ruffus Documentation

Release 2.6.2

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March 12, 2015

CHAPTER

ONE

START HERE:

1.1 Installation

`Ruffus` is a lightweight python module for building computational pipelines.

Note: Ruffus requires Python 2.6 or higher or Python 3.0 or higher

1.1.1 The easy way

Ruffus is available as an easy-install -able package on the Python Package Index.

```
sudo pip install ruffus --upgrade
```

This may also work for older installations:

```
easy_install -U ruffus
```

See below if `eady_install` is missing

1.1.2 The most up-to-date code:

- Download the latest sources or
- Check out the latest code from Google using git:

  ```
  git clone https://bunbun68@code.google.com/p/ruffus/ .
  ```

- Bleeding edge Ruffus development takes place on github:

  ```
  git clone git@github.com:bunbun/ruffus.git .
  ```

- To install after downloading, change to the , type:

  ```
  python ./setup.py install
  ```

1.1.3 Prequisites

1.1.4 Installing easy_install

If your system doesn't have `easy_install`, you can install one using a package manager, for example:

```
# ubuntu/linux mint
$ sudo apt-get install python-setuptools
$ or  sudo yum install python-setuptools
```

or manually:

```
sudo curl http://peak.telecommunity.com/dist/ez_setup.py | python
```

or manually:

```
wget peak.telecommunity.com/dist/ez_setup.py
sudo python ez_setup.py
```

1.1.5 Installing pip

If Pip is missing:

```
$ sudo easy_install -U pip
```

1.1.6 Graphical flowcharts The most up-to-date code:

Ruffus relies on the `dot` programme from Graphviz ("Graph visualisation") to make pretty flowchart representations of your pipelines in multiple graphical formats (e.g. `png`, `jpg`). The crossplatform Graphviz package can be downloaded here for Windows,

Linux, Macs and Solaris. For Fedora, try

```
yum list 'graphviz*'
```

For ubuntu / Debian, try

```
sudo apt-get install graphviz
```

1.2 Ruffus Manual: List of Chapters and Example code

Download as `pdf`.

- **Chapter 1**: *An introduction to basic Ruffus syntax*
- **Chapter 2**: *Transforming data in a pipeline with @transform*
- **Chapter 3**: *More on @transform-ing data*
- **Chapter 4**: *Creating files with @originate*
- **Chapter 5**: *Understanding how your pipeline works with pipeline_printout()*
- **Chapter 6**: *Running Ruffus from the command line with ruffus.cmdline*
- **Chapter 7**: *Displaying the pipeline visually with pipeline_printout_graph()*
- **Chapter 8**: *Specifying output file names with formatter() and regex()*
- **Chapter 9**: *Preparing directories for output with @mkdir*
- **Chapter 10**: *Checkpointing: Interrupted Pipelines and Exceptions*
- **Chapter 11**: *Pipeline topologies and a compendium of Ruffus decorators*

- **Chapter 12**: *Splitting up large tasks / files with @split*
- **Chapter 13**: *@merge multiple input into a single result*
- **Chapter 15**: *Logging progress through a pipeline*
- **Chapter 14**: *Multiprocessing, drmaa and Computation Clusters*
- **Chapter 16**: *@subdivide tasks to run efficiently and regroup with @collate*
- **Chapter 17**: *@combinations, @permutations and all versus all @product*
- **Chapter 18**: *Turning parts of the pipeline on and off at runtime with @active_if*
- **Chapter 20**: *Manipulating task inputs via string substitution with inputs() and add_inputs()*
- **Chapter 19**: *Signal the completion of each stage of our pipeline with @posttask*
- **Chapter 21**: *Esoteric: Generating parameters on the fly with @files*
- **Chapter 22**: *Esoteric: Running jobs in parallel without files using @parallel*
- **Chapter 23**: *Esoteric: Writing custom functions to decide which jobs are up to date with @check_if_uptodate*
- **Appendix 1** *Flow Chart Colours with pipeline_printout_graph*
- **Appendix 2** *Under the hood: How dependency works*
- **Appendix 3** *Exceptions thrown inside pipelines*
- **Appendix 4** *Names (keywords) exported from Ruffus*
- **Appendix 5**: *Legacy and deprecated syntax @files*
- **Appendix 6**: *Legacy and deprecated syntax @files_re*

Ruffus Manual: List of Example Code for Each Chapter:

- *Chapter 1: Python Code for An introduction to basic Ruffus syntax*
- *Chapter 1: Python Code for Transforming data in a pipeline with @transform*
- *Chapter 3: Python Code for More on @transform-ing data*
- *Chapter 4: Python Code for Creating files with @originate*
- *Chapter 5: Python Code for Understanding how your pipeline works with pipeline_printout(...)*
- *Chapter 7: Python Code for Displaying the pipeline visually with pipeline_printout_graph(...)*
- *Chapter 8: Python Code for Specifying output file names with formatter() and regex()*
- *Chapter 9: Python Code for Preparing directories for output with @mkdir()*
- *Chapter 10: Python Code for Checkpointing: Interrupted Pipelines and Exceptions*
- *Chapter 12: Python Code for Splitting up large tasks / files with @split*
- *Chapter 13: Python Code for @merge multiple input into a single result*
- *Chapter 14: Python Code for Multiprocessing, drmaa and Computation Clusters*
- *Chapter 15: Python Code for Logging progress through a pipeline*
- *Chapter 16: Python Code for @subdivide tasks to run efficiently and regroup with @collate*
- *Chapter 17: Python Code for @combinations, @permutations and all versus all @product*
- *Chapter 20: Python Code for Manipulating task inputs via string substitution using inputs() and add_inputs()*

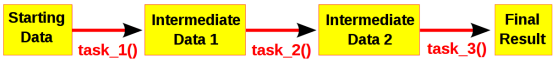
- *Chapter 21: Esoteric: Python Code for Generating parameters on the fly with @files*

1.3 Chapter 1: An introduction to basic *Ruffus* syntax

See also:

- *Manual Table of Contents*

1.3.1 Overview



Computational pipelines transform your data in stages until the final result is produced. One easy way to understand pipelines is by imagining your data flowing across a series of pipes until it reaches its final destination. Even quite complicated processes can be broken into simple stages. Of course, it helps to visualise the whole process.

Ruffus is a way of automating the plumbing in your pipeline: You supply the python functions which perform the data transformation, and tell *Ruffus* how these pipeline `task` functions are connected up. *Ruffus* will make sure that the right data flows down your pipeline in the right way at the right time.

Note: *Ruffus* refers to each stage of your pipeline as a *task*.

1.3.2 Importing *Ruffus*

The most convenient way to use *Ruffus* is to import the various names directly:

```
from ruffus import *
```

This will allow *Ruffus* terms to be used directly in your code. This is also the style we have adopted for this manual.

If any of these clash with names in your code, you can use qualified names instead:

```
import ruffus

ruffus.pipeline_printout("...")
```

Ruffus uses only standard python syntax.

There is no need to install anything extra or to have your script "preprocessed" to run your pipeline.

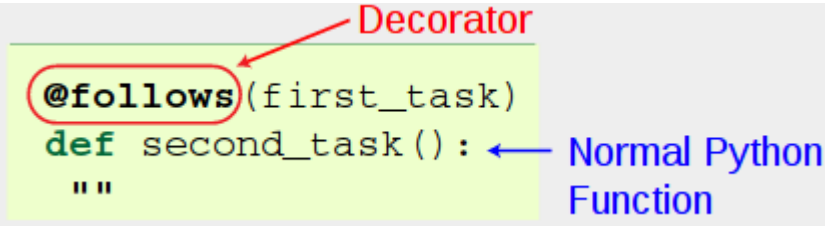
1.3.3 *Ruffus* decorators

To let *Ruffus* know that which python functions are part of your pipeline, they need to be tagged or annotated using *Ruffus* decorators .

Decorators have been part of the Python language since version 2.4. Common examples from the standard library include @staticmethod and classmethod.

decorators start with a `@` prefix, and take a number of parameters in parenthesis, much like in a function call.

decorators are placed before a normal python function.



Multiple decorators can be stacked as necessary in whichever order:

```
@follows(first_task)
@follows(another_task)
@originate(range(5))
def second_task():
    ""
```

Ruffus decorators do not otherwise alter the underlying function. These can still be called normally.

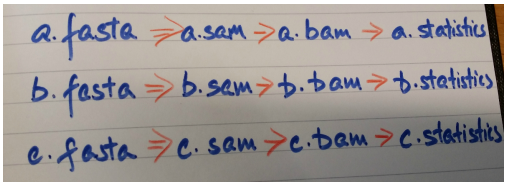
1.3.4 Your first *Ruffus* pipeline

1. Write down the file names

Ruffus is designed for data moving through a computational pipeline as a series of files.

It is also possible to use *Ruffus* pipelines without using intermediate data files but for your first efforts, it is probably best not to subvert its canonical design.

The first thing when designing a new *Ruffus* pipeline is to sketch out the set of file names for the pipeline on paper:



Here we have a number of DNA sequence files (`*.fasta`)

1. mapped to a genome (`*.sam`), and
2. compressed (`*.bam`) before being
3. summarised statistically (`*.statistics`)

The first striking thing is that all of the files following the same **consistent naming scheme**.

Note: The most important part of a Ruffus pipeline is to have a consistent naming scheme for your files. This allows you to build sane pipelines.

In this case, each of the files at the same stage share the same file extension, e.g. (`.sam`). This is usually the simplest and most sensible choice. (We shall see in later chapters that *Ruffus* supports more complicated naming patterns so long as they are consistent.)

2. Write the python functions for each stage

Next, we can sketch out the python functions which do the actual work for the pipeline.

Note:

1. These are normal python functions with the important proviso that
   (a) The first parameter contains the **Input** (file names)
   (b) The second parameter contains the **Output** (file names)

   You can otherwise supply as many parameters as is required.
2. Each python function should only take a *Single* **Input** at a time

   All the parallelism in your pipeline should be handled by *Ruffus*. Make sure each function analyses one thing at a time.

Ruffus refers to a pipelined function as a *task*.

The code for our three task functions look something like:

```
#
#   STAGE 1 fasta->sam
#
def map_dna_sequence(input_file,                # 1st parameter is Input
                     output_file):              # 2nd parameter is Output
    """
    Sketch of real mapping function
    We can do the mapping ourselves
        or call some other programme:
            os.system("stampy %s %s..." % (input_file, output_file))
    """
    ii = open(input_file)
    oo = open(output_file, "w")

#
#   STAGE 2 sam->bam
#
def compress_sam_file(input_file,               # Input  parameter
                      output_file):             # Output parameter
    """
    Sketch of real compression function
    """
    ii = open(input_file)
    oo = open(output_file, "w")

#
#   STAGE 3 bam->statistics
#
def summarise_bam_file(input_file,              # Input  parameter
                       output_file,             # Output parameter
                       extra_stats_parameter): # Any number of extra parameters as required
    """
    Sketch of real analysis function
    """
    ii = open(input_file)
    oo = open(output_file, "w")
```

If we were calling our functions manually, without the benefit of *Ruffus*, we would need the following sequence of calls:

```
# STAGE 1
map_dna_sequence("a.fasta", "a.sam")
map_dna_sequence("b.fasta", "b.sam")
map_dna_sequence("c.fasta", "c.sam")

# STAGE 2
compress_sam_file("a.sam", "a.bam")
compress_sam_file("b.sam", "b.bam")
compress_sam_file("c.sam", "c.bam")

# STAGE 3
summarise_bam_file("a.bam", "a.statistics")
summarise_bam_file("b.bam", "b.statistics")
summarise_bam_file("c.bam", "c.statistics")
```

3. Link the python functions into a pipeline

Ruffus makes exactly the same function calls on your behalf. However, first, we need to tell *Ruffus* what the arguments should be for each of the function calls.

- The **Input** is easy: This is either the starting file set (`*.fasta`) or whatever is produced by the previous stage.
- The **Output** file name is the same as the **Input** but with the appropriate extension.

These are specified using the *Ruffus* *@transform* decorator as follows:

```
from ruffus import *

starting_files = ["a.fasta", "b.fasta", "c.fasta"]

#
#   STAGE 1 fasta->sam
#
@transform(starting_files,                      # Input = starting files
           suffix(".fasta"),                    #         suffix = .fasta
           ".sam")                              # Output  suffix = .sam
def map_dna_sequence(input_file,
                     output_file):
    ii = open(input_file)
    oo = open(output_file, "w")

#
#   STAGE 2 sam->bam
#
@transform(map_dna_sequence,                    # Input = previous stage
           suffix(".sam"),                      #         suffix = .sam
           ".bam")                              # Output  suffix = .bam
def compress_sam_file(input_file,
                      output_file):
    ii = open(input_file)
    oo = open(output_file, "w")

#
#   STAGE 3 bam->statistics
```

```
#
@transform(compress_sam_file,                   # Input = previous stage
           suffix(".bam"),                      #         suffix = .bam
           ".statistics",                       # Output  suffix = .statistics
           "use_linear_model")                  # Extra statistics parameter
def summarise_bam_file(input_file,
                       output_file,
                       extra_stats_parameter):
    """
    Sketch of real analysis function
    """
    ii = open(input_file)
    oo = open(output_file, "w")
```

4. @transform syntax

1. The 1st parameter for *@transform* is the **Input**.
   This is either the set of starting data or the name of the previous pipeline function.
   Ruffus chains together the stages of a pipeline by linking the **Output** of the previous stage into the **Input** of the next.
2. The 2nd parameter is the current *suffix*
   (i.e. our **Input** file extensions of `".fasta"` or `".sam"` or `".bam"`)
3. The 3rd parameter is what we want our **Output** file name to be after *suffix* string substitution (e.g. `.fasta -> .sam`).
   This works because we are using a sane naming scheme for our data files.
4. Other parameters can be passed to `@transform` and they will be forwarded to our python pipeline function.

The functions that do the actual work of each stage of the pipeline remain unchanged. The role of *Ruffus* is to make sure each is called in the right order, with the right parameters, running in parallel (using multiprocessing if desired).

5. Run the pipeline!

Note: Key Ruffus Terminology:

A *task* is an annotated python function which represents a recipe or stage of your pipeline.

A *job* is each time your recipe is applied to a piece of data, i.e. each time *Ruffus* calls your function.

Each **task** or pipeline recipe can thus have many **jobs** each of which can work in parallel on different data.

Now we can run the pipeline with the *Ruffus* function *pipeline_run*:

```
pipeline_run()
```

This produces three sets of results in parallel, as you might expect:

```
>>> pipeline_run()
    Job  = [a.fasta -> a.sam] completed
    Job  = [b.fasta -> b.sam] completed
    Job  = [c.fasta -> c.sam] completed
Completed Task = map_dna_sequence
```

```
    Job  = [a.sam -> a.bam] completed
    Job  = [b.sam -> b.bam] completed
    Job  = [c.sam -> c.bam] completed
Completed Task = compress_sam_file
    Job  = [a.bam -> a.statistics, use_linear_model] completed
    Job  = [b.bam -> b.statistics, use_linear_model] completed
    Job  = [c.bam -> c.statistics, use_linear_model] completed
Completed Task = summarise_bam_file
```

To work out which functions to call, *pipeline_run* finds the **last** *task* function of your pipeline, then works out all the other functions this depends on, working backwards up the chain of dependencies automatically.

We can specify this end point of your pipeline explicitly:

```
>>> pipeline_run(target_tasks = [summarise_bam_file])
```

This allows us to only run part of the pipeline, for example:

```
>>> pipeline_run(target_tasks = [compress_sam_file])
```

Note: The *example code* can be copied and pasted into a python command shell.

1.4 Chapter 2: Transforming data in a pipeline with *@transform*

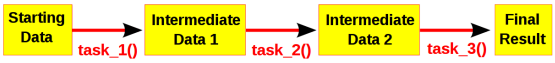
See also:

- *Manual Table of Contents*
- *@transform* syntax

Note: Remember to look at the example code:

- *Chapter 1: Python Code for Transforming data in a pipeline with @transform*

1.4.1 Review



Computational pipelines transform your data in stages until the final result is produced. Ruffus automates the plumbing in your pipeline. You supply the python functions which perform the data transformation, and tell Ruffus how these pipeline stages or *task* functions are connected together.

Note: The best way to design a pipeline is to:

- **write down the file names of the data as it flows across your pipeline**
- **write down the names of functions which transforms the data at each stage of the pipeline.**

1.4.2 Task functions as recipes

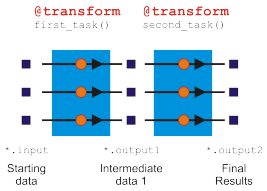
Each *task* function of the pipeline is a recipe or rule which can be applied repeatedly to our data.

For example, one can have

- a `compile()` *task* which will compile any number of source code files, or
- a `count_lines()` *task* which will count the number of lines in any file or
- an `align_dna()` *task* which will align the DNA of many chromosomes.

1.4.3 *@transform* is a 1 to 1 operation

`@transform` is a 1:1 operation because for each input, it generates one output.



This is obvious when you count the number of jobs at each step. In our example pipeline, there are always three jobs moving through in step at each stage (*task*).

Each **Input** or **Output** is not limited, however, to a single filename. Each job can accept, for example, a pair of files as its **Input**, or generate more than one file or a dictionary or numbers as its **Output**.

When each job outputs a pair of files, this does not generate two jobs downstream. It just means that the successive *task* in the pipeline will receive a list or tuple of files as its input parameter.

Note: The different sort of decorators in Ruffus determine the *topology* of your pipeline, i.e. how the jobs from different tasks are linked together seamlessly.

@transform always generates one **Output** for one **Input**.

In the later parts of the tutorial, we will encounter more decorators which can *split up*, or *join together* or *group* inputs.

In other words, using other decorators **Input** and **Output** can have **many to one**, **many to many** etc. relationships.

A pair of files as the Input

Let us rewrite our previous example so that the **Input** of the first task are matching pairs of DNA sequence files, processed in tandem.

```
from ruffus import *

starting_files = [("a.1.fastq", "a.2.fastq"),
                  ("a.1.fastq", "a.2.fastq"),
                  ("a.1.fastq", "a.2.fastq")]


#
#   STAGE 1 fasta->sam
#
@transform(starting_files,                      # Input = starting files
           suffix(".1.fastq"),                  #         suffix = .1.fastq
           ".sam")                              # Output  suffix = .sam
def map_dna_sequence(input_files,
                     output_file):
    # remember there are two input files now
    ii1 = open(input_files[0])
```

```
    ii2 = open(input_files[1])
    oo = open(output_file, "w")
```

The only changes are to the first task:

```
pipeline_run()
    Job  = [[a.1.fastq, a.2.fastq] -> a.sam] completed
    Job  = [[a.1.fastq, a.2.fastq] -> a.sam] completed
    Job  = [[a.1.fastq, a.2.fastq] -> a.sam] completed
Completed Task = map_dna_sequence
```

suffix always matches only the first file name in each **Input**.

1.4.4 Input and Output parameters

Ruffus chains together different tasks by taking the **Output** from one job and plugging it automatically as the **Input** of the next.

The first two parameters of each job are the **Input** and **Output** parameters respectively.

In the above example, we have:

```
>>> pipeline_run()
    Job  = [a.bam -> a.statistics, use_linear_model] completed
    Job  = [b.bam -> b.statistics, use_linear_model] completed
    Job  = [c.bam -> c.statistics, use_linear_model] completed
Completed Task = summarise_bam_file
```

Table 1.1: Parameters for summarise_bam_file()

Inputs	Outputs	Extra
"a.bam"	"a.statistics"	"use_linear_model"
"b.bam"	"b.statistics"	"use_linear_model"
"c.bam"	"c.statistics"	"use_linear_model"

Extra parameters are for the consumption of `summarise_bam_file()` and will not passed to the next task.

Ruffus was designed for pipelines which save intermediate data in files. This is not compulsory but saving your data in files at each step provides many advantages:

1. Ruffus can use file system time stamps to check if your pipeline is up to date
2. Your data is persistent across runs
3. This is a good way to pass large amounts of data across processes and computational nodes

Nevertheless, *all* the *task* parameters can include anything which suits your workflow, from lists of files, to numbers, sets or tuples. *Ruffus* imposes few constraints on what *you* would like to send to each stage of your pipeline.

Ruffus does, however, assume that if the **Input** and **Output** parameter contains strings, these will be interpreted as file names required by and produced by that job. As we shall see, the modification times of these file names indicate whether that part of the pipeline is up to date or needs to be rerun.

1.5 Chapter 3: More on `@transform`-ing data

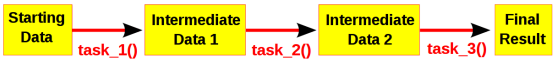
See also:

- *Manual Table of Contents*
- *@transform* syntax

Note: Remember to look at the example code:

- *Chapter 3: Python Code for More on @transform-ing data*

1.5.1 Review



Computational pipelines transform your data in stages until the final result is produced. *Ruffus* automates the plumbing in your pipeline. You supply the python functions which perform the data transformation, and tell *Ruffus* how these pipeline stages or *task* functions are connected together.

Note: The best way to design a pipeline is to:

- **write down the file names of the data as it flows across your pipeline**
- **write down the names of functions which transforms the data at each stage of the pipeline.**

Chapter 1: An introduction to basic Ruffus syntax described the bare bones of a simple *Ruffus* pipeline.

Using the *Ruffus* *@transform* decorator, we were able to specify the data files moving through our pipeline so that our specified task functions could be invoked.

This may seem like a lot of effort and complication for something so simple: a couple of simple python function calls we could have invoked ourselves. However, By letting *Ruffus* manage your pipeline parameters, you will get the following features for free:

1. Only out-of-date parts of the pipeline will be re-run
2. Multiple jobs can be run in parallel (on different processors if possible)
3. Pipeline stages can be chained together automatically. This means you can apply your pipeline just as easily to 1000 files as to 3.

1.5.2 Running pipelines in parallel

Even though three sets of files have been specified for our initial pipeline, and they can be processed completely independently, by default *Ruffus* runs each of them serially in succession.

To ask *Ruffus* to run them in parallel, all you have to do is to add a `multiprocess` parameter to `pipeline_run`:

```
>>> pipeline_run(multiprocess = 5)
```

In this case, we are telling *Ruffus* to run a maximum of 5 jobs at the same time. Since we only have three sets of data, that is as much parallelism as we are going to get...

1.5.3 Up-to-date jobs are not re-run unnecessarily

A job will be run only if the output file timestamps are out of date. If you ran our example code a second time, nothing would happen because all the work is already complete.

We can check the details by asking *Ruffus* for more `verbose` output

```
>>> pipeline_run(verbose = 4)
  Task = map_dna_sequence
    All jobs up to date
  Task = compress_sam_file
    All jobs up to date
  Task = summarise_bam_file
    All jobs up to date
```

Nothing happens because:

- `a.sam` was created later than `a.1.fastq` and `a.2.fastq`, and
- `a.bam` was created later than `a.sam` and
- `a.statistics` was created later than `a.bam`.

and so on...

Let us see what happens if we recreated the file `a.1.fastq` so that it appears as if 1 out of the original data files is out of

```
open("a.1.fastq", "w")
pipeline_run(multiprocess = 5)
```

The up to date jobs are cleverly ignored and only the out of date files are reprocessed.

```
>>> open("a.1.fastq", "w")
>>> pipeline_run(verbose=2)
    Job  = [[b.1.fastq, b.2.fastq] -> b.sam] # unnecessary: already up to date
    Job  = [[c.1.fastq, c.2.fastq] -> c.sam] # unnecessary: already up to date
    Job  = [[a.1.fastq, a.2.fastq] -> a.sam] completed
Completed Task = map_dna_sequence
    Job  = [b.sam -> b.bam] # unnecessary: already up to date
    Job  = [c.sam -> c.bam] # unnecessary: already up to date
    Job  = [a.sam -> a.bam] completed
Completed Task = compress_sam_file
    Job  = [b.bam -> b.statistics, use_linear_model] # unnecessary: already up to date
    Job  = [c.bam -> c.statistics, use_linear_model] # unnecessary: already up to date
    Job  = [a.bam -> a.statistics, use_linear_model] completed
Completed Task = summarise_bam_file
```

1.5.4 Defining pipeline tasks out of order

The examples so far assumes that all your pipelined tasks are defined in order. (`first_task` before `second_task`). This is usually the most sensible way to arrange your code.

If you wish to refer to tasks which are not yet defined, you can do so by quoting the function name as a string and wrapping it with the *indicator class output_from(...)* so that *Ruffus* knowns this is a *task* name, not a file name

```
#---------------------------------------------------------------
#
#   second task
#
#   task name string wrapped in output_from(...)
@transform(output_from("first_task"), suffix(".output.1"), ".output2")
def second_task(input_files, output_file):
    with open(output_file, "w"): pass
```

```
#---------------------------------------------------------------
#
#   first task
#
@transform(first_task_params, suffix(".start"),
                         [".output.1",
                          ".output.extra.1"],
                        "some_extra.string.for_example", 14)
def first_task(input_files, output_file_pair,
               extra_parameter_str, extra_parameter_num):
    for output_file in output_file_pair:
        with open(output_file, "w"):
            pass


#---------------------------------------------------------------
#
#       Run
#
pipeline_run([second_task])
```

You can also refer to tasks (functions) in other modules, in which case the full qualified name must be used:

```
@transform(output_from("other_module.first_task"), suffix(".output.1"), ".output2")
def second_task(input_files, output_file):
    pass
```

1.5.5 Multiple dependencies

Each task can depend on more than one antecedent simply by chaining to a list in *@transform*

```
#
# third_task depends on both first_task() and second_task()
#
@transform([first_task, second_task], suffix(".output.1"), ".output2")
def third_task(input_files, output_file):
    with open(output_file, "w"): pass
```

`third_task()` depends on and follows both `first_task()` and `second_task()`. However, these latter two tasks are independent of each other and can and will run in parallel. This can be clearly shown for our example if we added a little randomness to the run time of each job:

```
time.sleep(random.random())
```

The execution of `first_task()` and `second_task()` jobs will be interleaved and they finish in no particular order:

```
>>> pipeline_run([third_task], multiprocess = 6)
    Job  = [[job3.a.start, job3.b.start] -> [job3.a.output.1, job3.a.output.extra.1], some_e
    Job  = [[job6.a.start, job6.b.start] -> [job6.a.output.1, job6.a.output.extra.1], some_e
    Job  = [[job1.a.start, job1.b.start] -> [job1.a.output.1, job1.a.output.extra.1], some_e
    Job  = [[job4.a.start, job4.b.start] -> [job4.a.output.1, job4.a.output.extra.1], some_e
    Job  = [[job5.a.start, job5.b.start] -> [job5.a.output.1, job5.a.output.extra.1], some_e
Completed Task = second_task
    Job  = [[job2.a.start, job2.b.start] -> [job2.a.output.1, job2.a.output.extra.1], some_e
```

Note: See the *example code*

1.5.6 *@follows*

If there is some extrinsic reason one non-dependent task has to precede the other, then this can be specified explicitly using *@follows*:

```
#
#   @follows specifies a preceding task
#
@follows("first_task")
@transform(second_task_params, suffix(".start"),
                          [".output.1",
                           ".output.extra.1"],
                         "some_extra.string.for_example", 14)
def second_task(input_files, output_file_pair,
                extra_parameter_str, extra_parameter_num):
```

@follows specifies either a preceding task (e.g. `first_task`), or if it has not yet been defined, the name (as a string) of a task function (e.g. `"first_task"`).

With the addition of *@follows*, all the jobs of `second_task()` start *after* those from `first_task()` have finished:

```
>>> pipeline_run([third_task], multiprocess = 6)
    Job  = [[job2.a.start, job2.b.start] -> [job2.a.output.1, job2.a.output.extra.1], some_e
    Job  = [[job3.a.start, job3.b.start] -> [job3.a.output.1, job3.a.output.extra.1], some_e
    Job  = [[job1.a.start, job1.b.start] -> [job1.a.output.1, job1.a.output.extra.1], some_e
Completed Task = first_task
    Job  = [[job4.a.start, job4.b.start] -> [job4.a.output.1, job4.a.output.extra.1], some_e
    Job  = [[job6.a.start, job6.b.start] -> [job6.a.output.1, job6.a.output.extra.1], some_e
    Job  = [[job5.a.start, job5.b.start] -> [job5.a.output.1, job5.a.output.extra.1], some_e
Completed Task = second_task
```

1.5.7 Making directories automatically with *@follows* and *mkdir*

@follows is also useful for making sure one or more destination directories exist before a task is run.

Ruffus provides special syntax to support this, using the special *mkdir* indicator class. For example:

```
#
#   @follows specifies both a preceding task and a directory name
#
@follows("first_task", mkdir("output/results/here"))
@transform(second_task_params, suffix(".start"),
                          [".output.1",
                           ".output.extra.1"],
                         "some_extra.string.for_example", 14)
def second_task(input_files, output_file_pair,
                extra_parameter_str, extra_parameter_num):
```

Before `second_task()` is run, the `output/results/here` directory will be created if necessary.

1.5.8 Globs in the Input parameter

- As a syntactic convenience, *Ruffus* also allows you to specify a *glob* pattern (e.g. `*.txt`) in the **Input** parameter.
- *glob* patterns will be automatically specify all matching file names as the **Input**.
- Any strings within **Input** which contain the letters: `*?[]` will be treated as a *glob* pattern.

The first function in our initial *Ruffus* pipeline example could have been written as:

```
#
#   STAGE 1 fasta->sam
#
@transform("*.fasta",                           # Input = glob
           suffix(".fasta"),                    #         suffix = .fasta
           ".sam")                              # Output  suffix = .sam
def map_dna_sequence(input_file,
                     output_file):
    ""
```

1.5.9 Mixing Tasks and Globs in the Input parameter

glob patterns, references to tasks and file names strings can be mixed freely in (nested) python lists and tuples in the **Input** parameter.

For example, a task function can chain to the **Output** from multiple upstream tasks:

```
@transform([task1, task2,                       # Input = multiple tasks
            "aa*.fasta",                        #       + all files matching glob
            "zz.fasta"]                         #       + file name
           suffix(".fasta"),                    #         suffix = .fasta
           ".sam")                              # Output  suffix = .sam
def map_dna_sequence(input_file,
                     output_file):
    ""
```

In all cases, *Ruffus* tries to do the right thing, and to make the simple or obvious case require the simplest, least onerous syntax.

If sometimes *Ruffus* does not behave the way you expect, please write to the authors: it may be a bug!

Chapter 5: Understanding how your pipeline works with pipeline_printout(...) and *Chapter 6: Running Ruffus from the command line with ruffus.cmdline* will show you how to to make sure that your intentions are reflected in *Ruffus* code.

1.6 Chapter 4: Creating files with `@originate`

See also:

- *Manual Table of Contents*
- *@originate syntax in detail*

Note: Remember to look at the example code:

- *Chapter 4: Python Code for Creating files with @originate*

1.6.1 Simplifying our example with *@originate*

Our previous pipeline example started off with a set of files which we had to create first.

This is a common task: pipelines have to start *somewhere*.

Ideally, though, we would only want to create these starting files if they didn't already exist. In other words, we want a sort of `@transform` which makes files from nothing (`None`?).

This is exactly what *@originate* helps you to do.

Rewriting our pipeline with *@originate* gives the following three steps:

```
from ruffus import *

#---------------------------------------------------------------
#   create initial files
#
@originate([   ['job1.a.start', 'job1.b.start'],
               ['job2.a.start', 'job2.b.start'],
               ['job3.a.start', 'job3.b.start']    ])
def create_initial_file_pairs(output_files):
    # create both files as necessary
    for output_file in output_files:
        with open(output_file, "w") as oo: pass

#---------------------------------------------------------------
#   first task
@transform(create_initial_file_pairs, suffix(".start"), ".output.1")
def first_task(input_files, output_file):
    with open(output_file, "w"): pass


#---------------------------------------------------------------
#   second task
@transform(first_task, suffix(".output.1"), ".output.2")
def second_task(input_files, output_file):
    with open(output_file, "w"): pass

#
#       Run
#
pipeline_run([second_task])
```

```
    Job  = [None -> [job1.a.start, job1.b.start]] completed
    Job  = [None -> [job2.a.start, job2.b.start]] completed
    Job  = [None -> [job3.a.start, job3.b.start]] completed
Completed Task = create_initial_file_pairs
    Job  = [[job1.a.start, job1.b.start] -> job1.a.output.1] completed
    Job  = [[job2.a.start, job2.b.start] -> job2.a.output.1] completed
    Job  = [[job3.a.start, job3.b.start] -> job3.a.output.1] completed
Completed Task = first_task
    Job  = [job1.a.output.1 -> job1.a.output.2] completed
    Job  = [job2.a.output.1 -> job2.a.output.2] completed
    Job  = [job3.a.output.1 -> job3.a.output.2] completed
Completed Task = second_task
```

1.7 Chapter 5: Understanding how your pipeline works with *pipeline_printout(...)*

See also:

- *Manual Table of Contents*
- *pipeline_printout(...)* syntax
- *Python Code for this chapter*

Note:

- **Whether you are learning or developing ruffus pipelines, your best friend is** *pipeline_printout(...)* **This shows the exact parameters and files as they are passed through the pipeline.**
- **We also** *strongly* **recommend you use the** `Ruffus.cmdline` **convenience module which will take care of all the command line arguments for you. See** *Chapter 6: Running Ruffus from the command line with ruffus.cmdline*.

1.7.1 Printing out which jobs will be run

pipeline_printout(...) takes the same parameters as pipeline_run but just prints the tasks which are and are not up-to-date.

The `verbose` parameter controls how much detail is displayed.

Let us take the pipelined code we previously wrote in **Chapter 3** *More on @transform-ing data and @originate* but call *pipeline_printout(...)* instead of *pipeline_run(...)*. This lists the tasks which will be run in the pipeline:

```
>>> import sys
>>> pipeline_printout(sys.stdout, [second_task])

_____________________________________________
Tasks which will be run:

Task = create_initial_file_pairs
Task = first_task
Task = second_task
_____________________________________________
```

To see the input and output parameters of each job in the pipeline, try increasing the verbosity from the default (`1`) to `3` (See *code*)

This is very useful for checking that the input and output parameters have been specified correctly.

1.7.2 Determining which jobs are out-of-date or not

It is often useful to see which tasks are or are not up-to-date. For example, if we were to run the pipeline in full, and then modify one of the intermediate files, the pipeline would be partially out of date.

Let us start by run the pipeline in full but then modify `job1.a.output.1` so that the second task appears out-of-date:

```
pipeline_run([second_task])

# "touch" job1.stage1
open("job1.a.output.1", "w").close()
```

Run *pipeline_printout(...)* with a verbosity of 5.

This will tell you exactly why second_task(...) needs to be re-run: because job1.a.output.1 has a file modification time *after* job1.a.output.2 (highlighted):

```
>>> pipeline_printout(sys.stdout, [second_task], verbose = 5)

____________________________________________
Tasks which are up-to-date:

Task = create_initial_file_pairs
Task = first_task


____________________________________________


____________________________________________
Tasks which will be run:

Task = second_task
       Job  = [job1.a.output.1
             -> job1.a.output.2]
>>> # File modification times shown for out of date files
         Job needs update:
         Input files:
          * 22 Jul 2014 15:29:19.33: job1.a.output.1
         Output files:
          * 22 Jul 2014 15:29:07.53: job1.a.output.2

       Job  = [job2.a.output.1
             -> job2.a.output.2]
       Job  = [job3.a.output.1
             -> job3.a.output.2]


____________________________________________
```

N.B. At a verbosity of 5, even jobs which are up-to-date in second_task are displayed.

1.7.3 Verbosity levels

The verbosity levels for *pipeline_printout(...)* and *pipeline_run(...)* can be specified from verbose = 0 (print out nothing) to the extreme verbosity of verbose=6. A verbosity of above 10 is reserved for the internal debugging of Ruffus

- level **0** : *nothing*
- level **1** : *Out-of-date Task names*
- level **2** : *All Tasks (including any task function docstrings)*
- level **3** : *Out-of-date Jobs in Out-of-date Tasks, no explanation*
- level **4** : *Out-of-date Jobs in Out-of-date Tasks, with explanations and warnings*
- level **5** : *All Jobs in Out-of-date Tasks, (include only list of up-to-date tasks)*

- level **6** : *All jobs in All Tasks whether out of date or not*
- level **10**: *logs messages useful only for debugging ruffus pipeline code*

1.7.4 Abbreviating long file paths with `verbose_abbreviated_path`

Pipelines often produce interminable lists of deeply nested filenames. It would be nice to be able to abbreviate this to just enough information to follow the progress.

The `verbose_abbreviated_path` parameter specifies that *pipeline_printout(...)* and *pipeline_run(...)* only display

1. the `NNN` th top level sub-directories to be included, or that
2. the message to be truncated to a specified `MMM` characters (to fit onto a line, for example). `MMM` is specified by setting `verbose_abbreviated_path = -MMM`, i.e. negative values.

   Note that the number of characters specified is just the separate lengths of the input and output parameters, not the entire indented line. You many need to specify a smaller limit that you expect (e.g. `60` rather than *80*)

```
pipeline_printout(verbose_abbreviated_path = NNN)
pipeline_run(verbose_abbreviated_path = -MMM)
```

`verbose_abbreviated_path` defaults to `2`

For example:

Given `["aa/bb/cc/dddd.txt", "aaa/bbbb/cccc/eeed/eeee/ffff/gggg.txt"]`

```
# Original relative paths
"[aa/bb/cc/dddd.txt, aaa/bbbb/cccc/eeed/eeee/ffff/gggg.txt]"

# Full abspath
verbose_abbreviated_path = 0
"[/test/ruffus/src/aa/bb/cc/dddd.txt, /test/ruffus/src/aaa/bbbb/cccc/eeed/eeee/ffff/gggg.tx

# Specifed level of nested directories
verbose_abbreviated_path = 1
"[.../dddd.txt, .../gggg.txt]"

verbose_abbreviated_path = 2
"[.../cc/dddd.txt, .../ffff/gggg.txt]"

verbose_abbreviated_path = 3
"[.../bb/cc/dddd.txt, .../eeee/ffff/gggg.txt]"


# Truncated to MMM characters
verbose_abbreviated_path = -60
"<???> /bb/cc/dddd.txt, aaa/bbbb/cccc/eeed/eeee/ffff/gggg.txt]"
```

1.7.5 Getting a list of all tasks in a pipeline

If you just wanted a list of all tasks (Ruffus decorated function names), then you can just run Run *pipeline_get_task_names(...)*.

This doesn't touch any pipeline code or even check to see if the pipeline is connected up properly.

However, it is sometimes useful to allow users at the command line to choose from a list of possible tasks as a target.

1.8 Chapter 6: Running *Ruffus* from the command line with ruffus.cmdline

See also:

- *Manual table of Contents*

We find that much of our *Ruffus* pipeline code is built on the same template and this is generally a good place to start developing a new pipeline.

From version 2.4, *Ruffus* includes an optional `Ruffus.cmdline` module that provides support for a set of common command line arguments. This makes writing *Ruffus* pipelines much more pleasant.

1.8.1 Template for argparse

All you need to do is copy these 6 lines

```
import ruffus.cmdline as cmdline

parser = cmdline.get_argparse(description='WHAT DOES THIS PIPELINE DO?')

#   <<<---- add your own command line options like --input_file here
# parser.add_argument("--input_file")

options = parser.parse_args()

#  standard python logger which can be synchronised across concurrent Ruffus tasks
logger, logger_mutex = cmdline.setup_logging (__name__, options.log_file, options.verbose)

#   <<<----  pipelined functions go here

cmdline.run (options)
```

You are recommended to use the standard argparse module but the deprecated optparse module works as well. (See *below* for the template)

1.8.2 Command Line Arguments

`Ruffus.cmdline` by default provides these predefined options:

```
    -v, --verbose
        --version
    -L, --log_file

        # tasks
    -T, --target_tasks
        --forced_tasks
    -j, --jobs
        --use_threads
```

```
        # printout
    -n, --just_print

        # flow chart
        --flowchart
        --key_legend_in_graph
        --draw_graph_horizontally
        --flowchart_format


        # check sum
        --touch_files_only
        --checksum_file_name
        --recreate_database
```

1.8.3 1) Logging

The script provides for logging both to the command line:

```
myscript -v
myscript --verbose
```

and an optional log file:

```
# keep tabs on yourself
myscript --log_file /var/log/secret.logbook
```

Logging is ignored if neither `--verbose` or `--log_file` are specified on the command line

`Ruffus.cmdline` automatically allows you to write to a shared log file via a proxy from multiple processes. However, you do need to use `logging_mutex` for the log files to be synchronised properly across different jobs:

```
with logging_mutex:

    logger_proxy.info("Look Ma. No hands")
```

Logging is set up so that you can write

A) Only to the log file:

```
logger.info("A message")
```

B) Only to the display:

```
logger.debug("A message")
```

C) To both simultaneously:

```
from ruffus.cmdline import MESSAGE

logger.log(MESSAGE, "A message")
```

1.8.4 2) Tracing pipeline progress

This is extremely useful for understanding what is happening with your pipeline, what tasks and which jobs are up-to-date etc.

See *Chapter 5: Understanding how your pipeline works with pipeline_printout(...)*

To trace the pipeline, call script with the following options

```
# well-mannered, reserved
myscript --just_print
myscript -n

or

# extremely loquacious
myscript --just_print --verbose 5
myscript -n -v5
```

Increasing levels of verbosity (`--verbose` to `--verbose 5`) provide more detailed output

1.8.5 3) Printing a flowchart

This is the subject of *Chapter 7: Displaying the pipeline visually with pipeline_printout_graph(...)*.

Flowcharts can be specified using the following option:

```
myscript --flowchart xxxchart.svg
```

The extension of the flowchart file indicates what format the flowchart should take, for example, `svg`, `jpg` etc.

Override with `--flowchart_format`

1.8.6 4) Running in parallel on multiple processors

Optionally specify the number of parallel strands of execution and which is the last *target* task to run. The pipeline will run starting from any out-of-date tasks which precede the *target* and proceed no further beyond the *target*.

```
myscript --jobs 15 --target_tasks "final_task"
myscript -j 15
```

1.8.7 5) Setup checkpointing so that *Ruffus* knows which files are out of date

The *checkpoint file* uses to the value set in the environment (`DEFAULT_RUFFUS_HISTORY_FILE`).

If this is not set, it will default to `.ruffus_history.sqlite` in the current working directory.

Either can be changed on the command line:

```
myscript --checksum_file_name mychecksum.sqlite
```

Recreating checkpoints

Create or update the checkpoint file so that all existing files in completed jobs appear up to date

Will stop sensibly if current state is incomplete or inconsistent

```
myscript --recreate_database
```

Touch files

As far as possible, create empty files with the correct timestamp to make the pipeline appear up to date.

```
myscript --touch_files_only
```

1.8.8 6) Skipping specified options

Note that particular options can be skipped (not added to the command line), if they conflict with your own options, for example:

```
# see below for how to use get_argparse
parser = cmdline.get_argparse(  description='WHAT DOES THIS PIPELINE DO?',
                                # Exclude the following options: --log_file --key_legend_in_
                                ignored_args = ["log_file", "key_legend_in_graph"])
```

1.8.9 7) Specifying verbosity and abbreviating long paths

The verbosity can be specified on the command line

```
myscript --verbose 5

# verbosity of 5 + 1 = 6
myscript --verbose 5 --verbose

# verbosity reset to 2
myscript --verbose 5 --verbose --verbose 2
```

If the printed paths are too long, and need to be abbreviated, or alternatively, if you want see the full absolute paths of your input and output parameters, you can specify an extension to the verbosity. See the manual discussion of *verbose_abbreviated_path* for more details. This is specified as `--verbose VERBOSITY:VERBOSE_ABBREVIATED_PATH`. (No spaces!)

For example:

```
# verbosity of 4
myscript.py --verbose 4

# display three levels of nested directories
myscript.py --verbose 4:3

# restrict input and output parameters to 60 letters
myscript.py --verbose 4:-60
```

1.8.10 8) Displaying the version

Note that the version for your script will default to `"%(prog)s 1.0"` unless specified:

```
parser = cmdline.get_argparse(  description='WHAT DOES THIS PIPELINE DO?',
                                version = "my_programme.py v. 2.23")
```

1.8.11 Template for optparse

deprecated since python 2.7

```
#
#   Using optparse (new in python v 2.6)
#
from ruffus import *

parser = cmdline.get_optgparse(version="%prog 1.0", usage = "\n\n    %prog [options]")

#   <<<---- add your own command line options like --input_file here
# parser.add_option("-i", "--input_file", dest="input_file", help="Input file")

(options, remaining_args) = parser.parse_args()

#  logger which can be passed to ruffus tasks
logger, logger_mutex = cmdline.setup_logging ("this_program", options.log_file, options.verb

#   <<<----  pipelined functions go here

cmdline.run (options)
```

1.9 Chapter 7: Displaying the pipeline visually with *pipeline_printout_graph(...)*

See also:

- *Manual Table of Contents*
- *pipeline_printout_graph(...)* syntax
- *@graphviz(...)* syntax

Note: Remember to look at the example code:

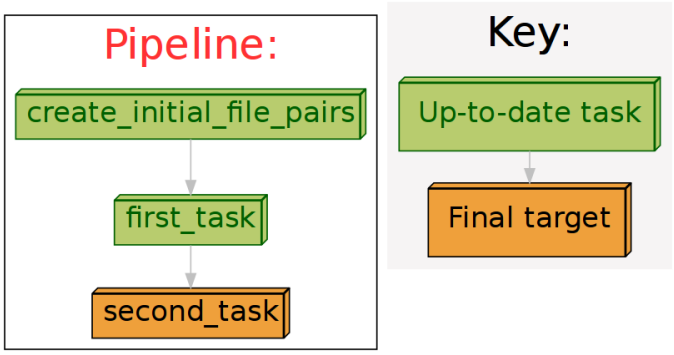
- *Chapter 7: Python Code for Displaying the pipeline visually with pipeline_printout_graph(...)*

1.9.1 Printing out a flowchart of our pipeline

It is all very well being able to trace the data flow through the pipeline as text. Sometimes, however, we need a bit of eye-candy!

We can see a flowchart for our fledgling pipeline by executing:

```
pipeline_printout_graph (    'flowchart.svg',
                             'svg',
                             [second_task],
                             no_key_legend = False)
```

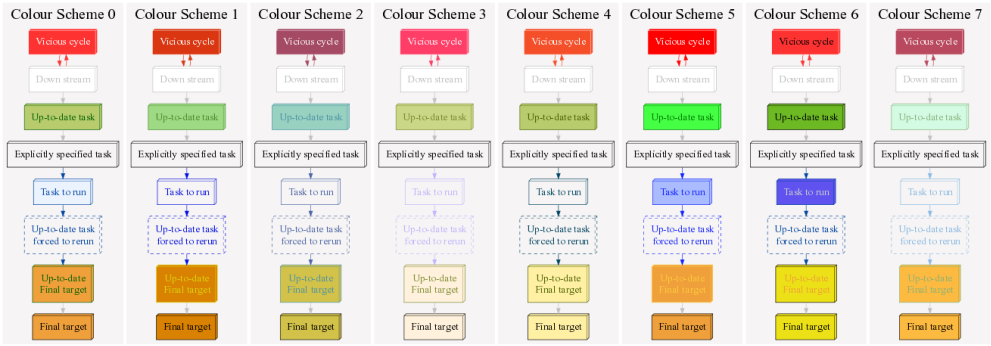


Flowcharts can be printed in a large number of formats including `jpg`, `svg`, `png` and `pdf`.

Note: Flowcharts rely on the `dot` programme from Graphviz.

Please make sure this is installed.

There are 8 standard colour schemes, but you can further customise all the colours to your satisfaction:



See *here* for example code.

1.9.2 Command line options made easier with `ruffus.cmdline`

If you are using `ruffus.cmdline`, then you can easily ask for a flowchart from the command line:

```
your_script.py --flowchart pipeline_flow_chart.png
```

The output format is deduced from the extension but can be specified manually:

```
# specify format. Otherwise, deduced from the extension
your_script.py --flowchart pipeline_flow_chart.png --flowchart_format png
```

Print the flow chart horizontally or vertically...

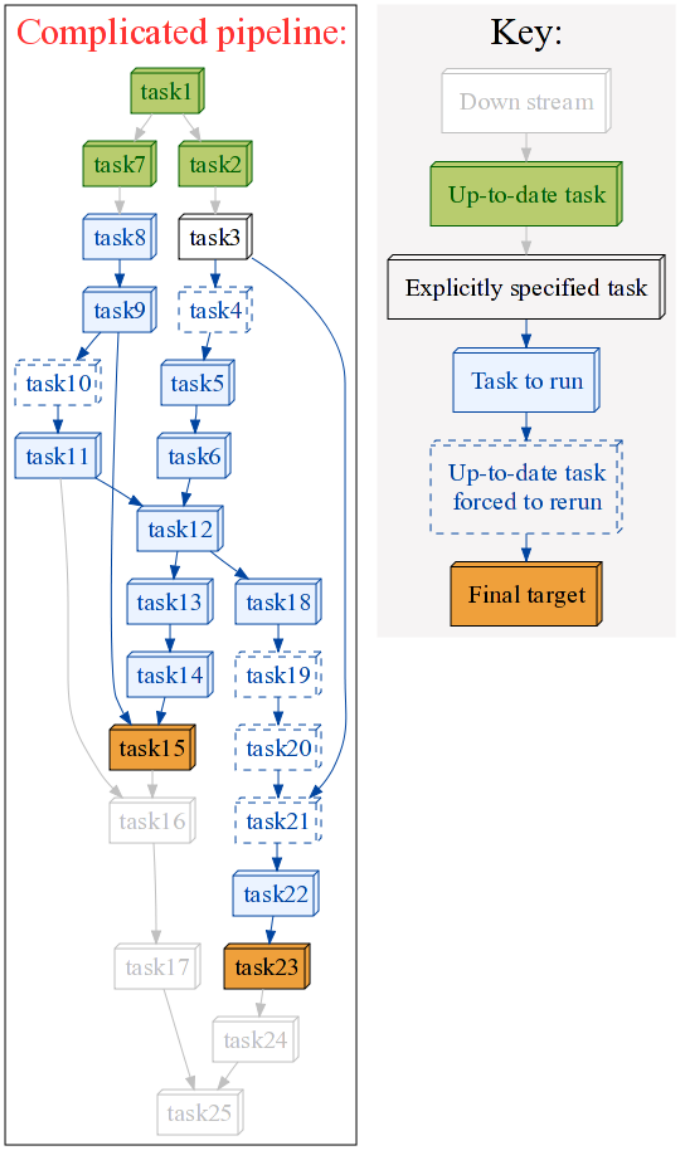
```
# flowchart proceeds from left to right , rather than from  top to bottom
your_script.py --flowchart pipeline_flow_chart.png --draw_graph_horizontally
```

...with or without a key legend

```
# Draw key legend
your_script.py --flowchart pipeline_flow_chart.png --key_legend_in_graph
```

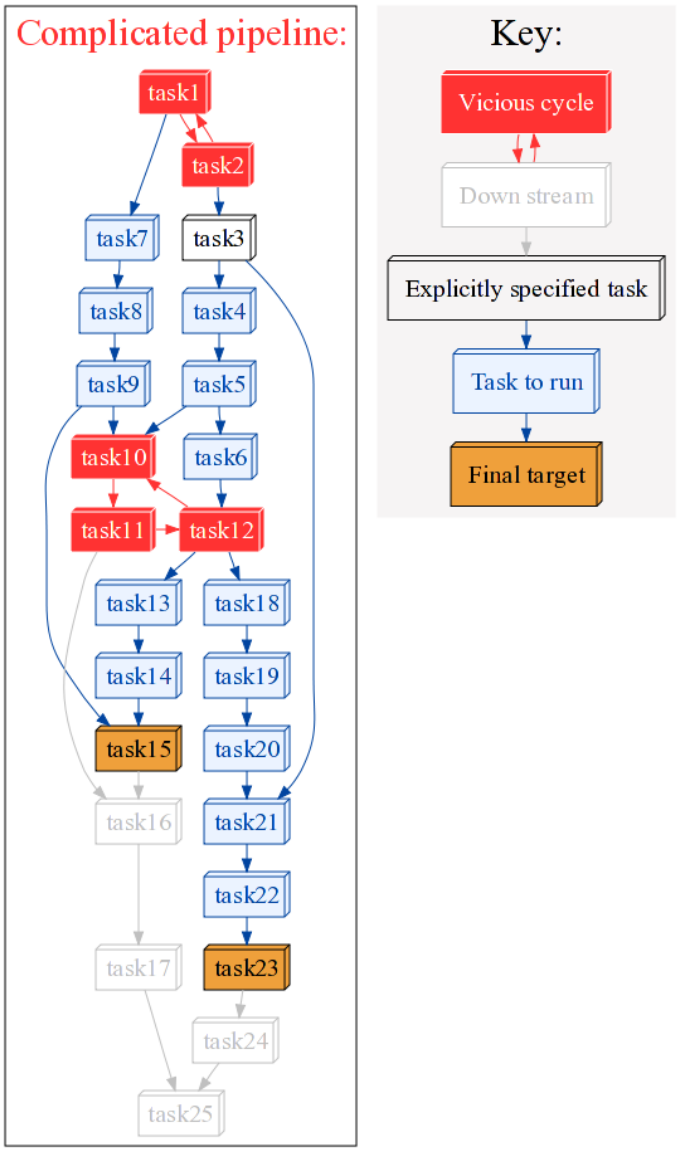
1.9.3 Horribly complicated pipelines!

Flowcharts are especially useful if you have really complicated pipelines, such as



1.9.4 Circular dependency errors in pipelines!

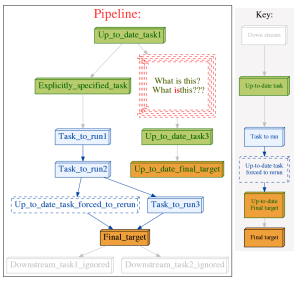
Especially, if the pipeline is not set up properly, and vicious circular dependencies are present:



1.9.5 `@graphviz`: Customising the appearance of each task

The graphic for each task can be further customised as you please by adding graphviz attributes such as the URL, shape, colour directly to that node using the decorator `@graphviz.

For example, we can customise the graphic for `myTask()` to look like:



by adding the requisite attributes as follows:

```
@graphviz(URL='"http://cnn.com"', fillcolor = '"#FFCCCC"',
                color = '"#FF0000"', pencolor='"#FF0000"', fontcolor='"#4B6000"',
                label_suffix = "???", label_prefix = "What is this?<BR/> ",
                label = "<What <FONT COLOR=\"red\">is</FONT>this>",
                shape= "component", height = 1.5, peripheries = 5,
                style="dashed")
def Up_to_date_task2(infile, outfile):
    pass

#   Can use dictionary if you wish...
graphviz_params = {"URL":"http://cnn.com", "fontcolor": '"#FF00FF"'}
@graphviz(**graphviz_params)
def myTask(input,output):
    pass
```

You can even using HTML formatting in task names, including specifying line wraps (as in the above example), using the `label` parameter. However, HTML labels **must** be enclosed in < and >.

```
    label = "<Line <BR/> wrapped task_name()>"
```

Otherwise, you can also opt to keep the task name and wrap it with a prefix and suffix:

```
    label_suffix = "??? ", label_prefix = ": What is this?"
```

The `URL` attribute allows the generation of clickable svg, and also client / server side image maps usable in web pages. See Graphviz documentation

1.10 Chapter 8: Specifying output file names with *formatter()* and *regex()*

See also:

- *Manual Table of Contents*
- *suffix()* syntax
- *formatter()* syntax
- *regex()* syntax

Note: Remember to look at the example code:

- *Chapter 8: Python Code for Specifying output file names with formatter() and regex()*

1.10.1 Review

Computational pipelines transform your data in stages until the final result is produced. The most straightforward way to use Ruffus is to hold the intermediate results after each stage in a series of files with related file names.

Part of telling Ruffus how these pipeline stages or *task* functions are connected together is to write simple rules for how to the file names for each stage follow on from each other. Ruffus helps you to specify these file naming rules.

Note: The best way to design a pipeline is to:

- **Write down the file names of the data as it flows across your pipeline.** Do these file names follow a *pattern* ?
- **Write down the names of functions which transforms the data at each stage of the pipeline.**

1.10.2 A different file name *suffix()* for each pipeline stage

The easiest and cleanest way to write Ruffus pipelines is to use a different suffix for each stage of your pipeline.

We used this approach in *Chapter 1: An introduction to basic Ruffus syntax* and in *code* from *Chapter 3: More on @transform-ing data*:

```
#Task Name:                    File suffices
_____________________________  ____________________
create_initial_file_pairs            *.start
first_task                           *.output.1
second_task                          *.output.2
```

There is a long standing convention of using file suffices to denote file type: For example, a **"compile"** task might convert **source** files of type `*.c` to **object** files of type `*.o`.

We can think of Ruffus tasks comprising :

- recipes in `@transform(...)` for transforming file names: changing `.c` to a `.o` (e.g. `AA.c -> AA.o BB.c -> BB.o`)
- recipes in a task function `def foo_bar()` for transforming your data: from **source** `.c` to **object** `.o`

Let us review the Ruffus syntax for doing this:

```
@transform( create_initial_file_pairs,   # Input:   Name of previous task(s)
            suffix(".start"),            # Matching suffix
            ".output.1")                 # Replacement string
def first_task(input_files, output_file):
    with open(output_file, "w"): pass
```

1. **Input**:

   The first parameter for `@transform` can be a mixture of one or more:

   - previous tasks (e.g. `create_initial_file_pairs`)
   - file names (all python strings are treated as paths)
   - glob specifications (e.g `*.c`, `/my/path/*.foo`)

   Each element provides an input for the task. So if the previous task `create_initial_file_pairs` has five outputs, the next `@transform` task will accept these as five separate inputs leading to five independent jobs.

2. *suffix()*:

The second parameter `suffix(".start")` must match the end of the first string in each input. For example, `create_initial_file_pairs` produces the list `['job1.a.start', 'job1.b.start']`, then `suffix(".start")` must matches the first string, i.e. `'job1.a.start'`. If the input is nested structure, this would be iterated through recursively to find the first string.

Note: Inputs which do not match the suffix are discarded altogether.

---

3. **Replacement**:

   The third parameter is the replacement for the suffix. The pair of input strings in the step3 example produces the following output parameter

```
input_parameters    = ['job1.a.start', 'job1.b.start']
matching_input      = 'job1.a.start'
output_parameter    = 'job1.a.output.1'
```

   When the pipeline is run, this results in the following equivalent call to `first_task(...)`:

```
first_task(['job1.a.start', 'job1.b.start'], 'job1.a.output.1'):
```

   The replacement parameter can itself be a list or any arbitrary complicated structure:

```
@transform(create_initial_file_pairs,            # Input
           suffix(".a.start"),                   # Matching suffix
           [".output.a.1", ".output.b.1", 45])   # Replacement list
def first_task(input_files, output_parameters):
    print "input_parameters = ", input_files
    print "output_parameters = ", output_parameters
```

   In which case, all the strings are used as replacements, other values are left untouched, and we obtain the following:

```
# job #1
input  =  ['job1.a.start',    'job1.b.start']
output =  ['job1.output.a.1', 'job1.output.b.1', 45]

# job #2
input  =  ['job2.a.start',    'job2.b.start']
output =  ['job2.output.a.1', 'job2.output.b.1', 45]

# job #3
input  =  ['job3.a.start',    'job3.b.start']
output =  ['job3.output.a.1', 'job3.output.b.1', 45]
```

   Note how task function is called with the value `45` *verbatim* because it is not a string.

1.10.3 *formatter()* manipulates pathnames and regular expression

suffix() replacement is the cleanest and easiest way to generate suitable output file names for each stage in a pipeline. Often, however, we require more complicated manipulations to specify our file names. For example,

- It is common to have to change directories from a *data* directory to a *working* directory as the first step of a pipeline.

- Data management can be simplified by separate files from each pipeline stage into their own directory.
- Information may have to be decoded from data file names, e.g. `"experiment373.IBM.03March2002.txt"`

Though *formatter()* is much more powerful, the principle and syntax are the same: we take string elements from the **Input** and perform some replacements to generate the **Output** parameters.

formatter()

- Allows easy manipulation of path subcomponents in the style of os.path.split(), and os.path.basename
- Uses familiar python string.format syntax (See string.format examples.)
- Supports optional regular expression (re) matches including named captures.
- Can refer to any file path (i.e. python string) in each input and is not limited like *suffix()* to the first string.
- Can even refer to individual letters within a match

Path name components

formatter() breaks down each input pathname into path name components which can then be recombined in whichever way by the replacement string.

Given an example string of :

```
input_string = "/directory/to/a/file.name.ext"
formatter()
```

the path components are:

- `basename`: The base name *excluding* extension, `"file.name"`
- `ext` : The extension, `".ext"`
- `path` : The dirname, `"/directory/to/a"`
- `subdir` : A list of sub-directories in the `path` in reverse order, `["a", "to", "directory", "/"]`
- `subpath` : A list of descending sub-paths in reverse order, `["/directory/to/a", "/directory/to", "/directory", "/"]`

The replacement string refers to these components by using python string.format style curly braces. `"{NAME}"`

We refer to an element from the Nth input string by index, for example:

- `"{ext[0]}"` is the extension of the first file name string in **Input**.
- `"{basename[1]}"` is the basename of the second file name in **Input**.
- `"{basename[1][0:3]}"` are the first three letters from the basename of the second file name in **Input**.

`subdir`, `subpath` were designed to help you navigate directory hierachies with the minimum of fuss. For example, you might want to graft a hierachical path to another location: `"{subpath[0][2]}/from/{subdir[0][0]}/{basename[0]}"` neatly replaces just one directory (`"to"`) in the path with another (`"from"`):

```
replacement_string = "{subpath[0][2]}/from/{subdir[0][0]}/{basename[0]}"

input_string    = "/directory/to/a/file.name.ext"
result_string   = "/directory/from/a/file.name.ext"
```

Filter and parse using regular expressions

Regular expression matches can be used with the similar syntax. Our example string can be parsed using the following regular expression:

```
input_string = "/directory/to/a/file.name.ext"
formatter(r"/directory/(.+)/(?P<MYFILENAME>)\.ext")
```

We capture part of the path using `(.+)`, and the base name using `(?P<MYFILENAME>)`. These matching subgroups can be referred to by index but for greater clarity the second named capture can also be referred to by name, i.e. `{MYFILENAME}`.

The regular expression components for the first string can thus be referred to as follows:

- `{0[0]}` : The entire match captured by index, `"/directory/to/a/file.name.ext"`
- `{1[0]}` : The first match captured by index, `"to/a"`
- `{2[0]}` : The second match captured by index, `"file.name"`
- `{MYFILENAME[0]}` : The match captured by name, `"file.name"`

If each input consists of a list of paths such as `['job1.a.start', 'job1.b.start', 'job1.c.start']`, we can match each of them separately by using as many regular expressions as necessary. For example:

```
input_string = ['job1.a.start', 'job1.b.start', 'job1.c.start']
# Regular expression matches for 1st, 2nd but not 3rd element
formatter(".+a.start", "b.start$")
```

Or if you only wanted regular expression matches for the second file name (string), pad with `None`:

```
input_string = ['job1.a.start', 'job1.b.start', 'job1.c.start']
# Regular expression matches for 2nd but not 1st or 3rd elements
formatter(None, "b.start$")
```

Using *@transform()* with *formatter()*

We can put these together in the following example:

```
from ruffus import *

#   create initial files
@originate([    ['job1.a.start', 'job1.b.start'],
                ['job2.a.start', 'job2.b.start'],
                ['job3.a.start', 'job3.c.start']    ])
def create_initial_file_pairs(output_files):
    # create both files as necessary
    for output_file in output_files:
        with open(output_file, "w") as oo: pass


#---------------------------------------------------------------
```

```
#
#   formatter
#

#   first task
@transform(create_initial_file_pairs,                                   # Input

           formatter(".+/job(?P<JOBNUMBER>\d+).a.start",                # Extract job number
                     ".+/job[123].b.start"),                            # Match only "b" files

           ["{path[0]}/jobs{JOBNUMBER[0]}.output.a.1",                  # Replacement list
            "{path[1]}/jobs{JOBNUMBER[0]}.output.b.1", 45])
def first_task(input_files, output_parameters):
    print "input_parameters = ", input_files
    print "output_parameters = ", output_parameters


#
#       Run
#
pipeline_run(verbose=0)
```

This produces:

```
input_parameters  =  ['job1.a.start',
                      'job1.b.start']
output_parameters =  ['/home/lg/src/temp/jobs1.output.a.1',
                      '/home/lg/src/temp/jobs1.output.b.1', 45]

input_parameters  =  ['job2.a.start',
                      'job2.b.start']
output_parameters =  ['/home/lg/src/temp/jobs2.output.a.1',
                      '/home/lg/src/temp/jobs2.output.b.1', 45]
```

Notice that `job3` has `'job3.c.start'` as the second file. This fails to match the regular expression and is discarded.

Note: Failed regular expression mismatches are ignored.

formatter() regular expressions are thus very useful in filtering out all files which do not match your specified criteria.

If your some of your task inputs have a mixture of different file types, a simple `Formatter(".txt$")`, for example, will make your code a lot simpler...

---

string substitution for "extra" arguments

The first two arguments for Ruffus task functions are special because they are the **Input** and **Output** parameters which link different stages of a pipeline.

Python strings in these arguments are names of data files whose modification times indicate whether the pipeline is up to date or not.

Other arguments to task functions are not passed down the pipeline but consumed. Any python strings they contain do not need to be file names. These extra arguments are very useful for passing data to pipelined tasks, such as shared values, loggers, programme options etc.

One helpful feature is that strings in these extra arguments are also subject to *formatter()* string substitution. This means you can leverage the parsing capabilities of Ruffus to decode any information about the pipeline data files, These might include the directories you are running in and parts of the file name.

For example, if we would want to know which files go with which "job number" in the previous example:

```
from ruffus import *

#   create initial files
@originate([    ['job1.a.start', 'job1.b.start'],
                ['job2.a.start', 'job2.b.start'],
                ['job3.a.start', 'job3.c.start']    ])
def create_initial_file_pairs(output_files):
    for output_file in output_files:
        with open(output_file, "w") as oo: pass


#---------------------------------------------------------------
#
#   print job number as an extra argument
#

#   first task
@transform(create_initial_file_pairs,                                   # Input

           formatter(".+/job(?P<JOBNUMBER>\d+).a.start",                # Extract job number
                     ".+/job[123].b.start"),                            # Match only "b" files

           ["{path[0]}/jobs{JOBNUMBER[0]}.output.a.1",                  # Replacement list
            "{path[1]}/jobs{JOBNUMBER[0]}.output.b.1"],

            "{JOBNUMBER[0]}"
def first_task(input_files, output_parameters, job_number):
    print job_number, ":", input_files


pipeline_run(verbose=0)
```

```
>>> pipeline_run(verbose=0)
1 : ['job1.a.start', 'job1.b.start']
2 : ['job2.a.start', 'job2.b.start']
```

Changing directories using *formatter()* in a zoo...

Here is a more fun example. We would like to feed the denizens of a zoo. Unfortunately, the file names for these are spread over several directories. Ideally, we would like their food supply to be grouped more sensibly. And, of course, we only want to feed the animals, not the plants.

I have colour coded the input and output files for this task to show how we would like to rearrange them:

```
crocodile/reptiles.wild.animals   ──►  reptiles/wild.crocodile.food
dog/mammals.tame.animals          ──►  mammals/tame.dog.food
dog/mammals.wild.animals          ──►  mammals/wild.dog.food
lion/mammals.handreared.animals   ──►  mammals/handreared.lion.food
lion/mammals.wild.animals         ──►  mammals/wild.lion.food
lion/mammals.wild.animals         ──►  mammals/wild.lion.food
Roses are not animals!
rose/flowering.handreared.plants  ──✗
```

```
from ruffus import *

#   Make directories
```

```
@mkdir(["tiger", "lion", "dog", "crocodile", "rose"])

@originate(
            #   List of animals and plants
            [    "tiger/mammals.wild.animals",
                "lion/mammals.wild.animals",
                "lion/mammals.handreared.animals",
                "dog/mammals.tame.animals",
                "dog/mammals.wild.animals",
                "crocodile/reptiles.wild.animals",
                "rose/flowering.handreared.plants"])
def create_initial_files(output_file):
    with open(output_file, "w") as oo: pass


#   Put different animals in different directories depending on their clade
@transform(create_initial_files,                                        # Input

           formatter(".+/(?P<clade>\w+).(?P<tame>\w+).animals"),        # Only animals: ignor

           "{subpath[0][1]}/{clade[0]}/{tame[0]}.{subdir[0][0]}.food", # Replacement

           "{subpath[0][1]}/{clade[0]}",                                # new_directory
           "{subdir[0][0]}",                                            # animal_name
           "{tame[0]}")                                                 # tameness
def feed(input_file, output_file, new_directory, animal_name, tameness):
    print "Food for the {tameness:11s} {animal_name:9s} = {output_file:90s} will be placed i

pipeline_run(verbose=0)
```

We can see that the food for each animal are now grouped by clade in the same directory, which makes a lot more sense...

Note how we used `subpath[0][1]` to move down one level of the file path to build a new file name.

```
>>> pipeline_run(verbose=0)
Food for the wild        crocodile = ./reptiles/wild.crocodile.food will be placed in ./rept
Food for the tame        dog       = ./mammals/tame.dog.food        will be placed in ./mamm
Food for the wild        dog       = ./mammals/wild.dog.food        will be placed in ./mamm
Food for the handreared  lion      = ./mammals/handreared.lion.food will be placed in ./mamm
Food for the wild        lion      = ./mammals/wild.lion.food       will be placed in ./mamm
Food for the wild        tiger     = ./mammals/wild.tiger.food      will be placed in ./mamm
```

1.10.4 *regex()* manipulates via regular expressions

If you are a hard core regular expressions fan, you may want to use *regex()* instead of *suffix()* or *formatter()*.

Note: *regex()* uses regular expressions like *formatter()* but

- It only matches the first file name in the input. As described above, *formatter()* can match any one or more of the input filename strings.
- It does not understand file paths so you may have to perform your own directory / file name parsing.
- String replacement uses syntax borrowed from re.sub(), rather than building a result from parsed regular expression (and file path) components

In general *formatter()* is more powerful and was introduced from version 2.4 is intended to be a more user friendly replacement for *regex()*.

Let us see how the previous zoo example looks with *regex()*:

formatter() code:

```
#   Put different animals in different directories depending on their clade
@transform(create_initial_files,                                          # Input

           formatter(".+/(?P<clade>\w+).(?P<tame>\w+).animals"),          # Only animals: ignor

           "{subpath[0][1]}/{clade[0]}/{tame[0]}.{subdir[0][0]}.food",    # Replacement

           "{subpath[0][1]}/{clade[0]}",                                  # new_directory
           "{subdir[0][0]}",                                              # animal_name
           "{tame[0]}")                                                   # tameness
def feed(input_file, output_file, new_directory, animal_name, tameness):
    print "Food for the {tameness:11s} {animal_name:9s} = {output_file:90s} will be placed i
```

regex() code:

```
#   Put different animals in different directories depending on their clade
@transform(create_initial_files,                                           # Input

           regex(r"(.*?/?)(\w+)/(?P<clade>\w+).(?P<tame>\w+).animals"), # Only animals: ignc

           r"\1/\g<clade>/\g<tame>.\2.food",                               # Replacement

           r"\1/\g<clade>",                                                # new_directory
           r"\2",                                                          # animal_name
           "\g<tame>")                                                     # tameness
def feed(input_file, output_file, new_directory, animal_name, tameness):
    print "Food for the {tameness:11s} {animal_name:9s} = {output_file:90s} will be placed i
```

The regular expression to parse the input file path safely was a bit hairy to write, and it is not clear that it handles all edge conditions (e.g. files in the root directory). Apart from that, if the limitations of *regex()* do not preclude its use, then the two approaches are not so different in practice.

1.11 Chapter 9: Preparing directories for output with *@mkdir()*

See also:

- *Manual Table of Contents*
- *@follows(mkdir()) syntax in detail*
- *@mkdir syntax in detail*

Note: Remember to look at the example code:

- *Chapter 9: Python Code for Preparing directories for output with @mkdir()*

1.11.1 Overview

In **Chapter 3**, we saw that we could use *@follows(mkdir())* to ensure that output directories exist:

```
#
#   create_new_files() @follows mkdir
#
@follows(mkdir("output/results/here"))
@originate(["output/results/here/a.start_file",
            "output/results/here/b.start_file"])
def create_new_files(output_file_pair):
    pass
```

This ensures that the decorated task follows (*@follows*) the making of the specified directory (`mkdir()`).

Sometimes, however, the **Output** is intended not for any single directory but a group of destinations depending on the parsed contents of **Input** paths.

1.11.2 Creating directories after string substitution in a zoo...

You may remember *this example* from **Chapter 8**:

We want to feed the denizens of a zoo. The original file names are spread over several directories and we group their food supply by the *clade* of the animal in the following manner:

```
crocodile/reptiles.wild.animals   ⟶  reptiles/wild.crocodile.food
dog/mammals.tame.animals          ⟶  mammals/tame.dog.food
dog/mammals.wild.animals          ⟶  mammals/wild.dog.food
lion/mammals.handreared.animals   ⟶  mammals/handreared.lion.food
lion/mammals.wild.animals         ⟶  mammals/wild.lion.food
lion/mammals.wild.animals         ⟶  mammals/wild.lion.food
Roses are not animals!
rose/flowering.handreared.plants  ✗
```

```
    #   Put different animals in different directories depending on their clade
    @transform(create_initial_files,                                        # Input

               formatter(".+/(?P<clade>\w+).(?P<tame>\w+).animals"),        # Only animals: ignor

               "{subpath[0][1]}/{clade[0]}/{tame[0]}.{subdir[0][0]}.food", # Replacement

               "{subpath[0][1]}/{clade[0]}",                                # new_directory
               "{subdir[0][0]}",                                            # animal_name
               "{tame[0]}")                                                 # tameness
    def feed(input_file, output_file, new_directory, animal_name, tameness):
        print "%40s -> %90s" % (input_file, output_file)
        # this blows up
        # open(output_file, "w")
```

The example code from **Chapter 8** is, however, incomplete. If we were to actually create the specified files we would realise that we had forgotten to create the destination directories `reptiles`, `mammals` first!

using *formatter()*

We could of course create directories manually. However, apart from being tedious and error prone, we have already gone to some lengths to parse out the diretories for *@transform*. Why don't we use the same logic to make the directories?

Can you see the parallels between the syntax for *@mkdir* and *@transform*?

```
    # create directories for each clade
    @mkdir(     create_initial_files,                                       # Input

               formatter(".+/(?P<clade>\w+).(?P<tame>\w+).animals"),        # Only animals: ignor
```

```
            "{subpath[0][1]}/{clade[0]})                                    # new_directory

    #   Put animals of each clade in the same directory
    @transform(create_initial_files,                                        # Input

               formatter(".+/(?P<clade>\w+).(?P<tame>\w+).animals"),        # Only animals: ignor

               "{subpath[0][1]}/{clade[0]}/{tame[0]}.{subdir[0][0]}.food", # Replacement

               "{subpath[0][1]}/{clade[0]}",                                # new_directory
               "{subdir[0][0]}",                                            # animal_name
               "{tame[0]}")                                                 # tameness
    def feed(input_file, output_file, new_directory, animal_name, tameness):
        print "%40s -> %90s" % (input_file, output_file)
        # this works now
        open(output_file, "w")
```

See the *example code*

using *regex()*

If you are particularly fond of using regular expression to parse file paths, you could also use *regex()*:

```
    # create directories for each clade
    @mkdir(     create_initial_files,                                       # Input

               regex(r"(.*?)/?(\w+)/(?P<clade>\w+).(?P<tame>\w+).animals"), # Only animals: ignc
               r"\1/\g<clade>")                                             # new_directory

    #   Put animals of each clade in the same directory
    @transform(create_initial_files,                                        # Input

               formatter(".+/(?P<clade>\w+).(?P<tame>\w+).animals"),        # Only animals: ignor

               "{subpath[0][1]}/{clade[0]}/{tame[0]}.{subdir[0][0]}.food", # Replacement

               "{subpath[0][1]}/{clade[0]}",                                # new_directory
               "{subdir[0][0]}",                                            # animal_name
               "{tame[0]}")                                                 # tameness
    def feed(input_file, output_file, new_directory, animal_name, tameness):
        print "%40s -> %90s" % (input_file, output_file)
        # this works now
        open(output_file, "w")
```

1.12 Chapter 10: Checkpointing: Interrupted Pipelines and Exceptions

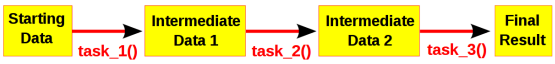
See also:

- *Manual Table of Contents*

Note: Remember to look at the example code:

- *Chapter 10: Python Code for Checkpointing: Interrupted Pipelines and Exceptions*

1.12.1 Overview



Computational pipelines transform your data in stages until the final result is produced.

By default, *Ruffus* uses file modification times for the **input** and **output** to determine whether each stage of a pipeline is up-to-date or not. But what happens when the task function is interrupted, whether from the command line or by error, half way through writing the output?

In this case, the half-formed, truncated and corrupt **Output** file will look newer than its **Input** and hence up-to-date.

1.12.2 Interrupting tasks

Let us try with an example:

```
from ruffus import *
import sys, time

#   create initial files
@originate(['job1.start'])
def create_initial_files(output_file):
    with open(output_file, "w") as oo: pass


#---------------------------------------------------------------
#
#   long task to interrupt
#
@transform(create_initial_files, suffix(".start"), ".output")
def long_task(input_files, output_file):
    with open(output_file, "w") as ff:
        ff.write("Unfinished...")
        # sleep for 2 seconds here so you can interrupt me
        sys.stderr.write("Job started. Press ^C to interrupt me now...\n")
        time.sleep(2)
        ff.write("\nFinished")
        sys.stderr.write("Job completed.\n")


#       Run
pipeline_run([long_task])
```

When this script runs, it pauses in the middle with this message:

```
Job started. Press ^C to interrupt me now...
```

If you interrupted the script by pressing Control-C at this point, you will see that `job1.output` contains only `Unfinished...`. However, if you should rerun the interrupted pipeline again, Ruffus ignores the corrupt, incomplete file:

```
>>> pipeline_run([long_task])
Job started. Press ^C to interrupt me now...
Job completed
```

And if you had run `pipeline_printout`:

```
>>> pipeline_printout(sys.stdout, [long_task], verbose=3)
_____________________________________
Tasks which will be run:

Task = long_task
       Job  = [job1.start
             -> job1.output]
         # Job needs update: Previous incomplete run leftover: [job1.output]
```

We can see that *Ruffus* magically knows that the previous run was incomplete, and that `job1.output` is detritus that needs to be discarded.

1.12.3 Checkpointing: only log completed jobs

All is revealed if you were to look in the working directory. *Ruffus* has created a file called `.ruffus_history.sqlite`. In this SQLite database, *Ruffus* logs only those files which are the result of a completed job, all other files are suspect. This file checkpoint database is a fail-safe, not a substitute for checking file modification times. If the **Input** or **Output** files are modified, the pipeline will rerun.

By default, *Ruffus* saves only file timestamps to the SQLite database but you can also add a checksum of the pipeline task function body or parameters. This behaviour can be controlled by setting the `checksum_level` parameter in `pipeline_run()`. For example, if you do not want to save any timestamps or checksums:

```
pipeline_run(checksum_level = 0)

CHECKSUM_FILE_TIMESTAMPS      = 0     # only rerun when the file timestamps are out of date
CHECKSUM_HISTORY_TIMESTAMPS   = 1     # Default: also rerun when the history shows a job as
CHECKSUM_FUNCTIONS            = 2     # also rerun when function body has changed
CHECKSUM_FUNCTIONS_AND_PARAMS = 3     # also rerun when function parameters or function body
```

Note: Checksums are calculated from the pickled string for the function code and parameters. If pickling fails, Ruffus will degrade gracefully to saving just the timestamp in the SQLite database.

1.12.4 Do not share the same checkpoint file across for multiple pipelines!

The name of the Ruffus python script is not saved in the checkpoint file along side timestamps and checksums. That means that you can rename your pipeline source code file without having to rerun the pipeline! The tradeoff is that if multiple pipelines are run from the same directory, and save their histories to the same SQlite database file, and if their file names overlap (all of these are bad ideas anyway!), this is bound to be a source of confusion.

Luckily, the name and path of the checkpoint file can be also changed for each pipeline

1.12.5 Setting checkpoint file names

Warning: Some file systems do not appear to support SQLite at all:
There are reports that SQLite databases have file locking problems on Lustre.
The best solution would be to keep the SQLite database on an alternate compatible file system away from the working directory if possible.

environment variable DEFAULT_RUFFUS_HISTORY_FILE

The name of the checkpoint file is the value of the environment variable DEFAULT_RUFFUS_HISTORY_FILE.

export DEFAULT_RUFFUS_HISTORY_FILE=/some/where/.ruffus_history.sqlite

This gives considerable flexibility, and allows a system-wide policy to be set so that all Ruffus checkpoint files are set logically to particular paths.

Note: It is your responsibility to make sure that the requisite destination directories for the checkpoint files exist beforehand!

Where this is missing, the checkpoint file defaults to `.ruffus_history.sqlite` in your working directory

Setting the checkpoint file name manually

This checkpoint file name can always be overridden as a parameter to Ruffus functions:

```
pipeline_run(history_file = "XXX")
pipeline_printout(history_file = "XXX")
pipeline_printout_graph(history_file = "XXX")
```

There is also built in support in `Ruffus.cmdline`. So if you use this module, you can simply add to your command line:

```
# use a custom checkpoint file
myscript --checksum_file_name .myscript.ruffus_history.sqlite
```

This takes precedence over everything else.

1.12.6 Useful checkpoint file name policies DEFAULT_RUFFUS_HISTORY_FILE

If the pipeline script is called `test/bin/scripts/run.me.py`, then these are the resulting checkpoint files locations:

Example 1: same directory, different name

If the environment variable is:

```
export DEFAULT_RUFFUS_HISTORY_FILE=.{basename}.ruffus_history.sqlite
```

Then the job checkpoint database for `run.me.py` will be `.run.me.ruffus_history.sqlite`

```
/test/bin/scripts/run.me.py
/common/path/for/job_history/scripts/.run.me.ruffus_history.sqlite
```

Example 2: Different directory, same name

```
export DEFAULT_RUFFUS_HISTORY_FILE=/common/path/for/job_history/.{basename}.ruffus_history.sqlit
```

```
/common/path/for/job_history/.run.me.ruffus_history.sqlite
```

Example 2: Different directory, same name but keep one level of subdirectory to disambiguate

```
export DEFAULT_RUFFUS_HISTORY_FILE=/common/path/for/job_history/{subdir[0]}/.{basename}.ruffus_h

/common/path/for/job_history/scripts/.run.me.ruffus_history.sqlite
```

Example 2: nested in common directory

```
export DEFAULT_RUFFUS_HISTORY_FILE=/common/path/for/job_history/{path}/.{basename}.ruffus_histor

/common/path/for/job_history/test/bin/scripts/.run.me.ruffus_history.sqlite
```

1.12.7 Regenerating the checkpoint file

Occasionally you may need to re-generate the checkpoint file.

This could be necessary:

- because you are upgrading from a previous version of Ruffus without checkpoint file support
- on the rare occasions when the SQLite file becomes corrupted and has to deleted
- if you wish to circumvent the file checking of Ruffus after making some manual changes!

To do this, it is only necessary to call `pipeline_run` appropriately:

```
CHECKSUM_REGENERATE = 2
pipeline(touch_files_only = CHECKSUM_REGENERATE)
```

Similarly, if you are using `Ruffus.cmdline`, you can call:

```
myscript --recreate_database
```

Note that this regenerates the checkpoint file to reflect the existing *Input*, *Output* files on disk. In other words, the onus is on you to make sure there are no half-formed, corrupt files. On the other hand, the pipeline does not need to have been previously run successfully for this to work. Essentially, Ruffus, pretends to run the pipeline, while logging all the files with consistent file modication times, stopping at the first tasks which appear out of date or incomplete.

1.12.8 Rules for determining if files are up to date

The following simple rules are used by *Ruffus*.

1. The pipeline stage will be rerun if:
   - If any of the **Input** files are new (newer than the **Output** files)
   - If any of the **Output** files are missing
2. In addition, it is possible to run jobs which create files from scratch.
   - If no **Input** file names are supplied, the job will only run if any *output* file is missing.
3. Finally, if no **Output** file names are supplied, the job will always run.

1.12.9 Missing files generate exceptions

If the *inputs* files for a job are missing, the task function will have no way to produce its *output*. In this case, a `MissingInputFileError` exception will be raised automatically. For example,

```
task.MissingInputFileError: No way to run job: Input file ['a.1'] does not exist
for Job = ["a.1" -> "a.2", "A file"]
```

1.12.10 Caveats: Coarse Timestamp resolution

Note that modification times have precision to the nearest second under some older file systems (ext2/ext3?). This may be also be true for networked file systems.

Ruffus supplements the file system time resolution by independently recording the timestamp at full OS resolution (usually to at least the millisecond) at job completion, when presumably the **Output** files will have been created.

However, *Ruffus* only does this if the discrepancy between file time and system time is less than a second (due to poor file system timestamp resolution). If there are large mismatches between the two, due for example to network time slippage, misconfiguration etc, *Ruffus* reverts to using the file system time and adds a one second delay between jobs (via `time.sleep()`) to make sure input and output file stamps are different.

If you know that your filesystem has coarse-grained timestamp resolution, you can always revert to this very conservative behaviour, at the prices of some annoying 1s pauses, by setting *pipeline_run(one_second_per_job = True)*

1.12.11 Flag files: Checkpointing for the paranoid

One other way of checkpointing your pipelines is to create an extra "flag" file as an additional **Output** file name. The flag file is only created or updated when everything else in the job has completed successfully and written to disk. A missing or out of date flag file then would be a sign for Ruffus that the task never completed properly in the first place.

This used to be much the best way of performing checkpointing in Ruffus and is still the most bulletproof way of proceeding. For example, even the loss or corruption of the checkpoint file, would not affect things greatly.

Nevertheless flag files are largely superfluous in modern *Ruffus*.

1.13 Chapter 11: Pipeline topologies and a compendium of *Ruffus* decorators

See also:

- *Manual Table of Contents*
- *decorators*

1.13.1 Overview

Computational pipelines transform your data in stages until the final result is produced.

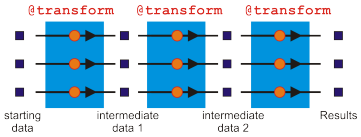
You can visualise your pipeline data flowing like water down a system of pipes. *Ruffus* has many ways of joining up your pipes to create different topologies.

Note: The best way to design a pipeline is to:

- **Write down the file names of the data as it flows across your pipeline.**
- **Draw lines between the file names to show how they should be connected together.**

1.13.2 *@transform*

So far, our data files have been flowing through our pipelines independently in lockstep.

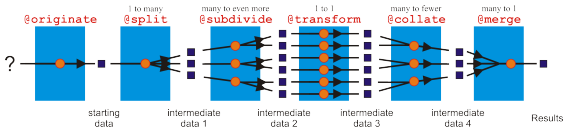


If we drew a graph of the data files moving through the pipeline, all of our flowcharts would look like something like this.

The *@transform* decorator connects up your data files in 1 to 1 operations, ensuring that for every **Input**, a corresponding **Output** is generated, ready to got into the next pipeline stage. If we start with three sets of starting data, we would end up with three final sets of results.

1.13.3 A bestiary of *Ruffus* decorators

Very often, we would like to transform our data in more complex ways, this is where other *Ruffus* decorators come in.



1.13.4 *@originate*

- Introduced in **Chapter 3** *More on @transform-ing data and @originate*, *@originate* generates **Output** files from scratch without the benefits of any **Input** files.

1.13.5 *@merge*

- A **many to one** operator.
- The last decorator at the far right to the figure, *@merge* merges multiple **Input** into one **Output**.

1.13.6 *@split*

- A **one to many** operator,
- *@split* is the evil twin of *@merge*. It takes a single set of **Input** and splits them into multiple smaller pieces.

- The best part of *@split* is that we don't necessarily have to decide ahead of time *how many* smaller pieces it should produce. If we have encounter a larger file, we might need to split it up into more fragments for greater parallelism.
- Since *@split* is a **one to many** operator, if you pass it **many** inputs (e.g. via *@transform*, it performs an implicit *@merge* step to make one set of **Input** that you can redistribute into a different number of pieces. If you are looking to split *each* **Input** into further smaller fragments, then you need *@subdivide*

1.13.7 *@subdivide*

- A **many to even more** operator.
- It takes each of multiple **Input**, and further subdivides them.
- Uses *suffix()*, *formatter()* or *regex()* to generate **Output** names from its **Input** files but like *@split*, we don't have to decide ahead of time *how many* smaller pieces each **Input** should be further divided into. For example, a large **Input** files might be subdivided into 7 pieces while the next job might, however, split its **Input** into just 4 pieces.

1.13.8 *@collate*

- A **many to fewer** operator.
- *@collate* is the opposite twin of `subdivide`: it takes multiple **Output** and groups or collates them into bundles of **Output**.
- *@collate* uses *formatter()* or *regex()* to generate **Output** names.
- All **Input** files which map to the same **Output** are grouped together into one job (one task function call) which produces one **Output**.

1.13.9 Combinatorics

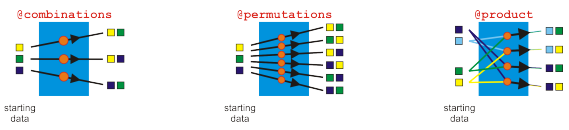
More rarely, we need to generate a set of **Output** based on a combination or permutation or product of the **Input**.

For example, in bioinformatics, we might need to look for all instances of a set of genes in the genomes of a different number of species. In other words, we need to find the *@product* of XXX genes x YYY species.

Ruffus provides decorators modelled on the "Combinatoric generators" in the Standard Python itertools library.

To use combinatoric decorators, you need to explicitly include them from *Ruffus*:

```
import ruffus
from ruffus import *
from ruffus.combinatorics import *
```



1.13.10 *@product*

- Given several sets of **Input**, it generates all versus all **Output**. For example, if there are four sets of **Input** files, *@product* will generate `WWW x XXX x YYY x ZZZ` **Output**.
- Uses *formatter* to generate unique **Output** names from components parsed from *any* parts of *any* specified files in all **Input** sets. In the above example, this allows the generation of `WWW x XXX x YYY x ZZZ` unique names.

1.13.11 *@combinations*

- Given one set of **Input**, it generates the combinations of r-length tuples among them.
- Uses *formatter* to generate unique **Output** names from components parsed from *any* parts of *any* specified files in all **Input** sets.
- For example, given **Input** called `A`, `B` and `C`, it will generate: `A-B`, `A-C`, `B-C`
- The order of **Input** items is ignored so either `A-B` or `B-A` will be included, not both
- Self-vs-self combinations (`A-A`) are excluded.

1.13.12 *@combinations_with_replacement*

- Given one set of **Input**, it generates the combinations of r-length tuples among them but includes self-vs-self conbinations.
- Uses *formatter* to generate unique **Output** names from components parsed from *any* parts of *any* specified files in all **Input** sets.
- For example, given **Input** called `A`, `B` and `C`, it will generate: `A-A`, `A-B`, `A-C`, `B-B`, `B-C`, `C-C`

1.13.13 *@permutations*

- Given one set of **Input**, it generates the permutations of r-length tuples among them. This excludes self-vs-self combinations but includes all orderings (`A-B` and `B-A`).
- Uses *formatter* to generate unique **Output** names from components parsed from *any* parts of *any* specified files in all **Input** sets.
- For example, given **Input** called `A`, `B` and `C`, it will generate: `A-A`, `A-B`, `A-C`, `B-A`, `B-C`, `C-A`, `C-B`

1.14 Chapter 12: Splitting up large tasks / files with @split

See also:

- *Manual Table of Contents*
- *@split* syntax
- *Example code for this chapter*

1.14.1 Overview

A common requirement in computational pipelines is to split up a large task into small jobs which can be run on different processors, (or sent to a computational cluster). Very often, the number of jobs depends dynamically on the size of the task, and cannot be known beforehand.

Ruffus uses the *@split* decorator to indicate that the *task* function will produce an indeterminate number of independent *Outputs* from a single *Input*.

1.14.2 Example: Calculate variance for a large list of numbers in parallel

Suppose we wanted to calculate the variance for 100,000 numbers, how can we parallelise the calculation so that we can get an answer as speedily as possible?

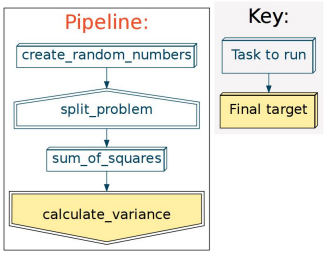
We need to

- break down the problem into manageable chunks
- solve these in parallel, possibly on a computational cluster and then
- merge the partial solutions back together for a final result.

To complicate things, we usually do not want to hard-code the number of parallel chunks beforehand. The degree of parallelism is often only apparent as we process our data.

Ruffus was designed to solve such problems which are common, for example, in bioinformatics and genomics.

A flowchart for our variance problem might look like this:



(In this toy example, we create our own starting data in `create_random_numbers()`.)

1.14.3 Output files for *@split*

The *Ruffus* decorator *@split* is designed specifically with this run-time flexibility in mind:

```
@split(create_random_numbers, "*.chunks")
def split_problem (input_file_names, output_files):
    pass
```

This will split the incoming `input_file_names` into `NNN` number of *outputs* where `NNN` is not pre-determined:

The *output* (second) parameter of *@split* often contains a *glob* pattern like the `*.chunks` above.

Only **after** the task function has completed, will Ruffus match the **Output** parameter (`*.chunks`) against the files which have been created by `split_problem()` (e.g. `1.chunks`, `2.chunks`, `3.chunks`)

1.14.4 Be careful in specifying Output globs

Note that it is your responsibility to keep the **Output** specification tight enough so that Ruffus does not pick up extraneous files.

You can specify multiple *glob* patterns to match *all* the files which are the result of the splitting task function. These can even cover different directories, or groups of file names. This is a more extreme example:

```
@split("input.file", ['a*.bits', 'b*.pieces', 'somewhere_else/c*.stuff'])
def split_function (input_filename, output_files):
    "Code to split up 'input.file'"
```

1.14.5 Clean up previous pipeline runs

Problem arise when the current directory contains results of previous pipeline runs.

- For example, if the previous analysis involved a large data set, there might be 3 chunks: `1.chunks`, `2.chunks`, `3.chunks`.
- In the current analysis, there might be a smaller data set which divides into only 2 chunks, `1.chunks` and `2.chunks`.
- Unfortunately, `3.chunks` from the previous run is still hanging around and will be included erroneously by the glob `*.chunks`.

Warning: Your first duty in *@split* tasks functions should be to clean up

To help you clean up thoroughly, Ruffus initialises the **output** parameter to all files which match specification.

The first order of business is thus invariably to cleanup (delete with `os.unlink`) all files in **Output**.

```
#---------------------------------------------------------------
#
#   split initial file
#
@split(create_random_numbers, "*.chunks")
def split_problem (input_file_names, output_files):
    """
        splits random numbers file into xxx files of chunk_size each
    """
    #
    #   clean up any files from previous runs
    #
    #for ff in glob.glob("*.chunks"):
    for ff in input_file_names:
        os.unlink(ff)
```

(The first time you run the example code, `*.chunks` will initialise `output_files` to an empty list.)

1.14.6 1 to many

@split is a one to many operator because its outputs are a list of *independent* items.

If *@split* generates 5 files, then this will lead to 5 jobs downstream.

This means we can just connect our old friend *@transform* to our pipeline and the results of *@split* will be analysed in parallel. This code should look familiar:

```
#---------------------------------------------------------------
#
#   Calculate sum and sum of squares for each chunk file
#
@transform(split_problem, suffix(".chunks"), ".sums")
def sum_of_squares (input_file_name, output_file_name):
    pass
```

Which results in output like this:

```
>>> pipeline_run()
    Job  = [[random_numbers.list] -> *.chunks] completed
Completed Task = split_problem
    Job  = [1.chunks -> 1.sums] completed
    Job  = [10.chunks -> 10.sums] completed
    Job  = [2.chunks -> 2.sums] completed
    Job  = [3.chunks -> 3.sums] completed
    Job  = [4.chunks -> 4.sums] completed
    Job  = [5.chunks -> 5.sums] completed
    Job  = [6.chunks -> 6.sums] completed
    Job  = [7.chunks -> 7.sums] completed
    Job  = [8.chunks -> 8.sums] completed
    Job  = [9.chunks -> 9.sums] completed
Completed Task = sum_of_squares
```

Have a look at the *Example code for this chapter*

1.14.7 Nothing to many

Normally we would use *@originate* to create files from scratch, for example at the beginning of the pipeline.

However, sometimes, it is not possible to determine ahead of time how many files you will be creating from scratch. *@split* can also be useful even in such cases:

```
from random import randint
from ruffus import *
import os

# Create between 2 and 5 files
@split(None, "*.start")
def create_initial_files(no_input_file, output_files):
    # cleanup first
    for oo in output_files:
        os.unlink(oo)
    # make new files
    for ii in range(randint(2,5)):
        open("%d.start" % ii, "w")

@transform(create_initial_files, suffix(".start"), ".processed")
def process_files(input_file, output_file):
    open(output_file, "w")

pipeline_run()
```

Giving:

```
>>> pipeline_run()
    Job  = [None -> *.start] completed
Completed Task = create_initial_files
    Job  = [0.start -> 0.processed] completed
    Job  = [1.start -> 1.processed] completed
Completed Task = process_files
```

1.15 Chapter 13: `@merge` multiple input into a single result

See also:

- *Manual Table of Contents*
- *@merge* syntax
- *Example code for this chapter*

1.15.1 Overview of *@merge*

The *previous chapter* explained how **Ruffus** allows large jobs to be split into small pieces with *@split* and analysed in parallel using for example, our old friend *@transform*.

Having done this, our next task is to recombine the fragments into a seamless whole.

This is the role of the *@merge* decorator.

1.15.2 *@merge* is a many to one operator

@transform tasks multiple *inputs* and produces a single *output*, **Ruffus** is again agnostic as to the sort of data contained within this single *output*. It can be a single (string) file name, an arbitrary complicated nested structure with numbers, objects etc. Or even a list.

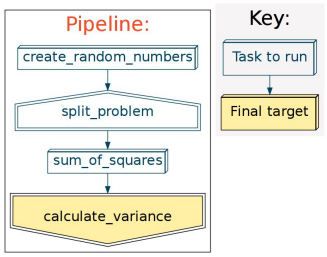
The main thing is that downstream tasks will interpret this output as a single entity leading to a single job.

@split and *@merge* are, in other words, about network topology.

Because of this *@merge* is also very useful for summarising the progress in our pipeline. At key selected points, we can gather data from the multitude of data or disparate *inputs* and *@merge* them to a single set of summaries.

1.15.3 Example: Combining partial solutions: Calculating variances

The *previous chapter* we had almost completed all the pieces of our flowchart:



What remains is to take the partial solutions from the different `.sums` files and turn these into the variance as follows:

```
variance = (sum_squared - sum * sum / N)/N
```

where `N` is the number of values

See the wikipedia entry for a discussion of why this is a very naive approach.

To do this, all we have to do is iterate through all the values in `*.sums`, add up the `sums` and `sum_squared`, and apply the above (naive) formula.

```
#
#   @merge files together
#
@merge(sum_of_squares, "variance.result")
def calculate_variance (input_file_names, output_file_name):
    """
    Calculate variance naively
    """
    #
    #   initialise variables
    #
    all_sum_squared = 0.0
    all_sum         = 0.0
    all_cnt_values  = 0.0
    #
    # added up all the sum_squared, and sum and cnt_values from all the chunks
    #
    for input_file_name in input_file_names:
        sum_squared, sum, cnt_values = map(float, open(input_file_name).readlines())
        all_sum_squared += sum_squared
        all_sum         += sum
        all_cnt_values  += cnt_values
    all_mean = all_sum / all_cnt_values
    variance = (all_sum_squared - all_sum * all_mean)/(all_cnt_values)
    #
    #   print output
    #
    open(output_file_name,  "w").write("%s\n" % variance)
```

This results in the following equivalent function call:

```
calculate_variance (["1.sums", "2.sums", "3.sums",
                     "4.sums", "5.sums", "6.sums",
                     "7.sums", "8.sums", "9.sums, "10.sums"], "variance.result")
```

and the following display:

```
>>> pipeline_run()
    Job  = [[1.sums, 10.sums, 2.sums, 3.sums, 4.sums, 5.sums, 6.sums, 7.sums, 8.sums, 9.sums
Completed Task = calculate_variance
```

The final result is in `variance.result`

Have a look at the *complete example code for this chapter*.

1.16 Chapter 14: Multiprocessing, drmaa and Computation Clusters

See also:

- *Manual Table of Contents*
- *@jobs_limit* syntax
- *pipeline_run()* syntax
- *drmaa_wrapper.run_job()* syntax

Note: Remember to look at the example code:

- *Chapter 14: Python Code for Multiprocessing, drmaa and Computation Clusters*

1.16.1 Overview

Multi Processing

Ruffus uses python multiprocessing to run each job in a separate process.

This means that jobs do *not* necessarily complete in the order of the defined parameters. Task hierachies are, of course, inviolate: upstream tasks run before downstream, dependent tasks.

Tasks that are independent (i.e. do not precede each other) may be run in parallel as well.

The number of concurrent jobs can be set in *pipeline_run*:

```
pipeline_run([parallel_task], multiprocess = 5)
```

If `multiprocess` is set to 1, then jobs will be run on a single process.

Data sharing

Running jobs in separate processes allows *Ruffus* to make full use of the multiple processors in modern computers. However, some multiprocessing guidelines should be borne in mind when writing *Ruffus* pipelines. In particular:

- Try not to pass large amounts of data between jobs, or at least be aware that this has to be marshalled across process boundaries.
- Only data which can be pickled can be passed as parameters to *Ruffus* task functions. Happily, that applies to almost any native Python data type. The use of the rare, unpicklable object will cause python to complain (fail) loudly when *Ruffus* pipelines are run.

1.16.2 Restricting parallelism with *@jobs_limit*

Calling *pipeline_run(multiprocess = NNN)* allows multiple jobs (from multiple independent tasks) to be run in parallel. However, there are some operations that consume so many resources that we might want them to run with less or no concurrency.

For example, we might want to download some files via FTP but the server restricts requests from each IP address. Even if the rest of the pipeline is running 100 jobs in parallel, the FTP downloading must be restricted to 2 files at a time. We would really like to keep the pipeline running as is, but let this one operation run either serially, or with little concurrency.

- *pipeline_run(multiprocess = NNN)* sets the pipeline-wide concurrency but
- *@jobs_limit(MMM)* sets concurrency at `MMM` only for jobs in the decorated task.

The optional name (e.g. `@jobs_limit(3, "ftp_download_limit")`) allows the same limit to be shared across multiple tasks. To be pedantic: a limit of `3` jobs at a time would be applied across all tasks which have a `@jobs_limit` named `"ftp_download_limit"`.

The *example code* uses up to 10 processes across the pipeline, but runs the `stage1_big` and `stage1_small` tasks 3 at a time (shared across both tasks). `stage2` jobs run 5 at a time.

1.16.3 Using `drmaa` to dispatch work to Computational Clusters or Grid engines from Ruffus jobs

Ruffus has been widely used to manage work on computational clusters or grid engines. Though Ruffus task functions cannot (yet!) run natively and transparently on remote cluster nodes, it is trivial to dispatch work across the cluster.

From version 2.4 onwards, Ruffus includes an optional helper module which interacts with python bindings for the widely used drmaa Open Grid Forum API specification. This allows jobs to dispatch work to a computational cluster and wait until it completes.

Here are the necessary steps

1) Use a shared drmaa session:

Before your pipeline runs:

```
#
#   start shared drmaa session for all jobs / tasks in pipeline
#
import drmaa
drmaa_session = drmaa.Session()
drmaa_session.initialize()
```

Cleanup after your pipeline completes:

```
#
#   pipeline functions go here
#
if __name__ == '__main__':
    drmaa_session.exit()
```

2) import `ruffus.drmaa_wrapper`

- The optional `ruffus.drmaa_wrapper` module needs to be imported explicitly:

```
# imported ruffus.drmaa_wrapper explicitly
from ruffus.drmaa_wrapper import run_job, error_drmaa_job
```

3) call *drmaa_wrapper.run_job()*

drmaa_wrapper.run_job() dispatches the work to a cluster node within a normal Ruffus job and waits for completion

This is the equivalent of os.system or subprocess.check_output but the code will run remotely as specified:

```
# ruffus.drmaa_wrapper.run_job
stdout_res, stderr_res  = run_job(cmd_str           = "touch " + output_file,
                                  job_name          = job_name,
                                  logger            = logger,
                                  drmaa_session     = drmaa_session,
                                  run_locally       = options.local_run,
                                  job_other_options = job_other_options)
```

The complete code is available *here*

- *drmaa_wrapper.run_job()* is a convenience wrapper around the python drmaa bindings RunJob function. It takes care of writing drmaa *job templates* for you.
- Each call creates a separate drmaa *job template*.

4) Use multithread: *pipeline_run(multithread = NNN)*

> **Warning:** *drmaa_wrapper.run_job()*
> **requires** `pipeline_run` *(multithread = NNN)*
> **and will not work with** `pipeline_run` *(multiprocess = NNN)*

Using multithreading rather than multiprocessing

- allows the drmaa session to be shared
- prevents "processing storms" which lock up the queue submission node when hundreds or thousands of grid engine / cluster commands complete at the same time.

```
pipeline_run (..., multithread = NNN, ...)
```

or if you are using ruffus.cmdline:

```
cmdline.run (options, multithread = options.jobs)
```

Normally multithreading reduces the amount of parallelism in python due to the python Global interpreter Lock (GIL). However, as the work load is almost entirely on another computer (i.e. a cluster / grid engine node) with a separate python interpreter, any cost benefit calculations of this sort are moot.

5) Develop locally

drmaa_wrapper.run_job() provides two convenience parameters for developing grid engine pipelines:

- commands can run locally, i.e. on the local machine rather than on cluster nodes:

```
run_job(cmd_str, run_locally = True)
```

- Output files can be touched, i.e. given the appearance of the work having being done without actually running the commands

```
run_job(cmd_str, touch_only = True)
```

1.16.4 Forcing a pipeline to appear up to date

Sometimes, we *know* that a pipeline has run to completion, that everything is up-to-date. However, Ruffus still insists on the basis of file modification times that you need to rerun.

For example, sometimes a trivial accounting modification needs to be made to a data file. Even though you know that this changes nothing in practice, Ruffus will detect the modification and ask to rerun everything from that point forwards.

One way to convince Ruffus that everything is fine is to manually touch all subsequent data files one by one in sequence so that the file timestamps follow the appropriate progression.

You can also ask *Ruffus* to do this automatically for you by running the pipeline in touch mode:

```
pipeline_run( touch_files_only = True)
```

pipeline_run will run your pipeline script normally working backwards from any specified final target, or else the last task in the pipeline. It works out where it should begin running, i.e. with the first out-of-date data files. After that point, instead of calling your pipeline task functions, each missing or out-of-date file is touch-ed in turn so that the file modification dates follow on successively.

This turns out to be useful way to check that your pipeline runs correctly by creating a series of dummy (empty files). However, *Ruffus* does not know how to read your mind to know which files to create from *@split* or *@subdivide* tasks.

Using *ruffus.cmdline* from version 2.4, you can just specify:

```
your script --touch_files_only [--other_options_of_your_own_etc]
```

1.17 Chapter 15: Logging progress through a pipeline

See also:

- *Manual Table of Contents*

Note: Remember to look at the *example code*

1.17.1 Overview

There are two parts to logging with **Ruffus**:

- Logging progress through the pipeline

  This produces the sort of output displayed in this manual:

  ```
  >>> pipeline_run([parallel_io_task])
  Task = parallel_io_task
      Job = ["a.1" -> "a.2", "A file"] completed
      Job = ["b.1" -> "b.2", "B file"] unnecessary: already up to date
  Completed Task = parallel_io_task
  ```

- Logging your own messages from within your pipelined functions.

  Because **Ruffus** may run each task function in separate process on a separate CPU (multiprocessing), some attention has to be paid to how to send and synchronise your log messages across process boundaries.

We shall deal with these in turn.

1.17.2 Logging task/job completion

By default, *Ruffus* logs each task and each job as it is completed to sys.stderr.

By default, Ruffus logs to `STDERR`: *pipeline_run(logger = stderr_logger)*.

If you want to turn off all tracking messages as the pipeline runs, apart from setting `verbose = 0`, you can also use the aptly named Ruffus `black_hole_logger`:

```
pipeline_run(logger = black_hole_logger)
```

Controlling logging verbosity

pipeline_run() currently has five levels of verbosity, set by the optional `verbose` parameter which defaults to 1:

```
verbose = 0: nothing
verbose = 1: logs completed jobs/tasks;
verbose = 2: logs up to date jobs in incomplete tasks
verbose = 3: logs reason for running job
verbose = 4: logs messages useful only for debugging ruffus pipeline code
```

`verbose` > 5 are intended for debugging **Ruffus** by the developers and the details are liable to change from release to release

1.17.3 Use *ruffus.cmdline*

As always, it is easiest to use *ruffus.cmdline*.

Set your script to

- write messages to `STDERR` with the `--verbose` option and
- to a log file with the `--log_file` option.

```
from ruffus import *

#  Python logger which can be synchronised across concurrent Ruffus tasks
logger, logger_mutex = cmdline.setup_logging (__name__, options.log_file, options.verbose)

@transform( ["job1.input"], suffix(".input"), ".output1"),
def first_task(input_file, output_file):
    pass

pipeline_run(logger=logger)
```

1.17.4 Customising logging

You can also specify exactly how logging works by providing a logging object to *pipeline_run()* . This log object should have `debug()` and `info()` methods.

Instead of writing your own, it is usually more convenient to use the python logging module which provides logging classes with rich functionality.

The *example code* sets up a logger to a rotating set of files

1.17.5 Log your own messages

You need to take a little care when logging your custom messages *within* your pipeline.

- If your Ruffus pipeline may run in parallel, make sure that logging is synchronised.
- If your Ruffus pipeline may run across separate processes, send your logging object across process boundaries.

logging objects can not be pickled and shared naively across processes. Instead, we need to create proxies which forward the logging to a single shared log.

The *ruffus.proxy_logger* module provides an easy way to share logging objects among jobs. This requires just two simple steps:

Note:

- This is a good template for sharing non-picklable objects across processes.

---

1. Set up logging

Things are easiest if you are using `ruffus.cmdline`:

```
#  standard python logger which can be synchronised across concurrent Ruffus tasks
logger, logger_mutex = cmdline.setup_logging (__name__, options.log_file, options.verbose)
```

Otherwise, manually:

```
from ruffus.proxy_logger import *
(logger,
 logging_mutex) = make_shared_logger_and_proxy (setup_std_shared_logger,
                                                "my_logger",
                                                {"file_name" :"/my/lg.log"})
```

2. Share the proxy

Now, pass:

- `logger` (which forwards logging calls across jobs) and
- `logging_mutex` (which prevents different jobs which are logging simultaneously from being jumbled up)

to each job:

```
@transform( initial_file,
            suffix(".input"),
            ".output1",
            logger, logging_mutex),          # pass log and synchronisation as parameters
def first_task(input_file, output_file,
            logger, logging_mutex):          # pass log and synchronisation as parameters
    pass

    # synchronise logging
```

```
    with logging_mutex:
        logger.info("Here we go logging...")
```

1.18 Chapter 16: *@subdivide* tasks to run efficiently and regroup with *@collate*

See also:

- *Manual Table of Contents*
- *@subdivide* syntax
- *@collate* syntax

1.18.1 Overview

In **Chapter 12** and **Chapter 13**, we saw how a large task can be *@split* into small jobs to be analysed efficiently in parallel. Ruffus can then *@merge* these back together to give a single, unified result.

This assumes that your pipeline is processing one item at a time. Usually, however, we will have, for example, 10 large pieces of data in play, each of which has to be subdivided into smaller pieces for analysis before being put back together.

This is the role of *@subdivide* and *@subdivide*.

Like *@split*, the number of output files *@subdivide* produces for *each* **Input** is not predetermined.

On the other hand, these output files should be named in such a way that they can later be grouped back together later using *@subdivide*.

This will be clearer with some worked examples.

1.18.2 *@subdivide* in parallel

Let us start from 3 files with varying number of lines. We wish to process these two lines at a time but we do not know ahead of time how long each file is:

```
from ruffus import *
import os, random, sys

# Create files a random number of lines
@originate(["a.start",
            "b.start",
            "c.start"])
def create_test_files(output_file):
    cnt_lines = random.randint(1,3) * 2
    with open(output_file, "w") as oo:
        for ii in range(cnt_lines):
            oo.write("data item = %d\n" % ii)
        print "        %s has %d lines" % (output_file, cnt_lines)


#
#   subdivide the input files into NNN fragment files of 2 lines each
#
```

```
@subdivide( create_test_files,
            formatter(),
            "{path[0]}/{basename[0]}.*.fragment",
            "{path[0]}/{basename[0]}")
def subdivide_files(input_file, output_files, output_file_name_stem):
    #
    #   cleanup any previous results
    #
    for oo in output_files:
        os.unlink(oo)
    #
    #   Output files contain two lines each
    #       (new output files every even line)
    #
    cnt_output_files = 0
    for ii, line in enumerate(open(input_file)):
        if ii % 2 == 0:
            cnt_output_files += 1
            output_file_name = "%s.%d.fragment" % (output_file_name_stem, cnt_output_files)
            output_file = open(output_file_name, "w")
            print "        Subdivide %s -> %s" % (input_file, output_file_name)
        output_file.write(line)


#
#   Analyse each fragment independently
#
@transform(subdivide_files, suffix(".fragment"), ".analysed")
def analyse_fragments(input_file, output_file):
    print "        Analysing %s -> %s" % (input_file, output_file)
    with open(output_file, "w") as oo:
        for line in open(input_file):
            oo.write("analysed " + line)
```

This produces the following output:

```
>>> pipeline_run(verbose = 1)
        a.start has 2 lines
    Job  = [None -> a.start] completed
        b.start has 6 lines
    Job  = [None -> b.start] completed
        c.start has 6 lines
    Job  = [None -> c.start] completed
Completed Task = create_test_files

        Subdivide a.start -> /home/lg/temp/a.1.fragment
    Job  = [a.start -> a.*.fragment, a] completed

        Subdivide b.start -> /home/lg/temp/b.1.fragment
        Subdivide b.start -> /home/lg/temp/b.2.fragment
        Subdivide b.start -> /home/lg/temp/b.3.fragment
    Job  = [b.start -> b.*.fragment, b] completed

        Subdivide c.start -> /home/lg/temp/c.1.fragment
        Subdivide c.start -> /home/lg/temp/c.2.fragment
        Subdivide c.start -> /home/lg/temp/c.3.fragment
    Job  = [c.start -> c.*.fragment, c] completed
```

```
Completed Task = subdivide_files

        Analysing /home/lg/temp/a.1.fragment -> /home/lg/temp/a.1.analysed
    Job  = [a.1.fragment -> a.1.analysed] completed
        Analysing /home/lg/temp/b.1.fragment -> /home/lg/temp/b.1.analysed
    Job  = [b.1.fragment -> b.1.analysed] completed

    [ ...SEE EXAMPLE CODE FOR MORE LINES ...]

Completed Task = analyse_fragments
```

`a.start` has two lines and results in a single `.fragment` file, while there are 3 `b.*.fragment` files because it has 6 lines. Whatever their origin, all of the different fragment files are treated equally in `analyse_fragments()` and processed (in parallel) in the same way.

1.18.3 Grouping using *@collate*

All that is left in our example is to reassemble the analysed fragments back together into 3 sets of results corresponding to the original 3 pieces of starting data.

This is straightforward by eye: the file names all have the same pattern: `[abc].*.analysed`:

```
a.1.analysed    ->   a.final_result
b.1.analysed    ->   b.final_result
b.2.analysed    ->   ..
b.3.analysed    ->   ..
c.1.analysed    ->   c.final_result
c.2.analysed    ->   ..
```

@collate does something similar:

1. Specify a string substitution e.g. `c.??.analysed -> c.final_result` and
2. Ask *ruffus* to group together any **Input** (e.g. `c.1.analysed`, `c.2.analysed`) that will result in the same **Output** (e.g. `c.final_result`)

```
#
#   ``XXX.??.analysed  -> XXX.final_result``
#   Group results using original names
#
@collate(   analyse_fragments,

            # split file name into [abc].NUMBER.analysed
            formatter("/(?P<NAME>[abc]+)\.\d+\.analysed$"),

            "{path[0]}/{NAME[0]}.final_result")
def recombine_analyses(input_file_names, output_file):
    with open(output_file, "w") as oo:
        for input_file in input_file_names:
            print "        Recombine %s -> %s" % (input_file, output_file)
            for line in open(input_file):
                oo.write(line)
```

This produces the following output:

```
        Recombine /home/lg/temp/a.1.analysed -> /home/lg/temp/a.final_result
    Job  = [[a.1.analysed] -> a.final_result] completed
        Recombine /home/lg/temp/b.1.analysed -> /home/lg/temp/b.final_result
        Recombine /home/lg/temp/b.2.analysed -> /home/lg/temp/b.final_result
```

```
        Recombine /home/lg/temp/b.3.analysed -> /home/lg/temp/b.final_result
    Job  = [[b.1.analysed, b.2.analysed, b.3.analysed] -> b.final_result] completed
        Recombine /home/lg/temp/c.1.analysed -> /home/lg/temp/c.final_result
        Recombine /home/lg/temp/c.2.analysed -> /home/lg/temp/c.final_result
        Recombine /home/lg/temp/c.3.analysed -> /home/lg/temp/c.final_result
    Job  = [[c.1.analysed, c.2.analysed, c.3.analysed] -> c.final_result] completed
Completed Task = recombine_analyses
```

Warning:

- **Input** file names are grouped together not in a guaranteed order.
  For example, the fragment files may not be sent to `recombine_analyses(input_file_names, ...)` in alphabetically or any other useful order.
  You may want to sort **Input** before concatenation.
- All **Input** are grouped together if they have both the same **Output** *and* **Extra** parameters. If any string substitution is specified in any of the other **Extra** parameters to *@subdivide*, they must give the same answers for **Input** in the same group.

1.19 Chapter 17: *@combinations*, *@permutations* and all versus all *@product*

See also:

- *Manual Table of Contents*
- *@combinations_with_replacement*
- *@combinations*
- *@permutations*
- *@product*
- *formatter()*

Note: Remember to look at the example code:

- *Chapter 17: Python Code for @combinations, @permutations and all versus all @product*

1.19.1 Overview

A surprising number of computational problems involve some sort of all versus all calculations. Previously, this would have required all the parameters to be supplied using a custom function on the fly with *@files*.

From version 2.4, *Ruffus* supports *@combinations_with_replacement*, *@combinations*, *@permutations*, *@product*.

These provide as far as possible all the functionality of the four combinatorics iterators from the standard python itertools functions of the same name.

1.19.2 Generating output with *formatter()*

String replacement always takes place via *formatter()*. Unfortunately, the other *Ruffus* workhorses of *regex()* and *suffix()* do not have sufficient syntactic flexibility.

Each combinatorics decorator deals with multiple sets of inputs whether this might be:

- a self-self comparison (such as *@combinations_with_replacement*, *@combinations*, *@permutations*) or,
- a self-other comparison (*@product*)

The replacement strings thus require an extra level of indirection to refer to parsed components.

1. The first level refers to which *set* of inputs.
2. The second level refers to which input file in any particular *set* of inputs.

For example, if the *inputs* are **[A1,A2],[B1,B2],[C1,C2] vs [P1,P2],[Q1,Q2],[R1,R2] vs [X1,X2],[Y1,Y2],[Z1,Z2]**, then `'{basename[2][0]}'` is the basename for

- the third set of inputs (**X,Y,Z**) and
- the first file name string in each **Input** of that set (**X1, Y1, Z1**)

1.19.3 All vs all comparisons with *@product*

@product generates the Cartesian **product** between sets of input files, i.e. all vs all comparisons.

The effect is analogous to a nested for loop.

@product can be useful, for example, in bioinformatics for finding the corresponding genes (orthologues) for a set of proteins in multiple species.

```
>>> from itertools import product
>>> # product('ABC', 'XYZ') --> AX AY AZ BX BY BZ CX CY CZ
>>> [ "".join(a) for a in product('ABC', 'XYZ')]
['AX', 'AY', 'AZ', 'BX', 'BY', 'BZ', 'CX', 'CY', 'CZ']
```

This example Calculates the **@product** of **A,B** and **P,Q** and **X,Y** files

```
from ruffus import *
from ruffus.combinatorics import *

#   Three sets of initial files
@originate([ 'a.start', 'b.start'])
def create_initial_files_ab(output_file):
    with open(output_file, "w") as oo: pass

@originate([ 'p.start', 'q.start'])
def create_initial_files_pq(output_file):
    with open(output_file, "w") as oo: pass

@originate([ ['x.1_start', 'x.2_start'],
             ['y.1_start', 'y.2_start'] ])
def create_initial_files_xy(output_file):
    with open(output_file, "w") as oo: pass

#   @product
@product(   create_initial_files_ab,        # Input
            formatter("(.start)$"),         # match input file set # 1
```

```
                create_initial_files_pq,        # Input
                formatter("(.start)$"),         # match input file set # 2

                create_initial_files_xy,        # Input
                formatter("(.start)$"),         # match input file set # 3

                "{path[0][0]}/"                 # Output Replacement string
                "{basename[0][0]}_vs_"          #
                "{basename[1][0]}_vs_"          #
                "{basename[2][0]}.product",     #

                "{path[0][0]}",                 # Extra parameter: path for 1st set of files, 1s

                ["{basename[0][0]}",            # Extra parameter: basename for 1st set of files
                 "{basename[1][0]}",            #                                  2nd
                 "{basename[2][0]}",            #                                  3rd
                 ])
    def product_task(input_file, output_parameter, shared_path, basenames):
        print "# basenames      = ", " ".join(basenames)
        print "input_parameter  = ", input_file
        print "output_parameter = ", output_parameter, "\n"


    #
    #       Run
    #
    pipeline_run(verbose=0)
```

This results in:

```
>>> pipeline_run(verbose=0)

# basenames      =  a p x
input_parameter  =  ('a.start', 'p.start', 'x.start')
output_parameter =  /home/lg/temp/a_vs_p_vs_x.product

# basenames      =  a p y
input_parameter  =  ('a.start', 'p.start', 'y.start')
output_parameter =  /home/lg/temp/a_vs_p_vs_y.product

# basenames      =  a q x
input_parameter  =  ('a.start', 'q.start', 'x.start')
output_parameter =  /home/lg/temp/a_vs_q_vs_x.product

# basenames      =  a q y
input_parameter  =  ('a.start', 'q.start', 'y.start')
output_parameter =  /home/lg/temp/a_vs_q_vs_y.product

# basenames      =  b p x
input_parameter  =  ('b.start', 'p.start', 'x.start')
output_parameter =  /home/lg/temp/b_vs_p_vs_x.product

# basenames      =  b p y
input_parameter  =  ('b.start', 'p.start', 'y.start')
output_parameter =  /home/lg/temp/b_vs_p_vs_y.product

# basenames      =  b q x
input_parameter  =  ('b.start', 'q.start', 'x.start')
```

```
output_parameter =  /home/lg/temp/b_vs_q_vs_x.product

# basenames      =  b q y
input_parameter  =  ('b.start', 'q.start', 'y.start')
output_parameter =  /home/lg/temp/b_vs_q_vs_y.product
```

1.19.4 Permute all k-tuple orderings of inputs without repeats using *@permutations*

Generates the permutations for all the elements of a set of Input (e.g. A B C D),

- r-length tuples of *input* elements
- excluding repeated elements (**A A**)
- and order of the tuples is significant (both **A B** and **B A**).

```
>>> from itertools import permutations
>>> # permutations('ABCD', 2) --> AB AC AD BA BC BD CA CB CD DA DB DC
>>> [ "".join(a) for a in permutations("ABCD", 2)]
['AB', 'AC', 'AD', 'BA', 'BC', 'BD', 'CA', 'CB', 'CD', 'DA', 'DB', 'DC']
```

This following example calculates the **@permutations** of **A,B,C,D** files

```
from ruffus import *
from ruffus.combinatorics import *

#   initial file pairs
@originate([ ['A.1_start', 'A.2_start'],
             ['B.1_start', 'B.2_start'],
             ['C.1_start', 'C.2_start'],
             ['D.1_start', 'D.2_start']])
def create_initial_files_ABCD(output_files):
    for output_file in output_files:
        with open(output_file, "w") as oo: pass

#   @permutations
@permutations(create_initial_files_ABCD,      # Input
              formatter(),                    # match input files

              # tuple of 2 at a time
              2,

              # Output Replacement string
              "{path[0][0]}/"
              "{basename[0][1]}_vs_"
              "{basename[1][1]}.permutations",

              # Extra parameter: path for 1st set of files, 1st file name
              "{path[0][0]}",

              # Extra parameter
              ["{basename[0][0]}",  # basename for 1st set of files, 1st file name
               "{basename[1][0]}",  #                                 2nd
               ])
def permutations_task(input_file, output_parameter, shared_path, basenames):
    print " - ".join(basenames)
```

```
#
#       Run
#
pipeline_run(verbose=0)
```

This results in:

```
>>> pipeline_run(verbose=0)

A - B
A - C
A - D
B - A
B - C
B - D
C - A
C - B
C - D
D - A
D - B
D - C
```

1.19.5 Select unordered k-tuples within inputs excluding repeated elements using *@combinations*

Generates the combinations for all the elements of a set of Input (e.g. A B C D),

- r-length tuples of *input* elements
- without repeated elements (**A A**)
- where order of the tuples is irrelevant (either **A B** or **B A**, not both).

@combinations can be useful, for example, in calculating a transition probability matrix for a set of states. The diagonals are meaningless "self-self" transitions which are excluded.

```
>>> from itertools import combinations
>>> # combinations('ABCD', 3) --> ABC ABD ACD BCD
>>> [ "".join(a) for a in combinations("ABCD", 3)]
['ABC', 'ABD', 'ACD', 'BCD']
```

This example calculates the **@combinations** of **A,B,C,D** files

```
from ruffus import *
from ruffus.combinatorics import *

#   initial file pairs
@originate([ ['A.1_start', 'A.2_start'],
             ['B.1_start', 'B.2_start'],
             ['C.1_start', 'C.2_start'],
             ['D.1_start', 'D.2_start']])
def create_initial_files_ABCD(output_files):
    for output_file in output_files:
        with open(output_file, "w") as oo: pass

#   @combinations
@combinations(create_initial_files_ABCD,      # Input
              formatter(),                    # match input files
```

```
                    # tuple of 3 at a time
                    3,

                    # Output Replacement string
                    "{path[0][0]}/"
                    "{basename[0][1]}_vs_"
                    "{basename[1][1]}_vs_"
                    "{basename[2][1]}.combinations",

                    # Extra parameter: path for 1st set of files, 1st file name
                    "{path[0][0]}",

                    # Extra parameter
                    ["{basename[0][0]}",  # basename for 1st set of files, 1st file name
                     "{basename[1][0]}",  #               2nd
                     "{basename[2][0]}",  #               3rd
                     ])
    def combinations_task(input_file, output_parameter, shared_path, basenames):
        print " - ".join(basenames)


    #
    #       Run
    #
    pipeline_run(verbose=0)
```

This results in:

```
>>> pipeline_run(verbose=0)
A - B - C
A - B - D
A - C - D
B - C - D
```

1.19.6 Select unordered k-tuples within inputs *including* repeated elements with *@combinations_with_replacement*

Generates the combinations_with_replacement for all the elements of a set of Input (e.g. A B C D),

- r-length tuples of *input* elements
- including repeated elements (**A A**)
- where order of the tuples is irrelevant (either **A B** or **B A**, not both).

@combinations_with_replacement can be useful, for example, in bioinformatics for finding evolutionary relationships between genetic elements such as proteins and genes. Self-self comparisons can be used a baseline for scaling similarity scores.

```
>>> from itertools import combinations_with_replacement
>>> # combinations_with_replacement('ABCD', 2) --> AA AB AC AD BB BC BD CC CD DD
>>> [ "".join(a) for a in combinations_with_replacement('ABCD', 2)]
['AA', 'AB', 'AC', 'AD', 'BB', 'BC', 'BD', 'CC', 'CD', 'DD']
```

This example calculates the **@combinations_with_replacement** of **A,B,C,D** files

```
from ruffus import *
from ruffus.combinatorics import *

#   initial file pairs
@originate([ ['A.1_start', 'A.2_start'],
             ['B.1_start', 'B.2_start'],
             ['C.1_start', 'C.2_start'],
             ['D.1_start', 'D.2_start']])
def create_initial_files_ABCD(output_files):
    for output_file in output_files:
        with open(output_file, "w") as oo: pass

#   @combinations_with_replacement
@combinations_with_replacement(create_initial_files_ABCD,    # Input
              formatter(),                                   # match input files

              # tuple of 2 at a time
              2,

              # Output Replacement string
              "{path[0][0]}/"
              "{basename[0][1]}_vs_"
              "{basename[1][1]}.combinations_with_replacement",

              # Extra parameter: path for 1st set of files, 1st file name
              "{path[0][0]}",

              # Extra parameter
              ["{basename[0][0]}",  # basename for 1st set of files, 1st file name
               "{basename[1][0]}",  #               2rd
               ])
def combinations_with_replacement_task(input_file, output_parameter, shared_path, basenames):
    print " - ".join(basenames)


#
#       Run
#
pipeline_run(verbose=0)
```

This results in:

```
>>> pipeline_run(verbose=0)
A - A
A - B
A - C
A - D
B - B
B - C
B - D
C - C
C - D
D - D
```

1.20 Chapter 18: Turning parts of the pipeline on and off at runtime with *@active_if*

See also:

- *Manual Table of Contents*
- *@active_if syntax in detail*

1.20.1 Overview

It is sometimes useful to be able to switch on and off parts of a pipeline. For example, a pipeline might have two difference code paths depending on the type of data it is being asked to analyse.

One surprisingly easy way to do this is to use a python `if` statement around particular task functions:

```
from ruffus import *

run_task1 = True

@originate(['a.foo', 'b.foo'])
def create_files(output_file):
    open(output_file, "w")


if run_task1:
    # might not run
    @transform(create_files, suffix(".foo"), ".bar")
    def foobar(input_file, output_file):
        open(output_file, "w")


@transform(foobar, suffix(".bar"), ".result")
def wrap_up(input_file, output_file):
        open(output_file, "w")


pipeline_run()
```

This simple solution has a number of drawbacks:

1. The on/off decision is a one off event that happens when the script is loaded. Ideally, we would like some flexibility, and postpone the decision until `pipeline_run()` is invoked.
2. When `if` is false, the entire task function becomes invisible, and if there are any downstream tasks, as in the above example, *Ruffus* will complain loudly about missing dependencies.

1.20.2 *@active_if* controls the state of tasks

- Switches tasks on and off at run time depending on its parameters
- Evaluated each time `pipeline_run`, `pipeline_printout` or `pipeline_printout_graph` is called.
- Dormant tasks behave as if they are up to date and have no output.

The Design and initial implementation were contributed by Jacob Biesinger

The following example shows its flexibility and syntax:

```
from ruffus import *
run_if_true_1 = True
run_if_true_2 = False
run_if_true_3 = True


#
#    task1
#
@originate(['a.foo', 'b.foo'])
def create_files(outfile):
    """
    create_files
    """
    open(outfile, "w").write(outfile + "\n")

#
#   Only runs if all three run_if_true conditions are met
#
#   @active_if determines if task is active
@active_if(run_if_true_1, lambda: run_if_true_2)
@active_if(run_if_true_3)
@transform(create_files, suffix(".foo"), ".bar")
def this_task_might_be_inactive(infile, outfile):
    open(outfile, "w").write("%s -> %s\n" % (infile, outfile))


# @active_if switches off task because run_if_true_2 == False
pipeline_run(verbose = 3)

# @active_if switches on task because all run_if_true conditions are met
run_if_true_2 = True
pipeline_run(verbose = 3)
```

The task starts off inactive:

```
>>> # @active_if switches off task "this_task_might_be_inactive" because run_if_true_2 == Fa
>>> pipeline_run(verbose = 3)

Task enters queue = create_files
create_files
    Job  = [None -> a.foo] Missing file [a.foo]
    Job  = [None -> b.foo] Missing file [b.foo]
    Job  = [None -> a.foo] completed
    Job  = [None -> b.foo] completed
Completed Task = create_files
Inactive Task = this_task_might_be_inactive
```

Now turn on the task:

```
>>> # @active_if switches on task "this_task_might_be_inactive" because all run_if_true cond
>>> run_if_true_2 = True
>>> pipeline_run(verbose = 3)

Task enters queue = this_task_might_be_inactive

    Job  = [a.foo -> a.bar] Missing file [a.bar]
    Job  = [b.foo -> b.bar] Missing file [b.bar]
```

```
        Job  = [a.foo -> a.bar] completed
        Job  = [b.foo -> b.bar] completed
Completed Task = this_task_might_be_inactive
```

1.21 Chapter 19: Signal the completion of each stage of our pipeline with *@posttask*

See also:

- *Manual Table of Contents*
- *@posttask* syntax

1.21.1 Overview

It is often useful to signal the completion of each task by specifying a specific action to be taken or function to be called. This can range from printing out some message, or touching some sentinel file, to emailing the author. This is particular useful if the *task* is a recipe apply to an unspecified number of parameters in parallel in different *job*s. If the task is never run, or if it fails, needless-to-say no task completion action will happen.

Ruffus uses the *@posttask* decorator for this purpose.

@posttask

We can signal the completion of each task by specifying one or more function(s) using *@posttask*

```
from ruffus import *

def task_finished():
    print "hooray"

@posttask(task_finished)
@originate("a.1")
def create_if_necessary(output_file):
    open(output_file, "w")

pipeline_run([create_if_necessary])
```

This is such a short function, we might as well write it in-line:

```
    @posttask(lambda: sys.stdout.write("hooray\n"))
    @originate("a.1")
    def create_if_necessary(output_file):
        open(output_file, "w")
```

Note: The function(s) provided to *@posttask* will be called if the pipeline passes through a task, even if none of its jobs are run because they are up-to-date. This happens when a upstream task is out-of-date, and the execution passes through this point in the pipeline. See the example in *Appendix 2: How dependency is checked* of this manual.

touch_file

One way to note the completion of a task is to create some sort of "flag" file. Each stage in a traditional `make` pipeline would contain a `touch completed.flag`.

This is such a useful idiom that *Ruffus* provides the shorthand *touch_file*:

```
from ruffus import *

@posttask(touch_file("task_completed.flag"))
@files(None, "a.1")
def create_if_necessary(input_file, output_file):
    open(output_file, "w")

pipeline_run()
```

Adding several post task actions

You can, of course, add more than one different action to be taken on completion of the task, either by stacking up as many *@posttask* decorators as necessary, or by including several functions in the same *@posttask*:

```
from ruffus import *

@posttask(print_hooray, print_whoppee)
@posttask(print_hip_hip, touch_file("sentinel_flag"))
@originate("a.1")
def create_if_necessary(output_file):
    open(output_file, "w")

pipeline_run()
```

1.22 Chapter 20: Manipulating task inputs via string substitution using *inputs()* and *add_inputs()*

See also:

- *Manual Table of Contents*
- *inputs()* syntax
- *add_inputs()* syntax

Note: Remember to look at the example code:

- *Chapter 20: Python Code for Manipulating task inputs via string substitution using inputs() and add_inputs()*

1.22.1 Overview

The previous chapters have been described how *Ruffus* allows the **Output** names for each job to be generated from the *Input* names via string substitution. This is how *Ruffus* can automatically chain multiple tasks in a pipeline together seamlessly.

Sometimes it is useful to be able to modify the **Input** by string substitution as well. There are two situations where this additional flexibility is needed:

1. You need to add additional prequisites or filenames to the **Input** of every single job
2. You need to add additional **Input** file names which are some variant of the existing ones.

Both will be much more obvious with some examples

1.22.2 Adding additional *input* prerequisites per job with *add_inputs()*

1. Example: compiling c++ code

Let us first compile some c++ (`"*.cpp"`) files using plain *@transform* syntax:

```
# source files exist before our pipeline
source_files = ["hasty.cpp", "tasty.cpp", "messy.cpp"]
for source_file in source_files:
    open(source_file, "w")

from ruffus import *

@transform(source_files, suffix(".cpp"), ".o")
def compile(input_filename, output_file):
    open(output_file, "w")

pipeline_run()
```

2. Example: Adding a common header file with *add_inputs()*

```
# source files exist before our pipeline
source_files = ["hasty.cpp", "tasty.cpp", "messy.cpp"]
for source_file in source_files:
    open(source_file, "w")

# common (universal) header exists before our pipeline
open("universal.h", "w")

from ruffus import *

# make header files
@transform(source_files, suffix(".cpp"), ".h")
def create_matching_headers(input_file, output_file):
    open(output_file, "w")

@transform(source_files, suffix(".cpp"),
                         # add header to the input of every job
            add_inputs("universal.h",
                         # add result of task create_matching_headers to the input of every job
                        create_matching_headers),
            ".o")
def compile(input_filename, output_file):
    open(output_file, "w")

pipeline_run()
```

```
    >>> pipeline_run()
```

```
    Job  = [hasty.cpp -> hasty.h] completed
    Job  = [messy.cpp -> messy.h] completed
    Job  = [tasty.cpp -> tasty.h] completed
Completed Task = create_matching_headers
    Job  = [[hasty.cpp, universal.h, hasty.h, messy.h, tasty.h] -> hasty.o] completed
    Job  = [[messy.cpp, universal.h, hasty.h, messy.h, tasty.h] -> messy.o] completed
    Job  = [[tasty.cpp, universal.h, hasty.h, messy.h, tasty.h] -> tasty.o] completed
Completed Task = compile
```

3. Example: Additional *Input* can be tasks

We can also add a task name to *add_inputs()*. This chains the **Output**, i.e. run time results, of any previous task as an additional **Input** to every single job in the task.

```
# make header files
@transform(source_files, suffix(".cpp"), ".h")
def create_matching_headers(input_file, output_file):
    open(output_file, "w")

@transform(source_files, suffix(".cpp"),
                         # add header to the input of every job
           add_inputs("universal.h",
                         # add result of task create_matching_headers to the input of every j
                        create_matching_headers),
           ".o")
def compile(input_filenames, output_file):
    open(output_file, "w")

pipeline_run()
```

```
>>> pipeline_run()
    Job  = [[hasty.cpp, universal.h, hasty.h, messy.h, tasty.h] -> hasty.o] completed
    Job  = [[messy.cpp, universal.h, hasty.h, messy.h, tasty.h] -> messy.o] completed
    Job  = [[tasty.cpp, universal.h, hasty.h, messy.h, tasty.h] -> tasty.o] completed
Completed Task = compile
```

4. Example: Add corresponding files using *add_inputs()* with *formatter* or *regex*

The previous example created headers corresponding to our source files and added them as the **Input** to the compilation. That is generally not what you want. Instead, what is generally need is a way to

1. Look up the exact corresponding header for the *specific* job, and not add all possible files to all jobs in a task. When compiling `hasty.cpp`, we just need to add `hasty.h` (and `universal.h`).
2. Add a pre-existing file name (`hasty.h` already exists. Don't create it via another task.)

This is a surprisingly common requirement: In bioinformatics sometimes DNA or RNA sequence files come singly in *.fastq and sometimes in matching pairs: `*1.fastq, *2.fastq` etc. In the latter case, we often need to make sure that both sequence files are being processed in tandem. One way is to take one file name (`*1.fastq`) and look up the other.

add_inputs() uses standard *Ruffus* string substitution via *formatter* and *regex* to lookup (generate) **Input** file names. (As a rule *suffix* only substitutes **Output** file names.)

```
@transform( source_files,
            formatter(".cpp$"),
                        # corresponding header for each source file
```

```
            add_inputs("{basename[0]}.h",
                       # add header to the input of every job
                       "universal.h"),
            "{basename[0]}.o")
def compile(input_filenames, output_file):
    open(output_file, "w")
```

This script gives the following output

```
>>> pipeline_run()
    Job  = [[hasty.cpp, hasty.h, universal.h] -> hasty.o] completed
    Job  = [[messy.cpp, messy.h, universal.h] -> messy.o] completed
    Job  = [[tasty.cpp, tasty.h, universal.h] -> tasty.o] completed
Completed Task = compile
```

1.22.3 Replacing all input parameters with *inputs()*

The previous examples all *added* to the set of **Input** file names. Sometimes it is necessary to replace all the **Input** parameters altogether.

5. Example: Running matching python scripts using *inputs()*

Here is a contrived example: we wish to find all cython/python files which have been compiled into corresponding c++ source files. Instead of compiling the c++, we shall invoke the corresponding python scripts.

Given three c++ files and their corresponding python scripts:

```
@transform( source_files,
            formatter(".cpp$"),

            # corresponding python file for each source file
            inputs("{basename[0]}.py"),

            "{basename[0]}.results")
def run_corresponding_python(input_filenames, output_file):
    open(output_file, "w")
```

The *Ruffus* code will call each python script corresponding to their c++ counterpart:

```
>>> pipeline_run()
    Job  = [hasty.py -> hasty.results] completed
    Job  = [messy.py -> messy.results] completed
    Job  = [tasty.py -> tasty.results] completed
Completed Task = run_corresponding_python
```

1.23 Chapter 21: Esoteric: Generating parameters on the fly with *@files*

See also:

- *Manual Table of Contents*
- *@files on-the-fly syntax in detail*

Note: Remember to look at the example code:

- *Chapter 21: Esoteric: Python Code for Generating parameters on the fly with @files*

1.23.1 Overview

The different *Ruffus* *decorators* connect up different tasks and generate *Output* (file names) from your *Input* in all sorts of different ways.

However, sometimes, none of them *quite* do exactly what you need. And it becomes necessary to generate your own *Input* and *Output* parameters on the fly.

Although this additional flexibility comes at the cost of a lot of extra inconvenient code, you can continue to leverage the rest of *Ruffus* functionality such as checking whether files are up to date or not.

1.23.2 *@files* syntax

To generate parameters on the fly, use the *@files* with a *generator* function which yields one list / tuple of parameters per job.

For example:

```
from ruffus import *

# generator function
def generate_parameters_on_the_fly():
    """
    returns one list of parameters per job
    """
    parameters = [
                        ['A.input', 'A.output', (1, 2)], # 1st job
                        ['B.input', 'B.output', (3, 4)], # 2nd job
                        ['C.input', 'C.output', (5, 6)], # 3rd job
                    ]
    for job_parameters in parameters:
        yield job_parameters

# tell ruffus that parameters should be generated on the fly
@files(generate_parameters_on_the_fly)
def pipeline_task(input, output, extra):
    open(output, "w").write(open(input).read())
    sys.stderr.write("%d + %d => %d\n" % (extra[0] , extra[1], extra[0] + extra[1]))

pipeline_run()
```

Produces:

Task = parallel_task 1 + 2 = 3 Job = [”A”, 1, 2] completed 3 + 4 = 7 Job = [”B”, 3, 4] completed 5 + 6 = 11 Job = [”C”, 5, 6] completed

Note: Be aware that the parameter generating function may be invoked *more than once*: * The first time to check if this part of the pipeline is up-to-date. * The second time when the pipeline task function is run.

The resulting custom *inputs*, *outputs* parameters per job are treated normally for the purposes of checking to see if jobs are up-to-date and need to be re-run.

1.23.3 A Cartesian Product, all vs all example

The *accompanying example* provides a more realistic reason why you would want to generate parameters on the fly. It is a fun piece of code, which generates N x M combinations from two sets of files as the *inputs* of a pipeline stage.

The *inputs* / *outputs* filenames are generated as a pair of nested for-loops to produce the N (outside loop) x M (inside loop) combinations, with the appropriate parameters for each job `yield`ed per iteration of the inner loop. The gist of this is:

```
#_____________________________________________________________________________
#
#   Generator function
#
#        N x M jobs
#_____________________________________________________________________________
def generate_simulation_params ():
    """
    Custom function to generate
    file names for gene/gwas simulation study
    """
    for sim_file in get_simulation_files():
        for (gene, gwas) in get_gene_gwas_file_pairs():
            result_file = "%s.%s.results" % (gene, sim_file)
            yield (gene, gwas, sim_file), result_file



@files(generate_simulation_params)
def gwas_simulation(input_files, output_file):
    "..."
```

If `get_gene_gwas_file_pairs()` produces:

```
['a.sim', 'b.sim', 'c.sim']
```

and `get_gene_gwas_file_pairs()` produces:

```
[('1.gene', '1.gwas'), ('2.gene', '2.gwas')]
```

then we would end up with `3` x `2` = `6` jobs and the following equivalent function calls:

```
gwas_simulation(('1.gene', '1.gwas', 'a.sim'), "1.gene.a.sim.results")
gwas_simulation(('2.gene', '2.gwas', 'a.sim'), "2.gene.a.sim.results")
gwas_simulation(('1.gene', '1.gwas', 'b.sim'), "1.gene.b.sim.results")
gwas_simulation(('2.gene', '2.gwas', 'b.sim'), "2.gene.b.sim.results")
gwas_simulation(('1.gene', '1.gwas', 'c.sim'), "1.gene.c.sim.results")
gwas_simulation(('2.gene', '2.gwas', 'c.sim'), "2.gene.c.sim.results")
```

The *accompanying code* looks slightly more complicated because of some extra bookkeeping.

You can compare this approach with the alternative of using *@product*:

```
#_____________________________________________________________________________
#
#        N x M jobs
#_____________________________________________________________________________
@product(   os.path.join(simulation_data_dir, "*.simulation"),
            formatter(),

            os.path.join(gene_data_dir, "*.gene"),
            formatter(),

            # add gwas as an input: looks like *.gene but with a differnt extension
            add_inputs("{path[1][0]/{basename[1][0]}.gwas")

            "{basename[0][0]}.{basename[1][0]}.results")    # output file
def gwas_simulation(input_files, output_file):
    "..."
```

1.24 Chapter 22: Esoteric: Running jobs in parallel without files using *@parallel*

See also:

- *Manual Table of Contents*
- *@parallel* syntax in detail

1.24.1 @parallel

@parallel supplies parameters for multiple **jobs** exactly like *@files* except that:

1. The first two parameters are not treated like *inputs* and *ouputs* parameters, and strings are not assumed to be file names
2. Thus no checking of whether each job is up-to-date is made using *inputs* and *outputs* files
3. No expansions of *glob* patterns or *output* from previous tasks is carried out.

This syntax is most useful when a pipeline stage does not involve creating or consuming any files, and you wish to forego the conveniences of *@files*, *@transform* etc.

The following code performs some arithmetic in parallel:

```
import sys
from ruffus import *
parameters = [
                ['A', 1, 2], # 1st job
                ['B', 3, 4], # 2nd job
                ['C', 5, 6], # 3rd job
            ]
@parallel(parameters)
def parallel_task(name, param1, param2):
    sys.stderr.write("    Parallel task %s: " % name)
    sys.stderr.write("%d + %d = %d\n" % (param1, param2, param1 + param2))

pipeline_run([parallel_task])
```

produces the following:

```
Task = parallel_task
    Parallel task A: 1 + 2 = 3
    Job = ["A", 1, 2] completed
    Parallel task B: 3 + 4 = 7
    Job = ["B", 3, 4] completed
    Parallel task C: 5 + 6 = 11
    Job = ["C", 5, 6] completed
```

1.25 Chapter 23: Esoteric: Writing custom functions to decide which jobs are up to date with *@check_if_uptodate*

See also:

- *Manual Table of Contents*
- *@check_if_uptodate syntax in detail*

1.25.1 @check_if_uptodate : Manual dependency checking

tasks specified with most decorators such as

- *@split*
- *@transform*
- *@merge*
- *@collate*
- *@collate*

have automatic dependency checking based on file modification times.

Sometimes, you might want to decide have more control over whether to run jobs, especially if a task does not rely on or produce files (i.e. with *@parallel*)

You can write your own custom function to decide whether to run a job. This takes as many parameters as your task function, and needs to return a tuple for whether an update is required, and why (i.e. `tuple(bool, str)`)

This simple example which creates the file `"a.1"` if it does not exist:

```
from ruffus import *
@originate("a.1")
def create_if_necessary(output_file):
    open(output_file, "w")

pipeline_run([])
```

could be rewritten more laboriously as:

```
from ruffus import *
import os
def check_file_exists(input_file, output_file):
    if os.path.exists(output_file):
        return False, "File already exists"
    return True, "%s is missing" % output_file
```

```
@parallel([[None, "a.1"]])
@check_if_uptodate(check_file_exists)
def create_if_necessary(input_file, output_file):
    open(output_file, "w")

pipeline_run([create_if_necessary])
```

Both produce the same output:

```
Task = create_if_necessary
    Job = [null, "a.1"] completed
```

Note: The function specified by *@check_if_uptodate* can be called more than once for each job.

See the *description here* of how *Ruffus* decides which tasks to run.

1.26 Appendix 1: Flow Chart Colours with *pipeline_printout_graph(...)*

See also:

- *Manual Table of Contents*
- *pipeline_printout_graph(...)*
- `Download code`
- *Code* for experimenting with colours

1.26.1 Flowchart colours

The appearance of *Ruffus* flowcharts produced by *pipeline_printout_graph* can be extensively customised.

This is mainly controlled by the *user_colour_scheme* (note UK spelling of "colour") parameter

Example:

Use colour scheme index = 1

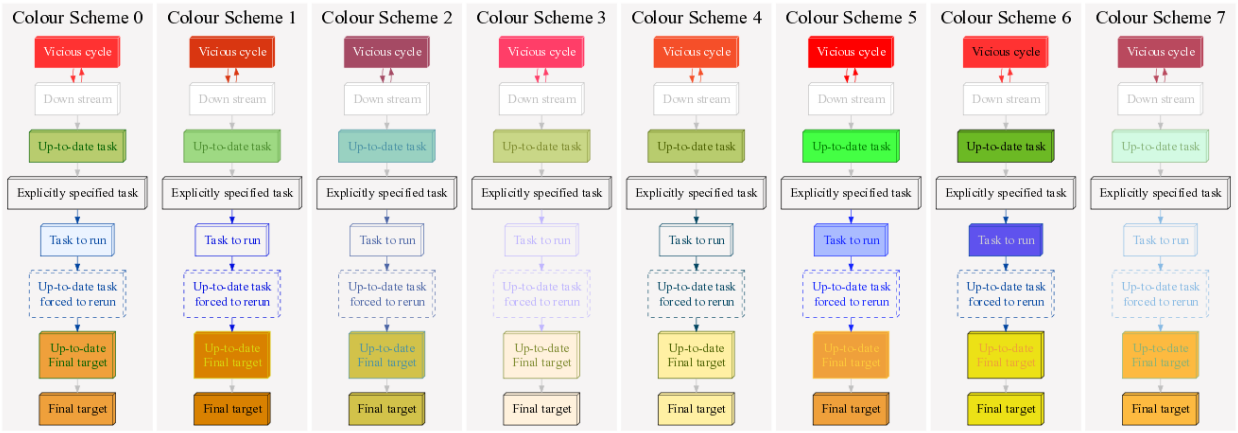
```
pipeline_printout_graph ("flowchart.svg", "svg", [final_task],
                         user_colour_scheme = {
                                                "colour_scheme_index" :1,
                                                "Pipeline"      :{"fontcolor" : '"#FF3232"' },
                                                "Key"           :{"fontcolor" : "Red",
                                                                  "fillcolor" : '"#F6F4F4"' },
                                                "Task to run"   :{"linecolor" : '"#0044A0"' },
                                                "Final target"  :{"fillcolor" : '"#EFA03B"',
                                                                  "fontcolor" : "black",
                                                                  "dashed"    : 0           }
                                               })
```

There are 8 colour schemes by setting `"colour_scheme_index"`:

```
pipeline_printout_graph ("flowchart.svg", "svg", [final_task],
                          user_colour_scheme = {"colour_scheme_index" :6})
```

These colours were chosen after much fierce arguments between the authors and friends, and much inspiration from http://kuler.adobe.com/#create/fromacolor. Please feel free to submit any additional sets of colours for our consideration.

(Click here for image in `svg`.)



1.27 Appendix 2: How dependency is checked

See also:

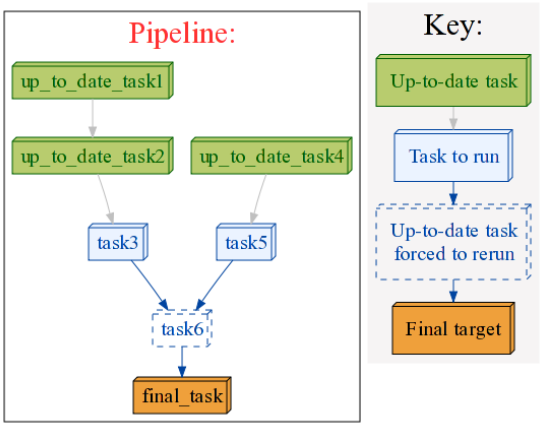
- *Manual Table of Contents*

1.27.1 Overview

How does *Ruffus* decide how to run your pipeline?

- In which order should pipelined functions be called?
- Which parts of the pipeline are up-to-date and do not need to be rerun?

Running all out-of-date tasks and dependents



By default, *Ruffus* will

- build a flow chart (dependency tree) of pipelined tasks (functions)
- start from the most ancestral tasks with the fewest dependencies (`task1` and `task4` in the flowchart above).
- walk up the tree to find the first incomplete / out-of-date tasks (i.e. `task3` and `task5`.
- start running from there

All down-stream (dependent) tasks will be re-run anyway, so we don't have to test whether they are up-to-date or not.

Note: This means that *Ruffus may* ask any task if their jobs are out of date more than once:

- once when deciding which parts of the pipeline have to be run
- once just before executing the task.

Ruffus tries to be clever / efficient, and does the minimal amount of querying.

Forced Reruns

Even if a pipeline stage appears to be up to date, you can always force the pipeline to include from one or more task functions.

This is particularly useful, for example, if the pipeline data hasn't changed but the analysis or computional code has.

```
pipeline_run(forcedtorun_tasks = [up_to_date_task1])
```

will run all tasks from `up_to_date_task1` to `final_task`

Both the "target" and the "forced" lists can include as many tasks as you wish. All dependencies are still carried out and out-of-date jobs rerun.

Esoteric option: Minimal Reruns

In the above example, if we were to delete the results of `up_to_date_task1`, *Ruffus* would rerun `up_to_date_task1`, `up_to_date_task2` and `task3`.

However, you might argue that so long as `up_to_date_task2` is up-to-date, and it is the only necessary prerequisite for `task3`, we should not be concerned about `up_to_date_task1`.

This is enabled with:

```
pipeline_run([task6], gnu_make_maximal_rebuild_mode = False)
```

This option walks down the dependency tree and proceeds no further when it encounters an up-to-date task (`up_to_date_task2`) whatever the state of what lies beyond it.

This rather dangerous option is useful if you don't want to keep all the intermediate files/results from upstream tasks. The pipeline will only not involve any incomplete tasks which precede an up-to-date result.

This is seldom what you intend, and you should always check that the appropriate stages of the pipeline are executed in the flowchart output.

1.28 Appendix 3: Exceptions thrown inside pipelines

1.28.1 Overview

The goal for *Ruffus* is that exceptions should just work *out-of-the-box* without any fuss. This is especially important for exceptions that come from your code which may be raised in a different process. Often multiple parallel operations (jobs or tasks) fail at the same time. *Ruffus* will forward each of these exceptions with the tracebacks so you can jump straight to the offending line.

This example shows separate exceptions from two jobs running in parallel:

```
from ruffus import *

@originate(["a.start", "b.start", "c.start", "d.start", "e.start"])
def throw_exceptions_here(output_file):
    raise Exception("OOPS")

pipeline_run(multiprocess = 2)

    >>> pipeline_run(multiprocess = 2)

    ruffus.ruffus_exceptions.RethrownJobError:

    Original exceptions:

        Exception #1
          'exceptions.Exception(OOPS)' raised in ...
           Task = def throw_exceptions_here(...):
           Job  = [None -> b.start]

        Traceback (most recent call last):
          File "/usr/local/lib/python2.7/dist-packages/ruffus/task.py", line 685, in run_pooled_
            return_value =  job_wrapper(param, user_defined_work_func, register_cleanup, touch_f
          File "/usr/local/lib/python2.7/dist-packages/ruffus/task.py", line 549, in job_wrapper
            job_wrapper_io_files(param, user_defined_work_func, register_cleanup, touch_files_on
          File "/usr/local/lib/python2.7/dist-packages/ruffus/task.py", line 504, in job_wrapper
            ret_val = user_defined_work_func(*(param[1:]))
          File "<stdin>", line 3, in throw_exceptions_here
        Exception: OOPS


        Exception #2
          'exceptions.Exception(OOPS)' raised in ...
           Task = def throw_exceptions_here(...):
           Job  = [None -> a.start]

        Traceback (most recent call last):
          File "/usr/local/lib/python2.7/dist-packages/ruffus/task.py", line 685, in run_pooled_
            return_value =  job_wrapper(param, user_defined_work_func, register_cleanup, touch_f
          File "/usr/local/lib/python2.7/dist-packages/ruffus/task.py", line 549, in job_wrapper
            job_wrapper_io_files(param, user_defined_work_func, register_cleanup, touch_files_on
          File "/usr/local/lib/python2.7/dist-packages/ruffus/task.py", line 504, in job_wrapper
            ret_val = user_defined_work_func(*(param[1:]))
          File "<stdin>", line 3, in throw_exceptions_here
        Exception: OOPS


.. image:: ../../images/manual_exceptions.png
```

1.28.2 Pipelines running in parallel accumulate Exceptions

As show above, by default *Ruffus* accumulates `NN` exceptions before interrupting the pipeline prematurely where `NN` is the specified parallelism for *pipeline_run(multiprocess = NN)*

This seems a fair tradeoff between being able to gather detailed error information for running jobs, and not wasting too much time for a task that is going to fail anyway.

1.28.3 Terminate pipeline immediately upon Exceptions

Set *pipeline_run(exceptions_terminate_immediately = True)*

To have all exceptions interrupt the pipeline immediately, invoke:

```
pipeline_run(exceptions_terminate_immediately = True)
```

For example, with this change, only a single exception will be thrown before the pipeline is interrupted:

```
from ruffus import *

@originate(["a.start", "b.start", "c.start", "d.start", "e.start"])
def throw_exceptions_here(output_file):
    raise Exception("OOPS")

pipeline_run(multiprocess = 2, exceptions_terminate_immediately = True)

>>> pipeline_run(multiprocess = 2)

ruffus.ruffus_exceptions.RethrownJobError:

Original exception:

    Exception #1
      'exceptions.Exception(OOPS)' raised in ...
       Task = def throw_exceptions_here(...):
       Job  = [None -> a.start]

    Traceback (most recent call last):
      [Tedious traceback snipped out!!!....]
    Exception: OOPS
```

raise `Ruffus.JobSignalledBreak`

The same can be accomplished on a finer scale by throwing the `Ruffus.JobSignalledBreak` Exception. Unlike other exceptions, this causes an immediate halt in pipeline execution. If there are other exceptions in play at that point, they will be rethrown in the main process but no new exceptions will be added.

```
from ruffus import *

@originate(["a.start", "b.start", "c.start", "d.start", "e.start"])
def throw_exceptions_here(output_file):
```

```
        raise JobSignalledBreak("OOPS")

    pipeline_run(multiprocess = 2)
```

1.28.4 Display exceptions as they occur

In the following example, the jobs throw exceptions at two second staggered intervals into the job. With `log_exceptions = True`, the exceptions are displayed as they occur even though the pipeline continues running.

logger.error(...) will be invoked with the string representation of the each exception, and associated stack trace.

The default logger prints to sys.stderr, but as usual can be changed to any class from the logging module or compatible object via *pipeline_run(logger = XXX)*

```
from ruffus import *
import time, os

@originate(["1.start", "2.start", "3.start", "4.start", "5.start"])
def throw_exceptions_here(output_file):
    delay = int(os.path.splitext(output_file)[0])
    time.sleep(delay * 2)
    raise JobSignalledBreak("OOPS")

pipeline_run(log_exceptions = True, multiprocess = 5)
```

1.29 Appendix 4: Names exported from Ruffus

See also:

- *Manual Table of Contents*

1.29.1 Ruffus Names

This is a list of all the names *Ruffus* makes available:

Category	Manual
Pipeline functions	
	pipeline_printout() (*Manual*)
	pipeline_printout() (*Manual*)
	pipeline_printout() (*Manual*)
Decorators	
	@active_if (*Manual*)
	@check_if_uptodate (*Manual*)
	@collate (*Manual*)
	@files (*Manual*)
	@follows (*Manual*)
	@jobs_limit (*Manual*)
	@merge (*Manual*)
	@mkdir (*Manual*)
	@originate (*Manual*)
	@parallel (*Manual*)
	@posttask (*Manual*)
	@split (*Manual*)
	@subdivide (*Manual*)
	@transform (*Manual*)
	@files_re (*Manual*)
Loggers	
	stderr_logger
	black_hole_logger
Parameter disambiguating Indicators	
	suffix (*Manual*)
	regex (*Manual*)
	formatter (*Manual*)
	inputs (*Manual*)
	inputs (*Manual*)
	touch_file (*Manual*)
	combine
	mkdir (*Manual*)
	output_from (*Manual*)
Decorators in ruffus.combinatorics	
	@combinations (*Manual*)
	@combinations_with_replacement (*Manual*)
	@permutations (*Manual*)
	@product (*Manual*)
Decorators in ruffus.cmdline	
	get_argparse
	setup_logging
	run
	MESSAGE

1.30 Appendix 5: @files: Deprecated syntax

Warning:
- **This is deprecated syntax which is no longer supported and should NOT be used in new code.**

See also:

- *Manual Table of Contents*
- *decorators*
- *@files* syntax in detail

1.30.1 Overview

The python functions which do the actual work of each stage or *task* of a *Ruffus* pipeline are written by you.
The role of *Ruffus* is to make sure these functions are called in the right order, with the right parameters, running in parallel using multiprocessing if desired.

The easiest way to specify parameters to *Ruffus task* functions is to use the *@files* decorator.

1.30.2 @files

Running this code:

```
from ruffus import *

@files('a.1', ['a.2', 'b.2'], 'A file')
def single_job_io_task(infile, outfiles, text):
    for o in outfiles: open(o, "w")

# prepare input file
open('a.1', "w")

pipeline_run()
```

Is equivalent to calling:

```
single_job_io_task('a.1', ['a.2', 'b.2'], 'A file')
```

And produces:

```
>>> pipeline_run()
    Job = [a.1 -> [a.2, b.2], A file] completed
Completed Task = single_job_io_task
```

Ruffus will automatically check if your task is up to date. The second time *pipeline_run()* is called, nothing will happen. But if you update `a.1`, the task will rerun:

```
>>> open('a.1', "w")
>>> pipeline_run()
    Job = [a.1 -> [a.2, b.2], A file] completed
Completed Task = single_job_io_task
```

See *chapter 2* for a more in-depth discussion of how *Ruffus* decides which parts of the pipeline are complete and up-to-date.

1.30.3 Running the same code on different parameters in parallel

Your pipeline may require the same function to be called multiple times on independent parameters. In which case, you can supply all the parameters to @files, each will be sent to separate jobs that may run in parallel if necessary. *Ruffus* will check if each separate *job* is up-to-date using the *inputs* and *outputs* (first two) parameters (See the *Up-to-date jobs are not re-run unnecessarily*).

For example, if a sequence (e.g. a list or tuple) of 5 parameters are passed to **@files**, that indicates there will also be 5 separate jobs:

```
from ruffus import *
parameters = [
                    [ 'job1.file'           ],          # 1st job
                    [ 'job2.file', 4        ],          # 2st job
                    [ 'job3.file', [3, 2]   ],          # 3st job
                    [ 67, [13, 'job4.file'] ],          # 4st job
                    [ 'job5.file'           ],          # 5st job
              ]
@files(parameters)
def task_file(*params):
    ""
```

Ruffus creates as many jobs as there are elements in `parameters`.
In turn, each of these elements consist of series of parameters which will be passed to each separate job.

Thus the above code is equivalent to calling:

```
task_file('job1.file')
task_file('job2.file', 4)
task_file('job3.file', [3, 2])
task_file(67, [13, 'job4.file'])
task_file('job5.file')
```

What `task_file()` does with these parameters is up to you!

The only constraint on the parameters is that *Ruffus* will treat any first parameter of each job as the *inputs* and any second as the *output*. Any strings in the *inputs* or *output* parameters (including those nested in sequences) will be treated as file names.

Thus, to pick the parameters out of one of the above jobs:

```
task_file(67, [13, 'job4.file'])
```

inputs == `67`
outputs == `[13, 'job4.file']`

The solitary output filename is `job4.file`

Checking if jobs are up to date

Usually we do not want to run all the stages in a pipeline but only where the input data has changed or is no longer up to date.
One easy way to do this is to check the modification times for files produced at each stage of the pipeline.

Let us first create our starting files `a.1` and `b.1`
We can then run the following pipeline function to create

- `a.2` from `a.1` and
- `b.2` from `b.1`

```
# create starting files
open("a.1", "w")
open("b.1", "w")


from ruffus import *
parameters = [
                    [ 'a.1', 'a.2', 'A file'], # 1st job
                    [ 'b.1', 'b.2', 'B file'], # 2nd job
              ]

@files(parameters)
def parallel_io_task(infile, outfile, text):
    # copy infile contents to outfile
    infile_text = open(infile).read()
    f = open(outfile, "w").write(infile_text + "\n" + text)

pipeline_run()
```

This produces the following output:

```
>>> pipeline_run()
    Job = [a.1 -> a.2, A file] completed
    Job = [b.1 -> b.2, B file] completed
Completed Task = parallel_io_task
```

If you called *pipeline_run()* again, nothing would happen because the files are up to date:
`a.2` is more recent than `a.1` and
`b.2` is more recent than `b.1`

However, if you subsequently modified `a.1` again:

```
open("a.1", "w")
pipeline_run(verbose = 1)
```

you would see the following:

```
>>> pipeline_run([parallel_io_task])
Task = parallel_io_task
    Job = ["a.1" -> "a.2", "A file"] completed
    Job = ["b.1" -> "b.2", "B file"] unnecessary: already up to date
Completed Task = parallel_io_task
```

The 2nd job is up to date and will be skipped.

1.31 Appendix 6: @files_re: Deprecated *syntax using regular expressions*

Warning:
- **This is deprecated syntax which is no longer supported and should NOT be used in new code.**

See also:

- *Manual Table of Contents*
- *decorators*
- *@files_re* syntax in detail

1.31.1 Overview

@files_re combines the functionality of @transform, @collate and @merge in one overloaded decorator.

This is the reason why its use is discouraged. **@files_re** syntax is far too overloaded and context-dependent to support its myriad of different functions.

The following documentation is provided to help maintain historical *Ruffus* usage.

Transforming input and output filenames

For example, the following code takes files from the previous pipeline task, and makes new output parameters with the `.sums` suffix in place of the `.chunks` suffix:

```
@transform(step_4_split_numbers_into_chunks, suffix(".chunks"), ".sums")
def step_5_calculate_sum_of_squares (input_file_name, output_file_name):
    #
    #   calculate sums and sums of squares for all values in the input_file_name
    #       writing to output_file_name
    ""
```

This can be written using @files_re equivalently:

```
@files_re(step_4_split_numbers_into_chunks, r".chunks", r".sums")
def step_5_calculate_sum_of_squares (input_file_name, output_file_name):
""
```

Collating many *inputs* into a single *output*

Similarly, the following code collects **inputs** from the same species in the same directory:

```
@collate('*.animals',                       # inputs = all *.animal files
            regex(r'mammals.([^.]+)'),      # regular expression
            r'\1/animals.in_my_zoo',        # single output file per species
            r'\1' )                         # species name
def capture_mammals(infiles, outfile, species):
    # summarise all animals of this species
    ""
```

This can be written using @files_re equivalently using the *combine* indicator:

```
@files_re('*.animals',                              # inputs = all *.animal files
            r'mammals.([^.]+)',                     # regular expression
            combine(r'\1/animals.in_my_zoo'),       # single output file per species
            r'\1' )                                 # species name
def capture_mammals(infiles, outfile, species):
    # summarise all animals of this species
    ""
```

Generating *input* and *output* parameter using regular expresssions

The following code generates additional *input* prerequisite file names which match the original *input* files.

We want each job of our `analyse()` function to get corresponding pairs of `xx.chunks` and `xx.red_indian` files when

`*.chunks` are generated by the task function `split_up_problem()` and `*.red_indian` are generated by the task function `make_red_indians()`:

```
@follows(make_red_indians)
@transform(split_up_problem,                    # starting set of *inputs*
            regex(r"(.*).chunks"),              # regular expression
            inputs([r"\g<0>",                   # xx.chunks
                    r"\1.red_indian"]),         # important.file
             r"\1.results"                      # xx.results
              )
def analyse(input_filenames, output_file_name):
    "Do analysis here"
```

The equivalent code using @files_re looks very similar:

```
@follows(make_red_indians)
@files_re( split_up_problem,            # starting set of *inputs*
           r"(.*).chunks",              # regular expression
           [r"\g<0>",                   # xx.chunks
            r"\1.red_indian"]),         # important.file
             r"\1.results")             # xx.results
def analyse(input_filenames, output_file_name):
    "Do analysis here"
```

Example code for:

1.32 Chapter 1: Python Code for An introduction to basic Ruffus syntax

See also:

- *Manual Table of Contents*
- *@transform syntax in detail*
- Back to **Chapter 1**: *An introduction to basic Ruffus syntax*

1.32.1 Your first Ruffus script

```
::

#
#   The starting data files would normally exist beforehand!
#       We create some empty files for this example
#
starting_files = ["a.fasta", "b.fasta", "c.fasta"]

for ff in starting_files:
    open(ff, "w")


from ruffus import *

#
#   STAGE 1 fasta->sam
#
@transform(starting_files,                      # Input = starting files
           suffix(".fasta"),                    #         suffix = .fasta
           ".sam")                              # Output  suffix = .sam
def map_dna_sequence(input_file,
                     output_file):
    ii = open(input_file)
    oo = open(output_file, "w")

#
#   STAGE 2 sam->bam
#
@transform(map_dna_sequence,                    # Input = previous stage
           suffix(".sam"),                      #         suffix = .sam
           ".bam")                              # Output  suffix = .bam
def compress_sam_file(input_file,
                      output_file):
    ii = open(input_file)
    oo = open(output_file, "w")

#
#   STAGE 3 bam->statistics
#
@transform(compress_sam_file,                   # Input = previous stage
           suffix(".bam"),                      #         suffix = .bam
           ".statistics",                       # Output  suffix = .statistics
           "use_linear_model")                  # Extra statistics parameter
def summarise_bam_file(input_file,
```

```
                        output_file,
                        extra_stats_parameter):
    """
    Sketch of real analysis function
    """
    ii = open(input_file)
    oo = open(output_file, "w")

pipeline_run()
```

1.32.2 Resulting Output

```
>>> pipeline_run()
    Job  = [a.fasta -> a.sam] completed
    Job  = [b.fasta -> b.sam] completed
    Job  = [c.fasta -> c.sam] completed
Completed Task = map_dna_sequence
    Job  = [a.sam -> a.bam] completed
    Job  = [b.sam -> b.bam] completed
    Job  = [c.sam -> c.bam] completed
Completed Task = compress_sam_file
    Job  = [a.bam -> a.statistics, use_linear_model] completed
    Job  = [b.bam -> b.statistics, use_linear_model] completed
    Job  = [c.bam -> c.statistics, use_linear_model] completed
Completed Task = summarise_bam_file
```

1.33 Chapter 1: Python Code for Transforming data in a pipeline with `@transform`

See also:

- *Manual Table of Contents*
- *@transform syntax in detail*
- Back to **Chapter 2**: *Transforming data in a pipeline with @transform*

1.33.1 Your first Ruffus script

```
#
#   The starting data files would normally exist beforehand!
#       We create some empty files for this example
#
starting_files = [("a.1.fastq", "a.2.fastq"),
                  ("b.1.fastq", "b.2.fastq"),
                  ("c.1.fastq", "c.2.fastq")]


for ff_pair in starting_files:
    open(ff_pair[0], "w")
    open(ff_pair[1], "w")
```

```
from ruffus import *

#
#   STAGE 1 fasta->sam
#
@transform(starting_files,                      # Input = starting files
           suffix(".1.fastq"),                  #         suffix = .1.fastq
           ".sam")                              # Output  suffix = .sam
def map_dna_sequence(input_files,
                     output_file):
    # remember there are two input files now
    ii1 = open(input_files[0])
    ii2 = open(input_files[1])
    oo = open(output_file, "w")

#
#   STAGE 2 sam->bam
#
@transform(map_dna_sequence,                    # Input = previous stage
           suffix(".sam"),                      #         suffix = .sam
           ".bam")                              # Output  suffix = .bam
def compress_sam_file(input_file,
                      output_file):
    ii = open(input_file)
    oo = open(output_file, "w")

#
#   STAGE 3 bam->statistics
#
@transform(compress_sam_file,                   # Input = previous stage
           suffix(".bam"),                      #         suffix = .bam
           ".statistics",                       # Output  suffix = .statistics
           "use_linear_model")                  # Extra statistics parameter
def summarise_bam_file(input_file,
                       output_file,
                       extra_stats_parameter):
    """
    Sketch of real analysis function
    """
    ii = open(input_file)
    oo = open(output_file, "w")

pipeline_run()
```

1.33.2 Resulting Output

```
>>> pipeline_run()
    Job  = [[a.1.fastq, a.2.fastq] -> a.sam] completed
    Job  = [[b.1.fastq, b.2.fastq] -> b.sam] completed
    Job  = [[c.1.fastq, c.2.fastq] -> c.sam] completed
Completed Task = map_dna_sequence
    Job  = [a.sam -> a.bam] completed
    Job  = [b.sam -> b.bam] completed
    Job  = [c.sam -> c.bam] completed
Completed Task = compress_sam_file
    Job  = [a.bam -> a.statistics, use_linear_model] completed
```

```
    Job  = [b.bam -> b.statistics, use_linear_model] completed
    Job  = [c.bam -> c.statistics, use_linear_model] completed
Completed Task = summarise_bam_file
```

1.34 Chapter 3: Python Code for More on `@transform`-ing data

See also:

- *Manual Table of Contents*
- *@transform syntax in detail*
- Back to **Chapter 3**: *More on @transform-ing data and @originate*

1.34.1 Producing several items / files per job

```
from ruffus import *

#---------------------------------------------------------------
#   Create pairs of input files
#
first_task_params = [
                     ['job1.a.start', 'job1.b.start'],
                     ['job2.a.start', 'job2.b.start'],
                     ['job3.a.start', 'job3.b.start'],
                    ]

for input_file_pairs in first_task_params:
    for input_file in input_file_pairs:
        open(input_file, "w")


#---------------------------------------------------------------
#
#   first task
#
@transform(first_task_params, suffix(".start"),
                        [".output.1",
                         ".output.extra.1"],
                       "some_extra.string.for_example", 14)
def first_task(input_files, output_file_pair,
               extra_parameter_str, extra_parameter_num):
    for output_file in output_file_pair:
        with open(output_file, "w"):
            pass


#---------------------------------------------------------------
#
#   second task
#
@transform(first_task, suffix(".output.1"), ".output2")
def second_task(input_files, output_file):
    with open(output_file, "w"): pass
```

```
#---------------------------------------------------------------
#
#       Run
#
pipeline_run([second_task])
```

Resulting Output

```
>>> pipeline_run([second_task])
    Job  = [[job1.a.start, job1.b.start] -> [job1.a.output.1, job1.a.output.extra.1], some_extra
    Job  = [[job2.a.start, job2.b.start] -> [job2.a.output.1, job2.a.output.extra.1], some_extra
    Job  = [[job3.a.start, job3.b.start] -> [job3.a.output.1, job3.a.output.extra.1], some_extra
Completed Task = first_task
    Job  = [[job1.a.output.1, job1.a.output.extra.1] -> job1.a.output2] completed
    Job  = [[job2.a.output.1, job2.a.output.extra.1] -> job2.a.output2] completed
    Job  = [[job3.a.output.1, job3.a.output.extra.1] -> job3.a.output2] completed
Completed Task = second_task
```

1.34.2 Defining tasks function out of order

```
from ruffus import *

#---------------------------------------------------------------
#   Create pairs of input files
#
first_task_params = [
                     ['job1.a.start', 'job1.b.start'],
                     ['job2.a.start', 'job2.b.start'],
                     ['job3.a.start', 'job3.b.start'],
                    ]

for input_file_pairs in first_task_params:
    for input_file in input_file_pairs:
        open(input_file, "w")



#---------------------------------------------------------------
#
#   second task defined first
#
#   task name string wrapped in output_from(...)
@transform(output_from("first_task"), suffix(".output.1"), ".output2")
def second_task(input_files, output_file):
    with open(output_file, "w"): pass


#---------------------------------------------------------------
#
#   first task
#
@transform(first_task_params, suffix(".start"),
                        [".output.1",
                         ".output.extra.1"],
```

```
                        "some_extra.string.for_example", 14)
def first_task(input_files, output_file_pair,
               extra_parameter_str, extra_parameter_num):
    for output_file in output_file_pair:
        with open(output_file, "w"):
            pass


#---------------------------------------------------------------
#
#       Run
#
pipeline_run([second_task])
```

Resulting Output

```
>>> pipeline_run([second_task])
    Job  = [[job1.a.start, job1.b.start] -> [job1.a.output.1, job1.a.output.extra.1], some_extra
    Job  = [[job2.a.start, job2.b.start] -> [job2.a.output.1, job2.a.output.extra.1], some_extra
    Job  = [[job3.a.start, job3.b.start] -> [job3.a.output.1, job3.a.output.extra.1], some_extra
Completed Task = first_task
    Job  = [[job1.a.output.1, job1.a.output.extra.1] -> job1.a.output2] completed
    Job  = [[job2.a.output.1, job2.a.output.extra.1] -> job2.a.output2] completed
    Job  = [[job3.a.output.1, job3.a.output.extra.1] -> job3.a.output2] completed
Completed Task = second_task
```

1.34.3 Multiple dependencies

```
from ruffus import *
import time
import random

#---------------------------------------------------------------
#   Create pairs of input files
#
first_task_params = [
                     ['job1.a.start', 'job1.b.start'],
                     ['job2.a.start', 'job2.b.start'],
                     ['job3.a.start', 'job3.b.start'],
                    ]
second_task_params = [
                     ['job4.a.start', 'job4.b.start'],
                     ['job5.a.start', 'job5.b.start'],
                     ['job6.a.start', 'job6.b.start'],
                    ]

for input_file_pairs in first_task_params + second_task_params:
    for input_file in input_file_pairs:
        open(input_file, "w")



#---------------------------------------------------------------
#
#   first task
```

```
#
@transform(first_task_params, suffix(".start"),
                         [".output.1",
                          ".output.extra.1"],
                        "some_extra.string.for_example", 14)
def first_task(input_files, output_file_pair,
               extra_parameter_str, extra_parameter_num):
    for output_file in output_file_pair:
        with open(output_file, "w"):
            pass
    time.sleep(random.random())



#---------------------------------------------------------------
#
#   second task
#
@transform(second_task_params, suffix(".start"),
                         [".output.1",
                          ".output.extra.1"],
                        "some_extra.string.for_example", 14)
def second_task(input_files, output_file_pair,
                extra_parameter_str, extra_parameter_num):
    for output_file in output_file_pair:
        with open(output_file, "w"):
            pass
    time.sleep(random.random())


#---------------------------------------------------------------
#
#   third task
#
#       depends on both first_task() and second_task()
@transform([first_task, second_task], suffix(".output.1"), ".output2")
def third_task(input_files, output_file):
    with open(output_file, "w"): pass


#---------------------------------------------------------------
#
#       Run
#
pipeline_run([third_task], multiprocess = 6)
```

Resulting Output

```
>>> pipeline_run([third_task], multiprocess = 6)
    Job  = [[job3.a.start, job3.b.start] -> [job3.a.output.1, job3.a.output.extra.1], some_extra
    Job  = [[job6.a.start, job6.b.start] -> [job6.a.output.1, job6.a.output.extra.1], some_extra
    Job  = [[job1.a.start, job1.b.start] -> [job1.a.output.1, job1.a.output.extra.1], some_extra
    Job  = [[job4.a.start, job4.b.start] -> [job4.a.output.1, job4.a.output.extra.1], some_extra
    Job  = [[job5.a.start, job5.b.start] -> [job5.a.output.1, job5.a.output.extra.1], some_extra
Completed Task = second_task
    Job  = [[job2.a.start, job2.b.start] -> [job2.a.output.1, job2.a.output.extra.1], some_extra
Completed Task = first_task
```

```
    Job  = [[job1.a.output.1, job1.a.output.extra.1] -> job1.a.output2] completed
    Job  = [[job2.a.output.1, job2.a.output.extra.1] -> job2.a.output2] completed
    Job  = [[job3.a.output.1, job3.a.output.extra.1] -> job3.a.output2] completed
    Job  = [[job4.a.output.1, job4.a.output.extra.1] -> job4.a.output2] completed
    Job  = [[job5.a.output.1, job5.a.output.extra.1] -> job5.a.output2] completed
    Job  = [[job6.a.output.1, job6.a.output.extra.1] -> job6.a.output2] completed
Completed Task = third_task
```

1.34.4 Multiple dependencies after @follows

```
from ruffus import *
import time
import random

#---------------------------------------------------------------
#   Create pairs of input files
#
first_task_params = [
                     ['job1.a.start', 'job1.b.start'],
                     ['job2.a.start', 'job2.b.start'],
                     ['job3.a.start', 'job3.b.start'],
                    ]
second_task_params = [
                     ['job4.a.start', 'job4.b.start'],
                     ['job5.a.start', 'job5.b.start'],
                     ['job6.a.start', 'job6.b.start'],
                    ]

for input_file_pairs in first_task_params + second_task_params:
    for input_file in input_file_pairs:
        open(input_file, "w")



#---------------------------------------------------------------
#
#   first task
#
@transform(first_task_params, suffix(".start"),
                        [".output.1",
                         ".output.extra.1"],
                       "some_extra.string.for_example", 14)
def first_task(input_files, output_file_pair,
               extra_parameter_str, extra_parameter_num):
    for output_file in output_file_pair:
        with open(output_file, "w"):
            pass
    time.sleep(random.random())



#---------------------------------------------------------------
#
#   second task
#
@follows("first_task")
```

```
@transform(second_task_params, suffix(".start"),
                        [".output.1",
                         ".output.extra.1"],
                       "some_extra.string.for_example", 14)
def second_task(input_files, output_file_pair,
                extra_parameter_str, extra_parameter_num):
    for output_file in output_file_pair:
        with open(output_file, "w"):
            pass
    time.sleep(random.random())


#---------------------------------------------------------------
#
#   third task
#
#       depends on both first_task() and second_task()
@transform([first_task, second_task], suffix(".output.1"), ".output2")
def third_task(input_files, output_file):
    with open(output_file, "w"): pass


#---------------------------------------------------------------
#
#       Run
#
pipeline_run([third_task], multiprocess = 6)
```

Resulting Output: `first_task` completes before `second_task`

```
>>> pipeline_run([third_task], multiprocess = 6)
    Job  = [[job2.a.start, job2.b.start] -> [job2.a.output.1, job2.a.output.extra.1], some_extra
    Job  = [[job3.a.start, job3.b.start] -> [job3.a.output.1, job3.a.output.extra.1], some_extra
    Job  = [[job1.a.start, job1.b.start] -> [job1.a.output.1, job1.a.output.extra.1], some_extra
Completed Task = first_task
    Job  = [[job4.a.start, job4.b.start] -> [job4.a.output.1, job4.a.output.extra.1], some_extra
    Job  = [[job6.a.start, job6.b.start] -> [job6.a.output.1, job6.a.output.extra.1], some_extra
    Job  = [[job5.a.start, job5.b.start] -> [job5.a.output.1, job5.a.output.extra.1], some_extra
Completed Task = second_task
    Job  = [[job1.a.output.1, job1.a.output.extra.1] -> job1.a.output2] completed
    Job  = [[job2.a.output.1, job2.a.output.extra.1] -> job2.a.output2] completed
    Job  = [[job3.a.output.1, job3.a.output.extra.1] -> job3.a.output2] completed
    Job  = [[job4.a.output.1, job4.a.output.extra.1] -> job4.a.output2] completed
    Job  = [[job5.a.output.1, job5.a.output.extra.1] -> job5.a.output2] completed
    Job  = [[job6.a.output.1, job6.a.output.extra.1] -> job6.a.output2] completed
```

1.35 Chapter 4: Python Code for Creating files with `@originate`

See also:

- *Manual Table of Contents*
- *@transform syntax in detail*
- Back to **Chapter 4**: *@originate*

1.35.1 Using `@originate`

```
from ruffus import *

#---------------------------------------------------------------
#   create initial files
#
@originate([   ['job1.a.start', 'job1.b.start'],
               ['job2.a.start', 'job2.b.start'],
               ['job3.a.start', 'job3.b.start']    ])
def create_initial_file_pairs(output_files):
    # create both files as necessary
    for output_file in output_files:
        with open(output_file, "w") as oo: pass

#---------------------------------------------------------------
#   first task
@transform(create_initial_file_pairs, suffix(".start"), ".output.1")
def first_task(input_files, output_file):
    with open(output_file, "w"): pass


#---------------------------------------------------------------
#   second task
@transform(first_task, suffix(".output.1"), ".output.2")
def second_task(input_files, output_file):
    with open(output_file, "w"): pass

#
#       Run
#
pipeline_run([second_task])
```

1.35.2 Resulting Output

```
    Job  = [None -> [job1.a.start, job1.b.start]] completed
    Job  = [None -> [job2.a.start, job2.b.start]] completed
    Job  = [None -> [job3.a.start, job3.b.start]] completed
Completed Task = create_initial_file_pairs
    Job  = [[job1.a.start, job1.b.start] -> job1.a.output.1] completed
    Job  = [[job2.a.start, job2.b.start] -> job2.a.output.1] completed
    Job  = [[job3.a.start, job3.b.start] -> job3.a.output.1] completed
Completed Task = first_task
    Job  = [job1.a.output.1 -> job1.a.output.2] completed
    Job  = [job2.a.output.1 -> job2.a.output.2] completed
    Job  = [job3.a.output.1 -> job3.a.output.2] completed
Completed Task = second_task
```

1.36 Chapter 5: Python Code for Understanding how your pipeline works with *pipeline_printout(...)*

See also:

- *Manual Table of Contents*

- *pipeline_printout(...)* syntax
- Back to **Chapter 5**: *Understanding how your pipeline works*

1.36.1 Display the initial state of the pipeline

```
from ruffus import *
import sys

#---------------------------------------------------------------
#   create initial files
#
@originate([   ['job1.a.start', 'job1.b.start'],
               ['job2.a.start', 'job2.b.start'],
               ['job3.a.start', 'job3.b.start']    ])
def create_initial_file_pairs(output_files):
    # create both files as necessary
    for output_file in output_files:
        with open(output_file, "w") as oo: pass

#---------------------------------------------------------------
#   first task
@transform(create_initial_file_pairs, suffix(".start"), ".output.1")
def first_task(input_files, output_file):
    with open(output_file, "w"): pass


#---------------------------------------------------------------
#   second task
@transform(first_task, suffix(".output.1"), ".output.2")
def second_task(input_files, output_file):
    with open(output_file, "w"): pass

pipeline_printout(sys.stdout, [second_task], verbose = 1)
pipeline_printout(sys.stdout, [second_task], verbose = 3)
```

1.36.2 Normal Output

```
>>> pipeline_printout(sys.stdout, [second_task], verbose = 1)

_____________________________________________
Tasks which will be run:

Task = create_initial_file_pairs
Task = first_task
Task = second_task
```

1.36.3 High Verbosity Output

```
>>> pipeline_printout(sys.stdout, [second_task], verbose = 4)

_____________________________________________
Tasks which will be run:
```

```
Task = create_initial_file_pairs
       Job  = [None
             -> job1.a.start
             -> job1.b.start]
         Job needs update: Missing files [job1.a.start, job1.b.start]
       Job  = [None
             -> job2.a.start
             -> job2.b.start]
         Job needs update: Missing files [job2.a.start, job2.b.start]
       Job  = [None
             -> job3.a.start
             -> job3.b.start]
         Job needs update: Missing files [job3.a.start, job3.b.start]

Task = first_task
       Job  = [[job1.a.start, job1.b.start]
             -> job1.a.output.1]
         Job needs update: Missing files [job1.a.start, job1.b.start, job1.a.output.1]
       Job  = [[job2.a.start, job2.b.start]
             -> job2.a.output.1]
         Job needs update: Missing files [job2.a.start, job2.b.start, job2.a.output.1]
       Job  = [[job3.a.start, job3.b.start]
             -> job3.a.output.1]
         Job needs update: Missing files [job3.a.start, job3.b.start, job3.a.output.1]

Task = second_task
       Job  = [job1.a.output.1
             -> job1.a.output.2]
         Job needs update: Missing files [job1.a.output.1, job1.a.output.2]
       Job  = [job2.a.output.1
             -> job2.a.output.2]
         Job needs update: Missing files [job2.a.output.1, job2.a.output.2]
       Job  = [job3.a.output.1
             -> job3.a.output.2]
         Job needs update: Missing files [job3.a.output.1, job3.a.output.2]

_____________________________________
```

1.36.4 Display the partially up-to-date pipeline

Run the pipeline, modify `job1.stage` so that the second task is no longer up-to-date and printout the pipeline stage again:

```
>>> pipeline_run([second_task], verbose=3)
Task enters queue = create_initial_file_pairs
    Job  = [None -> [job1.a.start, job1.b.start]]
    Job  = [None -> [job2.a.start, job2.b.start]]
    Job  = [None -> [job3.a.start, job3.b.start]]
    Job  = [None -> [job1.a.start, job1.b.start]] completed
    Job  = [None -> [job2.a.start, job2.b.start]] completed
    Job  = [None -> [job3.a.start, job3.b.start]] completed
Completed Task = create_initial_file_pairs
Task enters queue = first_task
    Job  = [[job1.a.start, job1.b.start] -> job1.a.output.1]
    Job  = [[job2.a.start, job2.b.start] -> job2.a.output.1]
    Job  = [[job3.a.start, job3.b.start] -> job3.a.output.1]
    Job  = [[job1.a.start, job1.b.start] -> job1.a.output.1] completed
```

```
    Job  = [[job2.a.start, job2.b.start] -> job2.a.output.1] completed
    Job  = [[job3.a.start, job3.b.start] -> job3.a.output.1] completed
Completed Task = first_task
Task enters queue = second_task
    Job  = [job1.a.output.1 -> job1.a.output.2]
    Job  = [job2.a.output.1 -> job2.a.output.2]
    Job  = [job3.a.output.1 -> job3.a.output.2]
    Job  = [job1.a.output.1 -> job1.a.output.2] completed
    Job  = [job2.a.output.1 -> job2.a.output.2] completed
    Job  = [job3.a.output.1 -> job3.a.output.2] completed
Completed Task = second_task


# modify job1.stage1
>>> open("job1.a.output.1", "w").close()
```

At a verbosity of 6, even jobs which are up-to-date will be displayed:

```
>>> pipeline_printout(sys.stdout, [second_task], verbose = 6)

_____________________________________________
Tasks which are up-to-date:

Task = create_initial_file_pairs
       Job  = [None
             -> job1.a.start
             -> job1.b.start]
       Job  = [None
             -> job2.a.start
             -> job2.b.start]
       Job  = [None
             -> job3.a.start
             -> job3.b.start]

Task = first_task
       Job  = [[job1.a.start, job1.b.start]
             -> job1.a.output.1]
       Job  = [[job2.a.start, job2.b.start]
             -> job2.a.output.1]
       Job  = [[job3.a.start, job3.b.start]
             -> job3.a.output.1]

_____________________________________________




_____________________________________________
Tasks which will be run:

Task = second_task
       Job  = [job1.a.output.1
             -> job1.a.output.2]
         Job needs update:
         Input files:
          * 22 Jul 2014 15:29:19.33: job1.a.output.1
         Output files:
          * 22 Jul 2014 15:29:07.53: job1.a.output.2
```

```
Job  = [job2.a.output.1
     -> job2.a.output.2]
Job  = [job3.a.output.1
     -> job3.a.output.2]
```

We can now see that the there is only one job in "second_task" which needs to be re-run because 'job1.stage1' has been modified after 'job1.stage2'

1.37 Chapter 7: Python Code for Displaying the pipeline visually with *pipeline_printout_graph(...)*

See also:

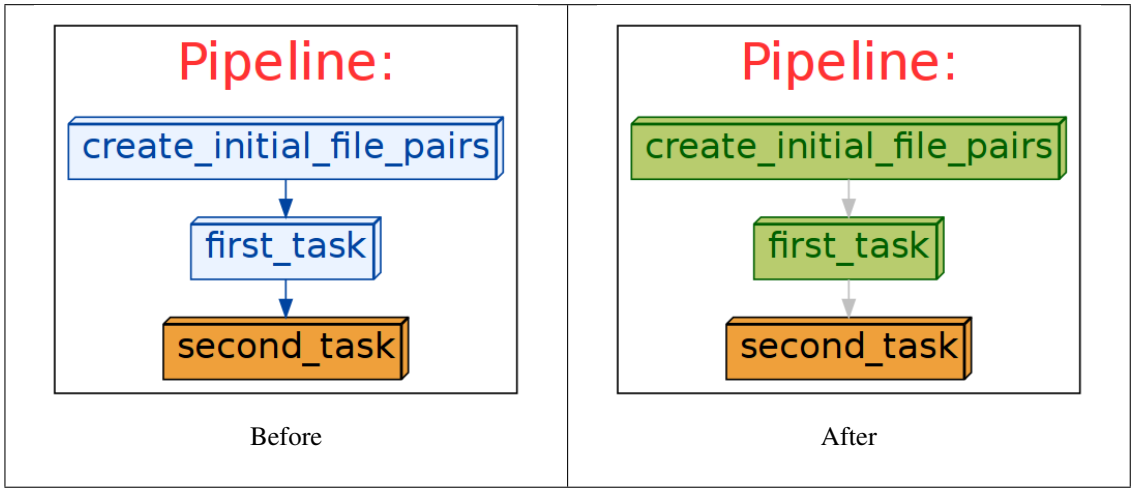
- *Manual Table of Contents*
- *pipeline_printout_graph(...)* syntax
- Back to **Chapter 7**: *Displaying the pipeline visually*

1.37.1 Code

```
from ruffus import *
import sys

#---------------------------------------------------------------
#   create initial files
#
@originate([   ['job1.a.start', 'job1.b.start'],
               ['job2.a.start', 'job2.b.start'],
               ['job3.a.start', 'job3.b.start']    ])
def create_initial_file_pairs(output_files):
    # create both files as necessary
    for output_file in output_files:
        with open(output_file, "w") as oo: pass

#---------------------------------------------------------------
#   first task
@transform(create_initial_file_pairs, suffix(".start"), ".output.1")
def first_task(input_files, output_file):
    with open(output_file, "w"): pass


#---------------------------------------------------------------
#   second task
@transform(first_task, suffix(".output.1"), ".output.2")
def second_task(input_files, output_file):
    with open(output_file, "w"): pass

#  Print graph before running pipeline

#---------------------------------------------------------------
#
#       Show flow chart and tasks before running the pipeline
```

```
#
print "Show flow chart and tasks before running the pipeline"
pipeline_printout_graph ( open("simple_tutorial_stage5_before.png", "w"),
                          "png",
                          [second_task],
                          minimal_key_legend=True)

#---------------------------------------------------------------
#
#       Run
#
pipeline_run([second_task])


# modify job1.stage1
open("job1.a.output.1", "w").close()


#  Print graph after everything apart from ``job1.a.output.1`` is update

#---------------------------------------------------------------
#
#       Show flow chart and tasks after running the pipeline
#
print "Show flow chart and tasks after running the pipeline"
pipeline_printout_graph ( open("simple_tutorial_stage5_after.png", "w"),
                          "png",
                          [second_task],
                          no_key_legend=True)
```

1.37.2 Resulting Flowcharts



1.38 Chapter 8: Python Code for Specifying output file names with *formatter()* and *regex()*

See also:

- *Manual Table of Contents*
- *suffix()* syntax
- *formatter()* syntax
- *regex()* syntax
- Back to **Chapter 8**: *Specifying output file names*

1.38.1 Example Code for *suffix()*

```
from ruffus import *

#---------------------------------------------------------------
#   create initial files
#
@originate([   ['job1.a.start', 'job1.b.start'],
               ['job2.a.start', 'job2.b.start'],
               ['job3.a.start', 'job3.b.start']    ])
def create_initial_file_pairs(output_files):
    # create both files as necessary
    for output_file in output_files:
        with open(output_file, "w") as oo: pass

#---------------------------------------------------------------
#
#   suffix
#
@transform(create_initial_file_pairs,             # name of previous task(s) (or list of files,
           suffix(".start"),                      # matching suffix of the "input file"
           [".output.a.1", 45, ".output.b.1"])    # resulting suffix
def first_task(input_files, output_parameters):
    print "  input_parameters  = ", input_files
    print "  output_parameters = ", output_parameters


#
#       Run
#
pipeline_run([first_task])
```

1.38.2 Example Code for *formatter()*

```
from ruffus import *

#   create initial files
@originate([   ['job1.a.start', 'job1.b.start'],
               ['job2.a.start', 'job2.b.start'],
               ['job3.a.start', 'job3.c.start']    ])
def create_initial_file_pairs(output_files):
```

```
    # create both files as necessary
    for output_file in output_files:
        with open(output_file, "w") as oo: pass


#---------------------------------------------------------------
#
#   formatter
#

#   first task
@transform(create_initial_file_pairs,                                   # Input

            formatter(".+/job(?P<JOBNUMBER>\d+).a.start",               # Extract job number
                      ".+/job[123].b.start"),                           # Match only "b" files

            ["{path[0]}/jobs{JOBNUMBER[0]}.output.a.1",                 # Replacement list
             "{path[1]}/jobs{JOBNUMBER[0]}.output.b.1", 45])
def first_task(input_files, output_parameters):
    print "input_parameters = ", input_files
    print "output_parameters = ", output_parameters


#
#       Run
#
pipeline_run(verbose=0)
```

1.38.3 Example Code for *formatter()* with replacements in *extra* arguments

```
from ruffus import *

#   create initial files
@originate([   ['job1.a.start', 'job1.b.start'],
               ['job2.a.start', 'job2.b.start'],
               ['job3.a.start', 'job3.c.start']    ])
def create_initial_file_pairs(output_files):
    for output_file in output_files:
        with open(output_file, "w") as oo: pass


#---------------------------------------------------------------
#
#   print job number as an extra argument
#

#   first task
@transform(create_initial_file_pairs,                                   # Input

            formatter(".+/job(?P<JOBNUMBER>\d+).a.start",               # Extract job number
                      ".+/job[123].b.start"),                           # Match only "b" files

            ["{path[0]}/jobs{JOBNUMBER[0]}.output.a.1",                 # Replacement list
             "{path[1]}/jobs{JOBNUMBER[0]}.output.b.1"],

             "{JOBNUMBER[0]}"
```

```
def first_task(input_files, output_parameters, job_number):
    print job_number, ":", input_files


pipeline_run(verbose=0)
```

1.38.4 Example Code for *formatter()* in Zoos

```
from ruffus import *

#   Make directories
@mkdir(["tiger", "lion", "dog", "crocodile", "rose"])

@originate(
            #   List of animals and plants
            [    "tiger/mammals.wild.animals",
                "lion/mammals.wild.animals",
                "lion/mammals.handreared.animals",
                "dog/mammals.tame.animals",
                "dog/mammals.wild.animals",
                "crocodile/reptiles.wild.animals",
                "rose/flowering.handreared.plants"])
def create_initial_files(output_file):
    with open(output_file, "w") as oo: pass


#   Put different animals in different directories depending on their clade
@transform(create_initial_files,                                        # Input

           formatter(".+/(?P<clade>\w+).(?P<tame>\w+).animals"),        # Only animals: ignore pl

           "{subpath[0][1]}/{clade[0]}/{tame[0]}.{subdir[0][0]}.food", # Replacement

           "{subpath[0][1]}/{clade[0]}",                                # new_directory
           "{subdir[0][0]}",                                            # animal_name
           "{tame[0]}")                                                 # tameness
def feed(input_file, output_file, new_directory, animal_name, tameness):
    print "Food for the {tameness:11s} {animal_name:9s} = {output_file:90s} will be placed in {n


pipeline_run(verbose=0)
```

Results in:

```
::

    >>> pipeline_run(verbose=0)
    Food for the wild        crocodile = ./reptiles/wild.crocodile.food will be placed in ./rept
    Food for the tame        dog       = ./mammals/tame.dog.food        will be placed in ./mamm
    Food for the wild        dog       = ./mammals/wild.dog.food        will be placed in ./mamm
    Food for the handreared  lion      = ./mammals/handreared.lion.food will be placed in ./mamm
    Food for the wild        lion      = ./mammals/wild.lion.food       will be placed in ./mamm
    Food for the wild        tiger     = ./mammals/wild.tiger.food      will be placed in ./mamm
```

1.38.5 Example Code for *regex()* in zoos

```
from ruffus import *

#   Make directories
@mkdir(["tiger", "lion", "dog", "crocodile", "rose"])

@originate(
            #   List of animals and plants
            [    "tiger/mammals.wild.animals",
                "lion/mammals.wild.animals",
                "lion/mammals.handreared.animals",
                "dog/mammals.tame.animals",
                "dog/mammals.wild.animals",
                "crocodile/reptiles.wild.animals",
                "rose/flowering.handreared.plants"])
def create_initial_files(output_file):
    with open(output_file, "w") as oo: pass



#   Put different animals in different directories depending on their clade
@transform(create_initial_files,                                        # Input

           regex(r"(.*?/?)(\w+)/(?P<clade>\w+).(?P<tame>\w+).animals"), # Only animals: ignore p

           r"\1/\g<clade>/\g<tame>.\2.food",                            # Replacement

           r"\1/\g<clade>",                                             # new_directory
           r"\2",                                                       # animal_name
           "\g<tame>")                                                  # tameness
def feed(input_file, output_file, new_directory, animal_name, tameness):
    print "Food for the {tameness:11s} {animal_name:9s} = {output_file:90s} will be placed in {n


pipeline_run(verbose=0)


Results in:

::

    >>> pipeline_run(verbose=0)
    Food for the wild        crocodile = reptiles/wild.crocodile.food will be placed in reptiles
    Food for the tame        dog       = mammals/tame.dog.food        will be placed in mammals
    Food for the wild        dog       = mammals/wild.dog.food        will be placed in mammals
    Food for the handreared  lion      = mammals/handreared.lion.food will be placed in mammals
    Food for the wild        lion      = mammals/wild.lion.food       will be placed in mammals
    Food for the wild        tiger     = mammals/wild.tiger.food      will be placed in mammals
```

1.39 Chapter 9: Python Code for Preparing directories for output with *@mkdir()*

See also:

- *Manual Table of Contents*

- *mkdir()* syntax
- *formatter()* syntax
- *regex()* syntax
- Back to **Chapter 9**: *Preparing directories for output with @mkdir()*

1.39.1 Code for *formatter()* Zoo example

```
from ruffus import *

#   Make directories
@mkdir(["tiger", "lion", "dog", "crocodile", "rose"])
@originate(
            #   List of animals and plants
            [    "tiger/mammals.wild.animals",
                "lion/mammals.wild.animals",
                "lion/mammals.handreared.animals",
                "dog/mammals.tame.animals",
                "dog/mammals.wild.animals",
                "crocodile/reptiles.wild.animals",
                "rose/flowering.handreared.plants"])
def create_initial_files(output_file):
    with open(output_file, "w") as oo: pass


# create directories for each clade
@mkdir(    create_initial_files,                                        # Input

           formatter(".+/(?P<clade>\w+).(?P<tame>\w+).animals"),        # Only animals: ignore pl

           "{subpath[0][1]}/{clade[0]}")                                # new_directory
#   Put different animals in different directories depending on their clade
@transform(create_initial_files,                                        # Input

           formatter(".+/(?P<clade>\w+).(?P<tame>\w+).animals"),        # Only animals: ignore pl

           "{subpath[0][1]}/{clade[0]}/{tame[0]}.{subdir[0][0]}.food", # Replacement

           "{subpath[0][1]}/{clade[0]}",                                # new_directory
           "{subdir[0][0]}",                                            # animal_name
           "{tame[0]}")                                                 # tameness
def feed(input_file, output_file, new_directory, animal_name, tameness):
        print "%40s -> %90s" % (input_file, output_file)
        # this works now
        open(output_file, "w")


pipeline_run(verbose=0)
```

1.39.2 Code for *regex()* Zoo example

```
from ruffus import *

#   Make directories
```

```
@mkdir(["tiger", "lion", "dog", "crocodile", "rose"])
@originate(
            #   List of animals and plants
            [    "tiger/mammals.wild.animals",
                 "lion/mammals.wild.animals",
                 "lion/mammals.handreared.animals",
                 "dog/mammals.tame.animals",
                 "dog/mammals.wild.animals",
                 "crocodile/reptiles.wild.animals",
                 "rose/flowering.handreared.plants"])
def create_initial_files(output_file):
    with open(output_file, "w") as oo: pass


# create directories for each clade
@mkdir(    create_initial_files,                                        # Input

           regex(r"(.*?/?)(\w+)/(?P<clade>\w+).(?P<tame>\w+).animals"), # Only animals: ignore p
           r"\g<clade>")                                               # new_directory
#   Put different animals in different directories depending on their clade
@transform(create_initial_files,                                         # Input

           regex(r"(.*?/?)(\w+)/(?P<clade>\w+).(?P<tame>\w+).animals"), # Only animals: ignore p

           r"\1\g<clade>/\g<tame>.\2.food",                            # Replacement

           r"\1\g<clade>",                                             # new_directory
           r"\2",                                                       # animal_name
           "\g<tame>")                                                  # tameness
def feed(input_file, output_file, new_directory, animal_name, tameness):
    print "%40s -> %90s" % (input_file, output_file)
    # this works now
    open(output_file, "w")


pipeline_run(verbose=0)
```

1.40 Chapter 10: Python Code for Checkpointing: Interrupted Pipelines and Exceptions

See also:

- *Manual Table of Contents*
- *Back to \new_manual.checkpointing.chapter_num\: Interrupted Pipelines and Exceptions*

1.40.1 Code for the "Interrupting tasks" example

```
from ruffus import *

from ruffus import *
import sys, time

#   create initial files
```

```
@originate(['job1.start'])
def create_initial_files(output_file):
    with open(output_file, "w") as oo: pass


#---------------------------------------------------------------
#
#   long task to interrupt
#
@transform(create_initial_files, suffix(".start"), ".output")
def long_task(input_files, output_file):
    with open(output_file, "w") as ff:
        ff.write("Unfinished...")
        # sleep for 2 seconds here so you can interrupt me
        sys.stderr.write("Job started. Press ^C to interrupt me now...\n")
        time.sleep(2)
        ff.write("\nFinished")
        sys.stderr.write("Job completed.\n")


#       Run
pipeline_run([long_task])
```

1.41 Chapter 12: Python Code for Splitting up large tasks / files with @split

See also:

- *Manual Table of Contents*
- *@split syntax in detail*
- Back to **Chapter 12**: *Splitting up large tasks / files with @split*

1.41.1 Splitting large jobs

```
from ruffus import *

NUMBER_OF_RANDOMS = 10000
CHUNK_SIZE = 1000


import random, os, glob

#---------------------------------------------------------------
#
#   Create random numbers
#
@originate("random_numbers.list")
def create_random_numbers(output_file_name):
    f = open(output_file_name, "w")
    for i in range(NUMBER_OF_RANDOMS):
        f.write("%g\n" % (random.random() * 100.0))

#---------------------------------------------------------------
```

```
#
#   split initial file
#
@split(create_random_numbers, "*.chunks")
def split_problem (input_file_names, output_files):
    """
        splits random numbers file into xxx files of chunk_size each
    """
    #
    #   clean up any files from previous runs
    #
    #for ff in glob.glob("*.chunks"):
    for ff in input_file_names:
        os.unlink(ff)
    #
    #
    #   create new file every chunk_size lines and
    #       copy each line into current file
    #
    output_file = None
    cnt_files = 0
    for input_file_name in input_file_names:
        for i, line in enumerate(open(input_file_name)):
            if i % CHUNK_SIZE == 0:
                cnt_files += 1
                output_file = open("%d.chunks" % cnt_files, "w")
            output_file.write(line)

#---------------------------------------------------------------
#
#   Calculate sum and sum of squares for each chunk file
#
@transform(split_problem, suffix(".chunks"), ".sums")
def sum_of_squares (input_file_name, output_file_name):
    output = open(output_file_name,  "w")
    sum_squared, sum = [0.0, 0.0]
    cnt_values = 0
    for line in open(input_file_name):
        cnt_values += 1
        val = float(line.rstrip())
        sum_squared += val * val
        sum += val
    output.write("%s\n%s\n%d\n" % (repr(sum_squared), repr(sum), cnt_values))

#---------------------------------------------------------------
#
#       Run
#
pipeline_run()
```

1.41.2 Resulting Output

```
>>> pipeline_run()
    Job  = [None -> random_numbers.list] completed
Completed Task = create_random_numbers
    Job  = [[random_numbers.list] -> *.chunks] completed
```

```
Completed Task = split_problem
    Job  = [1.chunks -> 1.sums] completed
    Job  = [10.chunks -> 10.sums] completed
    Job  = [2.chunks -> 2.sums] completed
    Job  = [3.chunks -> 3.sums] completed
    Job  = [4.chunks -> 4.sums] completed
    Job  = [5.chunks -> 5.sums] completed
    Job  = [6.chunks -> 6.sums] completed
    Job  = [7.chunks -> 7.sums] completed
    Job  = [8.chunks -> 8.sums] completed
    Job  = [9.chunks -> 9.sums] completed
Completed Task = sum_of_squares
```

1.42 Chapter 13: Python Code for `@merge` multiple input into a single result

See also:

- *Manual Table of Contents*
- *@merge syntax in detail*
- Back to **Chapter 13**: *Splitting up large tasks / files with @merge*

1.42.1 Splitting large jobs

```
from ruffus import *

NUMBER_OF_RANDOMS = 10000
CHUNK_SIZE = 1000


import random, os, glob

#---------------------------------------------------------------
#
#   Create random numbers
#
@originate("random_numbers.list")
def create_random_numbers(output_file_name):
    f = open(output_file_name, "w")
    for i in range(NUMBER_OF_RANDOMS):
        f.write("%g\n" % (random.random() * 100.0))

#---------------------------------------------------------------
#
#   split initial file
#
@split(create_random_numbers, "*.chunks")
def split_problem (input_file_names, output_files):
    """
        splits random numbers file into xxx files of chunk_size each
    """
    #
    #   clean up any files from previous runs
```

```
    #
    #for ff in glob.glob("*.chunks"):
    for ff in input_file_names:
        os.unlink(ff)
    #
    #
    #   create new file every chunk_size lines and
    #       copy each line into current file
    #
    output_file = None
    cnt_files = 0
    for input_file_name in input_file_names:
        for i, line in enumerate(open(input_file_name)):
            if i % CHUNK_SIZE == 0:
                cnt_files += 1
                output_file = open("%d.chunks" % cnt_files, "w")
            output_file.write(line)

#---------------------------------------------------------------
#
#   Calculate sum and sum of squares for each chunk file
#
@transform(split_problem, suffix(".chunks"), ".sums")
def sum_of_squares (input_file_name, output_file_name):
    output = open(output_file_name,  "w")
    sum_squared, sum = [0.0, 0.0]
    cnt_values = 0
    for line in open(input_file_name):
        cnt_values += 1
        val = float(line.rstrip())
        sum_squared += val * val
        sum += val
    output.write("%s\n%s\n%d\n" % (repr(sum_squared), repr(sum), cnt_values))

#---------------------------------------------------------------
#
#   Calculate variance from sums
#
@merge(sum_of_squares, "variance.result")
def calculate_variance (input_file_names, output_file_name):
    """
    Calculate variance naively
    """
    #
    #   initialise variables
    #
    all_sum_squared = 0.0
    all_sum         = 0.0
    all_cnt_values  = 0.0
    #
    # added up all the sum_squared, and sum and cnt_values from all the chunks
    #
    for input_file_name in input_file_names:
        sum_squared, sum, cnt_values = map(float, open(input_file_name).readlines())
        all_sum_squared += sum_squared
        all_sum         += sum
        all_cnt_values  += cnt_values
    all_mean = all_sum / all_cnt_values
```

```
    variance = (all_sum_squared - all_sum * all_mean)/(all_cnt_values)
    #
    #   print output
    #
    open(output_file_name,  "w").write("%s\n" % variance)

#---------------------------------------------------------------
#
#       Run
#
pipeline_run()
```

1.42.2 Resulting Output

```
>>> pipeline_run()
    Job  = [None -> random_numbers.list] completed
Completed Task = create_random_numbers
    Job  = [[random_numbers.list] -> *.chunks] completed
Completed Task = split_problem
    Job  = [1.chunks -> 1.sums] completed
    Job  = [10.chunks -> 10.sums] completed
    Job  = [2.chunks -> 2.sums] completed
    Job  = [3.chunks -> 3.sums] completed
    Job  = [4.chunks -> 4.sums] completed
    Job  = [5.chunks -> 5.sums] completed
    Job  = [6.chunks -> 6.sums] completed
    Job  = [7.chunks -> 7.sums] completed
    Job  = [8.chunks -> 8.sums] completed
    Job  = [9.chunks -> 9.sums] completed
Completed Task = sum_of_squares
    Job  = [[1.sums, 10.sums, 2.sums, 3.sums, 4.sums, 5.sums, 6.sums, 7.sums, 8.sums, 9.sums] ->
Completed Task = calculate_variance
```

1.43 Chapter 14: Python Code for Multiprocessing, `drmaa` and Computation Clusters

See also:

- *Manual Table of Contents*
- *@jobs_limit* syntax
- *pipeline_run()* syntax
- *drmaa_wrapper.run_job()* syntax
- Back to **Chapter 14**: *Multiprocessing, drmaa and Computation Clusters*

1.43.1 *@jobs_limit*

- First 2 tasks are constrained to a parallelism of 3 shared jobs at a time
- Final task is constrained to a parallelism of 5 jobs at a time

- The entire pipeline is constrained to a (theoretical) parallelism of 10 jobs at a time

```
from ruffus import *
import time

# make list of 10 files
@split(None, "*stage1")
def make_files(input_files, output_files):
    for i in range(10):
        if i < 5:
            open("%d.small_stage1" % i, "w")
        else:
            open("%d.big_stage1" % i, "w")

@jobs_limit(3, "ftp_download_limit")
@transform(make_files, suffix(".small_stage1"), ".stage2")
def stage1_small(input_file, output_file):
    print "FTP downloading %s ->Start" % input_file
    time.sleep(2)
    open(output_file, "w")
    print "FTP downloading %s ->Finished" % input_file

@jobs_limit(3, "ftp_download_limit")
@transform(make_files, suffix(".big_stage1"), ".stage2")
def stage1_big(input_file, output_file):
    print "FTP downloading %s ->Start" % input_file
    time.sleep(2)
    open(output_file, "w")
    print "FTP downloading %s ->Finished" % input_file

@jobs_limit(5)
@transform([stage1_small, stage1_big], suffix(".stage2"), ".stage3")
def stage2(input_file, output_file):
    print "Processing stage2 %s ->Start" % input_file
    time.sleep(2)
    open(output_file, "w")
    print "Processing stage2 %s ->Finished" % input_file

pipeline_run(multiprocess = 10, verbose = 0)
```

Giving:

```
>>> pipeline_run(multiprocess = 10, verbose = 0)

>>> # 3 jobs at a time, interleaved
FTP downloading 5.big_stage1 ->Start
FTP downloading 6.big_stage1 ->Start
FTP downloading 7.big_stage1 ->Start
FTP downloading 5.big_stage1 ->Finished
FTP downloading 8.big_stage1 ->Start
FTP downloading 6.big_stage1 ->Finished
FTP downloading 9.big_stage1 ->Start
FTP downloading 7.big_stage1 ->Finished
FTP downloading 0.small_stage1 ->Start
FTP downloading 8.big_stage1 ->Finished
FTP downloading 1.small_stage1 ->Start
FTP downloading 9.big_stage1 ->Finished
FTP downloading 2.small_stage1 ->Start
FTP downloading 0.small_stage1 ->Finished
```

```
FTP downloading 3.small_stage1 ->Start
FTP downloading 1.small_stage1 ->Finished
FTP downloading 4.small_stage1 ->Start
FTP downloading 2.small_stage1 ->Finished
FTP downloading 3.small_stage1 ->Finished
FTP downloading 4.small_stage1 ->Finished

>>> # 5 jobs at a time, interleaved
Processing stage2 0.stage2 ->Start
Processing stage2 1.stage2 ->Start
Processing stage2 2.stage2 ->Start
Processing stage2 3.stage2 ->Start
Processing stage2 4.stage2 ->Start
Processing stage2 0.stage2 ->Finished
Processing stage2 5.stage2 ->Start
Processing stage2 1.stage2 ->Finished
Processing stage2 6.stage2 ->Start
Processing stage2 2.stage2 ->Finished
Processing stage2 4.stage2 ->Finished
Processing stage2 7.stage2 ->Start
Processing stage2 8.stage2 ->Start
Processing stage2 3.stage2 ->Finished
Processing stage2 9.stage2 ->Start
Processing stage2 5.stage2 ->Finished
Processing stage2 7.stage2 ->Finished
Processing stage2 6.stage2 ->Finished
Processing stage2 8.stage2 ->Finished
Processing stage2 9.stage2 ->Finished
```

1.43.2 Using `ruffus.drmaa_wrapper`

```
#!/usr/bin/python
job_queue_name    = "YOUR_QUEUE_NAME_GOES_HERE"
job_other_options = "-P YOUR_PROJECT_NAME_GOES_HERE"

from ruffus import *
from ruffus.drmaa_wrapper import run_job, error_drmaa_job

parser = cmdline.get_argparse(description='WHAT DOES THIS PIPELINE DO?')

options = parser.parse_args()

#  logger which can be passed to multiprocessing ruffus tasks
logger, logger_mutex = cmdline.setup_logging (__name__, options.log_file, options.verbose)


#
#   start shared drmaa session for all jobs / tasks in pipeline
#
import drmaa
drmaa_session = drmaa.Session()
drmaa_session.initialize()

@originate(["1.chromosome", "X.chromosome"],
           logger, logger_mutex)
def create_test_files(output_file):
```

```
    try:
        stdout_res, stderr_res = "",""
        job_queue_name, job_other_options = get_queue_options()

        #
        #   ruffus.drmaa_wrapper.run_job
        #
        stdout_res, stderr_res  = run_job(cmd_str           = "touch " + output_file,
                                          job_name          = job_name,
                                          logger            = logger,
                                          drmaa_session     = drmaa_session,
                                          run_locally       = options.local_run,
                                          job_queue_name    = job_queue_name,
                                          job_other_options = job_other_options)

    # relay all the stdout, stderr, drmaa output to diagnose failures
    except error_drmaa_job as err:
        raise Exception("\n".join(map(str,
                          "Failed to run:"
                          cmd,
                          err,
                          stdout_res,
                          stderr_res)))


if __name__ == '__main__':
    cmdline.run (options, multithread = options.jobs)
    # cleanup drmaa
    drmaa_session.exit()
```

1.44 Chapter 15: Python Code for Logging progress through a pipeline

See also:

- *Manual Table of Contents*
- Back to **Chapter 15**: *Logging progress through a pipeline*

1.44.1 Rotating set of file logs

```
import logging
import logging.handlers

LOG_FILENAME = '/tmp/ruffus.log'

# Set up a specific logger with our desired output level
logger = logging.getLogger('My_Ruffus_logger')
logger.setLevel(logging.DEBUG)

# Rotate a set of 5 log files every 2kb
handler = logging.handlers.RotatingFileHandler(
              LOG_FILENAME, maxBytes=2000, backupCount=5)
```

```
# Add the log message handler to the logger
logger.addHandler(handler)

# Ruffus pipeline
from ruffus import *

# Start with some initial data file of yours...
initial_file = "job1.input"
open(initial_file, "w")

@transform( initial_file,
            suffix(".input"),
            ".output1"),
def first_task(input_file, output_file):
    "Some detailed description"
    pass

#   use our custom logging object
pipeline_run(logger=logger)
print open("/tmp/ruffus.log").read()
```

1.45 Chapter 16: Python Code for *@subdivide* tasks to run efficiently and regroup with *@collate*

See also:

- *Manual Table of Contents*
- *@jobs_limit* syntax
- *pipeline_run()* syntax
- *drmaa_wrapper.run_job()* syntax
- Back to **Chapter 16**: *:ref:'@subdivide tasks to run efficiently and regroup with @collate*

1.45.1 *@subdivide* and regroup with *@collate* example

```
from ruffus import *
import os, random, sys

# Create files a random number of lines
@originate(["a.start",
            "b.start",
            "c.start"])
def create_test_files(output_file):
    cnt_lines = random.randint(1,3) * 2
    with open(output_file, "w") as oo:
        for ii in range(cnt_lines):
            oo.write("data item = %d\n" % ii)
        print "        %s has %d lines" % (output_file, cnt_lines)


#
#   subdivide the input files into NNN fragment files of 2 lines each
```

```
    #
    @subdivide( create_test_files,
                formatter(),
                "{path[0]}/{basename[0]}.*.fragment",
                "{path[0]}/{basename[0]}")
    def subdivide_files(input_file, output_files, output_file_name_stem):
        #
        #   cleanup any previous results
        #
        for oo in output_files:
            os.unlink(oo)
        #
        #   Output files contain two lines each
        #       (new output files every even line)
        #
        cnt_output_files = 0
        for ii, line in enumerate(open(input_file)):
            if ii % 2 == 0:
                cnt_output_files += 1
                output_file_name = "%s.%d.fragment" % (output_file_name_stem, cnt_output_files)
                output_file = open(output_file_name, "w")
                print "        Subdivide %s -> %s" % (input_file, output_file_name)
            output_file.write(line)


    #
    #   Analyse each fragment independently
    #
    @transform(subdivide_files, suffix(".fragment"), ".analysed")
    def analyse_fragments(input_file, output_file):
        print "        Analysing %s -> %s" % (input_file, output_file)
        with open(output_file, "w") as oo:
            for line in open(input_file):
                oo.write("analysed " + line)


    #
    #   Group results using original names
    #
    @collate(   analyse_fragments,

                # split file name into [abc].NUMBER.analysed
                formatter("/(?P<NAME>[abc]+)\.\d+\.analysed$"),

                "{path[0]}/{NAME[0]}.final_result")
    def recombine_analyses(input_file_names, output_file):
        with open(output_file, "w") as oo:
            for input_file in input_file_names:
                print "        Recombine %s -> %s" % (input_file, output_file)
                for line in open(input_file):
                    oo.write(line)



    #pipeline_printout(sys.stdout, verbose = 3)
```

```
pipeline_run(verbose = 1)
```

Results in

```
>>> pipeline_run(verbose = 1)

        a.start has 2 lines
    Job  = [None -> a.start] completed
        b.start has 6 lines
    Job  = [None -> b.start] completed
        c.start has 6 lines
    Job  = [None -> c.start] completed
Completed Task = create_test_files

        Subdivide a.start -> /home/lg/temp/a.1.fragment
    Job  = [a.start -> a.*.fragment, a] completed
        Subdivide b.start -> /home/lg/temp/b.1.fragment
        Subdivide b.start -> /home/lg/temp/b.2.fragment
        Subdivide b.start -> /home/lg/temp/b.3.fragment
    Job  = [b.start -> b.*.fragment, b] completed
        Subdivide c.start -> /home/lg/temp/c.1.fragment
        Subdivide c.start -> /home/lg/temp/c.2.fragment
        Subdivide c.start -> /home/lg/temp/c.3.fragment
    Job  = [c.start -> c.*.fragment, c] completed
Completed Task = subdivide_files

        Analysing /home/lg/temp/a.1.fragment -> /home/lg/temp/a.1.analysed
    Job  = [a.1.fragment -> a.1.analysed] completed
        Analysing /home/lg/temp/b.1.fragment -> /home/lg/temp/b.1.analysed
    Job  = [b.1.fragment -> b.1.analysed] completed
        Analysing /home/lg/temp/b.2.fragment -> /home/lg/temp/b.2.analysed
    Job  = [b.2.fragment -> b.2.analysed] completed
        Analysing /home/lg/temp/b.3.fragment -> /home/lg/temp/b.3.analysed
    Job  = [b.3.fragment -> b.3.analysed] completed
        Analysing /home/lg/temp/c.1.fragment -> /home/lg/temp/c.1.analysed
    Job  = [c.1.fragment -> c.1.analysed] completed
        Analysing /home/lg/temp/c.2.fragment -> /home/lg/temp/c.2.analysed
    Job  = [c.2.fragment -> c.2.analysed] completed
        Analysing /home/lg/temp/c.3.fragment -> /home/lg/temp/c.3.analysed
    Job  = [c.3.fragment -> c.3.analysed] completed
Completed Task = analyse_fragments

        Recombine /home/lg/temp/a.1.analysed -> /home/lg/temp/a.final_result
    Job  = [[a.1.analysed] -> a.final_result] completed
        Recombine /home/lg/temp/b.1.analysed -> /home/lg/temp/b.final_result
        Recombine /home/lg/temp/b.2.analysed -> /home/lg/temp/b.final_result
        Recombine /home/lg/temp/b.3.analysed -> /home/lg/temp/b.final_result
    Job  = [[b.1.analysed, b.2.analysed, b.3.analysed] -> b.final_result] completed
        Recombine /home/lg/temp/c.1.analysed -> /home/lg/temp/c.final_result
        Recombine /home/lg/temp/c.2.analysed -> /home/lg/temp/c.final_result
        Recombine /home/lg/temp/c.3.analysed -> /home/lg/temp/c.final_result
    Job  = [[c.1.analysed, c.2.analysed, c.3.analysed] -> c.final_result] completed
Completed Task = recombine_analyses
```

1.46 Chapter 17: Python Code for *@combinations*, *@permutations* and all versus all *@product*

See also:

- *Manual Table of Contents*
- *@combinations_with_replacement*
- *@combinations*
- *@permutations*
- *@product*
- Back to **Chapter 17**: *Preparing directories for output with @combinatorics()*

1.46.1 Example code for *@product*

```
from ruffus import *
from ruffus.combinatorics import *

#   Three sets of initial files
@originate([ 'a.start', 'b.start'])
def create_initial_files_ab(output_file):
    with open(output_file, "w") as oo: pass

@originate([ 'p.start', 'q.start'])
def create_initial_files_pq(output_file):
    with open(output_file, "w") as oo: pass

@originate([ ['x.1_start', 'x.2_start'],
             ['y.1_start', 'y.2_start'] ])
def create_initial_files_xy(output_file):
    with open(output_file, "w") as oo: pass

#   @product
@product(   create_initial_files_ab,        # Input
            formatter("(.start)$"),         # match input file set # 1

            create_initial_files_pq,        # Input
            formatter("(.start)$"),         # match input file set # 2

            create_initial_files_xy,        # Input
            formatter("(.start)$"),         # match input file set # 3

            "{path[0][0]}/"                 # Output Replacement string
            "{basename[0][0]}_vs_"          #
            "{basename[1][0]}_vs_"          #
            "{basename[2][0]}.product",     #

            "{path[0][0]}",                 # Extra parameter: path for 1st set of files, 1st fi

            ["{basename[0][0]}",            # Extra parameter: basename for 1st set of files, 1s
             "{basename[1][0]}",            #                                  2nd
             "{basename[2][0]}",            #                                  3rd
             ])
def product_task(input_file, output_parameter, shared_path, basenames):
```

```
    print "# basenames      = ", " ".join(basenames)
    print "input_parameter  = ", input_file
    print "output_parameter = ", output_parameter, "\n"


#
#       Run
#
pipeline_run(verbose=0)
```

This results in:

```
>>> pipeline_run(verbose=0)

# basenames      =  a p x
input_parameter  =  ('a.start', 'p.start', 'x.start')
output_parameter =  /home/lg/temp/a_vs_p_vs_x.product

# basenames      =  a p y
input_parameter  =  ('a.start', 'p.start', 'y.start')
output_parameter =  /home/lg/temp/a_vs_p_vs_y.product

# basenames      =  a q x
input_parameter  =  ('a.start', 'q.start', 'x.start')
output_parameter =  /home/lg/temp/a_vs_q_vs_x.product

# basenames      =  a q y
input_parameter  =  ('a.start', 'q.start', 'y.start')
output_parameter =  /home/lg/temp/a_vs_q_vs_y.product

# basenames      =  b p x
input_parameter  =  ('b.start', 'p.start', 'x.start')
output_parameter =  /home/lg/temp/b_vs_p_vs_x.product

# basenames      =  b p y
input_parameter  =  ('b.start', 'p.start', 'y.start')
output_parameter =  /home/lg/temp/b_vs_p_vs_y.product

# basenames      =  b q x
input_parameter  =  ('b.start', 'q.start', 'x.start')
output_parameter =  /home/lg/temp/b_vs_q_vs_x.product

# basenames      =  b q y
input_parameter  =  ('b.start', 'q.start', 'y.start')
output_parameter =  /home/lg/temp/b_vs_q_vs_y.product
```

1.46.2 Example code for *@permutations*

```
from ruffus import *
from ruffus.combinatorics import *

#   initial file pairs
@originate([ ['A.1_start', 'A.2_start'],
             ['B.1_start', 'B.2_start'],
             ['C.1_start', 'C.2_start'],
             ['D.1_start', 'D.2_start']])
def create_initial_files_ABCD(output_files):
```

```
    for output_file in output_files:
        with open(output_file, "w") as oo: pass

#   @permutations
@permutations(create_initial_files_ABCD,      # Input
              formatter(),                    # match input files

              # tuple of 2 at a time
              2,

              # Output Replacement string
              "{path[0][0]}/"
              "{basename[0][1]}_vs_"
              "{basename[1][1]}.permutations",

              # Extra parameter: path for 1st set of files, 1st file name
              "{path[0][0]}",

              # Extra parameter
              ["{basename[0][0]}",  # basename for 1st set of files, 1st file name
               "{basename[1][0]}",  #                                 2nd
               ])
def permutations_task(input_file, output_parameter, shared_path, basenames):
    print " - ".join(basenames)


#
#       Run
#
pipeline_run(verbose=0)
```

This results in:

```
    >>> pipeline_run(verbose=0)

    A - B
    A - C
    A - D
    B - A
    B - C
    B - D
    C - A
    C - B
    C - D
    D - A
    D - B
    D - C
```

1.46.3 Example code for *@combinations*

```
from ruffus import *
from ruffus.combinatorics import *

#   initial file pairs
@originate([ ['A.1_start', 'A.2_start'],
             ['B.1_start', 'B.2_start'],
             ['C.1_start', 'C.2_start'],
```

```
            ['D.1_start', 'D.2_start']])
def create_initial_files_ABCD(output_files):
    for output_file in output_files:
        with open(output_file, "w") as oo: pass

#   @combinations
@combinations(create_initial_files_ABCD,      # Input
              formatter(),                    # match input files

              # tuple of 3 at a time
              3,

              # Output Replacement string
              "{path[0][0]}/"
              "{basename[0][1]}_vs_"
              "{basename[1][1]}_vs_"
              "{basename[2][1]}.combinations",

              # Extra parameter: path for 1st set of files, 1st file name
              "{path[0][0]}",

              # Extra parameter
              ["{basename[0][0]}",  # basename for 1st set of files, 1st file name
               "{basename[1][0]}",  #              2nd
               "{basename[2][0]}",  #              3rd
               ])
def combinations_task(input_file, output_parameter, shared_path, basenames):
    print " - ".join(basenames)


#
#       Run
#
pipeline_run(verbose=0)
```

This results in:

```
>>> pipeline_run(verbose=0)
A - B - C
A - B - D
A - C - D
B - C - D
```

1.46.4 Example code for *@combinations_with_replacement*

```
from ruffus import *
from ruffus.combinatorics import *

#   initial file pairs
@originate([ ['A.1_start', 'A.2_start'],
             ['B.1_start', 'B.2_start'],
             ['C.1_start', 'C.2_start'],
             ['D.1_start', 'D.2_start']])
def create_initial_files_ABCD(output_files):
    for output_file in output_files:
        with open(output_file, "w") as oo: pass
```

```
#   @combinations_with_replacement
@combinations_with_replacement(create_initial_files_ABCD,    # Input
               formatter(),                                  # match input files

               # tuple of 2 at a time
               2,

               # Output Replacement string
               "{path[0][0]}/"
               "{basename[0][1]}_vs_"
               "{basename[1][1]}.combinations_with_replacement",

               # Extra parameter: path for 1st set of files, 1st file name
               "{path[0][0]}",

               # Extra parameter
               ["{basename[0][0]}",  # basename for 1st set of files, 1st file name
                "{basename[1][0]}",  #              2rd
                ])
def combinations_with_replacement_task(input_file, output_parameter, shared_path, basenames):
    print " - ".join(basenames)


#
#       Run
#
pipeline_run(verbose=0)
```

This results in:

```
>>> pipeline_run(verbose=0)
A - A
A - B
A - C
A - D
B - B
B - C
B - D
C - C
C - D
D - D
```

1.47 Chapter 20: Python Code for Manipulating task inputs via string substitution using *inputs()* and *add_inputs()*

See also:

- *Manual Table of Contents*
- *inputs()* syntax
- *add_inputs()* syntax
- Back to **Chapter 20**: *Manipulating task inputs via string substitution*

1.47.1 Example code for adding additional *input* prerequisites per job with *add_inputs()*

1. Example: compiling c++ code

```
# source files exist before our pipeline
source_files = ["hasty.cpp", "tasty.cpp", "messy.cpp"]
for source_file in source_files:
    open(source_file, "w")

from ruffus import *

@transform(source_files, suffix(".cpp"), ".o")
def compile(input_filename, output_file):
    open(output_file, "w")

pipeline_run()
```

Giving:

```
    >>> pipeline_run()
        Job  = [hasty.cpp -> hasty.o] completed
        Job  = [messy.cpp -> messy.o] completed
        Job  = [tasty.cpp -> tasty.o] completed
    Completed Task = compile
```

2. Example: Adding a common header file with *add_inputs()*

```
# source files exist before our pipeline
source_files = ["hasty.cpp", "tasty.cpp", "messy.cpp"]
for source_file in source_files:
    open(source_file, "w")

# common (universal) header exists before our pipeline
open("universal.h", "w")

from ruffus import *

@transform( source_files, suffix(".cpp"),
            # add header to the input of every job
            add_inputs("universal.h"),
            ".o")
def compile(input_filename, output_file):
    open(output_file, "w")

pipeline_run()
```

Giving:

```
    >>> pipeline_run()
        Job  = [[hasty.cpp, universal.h] -> hasty.o] completed
        Job  = [[messy.cpp, universal.h] -> messy.o] completed
        Job  = [[tasty.cpp, universal.h] -> tasty.o] completed
    Completed Task = compile
```

3. Example: Additional *Input* can be tasks

```
# source files exist before our pipeline
source_files = ["hasty.cpp", "tasty.cpp", "messy.cpp"]
for source_file in source_files:
    open(source_file, "w")

# common (universal) header exists before our pipeline
open("universal.h", "w")

from ruffus import *

# make header files
@transform(source_files, suffix(".cpp"), ".h")
def create_matching_headers(input_file, output_file):
    open(output_file, "w")

@transform(source_files, suffix(".cpp"),
                        # add header to the input of every job
            add_inputs("universal.h",
                        # add result of task create_matching_headers to the input of every job
                       create_matching_headers),
            ".o")
def compile(input_filename, output_file):
    open(output_file, "w")

pipeline_run()
```

Giving:

```
    >>> pipeline_run()
        Job  = [hasty.cpp -> hasty.h] completed
        Job  = [messy.cpp -> messy.h] completed
        Job  = [tasty.cpp -> tasty.h] completed
    Completed Task = create_matching_headers
        Job  = [[hasty.cpp, universal.h, hasty.h, messy.h, tasty.h] -> hasty.o] completed
        Job  = [[messy.cpp, universal.h, hasty.h, messy.h, tasty.h] -> messy.o] completed
        Job  = [[tasty.cpp, universal.h, hasty.h, messy.h, tasty.h] -> tasty.o] completed
    Completed Task = compile
```

4. Example: Add corresponding files using *add_inputs()* with *formatter* or *regex*

```
# source files exist before our pipeline
source_files = ["hasty.cpp", "tasty.cpp", "messy.cpp"]
header_files = ["hasty.h", "tasty.h", "messy.h"]
for source_file in source_files + header_files:
    open(source_file, "w")

# common (universal) header exists before our pipeline
open("universal.h", "w")

from ruffus import *

@transform( source_files,
            formatter(".cpp$"),
                        # corresponding header for each source file
            add_inputs("{basename[0]}.h",
```

```
                        # add header to the input of every job
                        "universal.h"),
              "{basename[0]}.o")
def compile(input_filename, output_file):
    open(output_file, "w")

pipeline_run()
```

Giving:

```
    >>> pipeline_run()
        Job  = [[hasty.cpp, hasty.h, universal.h] -> hasty.o] completed
        Job  = [[messy.cpp, messy.h, universal.h] -> messy.o] completed
        Job  = [[tasty.cpp, tasty.h, universal.h] -> tasty.o] completed
    Completed Task = compile
```

1.47.2 Example code for replacing all input parameters with *inputs()*

5. Example: Running matching python scripts using *inputs()*

```
# source files exist before our pipeline
source_files = ["hasty.cpp", "tasty.cpp", "messy.cpp"]
python_files = ["hasty.py", "tasty.py", "messy.py"]
for source_file in source_files + python_files:
    open(source_file, "w")

# common (universal) header exists before our pipeline
open("universal.h", "w")

from ruffus import *

@transform( source_files,
            formatter(".cpp$"),
            # corresponding python file for each source file
            inputs("{basename[0]}.py"),

            "{basename[0]}.results")
def run_corresponding_python(input_filenames, output_file):
    open(output_file, "w")


pipeline_run()
```

Giving:

```
    >>> pipeline_run()
        Job  = [hasty.py -> hasty.results] completed
        Job  = [messy.py -> messy.results] completed
        Job  = [tasty.py -> tasty.results] completed
    Completed Task = run_corresponding_python
```

1.48 Chapter 21: Esoteric: Python Code for Generating parameters on the fly with *@files*

See also:

- *Manual Table of Contents*
- *@files on-the-fly syntax in detail*
- Back to **Chapter 21**: *Generating parameters on the fly*

1.48.1 Introduction

This script takes N pairs of input file pairs (with the suffices .gene and .gwas)
and runs them against M sets of simulation data (with the suffix .simulation)
A summary per input file pair is then produced

In pseudo-code:

STEP_1:

```
for n_file in NNN_pairs_of_input_files:
    for m_file in MMM_simulation_data:

        [n_file.gene,
         n_file.gwas,
         m_file.simulation] -> n_file.m_file.simulation_res
```

STEP_2:

```
for n_file in NNN_pairs_of_input_files:

    n_file.*.simulation_res -> n_file.mean
```

n = CNT_GENE_GWAS_FILES
m = CNT_SIMULATION_FILES

1.48.2 Code

```
from ruffus import *
import os

#88888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888

#   constants

#8888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888
working_dir             = "temp_NxM"
simulation_data_dir     = os.path.join(working_dir, "simulation")
gene_data_dir           = os.path.join(working_dir, "gene")
CNT_GENE_GWAS_FILES     = 2
CNT_SIMULATION_FILES    = 3
```

```
#888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888

#   imports

#888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888
import os, sys
from itertools import izip
import glob
#888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888

#   Functions


#888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888

#_____________________________________________________________________________________________________
#
#   get gene gwas file pairs
#
#_____________________________________________________________________________________________________
def get_gene_gwas_file_pairs(  ):
    """
    Helper function to get all *.gene, *.gwas from the direction specified
        in --gene_data_dir

    Returns
        file pairs with both .gene and .gwas extensions,
        corresponding roots (no extension) of each file
    """
    gene_files = glob.glob(os.path.join(gene_data_dir, "*.gene"))
    gwas_files = glob.glob(os.path.join(gene_data_dir, "*.gwas"))
    #
    common_roots = set(map(lambda x: os.path.splitext(os.path.split(x)[1])[0], gene_files))
    common_roots &=set(map(lambda x: os.path.splitext(os.path.split(x)[1])[0], gwas_files))
    common_roots = list(common_roots)
    #
    p = os.path; g_dir = gene_data_dir
    file_pairs = [[p.join(g_dir, x + ".gene"), p.join(g_dir, x + ".gwas")] for x in common_roots
    return file_pairs, common_roots

#_____________________________________________________________________________________________________
#
#   get simulation files
#
#_____________________________________________________________________________________________________
def get_simulation_files(  ):
    """
    Helper function to get all *.simulation from the direction specified
        in --simulation_data_dir
        Returns
            file with .simulation extensions,
            corresponding roots (no extension) of each file
    """
    simulation_files = glob.glob(os.path.join(simulation_data_dir, "*.simulation"))
    simulation_roots =map(lambda x: os.path.splitext(os.path.split(x)[1])[0], simulation_files)
    return simulation_files, simulation_roots
```

```
#88888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888

#   Main logic

#88888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888




#_____________________________________________________________________________________
#
#   setup_simulation_data
#
#_____________________________________________________________________________________

#
# mkdir: makes sure output directories exist before task
#
@follows(mkdir(gene_data_dir, simulation_data_dir))
def setup_simulation_data ():
    """
    create simulation files
    """
    for i in range(CNT_GENE_GWAS_FILES):
        open(os.path.join(gene_data_dir, "%03d.gene" % i), "w")
        open(os.path.join(gene_data_dir, "%03d.gwas" % i), "w")
    #
    # gene files without corresponding gwas and vice versa
    open(os.path.join(gene_data_dir, "orphan1.gene"), "w")
    open(os.path.join(gene_data_dir, "orphan2.gwas"), "w")
    open(os.path.join(gene_data_dir, "orphan3.gwas"), "w")
    #
    for i in range(CNT_SIMULATION_FILES):
        open(os.path.join(simulation_data_dir, "%03d.simulation" % i), "w")




#_____________________________________________________________________________________
#
#   cleanup_simulation_data
#
#_____________________________________________________________________________________
def try_rmdir (d):
    if os.path.exists(d):
        try:
            os.rmdir(d)
        except OSError:
            sys.stderr.write("Warning:\t%s is not empty and will not be removed.\n" % d)



def cleanup_simulation_data ():
    """
```

```
    cleanup files
    """
    sys.stderr.write("Cleanup working directory and simulation files.\n")
    #
    #   cleanup gene and gwas files
    #
    for f in glob.glob(os.path.join(gene_data_dir, "*.gene")):
        os.unlink(f)
    for f in glob.glob(os.path.join(gene_data_dir, "*.gwas")):
        os.unlink(f)
    try_rmdir(gene_data_dir)
    #
    #   cleanup simulation
    #
    for f in glob.glob(os.path.join(simulation_data_dir, "*.simulation")):
        os.unlink(f)
    try_rmdir(simulation_data_dir)
    #
    #   cleanup working_dir
    #
    for f in glob.glob(os.path.join(working_dir, "simulation_results", "*.simulation_res")):
        os.unlink(f)
    try_rmdir(os.path.join(working_dir, "simulation_results"))
    #
    for f in glob.glob(os.path.join(working_dir, "*.mean")):
        os.unlink(f)
    try_rmdir(working_dir)


#_____________________________________________________________________________________
#
#   Step 1:
#
#        for n_file in NNN_pairs_of_input_files:
#            for m_file in MMM_simulation_data:
#
#                [n_file.gene,
#                 n_file.gwas,
#                 m_file.simulation] -> working_dir/n_file.m_file.simulation_res
#
#_____________________________________________________________________________________
def generate_simulation_params ():
    """
    Custom function to generate
    file names for gene/gwas simulation study
    """
    simulation_files, simulation_file_roots    = get_simulation_files()
    gene_gwas_file_pairs, gene_gwas_file_roots =  get_gene_gwas_file_pairs()
    #
    for sim_file, sim_file_root in izip(simulation_files, simulation_file_roots):
        for (gene, gwas), gene_file_root in izip(gene_gwas_file_pairs, gene_gwas_file_roots):
            #
            result_file = "%s.%s.simulation_res" % (gene_file_root, sim_file_root)
            result_file_path = os.path.join(working_dir, "simulation_results", result_file)
            #
            yield [gene, gwas, sim_file], result_file_path, gene_file_root, sim_file_root, resul
```

```
#
# mkdir: makes sure output directories exist before task
#
@follows(mkdir(working_dir, os.path.join(working_dir, "simulation_results")))
@files(generate_simulation_params)
def gwas_simulation(input_files, result_file_path, gene_file_root, sim_file_root, result_file):
    """
    Dummy calculation of gene gwas vs simulation data
    Normally runs in parallel on a computational cluster
    """
    (gene_file,
    gwas_file,
    simulation_data_file) = input_files
    #
    simulation_res_file = open(result_file_path, "w")
    simulation_res_file.write("%s + %s -> %s\n" % (gene_file_root, sim_file_root, result_file))


#_____________________________________________________________________________________
#
#   Step 2:
#
#       Statistical summary per gene/gwas file pair
#
#        for n_file in NNN_pairs_of_input_files:
#            working_dir/simulation_results/n.*.simulation_res
#               -> working_dir/n.mean
#
#_____________________________________________________________________________________


@collate(gwas_simulation, regex(r"simulation_results/(\d+).\d+.simulation_res"), r"\1.mean")
@posttask(lambda : sys.stdout.write("\nOK\n"))
def statistical_summary (result_files, summary_file):
    """
    Simulate statistical summary
    """
    summary_file = open(summary_file, "w")
    for f in result_files:
        summary_file.write(open(f).read())



pipeline_run([setup_simulation_data], multiprocess = 5, verbose = 2)
pipeline_run([statistical_summary], multiprocess = 5, verbose = 2)

# uncomment to printout flowchar
#
# pipeline_printout(sys.stdout, [statistical_summary], verbose=2)
# graph_printout ("flowchart.jpg", "jpg", [statistical_summary])
#

cleanup_simulation_data ()
```

1.48.3 Resulting Output

```
>>> pipeline_run([setup_simulation_data], multiprocess = 5, verbose = 2)
    Make directories [temp_NxM/gene, temp_NxM/simulation] completed
Completed Task = setup_simulation_data_mkdir_1
    Job completed
Completed Task = setup_simulation_data


>>> pipeline_run([statistical_summary], multiprocess = 5, verbose = 2)
    Make directories [temp_NxM, temp_NxM/simulation_results] completed
Completed Task = gwas_simulation_mkdir_1
    Job = [[temp_NxM/gene/001.gene, temp_NxM/gene/001.gwas, temp_NxM/simulation/000.simulation]
    Job = [[temp_NxM/gene/000.gene, temp_NxM/gene/000.gwas, temp_NxM/simulation/000.simulation]
    Job = [[temp_NxM/gene/001.gene, temp_NxM/gene/001.gwas, temp_NxM/simulation/001.simulation]
    Job = [[temp_NxM/gene/000.gene, temp_NxM/gene/000.gwas, temp_NxM/simulation/001.simulation]
    Job = [[temp_NxM/gene/000.gene, temp_NxM/gene/000.gwas, temp_NxM/simulation/002.simulation]
    Job = [[temp_NxM/gene/001.gene, temp_NxM/gene/001.gwas, temp_NxM/simulation/002.simulation]
Completed Task = gwas_simulation
    Job = [[temp_NxM/simulation_results/000.000.simulation_res, temp_NxM/simulation_results/000.
    Job = [[temp_NxM/simulation_results/001.000.simulation_res, temp_NxM/simulation_results/001.
```

1.49 Appendix 1: Python code for Flow Chart Colours with *pipeline_printout_graph(...)*

See also:

- *Manual Table of Contents*
- *pipeline_printout_graph(...)*
- `Download code`
- Back to *Flowchart colours*

This example shows how flowchart colours can be customised.

1.49.1 Code

```
#!/usr/bin/env python
"""

    play_with_colours.py
    [--log_file PATH]
    [--verbose]

"""

################################################################################
#
#   play_with_colours.py
#
#
#   Copyright (c) 7/13/2010 Leo Goodstadt
#
```

```
#   Permission is hereby granted, free of charge, to any person obtaining a copy
#   of this software and associated documentation files (the "Software"), to deal
#   in the Software without restriction, including without limitation the rights
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#   LIABILITY, WHETHER IN AN ACTION OF CONTRACT, TORT OR OTHERWISE, ARISING FROM,
#   OUT OF OR IN CONNECTION WITH THE SOFTWARE OR THE USE OR OTHER DEALINGS IN
#   THE SOFTWARE.
################################################################################

import sys, os


#8888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888

#   options


#8888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888


from optparse import OptionParser
import StringIO

parser = OptionParser(version="%play_with_colours 1.0",
                      usage = "\n\n    play_with_colours "
                              "--flowchart FILE [options] "
                              "[--colour_scheme_index INT ] "
                              "[--key_legend_in_graph]")

#
#   pipeline
#
parser.add_option("--flowchart", dest="flowchart",
                  metavar="FILE",
                  type="string",
                  help="Don't actually run any commands; just print the pipeline "
                       "as a flowchart.")
parser.add_option("--colour_scheme_index", dest="colour_scheme_index",
                  metavar="INTEGER",
                  type="int",
                  help="Index of colour scheme for flow chart.")
parser.add_option("--key_legend_in_graph", dest="key_legend_in_graph",
                  action="store_true", default=False,
                  help="Print out legend and key for dependency graph.")

(options, remaining_args) = parser.parse_args()
if not options.flowchart:
    raise Exception("Missing mandatory parameter: --flowchart.\n")
```

```
#88888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888

#   imports

#88888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888

from ruffus import *
from ruffus.ruffus_exceptions import JobSignalledBreak

#88888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888

#   Pipeline

#88888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888


#
# up to date tasks
#
@check_if_uptodate (lambda : (False, ""))
def Up_to_date_task1(infile, outfile):
    pass

@check_if_uptodate (lambda : (False, ""))
@follows(Up_to_date_task1)
def Up_to_date_task2(infile, outfile):
    pass

@check_if_uptodate (lambda : (False, ""))
@follows(Up_to_date_task2)
def Up_to_date_task3(infile, outfile):
    pass


@check_if_uptodate (lambda : (False, ""))
@follows(Up_to_date_task3)
def Up_to_date_final_target(infile, outfile):
    pass


#
# Explicitly specified
#
@check_if_uptodate (lambda : (False, ""))
@follows(Up_to_date_task1)
def Explicitly_specified_task(infile, outfile):
    pass



#
# Tasks to run
```

```
#
@follows(Explicitly_specified_task)
def Task_to_run1(infile, outfile):
    pass


@follows(Task_to_run1)
def Task_to_run2(infile, outfile):
    pass

@follows(Task_to_run2)
def Task_to_run3(infile, outfile):
    pass

@check_if_uptodate (lambda : (False, ""))
@follows(Task_to_run2)
def Up_to_date_task_forced_to_rerun(infile, outfile):
    pass


#
# Final target
#
@follows(Up_to_date_task_forced_to_rerun, Task_to_run3)
def Final_target(infile, outfile):
    pass

#
# Ignored downstream
#
@follows(Final_target)
def Downstream_task1_ignored(infile, outfile):
    pass

@follows(Final_target)
def Downstream_task2_ignored(infile, outfile):
    pass









#8888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888

#   Main logic


#8888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888
from collections import defaultdict
custom_flow_chart_colour_scheme = defaultdict(dict)

#
```

```
    #   Base chart on this overall colour scheme index
    #
    custom_flow_chart_colour_scheme["colour_scheme_index"] = options.colour_scheme_index

    #
    #   Overriding colours
    #
    if options.colour_scheme_index is None:
        custom_flow_chart_colour_scheme["Vicious cycle"]["linecolor"]                   = '"#FF
        custom_flow_chart_colour_scheme["Pipeline"]["fontcolor"]                        = '"#FF
        custom_flow_chart_colour_scheme["Key"]["fontcolor"]                             = "blac
        custom_flow_chart_colour_scheme["Key"]["fillcolor"]                             = '"#F6
        custom_flow_chart_colour_scheme["Task to run"]["linecolor"]                     = '"#00
        custom_flow_chart_colour_scheme["Up-to-date"]["linecolor"]                      = "gray
        custom_flow_chart_colour_scheme["Final target"]["fillcolor"]                    = '"#EF
        custom_flow_chart_colour_scheme["Final target"]["fontcolor"]                    = "blac
        custom_flow_chart_colour_scheme["Final target"]["color"]                        = "blac
        custom_flow_chart_colour_scheme["Final target"]["dashed"]                       = 0
        custom_flow_chart_colour_scheme["Vicious cycle"]["fillcolor"]                   = '"#FF
        custom_flow_chart_colour_scheme["Vicious cycle"]["fontcolor"]                   = 'whit
        custom_flow_chart_colour_scheme["Vicious cycle"]["color"]                       = "whit
        custom_flow_chart_colour_scheme["Vicious cycle"]["dashed"]                      = 0
        custom_flow_chart_colour_scheme["Up-to-date task"]["fillcolor"]                 = '"#B8
        custom_flow_chart_colour_scheme["Up-to-date task"]["fontcolor"]                 = '"#00
        custom_flow_chart_colour_scheme["Up-to-date task"]["color"]                     = '"#00
        custom_flow_chart_colour_scheme["Up-to-date task"]["dashed"]                    = 0
        custom_flow_chart_colour_scheme["Down stream"]["fillcolor"]                     = "whit
        custom_flow_chart_colour_scheme["Down stream"]["fontcolor"]                     = "gray
        custom_flow_chart_colour_scheme["Down stream"]["color"]                         = "gray
        custom_flow_chart_colour_scheme["Down stream"]["dashed"]                        = 0
        custom_flow_chart_colour_scheme["Explicitly specified task"]["fillcolor"]       = "tran
        custom_flow_chart_colour_scheme["Explicitly specified task"]["fontcolor"]       = "blac
        custom_flow_chart_colour_scheme["Explicitly specified task"]["color"]           = "blac
        custom_flow_chart_colour_scheme["Explicitly specified task"]["dashed"]          = 0
        custom_flow_chart_colour_scheme["Task to run"]["fillcolor"]                     = '"#EE
        custom_flow_chart_colour_scheme["Task to run"]["fontcolor"]                     = '"#00
        custom_flow_chart_colour_scheme["Task to run"]["color"]                         = '"#00
        custom_flow_chart_colour_scheme["Task to run"]["dashed"]                        = 0
        custom_flow_chart_colour_scheme["Up-to-date task forced to rerun"]["fillcolor"] = 'tran
        custom_flow_chart_colour_scheme["Up-to-date task forced to rerun"]["fontcolor"] = '"#00
        custom_flow_chart_colour_scheme["Up-to-date task forced to rerun"]["color"]     = '"#00
        custom_flow_chart_colour_scheme["Up-to-date task forced to rerun"]["dashed"]    = 1
        custom_flow_chart_colour_scheme["Up-to-date Final target"]["fillcolor"]         = '"#EF
        custom_flow_chart_colour_scheme["Up-to-date Final target"]["fontcolor"]         = '"#00
        custom_flow_chart_colour_scheme["Up-to-date Final target"]["color"]             = '"#00
        custom_flow_chart_colour_scheme["Up-to-date Final target"]["dashed"]            = 0

    if __name__ == '__main__':
        pipeline_printout_graph (

                                        open(options.flowchart, "w"),
                                        # use flowchart file name extension to decide flowchart form
                                        #   e.g. svg, jpg etc.
                                        os.path.splitext(options.flowchart)[1][1:],

                                        # final targets
                                        [Final_target, Up_to_date_final_target],
```

```
                                    # Explicitly specified tasks
                                    [Explicitly_specified_task],

                                    # Do we want key legend
                                    no_key_legend   = not options.key_legend_in_graph,

                                    # Print all the task types whether used or not
                                    minimal_key_legend              = False,

                                    user_colour_scheme = custom_flow_chart_colour_scheme,
                                    pipeline_name = "Colour schemes")
```

CHAPTER

TWO

OVERVIEW:

2.1 Cheat Sheet

The `ruffus` module is a lightweight way to add support for running computational pipelines.

Each stage or **task** in a computational pipeline is represented by a python function
Each python function can be called in parallel to run multiple **jobs**.

2.1.1 1. Annotate functions with Ruffus decorators

Core

Decorator	Syntax	
@originate (*Manual*)	*@originate* (output_files, [extra_parameters,...])	
@split (*Manual*)	*@split* (tasks_or_file_names, output_files, [extra_parameters,...])	
@transform (*Manual*)	*@transform* (tasks_or_file_names, *suffix*(suffix_string), output_pattern, [extra_parameters,...]) *@transform* (tasks_or_file_names, *regex*(regex_pattern), output_pattern, [extra_parameters,...])	
@merge (*Manual*)	*@merge* (tasks_or_file_names, output, [extra_parameters,...])	
@posttask (*Manual*)	*@posttask* (signal_task_completion_function) *@posttask* (*touch_file*('task1.completed'))	

See *Decorators* for a complete list of decorators

2.1.2 2. Print dependency graph if necessary

- For a graphical flowchart in `jpg`, `svg`, `dot`, `png`, `ps`, `gif` formats:

```
pipeline_printout_graph ( "flowchart.svg")
```

- For a text printout of all jobs

```
pipeline_printout()
```

2.1.3 3. Run the pipeline

```
pipeline_run(multiprocess = N_PARALLEL_JOBS)
```

See *Decorators* for more decorators

2.2 Pipeline functions

There are only four functions for **Ruffus** pipelines:

- *pipeline_run* executes a pipeline
- *pipeline_printout* prints a list of tasks and jobs which will be run in a pipeline
- *pipeline_printout_graph* prints a schematic flowchart of pipeline tasks in various graphical formats
- *pipeline_get_task_names* returns a list of all task names in the pipeline

2.2.1 *pipeline_run*

pipeline_run (*target_tasks* = [], *forcedtorun_tasks* = [], *multiprocess* = 1, *logger* = stderr_logger, *gnu_make_maximal_rebuild_mode* = True, *verbose* =1, *runtime_data* = None, *one_second_per_job* = True, *touch_files_only* = False, *exceptions_terminate_immediately* = None, *log_exceptions* = None, *history_file* = None, *checksum_level* = None, *multithread* = 0, *verbose_abbreviated_path* = None)

Purpose:

Runs all specified pipelined functions if they or any antecedent tasks are incomplete or out-of-date.

Example:

```
#
#   Run task2 whatever its state, and also task1 and antecedents if they are incomplete
#   Do not log pipeline progress messages to stderr
#
pipeline_run([task1, task2], forcedtorun_tasks = [task2], logger = blackhole_logger)
```

Parameters:

- ***target_tasks*** Pipeline functions and any necessary antecedents (specified implicitly or with *@follows*) which should be invoked with the appropriate parameters if they are incomplete or out-of-date.
- ***forcedtorun_tasks*** Optional. These pipeline functions will be invoked regardless of their state. Any antecedents tasks will also be executed if they are out-of-date or incomplete.
- ***multiprocess*** Optional. The number of processes which should be dedicated to running in parallel independent tasks and jobs within each task. If `multiprocess` is set to 1, the pipeline will execute in the main process.
- ***multithread*** Optional. The number of threads which should be dedicated to running in parallel independent tasks and jobs within each task. Should be used only with drmaa. Otherwise the CPython global interpreter lock (GIL) will slow down your pipeline
- ***logger*** For logging messages indicating the progress of the pipeline in terms of tasks and jobs. Defaults to outputting to sys.stderr. Setting `logger=blackhole_logger` will prevent any logging output.
- ***gnu_make_maximal_rebuild_mode***

  Warning: This is a dangerous option. Use rarely and with caution

  Optional parameter governing how **Ruffus** determines which part of the pipeline is out of date and needs to be re-run. If set to `False`, **ruffus** will work back from the `target_tasks` and only execute the pipeline after the first up-to-date tasks that it encounters. For example, if there are four tasks:

```
#
#   task1 -> task2 -> task3 -> task4 -> task5
#
target_tasks = [task5]
```

If `task3()` is up-to-date, then only `task4()` and `task5()` will be run. This will be the case even if `task2()` and `task1()` are incomplete.

This allows you to remove all intermediate results produced by `task1 -> task3`.

- ***verbose*** Optional parameter indicating the verbosity of the messages sent to `logger`: (Defaults to level 1 if unspecified)
  - level **0** : *nothing*
  - level **1** : *Out-of-date Task names*
  - level **2** : *All Tasks (including any task function docstrings)*
  - level **3** : *Out-of-date Jobs in Out-of-date Tasks, no explanation*
  - level **4** : *Out-of-date Jobs in Out-of-date Tasks, with explanations and warnings*
  - level **5** : *All Jobs in Out-of-date Tasks, (include only list of up-to-date tasks)*
  - level **6** : *All jobs in All Tasks whether out of date or not*
  - level **10**: *logs messages useful only for debugging ruffus pipeline code*

  `verbose >= 10` are intended for debugging **Ruffus** by the developers and the details are liable to change from release to release
- ***runtime_data*** Experimental feature for passing data to tasks at run time
- ***one_second_per_job*** To work around poor file timepstamp resolution for some file systems. Defaults to True if checksum_level is 0 forcing Tasks to take a minimum of 1 second to complete. If your file system has coarse grained time stamps, you can turn on this delay by setting *one_second_per_job* to `True`
- ***touch_files_only*** Create or update output files only to simulate the running of the pipeline. Does not invoke real task functions to run jobs. This is most useful to force a pipeline to acknowledge that a particular part is now up-to-date.

  This will not work properly if the identities of some files are not known before hand, and depend on run time. In other words, not recommended if `@split` or custom parameter generators are being used.
- ***exceptions_terminate_immediately*** Exceptions cause immediate termination of the pipeline.
- ***log_exceptions*** Print exceptions to the logger as soon as they occur.
- ***history_file*** The database file which stores checksums and file timestamps for input/output files. Defaults to `.ruffus_history.sqlite` if unspecified
- ***checksum_level*** Several options for checking up-to-dateness are available: Default is level 1.
  - level 0 : Use only file timestamps
  - level 1 : above, plus timestamp of successful job completion
  - level 2 : above, plus a checksum of the pipeline function body
  - level 3 : above, plus a checksum of the pipeline function default arguments and the additional arguments passed in by task decorators
- ***verbose_abbreviated_path*** Whether input and output paths are abbreviated. Defaults to 2 if unspecified
  - level 0: The full (expanded, abspath) input or output path

- level > 1: The number of subdirectories to include. Abbreviated paths are prefixed with `[,,,]/`
- level < 0: Input / Output parameters are truncated to `MMM` letters where `verbose_abbreviated_path ==-MMM`. Subdirectories are first removed to see if this allows the paths to fit in the specified limit. Otherwise abbreviated paths are prefixed by `<???>`

2.2.2 *pipeline_printout*

pipeline_printout (*output_stream* = sys.stdout, *target_tasks* = [], *forcedtorun_tasks* = [], *verbose* = 1, *indent* = 4, *gnu_make_maximal_rebuild_mode* = True, *wrap_width* = 100, *runtime_data* = None, *checksum_level* = None, *history_file* = None, *verbose_abbreviated_path* = None)

Purpose:

Prints out all the pipelined functions which will be invoked given specified `target_tasks` without actually running the pipeline. Because this is a simulation, some of the job parameters may be incorrect. For example, the results of a *@split* operation is not predetermined and will only be known after the pipelined function splits up the original data. Parameters of all downstream pipelined functions will be changed depending on this initial operation.

Example:

```
#
#   Simulate running task2 whatever its state, and also task1 and antecedents
#     if they are incomplete
#   Print out results to STDOUT
#
pipeline_printout(sys.stdout, [task1, task2], forcedtorun_tasks = [task2], verbose = 1)
```

Parameters:

- ***output_stream*** Where to printout the results of simulating the running of the pipeline.
- ***target_tasks*** As in *pipeline_run*: Pipeline functions and any necessary antecedents (specified implicitly or with *@follows*) which should be invoked with the appropriate parameters if they are incomplete or out-of-date.
- ***forcedtorun_tasks*** As in *pipeline_run*:These pipeline functions will be invoked regardless of their state. Any antecedents tasks will also be executed if they are out-of-date or incomplete.
- ***verbose*** Optional parameter indicating the verbosity of the messages sent to `logger`: (Defaults to level 4 if unspecified)
  - level **0** : *nothing*
  - level **1** : *Out-of-date Task names*
  - level **2** : *All Tasks (including any task function docstrings)*
  - level **3** : *Out-of-date Jobs in Out-of-date Tasks, no explanation*
  - level **4** : *Out-of-date Jobs in Out-of-date Tasks, with explanations and warnings*
  - level **5** : *All Jobs in Out-of-date Tasks, (include only list of up-to-date tasks)*
  - level **6** : *All jobs in All Tasks whether out of date or not*
  - level **10**: *logs messages useful only for debugging ruffus pipeline code*

  `verbose >= 10` are intended for debugging **Ruffus** by the developers and the details are liable to change from release to release
- ***indent*** Optional parameter governing the indentation when printing out the component job parameters of each task function.

- ***gnu_make_maximal_rebuild_mode***

  Warning: This is a dangerous option. Use rarely and with caution

  See explanation in *pipeline_run*.

- ***wrap_width*** Optional parameter governing the length of each line before it starts wrapping around.
- ***runtime_data*** Experimental feature for passing data to tasks at run time
- ***history_file*** The database file which stores checksums and file timestamps for input/output files. Defaults to `.ruffus_history.sqlite` if unspecified
- ***checksum_level*** Several options for checking up-to-dateness are available: Default is level 1.
  - level 0 : Use only file timestamps
  - level 1 : above, plus timestamp of successful job completion
  - level 2 : above, plus a checksum of the pipeline function body
  - level 3 : above, plus a checksum of the pipeline function default arguments and the additional arguments passed in by task decorators
- ***verbose_abbreviated_path*** Whether input and output paths are abbreviated. Defaults to 2 if unspecified
  - level 0: The full (expanded, abspath) input or output path
  - level > 1: The number of subdirectories to include. Abbreviated paths are prefixed with `[,,,]/`
  - level < 0: Input / Output parameters are truncated to `MMM` letters where `verbose_abbreviated_path ==-MMM`. Subdirectories are first removed to see if this allows the paths to fit in the specified limit. Otherwise abbreviated paths are prefixed by `<???>`

2.2.3 *pipeline_printout_graph*

pipeline_printout_graph (*stream*, *output_format* = None, *target_tasks* = [], *forcedtorun_tasks* = [], *ignore_upstream_of_target* = False, *skip_uptodate_tasks* = False, *gnu_make_maximal_rebuild_mode* = True, *test_all_task_for_update* = True, *no_key_legend* = False, *minimal_key_legend* = True, *user_colour_scheme* = None, *pipeline_name* = "Pipeline", *size* = (11,8), *dpi* = 120, *runtime_data* = None, *checksum_level* = None, *history_file* = None)

Purpose:

Prints out flowchart of all the pipelined functions which will be invoked given specified `target_tasks` without actually running the pipeline.

See *Flowchart colours*

Example:

```
pipeline_printout_graph("flowchart.jpg", "jpg", [task1, task16],
                            forcedtorun_tasks = [task2],
                            no_key_legend = True)
```

Customising appearance:

The *user_colour_scheme* parameter can be used to change flowchart colours. This allows the default *Colour Schemes* to be set. An example of customising flowchart appearance is available *(see code)* .

Parameters:

- ***stream*** The file or file-like object to which the flowchart should be printed. If a string is provided, it is assumed that this is the name of the output file which will be opened automatically.

- ***output_format*** If missing, defaults to the extension of the *stream* file name (i.e. `jpg` for `a.jpg`)

  If the programme `dot` can be found on the executio path, this can be any number of formats supported by Graphviz, including, for example, `jpg`, `png`, `pdf`, `svg` etc.
  Otherwise, **ruffus** will only output without error in the dot format, which is a plain-text graph description language.

- ***target_tasks*** As in *pipeline_run*: Pipeline functions and any necessary antecedents (specified implicitly or with *@follows*) which should be invoked with the appropriate parameters if they are incomplete or out-of-date.
- ***forcedtorun_tasks*** As in *pipeline_run*:These pipeline functions will be invoked regardless of their state. Any antecedents tasks will also be executed if they are out-of-date or incomplete.
- ***draw_vertically*** Draw flowchart in vertical orientation
- ***ignore_upstream_of_target*** Start drawing flowchart from specified target tasks. Do not draw tasks which are downstream (subsequent) to the targets.
- ***ignore_upstream_of_target*** Do not draw up-to-date / completed tasks in the flowchart unless they are lie on the execution path of the pipeline.
- ***gnu_make_maximal_rebuild_mode***

  Warning: This is a dangerous option. Use rarely and with caution

  See explanation in *pipeline_run*.
- ***test_all_task_for_update***

  Indicates whether intermediate tasks are out of date or not. Normally **Ruffus** will stop checking dependent tasks for completion or whether they are out-of-date once it has discovered the maximal extent of the pipeline which has to be run.
  For displaying the flow of the pipeline, this is hardly very informative.
- ***no_key_legend*** Do not include key legend explaining the colour scheme of the flowchart.
- ***minimal_key_legend*** Do not include unused task types in key legend.
- ***user_colour_scheme*** Dictionary specifying colour scheme for flowchart

  See complete *list of Colour Schemes*.

  Colours can be names e.g. `"black"` or quoted hex e.g. `'"#F6F4F4"'` (note extra quotes)
  Default values will be used unless specified

key	Subkey	
– 'colour_scheme_index'	index of default colour scheme, 0-7, defaults to 0 unless specified	
– 'Final target' – 'Explicitly specified task' – 'Task to run' – 'Down stream' – 'Up-to-date Final target' – 'Up-to-date task forced to rerun' – 'Up-to-date task' – 'Vicious cycle'	– 'fillcolor' – 'fontcolor' – 'color' – 'dashed' = 0/1	Colours / attributes for each task type
– 'Vicious cycle' – 'Task to run' – 'Up-to-date'	– 'linecolor'	Colours for arrows between tasks
– 'Pipeline'	– 'fontcolor'	Flowchart title colour
– 'Key'	– 'fontcolor' – 'fillcolor'	Legend colours

Example:

Use colour scheme index = 1

```
pipeline_printout_graph ("flowchart.svg", "svg", [final_task],
                         user_colour_scheme = {
                                                "colour_scheme_index" :1,
                                                "Pipeline"      :{"fontcolor" : '"#FF323
                                                "Key"           :{"fontcolor" : "Red",
                                                                  "fillcolor" : '"#F6F4F
                                                "Task to run"   :{"linecolor" : '"#0044A
                                                "Final target"  :{"fillcolor" : '"#EFA03
                                                                  "fontcolor" : "black",
                                                                  "dashed"    : 0
                                               })
```

- ***pipeline_name*** Specify title for flowchart
- ***size*** Size in inches for flowchart
- ***dpi*** Resolution in dots per inch. Ignored for svg output
- ***runtime_data*** Experimental feature for passing data to tasks at run time
- ***history_file*** The database file which stores checksums and file timestamps for input/output files. Defaults to `.ruffus_history.sqlite` if unspecified
- ***checksum_level*** Several options for checking up-to-dateness are available: Default is level 1.

- level 0 : Use only file timestamps
- level 1 : above, plus timestamp of successful job completion
- level 2 : above, plus a checksum of the pipeline function body
- level 3 : above, plus a checksum of the pipeline function default arguments and the additional arguments passed in by task decorators

2.2.4 *pipeline_get_task_names*

pipeline_get_task_names ()

Purpose:

Returns a list of all task names in the pipeline without running the pipeline or checking to see if the tasks are connected correctly

Example:

Given:

```
from ruffus import *

@originate([])
def create_data(output_files):
    pass

@transform(create_data, suffix(".txt"), ".task1")
def task1(input_files, output_files):
    pass

@transform(task1, suffix(".task1"), ".task2")
def task2(input_files, output_files):
    pass
```

Produces a list of three task names:

```
>>> pipeline_get_task_names ()
['create_data', 'task1', 'task2']
```

2.3 drmaa functions

`drmaa_wrapper` is not exported automatically by ruffus and must be specified explicitly:

```
# imported ruffus.drmaa_wrapper explicitly
from ruffus.drmaa_wrapper import run_job, error_drmaa_job
```

2.3.1 *run_job*

run_job (*cmd_str*, *job_name* = None, *job_other_options* = None, *job_script_directory* = None, *job_environment* = None, *working_directory* = None, *logger* = None, *drmaa_session* = None, *retain_job_scripts* = False, *run_locally* = False, *output_files* = None, *touch_only* = False)

Purpose:

ruffus.drmaa_wrapper.run_job dispatches a command with arguments to a cluster or Grid Engine node and waits for the command to complete.

It is the semantic equivalent of calling os.system or subprocess.check_output.

Example:

```
from ruffus.drmaa_wrapper import run_job, error_drmaa_job
import drmaa
my_drmaa_session = drmaa.Session()
my_drmaa_session.initialize()

run_job("ls",
        job_name = "test",
        job_other_options="-P mott-flint.prja -q short.qa",
        job_script_directory = "test_dir",
        job_environment={ 'BASH_ENV' : '~/.bashrc' },
        retain_job_scripts = True, drmaa_session=my_drmaa_session)
run_job("ls",
        job_name = "test",
        job_other_options="-P mott-flint.prja -q short.qa",
        job_script_directory = "test_dir",
        job_environment={ 'BASH_ENV' : '~/.bashrc' },
        retain_job_scripts = True,
        drmaa_session=my_drmaa_session,
        working_directory = "/gpfs1/well/mott-flint/lg/src/oss/ruffus/doc")

#
#   catch exceptions
#
try:
    stdout_res, stderr_res  = run_job(cmd,
                                      job_name          = job_name,
                                      logger            = logger,
                                      drmaa_session     = drmaa_session,
                                      run_locally       = options.local_run,
                                      job_other_options = get_queue_name())

# relay all the stdout, stderr, drmaa output to diagnose failures
except error_drmaa_job as err:
    raise Exception("\n".join(map(str,
                          ["Failed to run:",
                           cmd,
                           err,
                           stdout_res,
                           stderr_res])))

my_drmaa_session.exit()
```

Parameters:

- *cmd_str*

  The command which will be run remotely including all parameters

- *job_name*

  A descriptive name for the command. This will be displayed by SGE qstat, for example. Defaults to "ruffus_job"

- *job_other_options*

Other drmaa parameters can be passed verbatim as a string.

Examples for SGE include project name (`-P project_name`), parallel environment (`-pe parallel_environ`), account (`-A account_string`), resource (`-l resource=expression`), queue name (`-q a_queue_name`), queue priority (`-p 15`).

These are parameters which you normally need to include when submitting jobs interactively, for example via SGE qsub or SLURM (srun)

- *job_script_directory*

  The directory where drmaa temporary script files will be found. Defaults to the current working directory.

- *job_environment*

  A dictionary of key / values with environment variables. E.g. `"{'BASH_ENV': '~/.bashrc'}"`

- *working_directory*
  - Sets the working directory.
  - Should be a fully qualified path.
  - Defaults to the current working directory.

- *retain_job_scripts*

  Do not delete temporary script files containg drmaa commands. Useful for debugging, running on the command line directly, and can provide a useful record of the commands.

- *logger*

  For logging messages indicating the progress of the pipeline in terms of tasks and jobs. Takes objects with the standard python logging module interface.

- *drmaa_session*

  A shared drmaa session created and managed separately.

  In the main part of your **Ruffus** pipeline script somewhere there should be code looking like this:

  ```
  #
  #   start shared drmaa session for all jobs / tasks in pipeline
  #
  import drmaa
  drmaa_session = drmaa.Session()
  drmaa_session.initialize()


  #
  #   pipeline functions
  #

  if __name__ == '__main__':
      cmdline.run (options, multithread = options.jobs)
      drmaa_session.exit()
  ```

- *run_locally*

  Runs commands locally using the standard python subprocess module rather than dispatching remotely. This allows scripts to be debugged easily

- *touch_only*

Create or update *Output files* only to simulate the running of the pipeline. Does not dispatch commands remotely or locally. This is most useful to force a pipeline to acknowledge that a particular part is now up-to-date.

See also: *pipeline_run(touch_files_only=True)*

- *output_files*

  Output files which will be created or updated if *touch_only* =`True`

2.4 Installation

`Ruffus` is a lightweight python module for building computational pipelines.

Note: Ruffus requires Python 2.6 or higher or Python 3.0 or higher

2.4.1 The easy way

Ruffus is available as an easy-install -able package on the Python Package Index.

```
sudo pip install ruffus --upgrade
```

This may also work for older installations:

```
easy_install -U ruffus
```

See below if `eady_install` is missing

2.4.2 The most up-to-date code:

- Download the latest sources or
- Check out the latest code from Google using git:

```
git clone https://bunbun68@code.google.com/p/ruffus/ .
```

- Bleeding edge Ruffus development takes place on github:

```
git clone git@github.com:bunbun/ruffus.git .
```

- To install after downloading, change to the , type:

```
python ./setup.py install
```

2.4.3 Prequisites

2.4.4 Installing easy_install

If your system doesn't have `easy_install`, you can install one using a package manager, for example:

```
# ubuntu/linux mint
$ sudo apt-get install python-setuptools
$ or  sudo yum install python-setuptools
```

or manually:

```
sudo curl http://peak.telecommunity.com/dist/ez_setup.py | python
```

or manually:

```
wget peak.telecommunity.com/dist/ez_setup.py
sudo python ez_setup.py
```

2.4.5 Installing pip

If Pip is missing:

```
$ sudo easy_install -U pip
```

2.4.6 Graphical flowcharts The most up-to-date code:

Ruffus relies on the `dot` programme from Graphviz ("Graph visualisation") to make pretty flowchart representations of your pipelines in multiple graphical formats (e.g. `png`, `jpg`). The crossplatform Graphviz package can be downloaded here for Windows,

Linux, Macs and Solaris. For Fedora, try

```
yum list 'graphviz*'
```

For ubuntu / Debian, try

```
sudo apt-get install graphviz
```

2.5 Design & Architecture

The *ruffus* module has the following design goals:

- Simplicity.
- Intuitive
- Lightweight
- Unintrusive
- Flexible/Powerful

Computational pipelines, especially in science, are best thought of in terms of data flowing through successive, dependent stages (**ruffus** calls these *task*s). Traditionally, files have been used to link pipelined stages together. This means that computational pipelines can be managed using traditional software construction (*build*) systems.

2.5.1 *GNU Make*

The grand-daddy of these is UNIX make. GNU make is ubiquitous in the linux world for installing and compiling software. It has been widely used to build computational pipelines because it supports:

- Stopping and restarting computational processes
- Running multiple, even thousands of jobs in parallel

Deficiencies of *make* / *gmake*

However, make and GNU make use a specialised (domain-specific) language, which has is been much criticised because of poor support for modern programming languages features, such as variable scope, pattern matching, debugging. Make scripts require large amounts of often obscure shell scripting and makefiles can quickly become unmaintainable.

2.5.2 *Scons*, *Rake* and other *Make* alternatives

Many attempts have been made to produce a more modern version of make, with less of its historical baggage. These include the Java-based Apache ant which is specified in xml.

More interesting are a new breed of build systems whose scripts are written in modern programming languages, rather than a specially-invented "build" specificiation syntax. These include the Python scons, Ruby rake and its python port Smithy.

The great advantages are that computation pipelines do not need to be artificially parcelled out between (the often second-class) workflow management code, and the logic which does the real computation in the pipeline. It also means that workflow management can use all the standard language and library features, for example, to read in directories, match file names using regular expressions and so on.

Ruffus is much like scons in that the modern dynamic programming language python is used seamlessly throughout its pipeline scripts.

Implicit dependencies: disadvantages of *make* / *scons* / *rake*

Although Python scons and Ruby rake are in many ways more powerful and easier to use for building software, they are still an imperfect fit to the world of computational pipelines.

This is a result of the way dependencies are specified, an essential part of their design inherited from GNU make.

The order of operations in all of these tools is specified in a *declarative* rather than *imperative* manner. This means that the sequence of steps that a build should take are not spelled out explicity and directly. Instead recipes are provided for turning input files of each type to another.

So, for example, knowing that `a->b`, `b->c`, `c->d`, the build system can infer how to get from `a` to `d` by performing the necessary operations in the correct order.

This is immensely powerful for three reasons:

1. The plumbing, such as dependency checking, passing output from one stage to another, are handled automatically by the build system. (This is the whole point!)
2. The same *recipe* can be re-used at different points in the build.
3. Intermediate files do not need to be retained.

   Given the automatic inference that `a->b->c->d`, we don't need to keep `b` and `c` files around once `d` has been produced.

The disadvantage is that because stages are specified only indirectly, in terms of file name matches, the flow through a complex build or a pipeline can be difficult to trace, and nigh impossible to debug when there are problems.

Explicit dependencies in *Ruffus*

Ruffus takes a different approach. The order of operations is specified explicitly rather than inferred indirectly from the input and output types. So, for example, we would explicitly specify three successive and linked operations `a->b`, `b->c`, `c->d`. The build system knows that the operations always proceed in this order.

Looking at a **Ruffus** script, it is always clear immediately what is the succession of computational steps which will be taken.

Ruffus values clarity over syntactic cleverness.

Static dependencies: What *make* / *scons* / *rake* can't do (easily)

GNU make, scons and rake work by infer a static dependency (diacyclic) graph between all the files which are used by a computational pipeline. These tools locate the target that they are supposed to build and work backward through the dependency graph from that target, rebuilding anything that is out of date.This is perfect for building software, where the list of files data files can be computed **statically** at the beginning of the build.

This is not ideal matches for scientific computational pipelines because:

- Though the *stages* of a pipeline (i.e. *compile* or *DNA alignment*) are invariably well-specified in advance, the number of operations (*job*s) involved at each stage may not be.

- A common approach is to break up large data sets into manageable chunks which can be operated on in parallel in computational clusters or farms (See embarassingly parallel problems).

  This means that the number of parallel operations or jobs varies with the data (the number of manageable chunks), and dependency trees cannot be calculated statically beforehand.

Computational pipelines require **dynamic** dependencies which are not calculated up-front, but at each stage of the pipeline

This is a *known* issue with traditional build systems each of which has partial strategies to work around this problem:

- gmake always builds the dependencies when first invoked, so dynamic dependencies require (complex!) recursive calls to gmake
- Rake dependencies unknown prior to running tasks.
- Scons: Using a Source Generator to Add Targets Dynamically

Ruffus explicitly and straightforwardly handles tasks which produce an indeterminate (i.e. runtime dependent) number of output, using its **@split**, **@transform**, **merge** function annotations.

2.5.3 Managing pipelines stage-by-stage using Ruffus

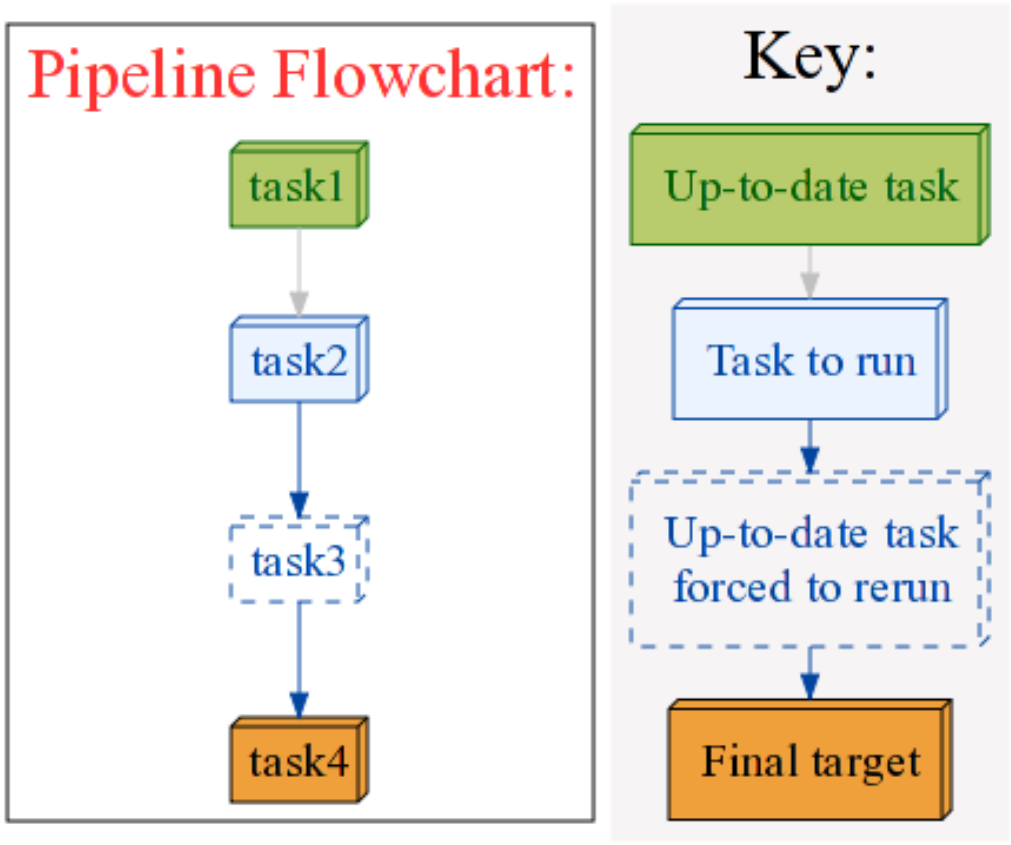
Ruffus manages pipeline stages directly.

1. The computational operations for each stage of the pipeline are written by you, in separate python functions.

   (These correspond to gmake pattern rules)

2. The dependencies between pipeline stages (python functions) are specified up-front.

These can be displayed as a flow chart.



3. **Ruffus** makes sure pipeline stage functions are called in the right order, with the right parameters, running in parallel using multiprocessing if necessary.
4. Data file timestamps can be used to automatically determine if all or any parts of the pipeline are out-of-date and need to be rerun.
5. Separate pipeline stages, and operations within each pipeline stage, can be run in parallel provided they are not inter-dependent.

Another way of looking at this is that **ruffus** re-constructs datafile dependencies dynamically on-the-fly when it gets to each stage of the pipeline, giving much more flexibility.

Disadvantages of the Ruffus design

Are there any disadvantages to this trade-off for additional clarity?

1. Each pipeline stage needs to take the right input and output. For example if we specified the steps in the wrong order: `a->b`, `c->d`, `b->c`, then no useful output would be produced.
2. We cannot re-use the same recipes in different parts of the pipeline
3. Intermediate files need to be retained.

In our experience, it is always obvious when pipeline operations are in the wrong order, precisely because the order of computation is the very essense of the design of each pipeline. Ruffus produces extra diagnostics when no output is created in a pipeline stage (usually happens for incorrectly specified regular

expressions.)

Re-use of recipes is as simple as an extra call to common function code.

Finally, some users have proposed future enhancements to **Ruffus** to handle unnecessary temporary / intermediate files.

2.5.4 Alternatives to Ruffus

A comparison of more make-like tools is available from Ian Holmes' group.

Build systems include:

- GNU make
- scons
- ant
- rake

There are also complete workload managements systems such as Condor. Various bioinformatics pipelines are also available, including that used by the leading genome annotation website Ensembl, Pegasys, GPIPE, Taverna, Wildfire, MOWserv, Triana, Cyrille2 etc. These all are either hardwired to specific databases, and tasks, or have steep learning curves for both the scientist/developer and the IT system administrators.

Ruffus is designed to be lightweight and unintrusive enough to use for writing pipelines with just 10 lines of code.

See also:

Bioinformatics workload managements systems

Condor: http://www.cs.wisc.edu/condor/description.html

Ensembl Analysis pipeline: http://www.ncbi.nlm.nih.gov/pubmed/15123589

Pegasys: http://www.ncbi.nlm.nih.gov/pubmed/15096276

GPIPE: http://www.biomedcentral.com/pubmed/15096276

Taverna: http://www.ncbi.nlm.nih.gov/pubmed/15201187

Wildfire: http://www.biomedcentral.com/pubmed/15788106

MOWserv: http://www.biomedcentral.com/pubmed/16257987

Triana: http://dx.doi.org/10.1007/s10723-005-9007-3

Cyrille2: http://www.biomedcentral.com/1471-2105/9/96

Acknowledgements

- Bruce Eckel's insightful article on A Decorator Based Build System was the obvious inspiration for the use of decorators in *Ruffus*.

The rest of the *Ruffus* takes uses a different approach. In particular:

1. *Ruffus* uses task-based not file-based dependencies

2. *Ruffus* tries to have minimal impact on the functions it decorates.

   Bruce Eckel's design wraps functions in "rule" objects.

   Ruffus tasks are added as attributes of the functions which can be still be called normally. This is how *Ruffus* decorators can be layered in any order onto the same task.

- Languages like c++ and Java would probably use a "mixin" approach. Python's easy support for reflection and function references, as well as the necessity of marshalling over process boundaries, dictated the internal architecture of *Ruffus*.
- The Boost Graph library for text book implementations of directed graph traversals.
- Graphviz. Just works. Wonderful.
- Andreas Heger, Christoffer Nellåker and Grant Belgard for driving Ruffus towards ever simpler syntax.

2.6 Major Features added to Ruffus

Note: See *To do list* for future enhancements to Ruffus

2.6.1 version 2.6

12th March 2015

1) Bug fixes

- `pipeline_printout_graph()` incompatibility with python3 fixed
- checkpointing did not work correctly with *@split(...)* and *@subdivide(...)*

2) *@transform '(..., suffix("xxx"),* output_dir *= "/new/output/path")*

Thanks to the suggestion of Milan Simonovic.

@transform(..., suffix(...)) has easy to understand syntax and takes care of all the common use cases of Ruffus.

However, when we need to place the output in a different directories, we suddenly have to plunge into the deep end and parse file paths using *regex()* or *formatter()*.

Now, *@transform* takes an optional `output_dir` named parameter so that we can continue to use *suffix()* even when the output needs to go into a new directory.

```
#
#   input/a.fasta -> output/a.sam
#   input/b.fasta -> output/b.sam
#
starting_files = ["input/a.fasta","input/b.fasta"]
@transform(starting_files,
           suffix('.fasta'),
           '.sam',
           output_dir = "output")
def map_dna_sequence(input_file, output_file) :
    pass
```

See example `test\test_suffix_output_dir.py`

2) Named parameters

Decorators can take named parameters.

These are self documenting, and improve clarity.

Note that the usual Python rules for function parameters apply:

- Positional arguments must precede named arguments
- Named arguments cannot be used to fill in for "missing" positional arguments

For example the following two functions are identical:

Positional parameters:

```
@merge(prev_task, ["a.summary", "b.summary"], 14, "extra_info", {"a":45, "b":5})
def merge_task(inputs, outputs, extra_num, extra_str, extra_dict):
    pass
```

Named parameters:

```
# new style is a bit clearer
@merge(input   = prev_task,
       output  = ["a.summary", "b.summary"],
       extras  = [14, "extra_info", {"a":45, "b":5}]
       )
def merge_task(inputs, outputs, extra_num, extra_str, extra_dict):
    pass
```

Warning: `,extras=` takes all the *extras* parameters (`14, "extra_info", {"a":45, "b":5}`) as a single list

- ***@split(...)*** **and** ***@merge(...)***
  - *input*
  - *output*
  - [*extras*]
- ***@transform(...)*** **and** ***@mkdir(...)***
  - *input*
  - *filter*
  - [*replace_inputs* or *add_inputs*]
  - *output*
  - [*extras*]
  - [*output_dir*]
- ***@collate(...)*** **and** ***@subdivide(...)***
  - *input*
  - *filter*
  - *output*

  - [*extras*]
- *@originate(...)*
  - *output*
  - [*extras*]
- *@product(...)*, *@permutations(...)*, *@combinations(...)*, **and** *@combinations_with_replacement(...)*
  - *input*
  - *filter*
  - [*input2...NNN*] (only for `product`)
  - [*filter2...NNN*] (only for `product`) where NNN is an incrementing number
  - *tuple_size* (except for `product`)
  - [*replace_inputs* or *add_inputs*]
  - *output*
  - [*extras*]

3) New object orientated syntax for Ruffus

Ruffus Pipelines can now be created directly using the new `Pipeline` and `Task` objects instead of via decorators.

```
# make ruffus pipeline
my_pipeline = Pipeline(name = "test")
my_pipeline.transform(task_func  = map_dna_sequence,
                      input      = starting_files,
                      filter     = suffix('.fasta'),
                      output     = '.sam',
                      output_dir = "output")

my_pipeline.run()
```

This new syntax is fully compatible and inter-operates with traditional Ruffus syntax using decorators.

Apart from cosmetic changes, the new syntax allows different instances of modular Ruffus sub-pipelines to be defined separately, in different python modules and then joined together flexible at runtime.

The new syntax and discussion are introduced *here*.

2.6.2 version 2.5

6th August 2014

1) Python3 compatability (but at least python 2.6 is now required)

Ruffus v2.5 is now python3 compatible. This has required surprisingly many changes to the codebase. Please report any bugs to me.

Note: Ruffus now requires at least python 2.6

It proved to be impossible to support python 2.5 and python 3.x at the same time.

2) Ctrl-C interrupts

Ruffus now mostly(!) terminates gracefully when interrupted by Ctrl-C .

Please send me bug reports for when this doesn't work with a minimally reproducible case.

This means that, in general, if an `Exception` is thrown during your pipeline but you don't want to wait for the rest of the jobs to complete, you can still press Ctrl-C at any point. Note that you may still need to clean up spawned processes, for example, using `qdel` if you are using `Ruffus.drmaa_wrapper`

3) Customising flowcharts in pipeline_printout_graph() with `@graphviz`

Contributed by Sean Davis, with improved syntax via Jake Biesinger

The graphics for each task can have its own attributes (URL, shape, colour) etc. by adding graphviz attributes using the `@graphviz` decorator.

- This allows HTML formatting in the task names (using the `label` parameter as in the following example). HTML labels **must** be enclosed in < and >. E.g.

```
label = "<Line <BR/> wrapped task_name()>"
```

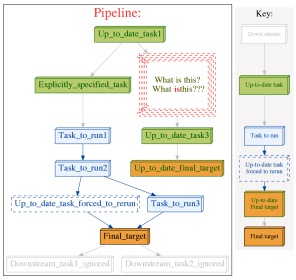
- You can also opt to keep the task name and wrap it with a prefix and suffix:

```
label_suffix = "??? ", label_prefix = ": What is this?"
```

- The `URL` attribute allows the generation of clickable svg, and also client / server side image maps usable in web pages. See Graphviz documentation

Example:

```
@graphviz(URL='"http://cnn.com"', fillcolor = '"#FFCCCC"',
                color = '"#FF0000"', pencolor='"#FF0000"', fontcolor='"#4B6000"',
                label_suffix = "???", label_prefix = "What is this?<BR/> ",
                label = "<What <FONT COLOR=\"red\">is</FONT>this>",
                shape= "component", height = 1.5, peripheries = 5,
                style="dashed")
def Up_to_date_task2(infile, outfile):
    pass

#   Can use dictionary if you wish...
graphviz_params = {"URL":"http://cnn.com", "fontcolor": '"#FF00FF"'}
@graphviz(**graphviz_params)
def myTask(input,output):
    pass
```



4. Consistent verbosity levels

The verbosity levels are now more fine-grained and consistent between pipeline_printout and pipeline_run. Note that At verbosity > 2, `pipeline_run` outputs lists of up-to-date tasks before running the pipeline. Many users who defaulted to using a verbosity of 3 may want to move up to `verbose = 4`.

- **level 0** : *Nothing*
- **level 1** : *Out-of-date Task names*
- **level 2** : *All Tasks (including any task function docstrings)*
- **level 3** : *Out-of-date Jobs in Out-of-date Tasks, no explanation*
- **level 4** : *Out-of-date Jobs in Out-of-date Tasks, with explanations and warnings*
- **level 5** : *All Jobs in Out-of-date Tasks, (include only list of up-to-date tasks)*
- **level 6** : *All jobs in All Tasks whether out of date or not*
- **level 10**: *Logs messages useful only for debugging ruffus pipeline code*
- Defaults to **level 4** for pipeline_printout: *Out of date jobs, with explanations and warnings*
- Defaults to **level 1** for pipeline_run: *Out-of-date Task names*

5. Allow abbreviated paths from `pipeline_run` or `pipeline_printout`

Note: Please contact me with suggestions if you find the abbreviations useful but "aesthetically challenged"!

Some pipelines produce interminable lists of long filenames. It would be nice to be able to abbreviate this to just enough information to follow the progress.

Ruffus now allows either

1. Only the nth top level sub-directories to be included
2. The message to be truncated to a specified number of characters (to fit on a line, for example)

   Note that the number of characters specified is the separate length of the input and output parameters, not the entire message. You many need to specify a smaller limit that you expect (e.g. `60` rather than *80*)

```
pipeline_printout(verbose_abbreviated_path = NNN)
pipeline_run(verbose_abbreviated_path = -MMM)
```

The `verbose_abbreviated_path` parameter restricts the length of input / output file paths to either

- NNN levels of nested paths
- A total of MMM characters, MMM is specified by setting `verbose_abbreviated_path` to -MMM (i.e. negative values)

`verbose_abbreviated_path` defaults to `2`

For example:

Given `["aa/bb/cc/dddd.txt", "aaa/bbbb/cccc/eeed/eeee/ffff/gggg.txt"]`

```
# Original relative paths
"[aa/bb/cc/dddd.txt, aaa/bbbb/cccc/eeed/eeee/ffff/gggg.txt]"

# Full abspath
verbose_abbreviated_path = 0
"[/test/ruffus/src/aa/bb/cc/dddd.txt, /test/ruffus/src/aaa/bbbb/cccc/eeed/eeee/ffff/gggg.tx

# Specifed level of nested directories
verbose_abbreviated_path = 1
"[.../dddd.txt, .../gggg.txt]"

verbose_abbreviated_path = 2
"[.../cc/dddd.txt, .../ffff/gggg.txt]"

verbose_abbreviated_path = 3
"[.../bb/cc/dddd.txt, .../eeee/ffff/gggg.txt]"


# Truncated to MMM characters
verbose_abbreviated_path = -60
"<???> /bb/cc/dddd.txt, aaa/bbbb/cccc/eeed/eeee/ffff/gggg.txt]"
```

If you are using `ruffus.cmdline`, the abbreviated path lengths can be specified on the command line as an extension to the verbosity:

```
# verbosity of 4
yourscript.py --verbose 4

# display three levels of nested directories
yourscript.py --verbose 4:3

# restrict input and output parameters to 60 letters
yourscript.py --verbose 4:-60
```

The number after the colon is the abbreviated path length

Other changes

- BUG FIX: Output producing wild cards was not saved in the checksum files!!!
- BUG FIX: @mkdir bug under Windows. Thanks to Sean Turley. (Aargh! Different exceptions are thrown in Windows vs. Linux for the same condition!)
- Added *pipeline_get_task_names(...)* which returns all task name as a list of strings. Thanks to Clare Sloggett

2.6.3 version 2.4.1

26th April 2014

- Breaking changes to drmaa API suggested by Bernie Pope to ensure portability across different drmaa implementations (SGE, SLURM etc.)

2.6.4 version 2.4

4th April 2014

Additions to `ruffus` namespace

- *formatter()* (*syntax*)
- *originate()* (*syntax*)
- *subdivide()* (*syntax*)

Installation: use pip

```
sudo pip install ruffus --upgrade
```

1) Command Line support

The optional `Ruffus.cmdline` module provides support for a set of common command line arguments which make writing *Ruffus* pipelines much more pleasant. See *manual*

2) Check pointing

- Contributed by **Jake Biesinger**
- See *Manual*
- Uses a fault resistant sqlite database file to log i/o files, and additional checksums
- defaults to checking file timestamps stored in the current directory (`ruffus_utilility.RUFFUS_HISTORY_FILE = '.ruffus_history.sqlite'`)
- *pipeline_run(..., checksum_level = N, ...)*
  - level 0 = CHECKSUM_FILE_TIMESTAMPS : Classic mode. Use only file timestamps (no checksum file will be created)
  - level 1 = CHECKSUM_HISTORY_TIMESTAMPS : Also store timestamps in a database after successful job completion
  - level 2 = CHECKSUM_FUNCTIONS : As above, plus a checksum of the pipeline function body
  - level 3 = CHECKSUM_FUNCTIONS_AND_PARAMS : As above, plus a checksum of the pipeline function default arguments and the additional arguments passed in by task decorators
  - defaults to level 1
- Can speed up trivial tasks: Previously Ruffus always added an extra 1 second pause between tasks to guard against file systems (Ext3, FAT, some NFS) with low timestamp granularity.

3) *subdivide()* (*syntax*)

- Take a list of input jobs (like *@transform*) but further splits each into multiple jobs, i.e. it is a **many->even more** relationship
- synonym for the deprecated `@split(..., regex(), ...)`

4) *mkdir()* (*syntax*) with *formatter()*, *suffix()* and *regex()*

- allows directories to be created depending on runtime parameters or the output of previous tasks
- behaves just like *@transform* but with its own (internal) function which does the actual work of making a directory
- Previous behavior is retained:`mkdir` continues to work seamlessly inside *@follows*

5) *originate()* (*syntax*)

- Generates output files without dependencies from scratch (*ex nihilo*!)
- For first step in a pipeline
- Task function obviously only takes output and not input parameters. (There *are* no inputs!)
- synonym for *@split(None,...)*
- See *Summary* / *Manual*

6) New flexible *formatter()* (*syntax*) alternative to *regex()* & *suffix()*

- Easy manipulation of path subcomponents in the style of os.path.split()
- Regular expressions are no longer necessary for path manipulation
- Familiar python syntax
- Optional regular expression matches
- Can refer to any in the list of N input files (not only the first file as for `regex(...)`)
- Can even refer to individual letters within a match

7) Combinatorics (all vs. all decorators)

- *@product* (See itertools.product)
- *@permutations* (See itertools.permutations)
- *@combinations* (See itertools.combinations)
- *@combinations_with_replacement* (See itertools.combinations_with_replacement)
- in optional *combinatorics* module
- Only *formatter()* provides the necessary flexibility to construct the output. (*suffix()* and *regex()* are not supported.)
- See *Summary* / *Manual*

8) drmaa support and multithreading:

- *ruffus.drmaa_wrapper.run_job()* (*syntax*)
- Optional helper module allows jobs to dispatch work to a computational cluster and wait until it completes.
- Requires `multithread` rather than `multiprocess`

9) `pipeline_run(...)` and exceptions

See *Manual*

- Optionally terminate pipeline after first exception
- Display exceptions without delay

10) Miscellaneous

Better error messages for `formatter()`, `suffix()` and `regex()` for `pipeline_printout(..., verbose >= 3`

- Error messages for showing mismatching regular expression and offending file name
- Wrong capture group names or out of range indices will raise informative Exception

2.6.5 version 2.3

1st September, 2013

- **`@active_if` turns off tasks at runtime** The Design and initial implementation were contributed by Jacob Biesinger

  Takes one or more parameters which can be either booleans or functions or callable objects which return True / False:

  ```
  run_if_true_1 = True
  run_if_true_2 = False

  @active_if(run_if_true, lambda: run_if_true_2)
  def this_task_might_be_inactive():
      pass
  ```

  The expressions inside @active_if are evaluated each time `pipeline_run`, `pipeline_printout` or `pipeline_printout_graph` is called.

  Dormant tasks behave as if they are up to date and have no output.

- **Command line parsing**
  - Supports both argparse (python 2.7) and optparse (python 2.6):
  - `Ruffus.cmdline` module is optional.
  - See *manual*
- **Optionally terminate pipeline after first exception** To have all exceptions interrupt immediately:

  ```
  pipeline_run(..., exceptions_terminate_immediately = True)
  ```

  By default ruffus accumulates `NN` errors before interrupting the pipeline prematurely. `NN` is the specified parallelism for `pipeline_run(..., multiprocess = NN)`.

  Otherwise, a pipeline will only be interrupted immediately if exceptions of type `ruffus.JobSignalledBreak` are thrown.

- Display exceptions without delay

By default, Ruffus re-throws exceptions in ensemble after pipeline termination.

To see exceptions as they occur:

```
pipeline_run(..., log_exceptions = True)
```

`logger.error(...)` will be invoked with the string representation of the each exception, and associated stack trace.

The default logger prints to sys.stderr, but this can be changed to any class from the logging module or compatible object via `pipeline_run(..., logger = ???)`

- Improved `pipeline_printout()`
  - *@split* operations now show the 1->many output in pipeline_printout

    This make it clearer that `@split` is creating multiple output parameters (rather than a single output parameter consisting of a list):

    ```
    Task = split_animals
         Job = [None
               -> cows
               -> horses
               -> pigs
                , any_extra_parameters]
    ```

  - File date and time are displayed in human readable form and out of date files are flagged with asterisks.

2.6.6 version 2.2

22nd July, 2010

- Simplifying **@transform** syntax with **suffix(...)**

  Regular expressions within ruffus are very powerful, and can allow files to be moved from one directory to another and renamed at will.

  However, using consistent file extensions and `@transform(..., suffix(...))` makes the code much simpler and easier to read.

  Previously, `suffix(...)` did not cooperate well with `inputs(...)`. For example, finding the corresponding header file (".h") for the matching input required a complicated `regex(...)` regular expression and `input(...)`. This simple case, e.g. matching "something.c" with "something.h", is now much easier in Ruffus.

  For example:

  ```
  source_files = ["something.c", "more_code.c"]
  @transform(source_files, suffix(".c"), add_inputs(r"\1.h", "common.h"), ".o")
  def compile(input_files, output_file):
      ( source_file,
        header_file,
        common_header) = input_files
      # call compiler to make object file
  ```

  This is equivalent to calling:

```
compile(["something.c", "something.h", "common.h"], "something.o")
compile(["more_code.c", "more_code.h", "common.h"], "more_code.o")
```

The `\1` matches everything *but* the suffix and will be applied to both `glob`s and file names.

For simplicity and compatibility with previous versions, there is always an implied r"1" before the output parameters. I.e. output parameters strings are *always* substituted.

- Tasks and glob in **inputs(...)** and **add_inputs(...)**

  `glob`s and tasks can be added as the prerequisites / input files using `inputs(...)` and `add_inputs(...)`. `glob` expansions will take place when the task is run.

- Advanced form of **@split** with **regex**:

  The standard `@split` divided one set of inputs into multiple outputs (the number of which can be determined at runtime).

  This is a `one->many` operation.

  An advanced form of `@split` has been added which can split each of several files further.

  In other words, this is a `many->"many more"` operation.

  For example, given three starting files:

  ```
  original_files = ["original_0.file",
                    "original_1.file",
                    "original_2.file"]
  ```

  We can split each into its own set of sub-sections:

  ```
  @split(original_files,
     regex(r"starting_(\d+).fa"),                          # match starting files
           r"files.split.\1.*.fa"                          # glob pattern
           r"\1")                                          # index of original file
  def split_files(input_file, output_files, original_index):
      """
          Code to split each input_file
              "original_0.file" -> "files.split.0.*.fa"
              "original_1.file" -> "files.split.1.*.fa"
              "original_2.file" -> "files.split.2.*.fa"
      """
  ```

  This is, conceptually, the reverse of the @collate(...) decorator

- Ruffus will complain about unescaped regular expression special characters:

  Ruffus uses "\1" and "\2" in regular expression substitutions. Even seasoned python users may not remember that these have to be 'escaped' in strings. The best option is to use 'raw' python strings e.g.

  ```
  r"\1_substitutes\2correctly\3four\4times"
  ```

  Ruffus will throw an exception if it sees an unescaped "\1" or "\2" in a file name, which should catch most of these bugs.

- Prettier output from *pipeline_printout_graph*

Changed to nicer colours, symbols etc. for a more professional look. @split and @merge tasks now look different from @transform. Colours, size and resolution are now fully customisable:

```
pipeline_printout_graph( #...
                         user_colour_scheme = {
                                                "colour_scheme_index":1,
                                                "Task to run"  : {"fillcolor":"blue"},
                                                 pipeline_name : "My flowchart",
                                                 size          : (11,8),
                                                 dpi           : 120)})
```

An SVG bug in firefox has been worked around so that font size are displayed correctly.

2.6.7 version 2.1.1

- **@transform(.., add_inputs(...))** `add_inputs(...)` allows the addition of extra input dependencies / parameters for each job.

  Unlike `inputs(...)`, the original input parameter is retained:

  ```
  from ruffus import *
  @transform(["a.input", "b.input"], suffix(".input"), add_inputs("just.1.more","just.2.mo
  def task(i, o):
  ""
  ```

  Produces:

  ```
  Job = [[a.input, just.1.more, just.2.more] ->a.output]
  Job = [[b.input, just.1.more, just.2.more] ->b.output]
  ```

  Like `inputs`, `add_inputs` accepts strings, tasks and `glob` s This minor syntactic change promises add much clarity to Ruffus code. `add_inputs()` is available for `@transform`, `@collate` and `@split`

2.6.8 version 2.1.0

- **@jobs_limit** Some tasks are resource intensive and too many jobs should not be run at the same time. Examples include disk intensive operations such as unzipping, or downloading from FTP sites.

  Adding:

  ```
  @jobs_limit(4)
  @transform(new_data_list, suffix(".big_data.gz"), ".big_data")
  def unzip(i, o):
    "unzip code goes here"
  ```

  would limit the unzip operation to 4 jobs at a time, even if the rest of the pipeline runs highly in parallel.

  (Thanks to Rob Young for suggesting this.)

2.6.9 version 2.0.10

- **touch_files_only** option for **pipeline_run**

When the pipeline runs, task functions will not be run. Instead, the output files for each job (in each task) will be `touch`-ed if necessary. This can be useful for simulating a pipeline run so that all files look as if they are up-to-date.

Caveats:

- This may not work correctly where output files are only determined at runtime, e.g. with **@split**
- Only the output from pipelined jobs which are currently out-of-date will be `touch`-ed. In other words, the pipeline runs *as normal*, the only difference is that the output files are `touch`-ed instead of being created by the python task functions which would otherwise have been called.

- Parameter substitution for **inputs(...)**

The **inputs(...)** parameter in **@transform**, **@collate** can now take tasks and `glob` s, and these will be expanded appropriately (after regular expression replacement).

For example:

```
@transform("dir/a.input", regex(r"(.*)\/(.+).input"),
               inputs((r"\1/\2.other", r"\1/*.more")), r"elsewhere/\2.output")
def task1(i, o):
  """
  Some pipeline task
  """
```

Is equivalent to calling:

```
task1(("dir/a.other", "dir/1.more", "dir/2.more"), "elsewhere/a.output")
```

Here:

```
r"\1/*.more"
```

is first converted to:

```
r"dir/*.more"
```

which matches:

```
"dir/1.more"
"dir/2.more"
```

2.6.10 version 2.0.9

- Better display of logging output
- Advanced form of **@split** This is an experimental feature.

Hitherto, **@split** only takes 1 set of input (tasks/files/`glob` s) and split these into an indeterminate number of output.

This is a one->many operation.

Sometimes it is desirable to take multiple input files, and split each of them further.

This is a many->many (more) operation.

It is possible to hack something together using **@transform** but downstream tasks would not aware that each job in **@transform** produces multiple outputs (rather than one input, one output per job).

The syntax looks like:

```
@split(get_files, regex(r"(.+).original"), r"\1.*.split")
def split_files(i, o):
     pass
```

If `get_files()` returned `A.original`, `B.original` and `C.original`, `split_files()` might lead to the following operations:

```
A.original
        -> A.1.original
        -> A.2.original
        -> A.3.original
B.original
        -> B.1.original
        -> B.2.original
C.original
        -> C.1.original
        -> C.2.original
        -> C.3.original
        -> C.4.original
        -> C.5.original
```

Note that each input (`A/B/C.original`) can produce a number of output, the exact number of which does not have to be pre-determined. This is similar to **@split**

Tasks following `split_files` will have ten inputs corresponding to each of the output from `split_files`.

If **@transform** was used instead of **@split**, then tasks following `split_files` would only have 3 inputs.

2.6.11 version 2.0.8

- File names can be in unicode
- File systems with 1 second timestamp granularity no longer cause problems.

2.6.12 version 2.0.2

- Much prettier /useful output from *pipeline_printout*
- New tutorial / manual

2.6.13 version 2.0

- Revamped documentation:
  - Rewritten tutorial
  - Comprehensive manual
  - New syntax help
- Major redesign. New decorators include
  - *@split*
  - *@transform*
  - *@merge*
  - *@collate*

- Major redesign. Decorator *inputs* can mix
  - Output from previous tasks
  - *glob* patterns e.g. `*.txt`
  - Files names
  - Any other data type

2.6.14 version 1.1.4

Tasks can get their input by automatically chaining to the output from one or more parent tasks using *@files_re*

2.6.15 version 1.0.7

Added *proxy_logger* module for accessing a shared log across multiple jobs in different processes.

2.6.16 version 1.0

Initial Release in Oxford

2.7 Fixed Bugs

Full list at "Latest Changes wiki entry"

2.8 New Object orientated syntax for Ruffus in Version 2.6

Ruffus Pipelines can now be created and manipulated directly using Pipeline and Task objects instead of via decorators.

Note: You may want to go through the *worked_example* first.

2.8.1 Syntax

This traditional Ruffus code:

```
from ruffus import *

# task function
starting_files = ["input/a.fasta","input/b.fasta"]
@transform(input      = starting_files,
           filter     = suffix('.fasta'),
           output     = '.sam',
           output_dir = "output")
def map_dna_sequence(input_file, output_file) :
    pass

pipeline_run()
```

Can also be written as:

```
from ruffus import *

# undecorated task function
def map_dna_sequence(input_file, output_file) :
    pass

starting_files = ["input/a.fasta","input/b.fasta"]

#   make ruffus Pipeline() object
my_pipeline = Pipeline(name = "test")
my_pipeline.transform(task_func  = map_dna_sequence,
                      input      = starting_files,
                      filter     = suffix('.fasta'),
                      output     = '.sam',
                      output_dir = "output")

my_pipeline.run()
```

The two different syntax are almost identical:
The first parameter **task_func=**`your_python_function` is mandatory.
Otherwise, all other parameters are in the same order as before, and can be given by position or as named arguments.

2.8.2 Advantages

These are some of the advantages of the new syntax:

1. **Pipeline topology is assembled in one place**

   This is a matter of personal preference.

   Nevertheless, using decorators to locally annotate python functions with pipeline parameters arguably helps separation of concerns.

2. **Pipelines can be created** *on the fly*

   For example, using parameters parsed from configuration files.

   Ruffus pipelines no longer have to be defined at global scope.

3. **Reuse common sub-pipelines**

   Shared sub pipelines can be created from discrete python modules and joined together as needed. Bioinformaticists may have "mapping", "aligning", "variant-calling" sub-pipelines etc.

4. **Multiple Tasks can share the same python function**

   Tasks are normally referred to by their associated functions (as with decoratored Ruffus tasks). However, you can also disambiguate Tasks by specifying their name directly.

5. **Pipeline topology can be specified at run time**

   Some (especially bioinformatics) tasks require binary merging. This can be very inconvenient.

   For example, if we have 8 data files, we need three successive rounds of merging (8->4->2->1) or three tasks) to produce the output. But if we are given 10 data files, we now find that we needed to have four tasks for four rounds of merging (10->5->3->2->1).

There was previously no easy way to arrange different Ruffus topologies in response to the data. Now we can add as many extra merging tasks to our pipeline (all sharing the same underlying python function) as needed.

2.8.3 Compatability

- The changes are fully backwards compatibile. All valid Ruffus code continues to work
- Decorators and `Pipeline` objects can be used interchangeably:

Decorated functions are automatically part of a default constructed `Pipeline` named `"main"`.

```
main_pipeline = Pipeline.pipelines["main"]
```

In the following example, a pipeline using the Ruffus with classes syntax (1) and (3) has a traditionally decorated task function in the middle (2).

```
from ruffus import *

# get default pipeline
main_pipeline = Pipeline.pipelines["main"]

# undecorated task functions
def compress_sam_to_bam(input_file, output_file) :
    open(output_file, "w").close()

def create_files(output_file) :
    open(output_file, "w").close()


#
#   1. Ruffus with classes
#
starting_files = main_pipeline.originate(create_files, ["input/a.fasta","input/b.fasta"])\
    .follows(mkdir("input", "output"))

#
#   2. Ruffus with python decorations
#
@transform(starting_files,
           suffix('.fasta'),
           '.sam',
           output_dir = "output")
def map_dna_sequence(input_file, output_file) :
    open(output_file, "w").close()


#
#   3. Ruffus with classes
#
main_pipeline.transform(task_func   = compress_sam_to_bam,
                        input       = map_dna_sequence,
                        filter      = suffix(".sam"),
                        output      = ".bam")

# main_pipeline.run()
#    or
pipeline_run()
```

2.8.4 Class methods

The **ruffus.Pipeline** class has the following self-explanatory methods:

```
Pipeline.run(...)
Pipeline.printout(...)
Pipeline.printout_graph(...)
```

These methods return a **ruffus.Task** object

```
Pipeline.originate(...)
Pipeline.transform(...)
Pipeline.split(...)
Pipeline.merge(...)
Pipeline.mkdir(...)

Pipeline.collate(...)
Pipeline.subdivide(...)

Pipeline.combinations(...)
Pipeline.combinations_with_replacement(...)
Pipeline.product(...)
Pipeline.permutations(...)

Pipeline.follows(...)
Pipeline.check_if_uptodate(...)
Pipeline.graphviz(...)

Pipeline.files(...)
Pipeline.parallel(...)
```

A Ruffus **Task** can be modified with the following methods

```
Task.active_if(...)
Task.check_if_uptodate(...)
Task.follows(...)
Task.graphviz(...)
Task.jobs_limit(...)
Task.mkdir(...)
Task.posttask(...)
```

2.8.5 Call chaining

The syntax is designed to allow call chaining:

```
Pipeline.transform(...)\
    .mkdir(follows(...))\
    .active_if(...)\
    .graphviz(...)
```

2.8.6 Referring to Tasks

Ruffus pipelines are chained together or specified by referring to each stage or Task.

(1) and (2) are ways to referring to tasks that Ruffus has always supported.

(3) - (6) are new to Ruffus v 2.6 but apply to both using decorators or the new Ruffus with classes syntax.

1) Python function

```
@transform(prev_task, ...)
def next_task():
    pass

pipeline.transform(input = next_task, ...)
```

2) Python function name (using *output_from*)

```
pipeline.transform(input = output_from("prev_task"), ...)
```

Note: The above (1) and (2) only work if the Python function specifies the task unambiguously in a pipeline. If you reuse the same Python function for multiple tasks, use the following methods.

Ruffus will complain with Exceptions if your code is ambiguous.

---

3) Task object

```
prev_task = pipeline.transform(...)

# prev_task is a Task object
next_task = pipeline.transform(input = prev_task, ....)
```

4) Task name (using *output_from*)

```
# name this task "prev_task"
pipeline.transform(name = "prev_task",...)

pipeline.transform(input = output_from("prev_task"), ....)
```

Note: Tasks from other pipelines can be referred to using full qualified names in the **pipeline**::*task* format

```
pipeline.transform(input = output_from("other_pipeline::prev_task"), ....)
```

---

5) Pipeline

When we are assembling our pipeline from sub-pipelines (especially those in other modules which other people might have written) it is inconvenient to break encapsulation to find out the component **Task** of the subpipeline.

In which case, the sub-pipeline author can assign particular tasks to the **head** and **tail** of the pipeline. The pipeline will be an alias for these:

```
# Note: these functions take lists
sub_pipeline.set_head_tasks([first_task])
sub_pipeline.set_tail_tasks([last_task])

# first_task.set_input(...)
sub_pipeline.set_input(input = "*.txt")
```

```
# (input = last_task,...)
main_pipeline.transform(input = sub_pipeline, ....)
```

If you don't have access to a pipeline object, you can look it up via the Pipeline object

```
    # This is the default "main" pipeline which holds decorated task functions
    main_pipeline = Pipeline.pipelines["main"]

    my_pipeline = Pipeline("test")

    alias_to_my_pipeline = Pipeline.pipelines["test"]
```

6) Lookup Task via the Pipeline

We can ask a Pipeline to lookup task names, functions and function names for us.

```
# Lookup task name
pipeline.transform(input = pipeline["prev_task"], ....)

# Lookup via python function
pipeline.transform(input = pipeline[python_function], ....)

# Lookup via python function name
pipeline.transform(input = pipeline["python_function_name"], ....)
```

This is straightforward if the lookup is unambiguous for the pipeline.

If the names are not found in the pipeline, Ruffus will look across all pipelines.

Any ambiguities will result in an immediate error.

In extremis, you can use pipeline qualified names

```
# Pipeline qualified task name
pipeline.transform(input = pipeline["other_pipeline::prev_task"], ....)
```

Note: All this will be much clearer going through the *worked_example*.

2.9 Worked Example for New Object orientated syntax for Ruffus in Version 2.6

Ruffus Pipelines can now be created and manipulated directly using Pipeline and Task objects instead of via decorators.

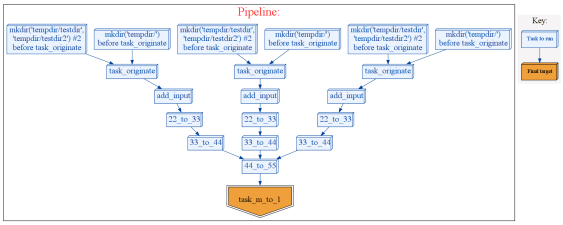
For clarity, we use named parameters in this example. You can just as easily pass all parameters by position.

2.9.1 Worked example

Note: Remember to look at the example code:

- *Python Code for: New Object orientated syntax for Ruffus in Version 2.6*

This example pipeline is a composite of three separately subpipelines each created by a python function `make_pipeline1()` which is joined to another subpipeline created by `make_pipeline2()`



Although there are 13 different stages to this pipeline, we are using the same three python functions (but supplying them with different data).

```
def task_originate(o):
    #   Makes new files
    ...

def task_m_to_1(i, o):
    #   Merges files together
    ...

def task_1_to_1(i, o):
    # One input per output
    ...
```

Pipeline factory

Let us start with a python function which makes a full formed sub pipeline useable as a modular building block

```
# Pipelines need to have a unique name
def make_pipeline1(pipeline_name,
                   starting_file_names):
    pass
```

Note that we are passing the pipeline name as the first parameter.

All pipelines must have unique names

```
test_pipeline = Pipeline(pipeline_name)

new_task = test_pipeline.originate(task_func = task_originate,
                                   output = starting_file_names)\
                        .follows(mkdir(tempdir), mkdir(tempdir + "testdir", tempdir + "testdir2"
                        .posttask(touch_file(tempdir + "testdir/whatever.txt"))
```

A new task is returned from `test_pipeline.originate(...)` which is then modified via `.follows(...)` and `.posttask(...)`. This is familiar Ruffus syntax only slightly rearranged.

We can change the `output=starting_file_names` later using `set_output()` but sometimes it is just more convenient to pass this as a parameter to the pipeline factory function.

Note: The first, mandatory parameter is `task_func = task_originate` which is the python function for this task

---

Three different ways of referring to input Tasks

Just as in traditional Ruffus, Pipelines are created by setting the **input** of one task to (the **output** of) its predecessor.

```
test_pipeline.transform(task_func   = task_m_to_1,
                        name        = "add_input",
                        #   Lookup Task from function task_originate()
                        #       Needs to be unique in the pipeline
                        input       = task_originate,
                        filter      = regex(r"(.*)"),
                        add_inputs  = add_inputs(tempdir + "testdir/whatever.txt"),
                        output      = r"\1.22")
test_pipeline.transform(task_func   = task_1_to_1,
                        name        = "22_to_33",
                        # Lookup Task from unique Task name = "add_input"
                        #   Function name is not unique in the pipeline
                        input       = output_from("add_input"),
                        filter      = suffix(".22"),
                        output      = ".33")
tail_task = test_pipeline.transform(task_func   = task_1_to_1,
                                    name        = "33_to_44",
                                    # Ask test_pipeline to lookup Task name = "22_to_33"
                                    input       = test_pipeline["22_to_33"],
                                    filter      = suffix(".33"),
                                    output      = ".44")
```

Head and Tail Tasks

```
#   Set the tail task: test_pipeline can be used as an input
#       without knowing the details of task names
#
#   Use Task object=tail_task directly
test_pipeline.set_tail_tasks([tail_task])

#   Set the head task: we can feed input into test_pipeline
#       without knowing the details of task names
test_pipeline.set_head_tasks([test_pipeline[task_originate]])

return test_pipeline
```

By calling `set_tail_tasks` and `set_head_tasks` to assign the first and last stages of `test_pipeline`, we can later use `test_pipeline` without knowing its component Tasks.

The last step is to return the fully formed pipeline instance

Another Pipeline factory

```
#
#   Returns a fully formed sub pipeline useable as a building block
#
def make_pipeline2( pipeline_name = "pipeline2", do_not_define_head_task = False):
    test_pipeline2 = Pipeline(pipeline_name)
    test_pipeline2.transform(task_func   = task_1_to_1,
                             # task name
                            name        = "44_to_55",
```

```
                                # placeholder: will be replaced later with set_input()
                            input       = None,
                            filter      = suffix(".44"),
                            output      = ".55")
    test_pipeline2.merge(   task_func   = task_m_to_1,
                            input       = test_pipeline2["44_to_55"],
                            output      = tempdir + "final.output",)
    # Lookup task using function name
    #   This is unique within pipeline2
    test_pipeline2.set_tail_tasks([test_pipeline2[task_m_to_1]])

    # Lookup task using task name
    test_pipeline2.set_head_tasks([test_pipeline2["44_to_55"]])

    return test_pipeline2
```

make_pipeline2() looks very similar to make_pipeline1 except that the input for the **head** task is left blank for assigning later

Note that we can use `task_m_to_1` to look up a Task (`test_pipeline2[task_m_to_1]`) even though this function is also used by test_pipeline. There is no ambiguity so long as only one task in `test_pipeline2` uses this python function.

Creating multiple copies of a pipeline

Let us call `make_pipeline1()` to make two completely independent pipelines (`"pipeline1a"` and `"pipeline1b"`)

```
#   First two pipelines are created as separate instances by make_pipeline1()
pipeline1a = make_pipeline1(pipeline_name = "pipeline1a", starting_file_names = [tempdir + ss fo
pipeline1b = make_pipeline1(pipeline_name = "pipeline1b", starting_file_names = [tempdir + ss fo
```

We can also create a new instance of a pipeline by **"cloning"** an existing pipeline

```
#   pipeline1c is a clone of pipeline1b
pipeline1c = pipeline1b.clone(new_name = "pipeline1c")
```

Because `"pipeline1c"` is a clone of `"pipeline1b"`, it shares exactly the same parameters. Let us change this by giving `"pipeline1c"` its own starting files.

We can do this for normal (e.g. **transform**, **split**, **merge** etc) tasks by calling

```
transform_task.set_input(input = xxx)
```

@originate doesn't take **input** but creates results specified in the **output** parameter. To finish setting up `pipeline1c`:

```
#   Set the "originate" files for pipeline1c to ("e.1" and "f.1")
#       Otherwise they would use the original ("c.1", "d.1")
pipeline1c.set_output(output = [tempdir + ss for ss in ("e.1", "f.1")])
```

We only create one copy of `pipeline2`

```
pipeline2 = make_pipeline2()
```

Connecting pipelines together

Because we have previously assigned **head** and **tail** tasks, we can easily join the pipelines together:

```
#   Join all pipeline1a-c to pipeline2
pipeline2.set_input(input = [pipeline1a, pipeline1b, pipeline1c])
```

Running a composite pipeline

Ruffus automatically follows the antecedent dependencies of each task even if they are from another pipeline.

This means that you can run composite pipelines seamlessly, without any effort:

```
# Only runs pipeline1a
pipeline1a.run()

# Runs pipeline1a,b,c -> pipeline2
pipeline2.run(multiprocess = 10, verbose = 0)
```

Note: Remember to look at the example code:

- *Python Code for: New Object orientated syntax for Ruffus in Version 2.6*

2.10 Python Code for: New Object orientated syntax for Ruffus in Version 2.6

See also:

- *new_syntax.worked_example*

This code is from `test/test_subpipeline.py` in the **Ruffus** distribution

```
#!/usr/bin/env python
from __future__ import print_function
"""
    test_subpipeline.py

        Demonstrates the new Ruffus syntax in version 2.6
"""

import os
import sys

# add grandparent to search path for testing
grandparent_dir = os.path.abspath(os.path.join(os.path.dirname(__file__), "..", ".."))
sys.path.insert(0, grandparent_dir)

import ruffus
from ruffus import add_inputs, suffix, mkdir, regex, Pipeline, output_from, touch_file
print("\tRuffus Version = ", ruffus.__version__)

#888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888

#   imports


#8888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888
import shutil
```

```
def touch (outfile):
    with open(outfile, "w"):
        pass


#888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888

#   Tasks


#888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888
tempdir = "tempdir/"
def task_originate(o):
    """
    Makes new files
    """
    touch(o)

def task_m_to_1(i, o):
    """
    Merges files together
    """
    with open(o, "w") as o_file:
        for f in sorted(i):
            with open(f) as ii:
                o_file.write(f +"=" + ii.read() + "; ")

def task_1_to_1(i, o):
    """
    1 to 1 for transform
    """
    with open(o, "w") as o_file:
        with open(i) as ii:
            o_file.write(i +"+" + ii.read())

DEBUG_do_not_define_tail_task = False
DEBUG_do_not_define_head_task = False

import unittest

#
#   Returns a fully formed sub pipeline useable as a building block
#
def make_pipeline1(pipeline_name,   # Pipelines need to have a unique name
                   starting_file_names):
    test_pipeline = Pipeline(pipeline_name)

    #   We can change the starting files later using
    #           set_input() for transform etc.
    #       or set_output() for originate
    #   But it can be more convenient to just pass this to the function making the pipeline
    #
    test_pipeline.originate(task_originate, starting_file_names)\
        .follows(mkdir(tempdir), mkdir(tempdir + "testdir", tempdir + "testdir2"))\
        .posttask(touch_file(tempdir + "testdir/whatever.txt"))
    test_pipeline.transform(task_func   = task_m_to_1,
                            name        = "add_input",
```

```
                                # Lookup Task from function name task_originate()
                                #   So long as this is unique in the pipeline
                                input       = task_originate,
                                filter      = regex(r"(.*)"),
                                add_inputs  = add_inputs(tempdir + "testdir/whatever.txt"),
                                output      = r"\1.22")
    test_pipeline.transform(task_func   = task_1_to_1,
                                name        = "22_to_33",
                                # Lookup Task from Task name
                                #   Function name is not unique in the pipeline
                                input       = output_from("add_input"),
                                filter      = suffix(".22"),
                                output      = ".33")
    tail_task = test_pipeline.transform(task_func   = task_1_to_1,
                                        name        = "33_to_44",
                                        # Ask Pipeline to lookup Task from Task name
                                        input       = test_pipeline["22_to_33"],
                                        filter      = suffix(".33"),
                                        output      = ".44")

    #   Set the tail task so that users of my sub pipeline can use it as a dependency
    #       without knowing the details of task names
    #
    #   Use Task() object directly without having to lookup
    test_pipeline.set_tail_tasks([tail_task])

    #   If we try to connect a Pipeline without tail tasks defined, we have to
    #       specify the exact task within the Pipeline.
    #   Otherwise Ruffus will not know which task we mean and throw an exception
    if DEBUG_do_not_define_tail_task:
        test_pipeline.set_tail_tasks([])

    # Set the head task so that users of my sub pipeline send input into it
    #   without knowing the details of task names
    test_pipeline.set_head_tasks([test_pipeline[task_originate]])

    return test_pipeline

#
#   Returns a fully formed sub pipeline useable as a building block
#
def make_pipeline2( pipeline_name = "pipeline2"):
    test_pipeline2 = Pipeline(pipeline_name)
    test_pipeline2.transform(task_func   = task_1_to_1,
                             # task name
                                name        = "44_to_55",
                                # placeholder: will be replaced later with set_input()
                                input       = None,
                                filter      = suffix(".44"),
                                output      = ".55")
    test_pipeline2.merge(   task_func   = task_m_to_1,
                                input       = test_pipeline2["44_to_55"],
                                output      = tempdir + "final.output",)

    # Set head and tail
    test_pipeline2.set_tail_tasks([test_pipeline2[task_m_to_1]])
    if not DEBUG_do_not_define_head_task:
        test_pipeline2.set_head_tasks([test_pipeline2["44_to_55"]])
```

```
    return test_pipeline2


def run_pipeline():

    #   First two pipelines are created as separate instances by the make_pipeline1 function
    pipeline1a = make_pipeline1(pipeline_name = "pipeline1a", starting_file_names = [tempdir + s
    pipeline1b = make_pipeline1(pipeline_name = "pipeline1b", starting_file_names = [tempdir + s

    #   The Third pipeline is a clone of pipeline1b
    pipeline1c = pipeline1b.clone(new_name = "pipeline1c")

    #   Set the "originate" files for pipeline1c to ("e.1" and "f.1")
    #       Otherwise they would use the original ("c.1", "d.1")
    pipeline1c.set_output(output = [])
    pipeline1c.set_output(output = [tempdir + ss for ss in ("e.1", "f.1")])

    #   Join all pipeline1a-c to pipeline2
    pipeline2 = make_pipeline2()
    pipeline2.set_input(input = [pipeline1a, pipeline1b, pipeline1c])


    pipeline2.printout_graph("test.svg", "svg", [task_m_to_1])
    pipeline2.printout(verbose = 0)
    pipeline2.run(multiprocess = 10, verbose = 0)


class Test_task(unittest.TestCase):

    def tearDown (self):
        """
        """
        try:
            shutil.rmtree(tempdir)
        except:
            pass


    def test_subpipelines (self):

        run_pipeline()

        # Check that the output reflecting the pipeline topology is correct.
        correct_output = 'tempdir/a.1.55=tempdir/a.1.44+tempdir/a.1.33+tempdir/a.1.22+tempdir/a.
                         'tempdir/b.1.55=tempdir/b.1.44+tempdir/b.1.33+tempdir/b.1.22+tempdir/b.
                         'tempdir/c.1.55=tempdir/c.1.44+tempdir/c.1.33+tempdir/c.1.22+tempdir/c.
                         'tempdir/d.1.55=tempdir/d.1.44+tempdir/d.1.33+tempdir/d.1.22+tempdir/d.
                         'tempdir/e.1.55=tempdir/e.1.44+tempdir/e.1.33+tempdir/e.1.22+tempdir/e.
                         'tempdir/f.1.55=tempdir/f.1.44+tempdir/f.1.33+tempdir/f.1.22+tempdir/f.
        with open(tempdir + "final.output") as real_output:
            real_output_str = real_output.read()
        self.assertEqual(correct_output, real_output_str)



if __name__ == '__main__':
    unittest.main()
```

2.11 Where I see Ruffus going

These are the future enhancements I would like to see in Ruffus:

- **Simpler syntax**
  - Extremely pared down syntax where strings are interpreted as commands (like gmake) but with full Ruffus support / string interpolation etc.
  - More powerful non-decorator OOP syntax
  - More customisation points for your own syntax / database use
- **Better support for Computational clusters / larger scale pipelines**
  - Running jobs out of sequence
  - Long running pipeline where input can be added later
  - Restarting failed jobs robustly
  - Finding out why jobs fail
  - Does Ruffus scale to thousands of parallel jobs. What are the bottlenecks?
- **Better displays of progress**
  - Query which tasks / jobs are being run
  - GUI displays
- **Dynamic control during pipeline progress**
  - Turn tasks on and off
  - Pause pipelines
  - Pause jobs
  - Change priorities
- **Better handling of data**
  - Can we read and write from databases instead of files?
  - Can we cleanup files but preserve history?

2.12 In up coming release:

2.12.1 Todo: document `output_from()`

2.12.2 Todo: document new syntax

2.12.3 Todo: Log the progress through the pipeline in a machine parsable format

Standard parsable format for reporting the state of the pipeline enhancement

- Timestamped text file
- Timestamped Database

2.12.4 Todo: either_or: Prevent failed jobs from propagating further

Motivating example:

```
@transform(prevtask, suffix(".txt"),  either_or(".failed", ".succeed"))
def task(input_file, output_files):
    succeed_file_name, failed_file_name = output_files
    if not run_operation(input_file, succeed_file_name):
        # touch failed file
        with open(failed_file_name, "w") as faile_file:
            pass
```

2.12.5 Todo: (bug fix) pipeline_printout_graph should print inactive tasks

2.12.6 Todo: Mark input strings as non-file names, and add support for dynamically returned parameters

1. Use indicator object.
2. What is a good name? "`output_from()`", "`NOT_FILE_NAME`" :-)
3. They will still participate in suffix, formatter and regex replacement

Bernie Pope suggests that we should generalise this:

If any object in the input parameters is a (non-list/tuple) class instance, check (getattr) whether it has a `ruffus_params()` function. If it does, call it to obtain a list which is substituted in place. If there are string nested within, these will also take part in Ruffus string substitution. Objects with `ruffus_params()` always "decay" to the results of the function call

`output_from` would be a simple wrapper which returns the internal string via `ruffus_params()`

```
class output_from (object):
    def __init__(self, str):
        self.str = str
    def ruffus_params(self):
        return [self.str]
```

Returning a list should be like wildcards and should not introduce an unnecessary level of indirection for output parameters, i.e. suffix(".txt") or formatter() / "{basename[0]}" should work.

Check!

2.13 Future Changes to Ruffus

I would appreciated feedback and help on all these issues and where next to take *ruffus*.

Future Changes are features where we more or less know where we are going and how to get there.

Planned Improvements describes features we would like in Ruffus but where the implementation or syntax has not yet been (fully) worked out.

If you have suggestions or contributions, please either write to me (ruffus_lib at llew.org.uk) or send a pull request via the git site.

2.13.1 Todo: Replacements for formatter(), suffix(), regex()

formatter etc. should be self contained objects derived from a single base class with behaviour rather than empty tags used for dispatching to functions

The design is better fit by and should be switched over to an inheritance scheme

2.13.2 Todo: Allow "extra" parameters to be used in output substitution

Formatter substitution can refer to the original elements in the input and extra parameters (without converting them to strings either). This refers to the original (nested) data structure.

This will allow normal python datatypes to be handed down and slipstreamed into a pipeline more easily.

The syntax would use Ruffus (> version 2.4) formatter:

```
@transform( ..., formatter(), [
                                  "{EXTRAS[0][1][3]}",     # EXTRAS
                                  "[INPUTS[1][2]]"],...)   # INPUTS
def taskfunc():
    pass
```

`EXTRA` and `INPUTS` indicate that we are referring to the input and extra parameters.

These are the full (nested) parameters in all their original form. In the case of the input parameters, this obvious depends on the decorator, so

```
@transform(["a.text", [1, "b.text"]], formatter(), "{INPUTS[0][0]}")
def taskfunc():
    pass
```

would give

```
job #1
   input  == "a.text"
   output == "a"

job #2
   input  == [1, "b.text"]
   output == 1
```

The entire string must consist of `INPUTS` or `EXTRAS` followed by optionally N levels of square brackets. i.e. They must match `"(INPUTS|EXTRAS)(\[\d+\])+"`

No string conversion takes place.

For `INPUTS` or `EXTRAS` which have objects with a `ruffus_params()` function (see Todo item above), the original object rather than the result of `ruffus_params()` is forwarded.

2.13.3 Todo: Extra signalling before and after each task and job

```
@prejob(custom_func)
@postjob(custom_func)
def task():
    pass
```

`@prejob` / `@postjob` would be run in the child processes.

2.13.4 Todo: `@split` / `@subdivide` returns the actual output created

- **overrides** (not replaces) wild cards.
- Returns a list, each with output and extra paramters.
- Won't include extraneous files which were not created in the pipeline but which just happened to match the wild card
- We should have `ruffus_output_params`, `ruffus_extra_params` wrappers for clarity:

```
@split("a.file", "*.txt")
def split_into_txt_files(input_file, output_files):
    output_files = ["a.txt", "b.txt", "c.txt"]
    for output_file_name in output_files:
        with open(output_file_name, "w") as oo:
            pass
    return [
            ruffus_output("a.file"),
            [ruffus_output(["b.file", "c.file"]), ruffus_extras(13, 14)],
            ]
```

- Consider yielding?

Checkpointing

- If checkpoint file is used, the actual files are saved and checked the next time
- If no files are generated, no files are checked the next time...
- The output files do not have to match the wildcard though we can output a warning message if that happens... This is obviously dangerous because the behavior will change if the pipeline is rerun without using the checkpoint file
- What happens if the task function changes?

2.13.5 Todo: New decorators

Todo: `@originate`

Each (serial) invocation returns lists of output parameters until returns None. (Empty list = `continue`, None = `break`).

Todo: `@recombine`

Like `@collate` but automatically regroups jobs which were a result of a previous `@subdivide` / `@split` (even after intervening `@transform`)

This is the only way job trickling can work without stalling the pipeline: We would know how many jobs were pending for each `@recombine` job and which jobs go together.

2.13.6 Todo: Bioinformatics example to end all examples

Uses

- `@product`

- `@subdivide`
- `@transform`
- `@collate`
- `@merge`

2.13.7 Todo: Allow the next task to start before all jobs in the previous task have finished

Jake (Biesinger) calls this **Job Trickling**!

- A single long running job no longer will hold up the entire pipeline
- Calculates dependencies dynamically at the job level.
- Goal is to have a long running (months) pipeline to which we can keep adding input...
- We can choose between prioritising completion of the entire pipeline for some jobs (depth first) or trying to complete as many tasks as possible (breadth first)

Converting to per-job rather than per task dependencies

Some decorators prevent per job (rather than per task) dependency calculations, and will call a pipeline stall until the dependent tasks are completed (the current situation):

- **Some types of jobs unavoidably depend on an entire previous task completing:**
  - `add_inputs()`, `inputs()`
  - `@merge`
  - `@split` (implicit `@merge`)
- **`@split`, `@originate` produce variable amount of output at runtime and must be completed before the next task c**
  - Should `yield` instead of return?
- **`@collate` needs to pattern match all the inputs of a previous task**
  - Replace `@collate` with `@recombine` which "remembers" and reverses the results of a previous `@subdivide` or `@split`
  - Jobs need unique job_id tag
  - Jobs are assigned (nested) grouping id which accompany them down the pipeline after `@subdivide` / `@split` and are removed after `@recombine`
  - Should have a count of jobs so we always know *when* an "input slot" is full
- Funny "single file" mode for `@transform`, `@files` needs to be regularised so it is a syntactic (front end) convenience (oddity!) and not plague the inards of ruffus

Breaking change: to force the entirety of the previous task to complete before the next one, use `@follows`

Implementation

- "Push" model. Completing jobs "check in" their outputs to "input slots" for all the sucessor jobs.
- When "input slots" are full for any job, it is put on the dispatch queue to be run.
- The priority (depth first or breadth first) can be set here.
- `pipeline_run` / `Pipeline_printout` create a task dependency tree structure (from decorator dependencies) (a runtime pipeline object)
- Each task in the pipeline object knows which other tasks wait on it.
- When output is created by a job, it sends messages to (i.e. function calls) all dependent tasks in the pipeline object with the new output
- Sets of output such as from `@split` and `@subdivide` and `@originate` have a terminating condition and/or a associated count (# of output)
- Tasks in the pipeline object forward incoming inputs to task input slots (for slots common to all jobs in a task: `@inputs`, `@add_inputs`) or to slots in new jobs in the pipeline object
- When all slots are full in each job, this triggers putting the job parameters onto the job submission queue
- The pipeline object should allow Ruffus to be reentrant?

2.13.8 Todo: Allow checkpoint files to be moved

Allow checkpoint files to be "rebased" so that moving the working directory of the pipeline does not invalidate all the files.

We need some sort of path search and replace mechanism which handles conflicts, and probably versioning?

2.13.9 Todo: Remove intermediate files

Often large intermediate files are produced in the middle of a pipeline which could be removed. However, their absence would cause the pipeline to appear out of date. What is the best way to solve this?

In gmake, all intermediate files which are not marked `.PRECIOUS` are deleted.

We can similar mark out all tasks producing intermediate files so that all their output file can be deleted using an `@intermediate/provisional/transient/temporary/interim/ephemeral` decorator.

The tricky part of the design is how to delete files without disrupting our ability to build the original file dependency DAG, and hence check which tasks have up-to-date output when the pipeline is run again.

1. We can just work back from upstream/downstream files and ignore the intermediate files as gmake does. However, the increased power of Ruffus makes this very fragile: In gmake, the DAG is entirely specified by the specified destination files. In Ruffus, the number of task files is indeterminate, and can be changed at run time (see @split and @subdivide)
2. We can save the filenames into the checksum file before deleting them
3. We can leave the files in place files but zero out their contents. It is probably best to write a small magic text value to the file, e.g. "RUFFUS_ZEROED_FILE", so that we are not confused by real files of zero size.

In practice (2) and (3) should be combined for safety.

1. pipeline_cleaunup() will print out a list of files to be zeroed, or a list of commands to zero files or just do it for you
2. When rerunning, we can force files to be recreated using `pipeline_run(..., forcedtorun_tasks,...)`, and Ruffus will track back through lists of dependencies and recreate all "zeroed" files.

2.14 Planned Improvements to Ruffus

- `@split` needs to be able to specify at run time the number of resulting jobs without using wild cards
- legacy support for wild cards and file names.

2.14.1 Planned: Running python code (task functions) transparently on remote cluster nodes

Wait until next release.

Will bump Ruffus to v.3.0 if can run python jobs transparently on a cluster!

abstract out `task.run_pooled_job_without_exceptions()` as a function which can be supplied to `pipeline_run`

Common "job" interface:

- marshalled arguments
- marshalled function
- submission timestamp

Returns

- completion timestamp
- returned values
- exception

1. Full version use libpythongrid? * http://zguide.zeromq.org/page:all * Christian Widmer <ckwidmer@gmail.com> * Cheng Soon Ong <chengsoon.ong@unimelb.edu.au> * https://code.google.com/p/pythongrid/source/browse/#git%2Fpythongrid * Probably not good to base Ruffus entirely on libpythongrid to minimise dependencies, the use of sophisticated configuration policies etc.
2. Start with light-weight file-based protocol * specify where the scripts should live * use drmaa to start jobs * have executable ruffus module which knows how to load deserialise (unmarshall) function / parameters from disk. This would be what drmaa starts up, given the marshalled data as an argument * time stamp * "heart beat" to check that the job is still running
3. Next step: socket-based protocol * use specified master port in ruffus script * start remote processes using drmaa * child receives marshalled data and the address::port in the ruffus script (head node) to initiate hand shake or die * process recycling: run successive jobs on the same remote process for reduced overhead, until exceeds max number of jobs on the same process, min/max time on the same process * resubmit if die (Don't do sophisticated stuff like libpythongrid).

2.14.2 Planned: Custom parameter generator

Request on mailing list

> I've often wished that I could use an arbitrary function to process the input filepath instead of just a regex.
>
> ```
> def f(inputs, outputs, extra_param1, extra_param2):
>     # do something to generate parameters
>     return new_output_param, new_extra_param1, new_extra_param2
> ```
>
> now f() can be used inside a Ruffus decorator to generate the outputs from inputs, instead of being forced to use a regex for the job.
>
> Cheers, Bernie.

Leverages built-in Ruffus functionality. Don't have to write entire parameter generation from scratch.

- Gets passed an iterator where you can do a for loop to get input parameters / a flattened list of files
- Other parameters are forwarded as is
- The duty of the function is to `yield` input, output, extra parameters

Simple to do but how do we prevent this from being a job-trickling barrier?

Postpone until we have an initial design for job-trickling: Ruffus v.4 ;-(

2.14.3 Planned: Ruffus GUI interface.

Desktop (PyQT or web-based solution?) I'd love to see an svg pipeline picture that I could actually interact with

2.14.4 Planned: Non-decorator / Function interface to Ruffus

2.14.5 Planned: @retry_on_error(NUM_OF_RETRIES)

2.14.6 Planned: Clean up

The plan is to store the files and directories created via a standard interface.

The placeholders for this are a function call `register_cleanup`.

Jobs can specify the files they created and which need to be deleted by returning a list of file names from the job function.

So:

```
raise Exception = Error

return False = halt pipeline now

return string / list of strings = cleanup files/directories later

return anything else = ignored
```

The cleanup file/directory store interface can be connected to a text file or a database.

The cleanup function would look like this:

```
pipeline_cleanup(cleanup_log("../cleanup.log"), [instance ="october19th" ])
pipeline_cleanup(cleanup_msql_db("user", "password", "hash_record_table"))
```

The parameters for where and how to store the list of created files could be similarly passed to pipeline_run as an extra parameter:

```
pipeline_run(cleanup_log("../cleanup.log"), [instance ="october19th" ])
pipeline_run(cleanup_msql_db("user", "password", "hash_record_table"))
```

where *cleanup_log* and *cleanup_msql_db* are classes which have functions for

1. storing file
2. retrieving file
3. clearing entries

- Files would be deleted in reverse order, and directories after files.
- By default, only empty directories would be removed.

  But this could be changed with a `--forced_remove_dir` option
- An `--remove_empty_parent_directories` option would be supported by os.removedirs(path).

2.15 Implementation Tips

2.15.1 Items remaining for current release

Code

1. update_checksum_level_on_tasks(checksum_level) is non reentrant
2. `Task.description_with_args_placeholder` needs to only fill in placeholders at the last minute Otherwise cloned pipelines will have the wrong name

Unit tests

1. output_dir for @mkdir
2. When are things defined / linked up
3. When can we join up Pipelines / tasks / set_input()?
4. Sub pipeline
5. Whether setup occurs `pipeline_run()` where `target_tasks` and `forcedtorun_tasks` are in different linked or unlinked pipelines
6. name lookup
7. Task (dependency) parsing inside @transform, pipeline.transform(input = , add_inputs, replace_inputs =), pipeline.split(..., output=)
8. `mkdir()` should not be allowed inside input parameters apart from @follows
9. Cannot dependency cannot be self
10. `Pipeline.clone()`

11. `Task.set_input()`
12. `@product` `set_input` should take (`input`, `input2`...)

2.15.2 Release

- Change `ruffus_version.py`
- Rebuild pdf and copy it to `doc/static_data`

    cd doc make latexpdf cp _build/latex/ruffus.pdf static_data

- Rebuild documentation:

```
make htmlsync
```

- tag git with, for example:

```
git tag -a v2.6 -m "Version 2.6"
```

- Upload to pypi:

```
python setup.py sdist --format=gztar upload
```

- Upload to repository:

```
git push googlecode
git push
```

2.15.3 blogger

```
.article-content h2 {color: #ad3a2b}
.article-content h3 {color: #0100b4}
    #header .header-bar .title h1
    {
    background-image: url('http://www.ruffus.org.uk/_static/small_logo.png');
    background-repeat: no-repeat;
    background-position: left;
    }
```

2.15.4 dbdict.py

This is an sqlite backed dictionary originally written by Jacob Sondergaard and contributed by Jake Biesinger who added automatic pickling of python objects.

The pickling code was refactored out by Leo Goodstadt into separate functions as part of the preparation to make Ruffus python3 ready.

Python original saved (pickled) objects as 7 bit ASCII strings. Later formats (protocol = -1 is the latest format) uses 8 bit strings and are rather more efficient.

These then need to be saved as BLOBs to sqlite3 rather than normal strings. We can signal this by wrapping the pickled string in a object providing a "buffer interface". This is `buffer` in python2.6/2.7 and `memoryview` in python3.

http://bugs.python.org/issue7723 suggests there is no portable python2/3 way to write blobs to Sqlite without these two incompatible wrappers. This would require conditional compilation:

```
if sys.hexversion >= 0x03000000:
    value = memoryview(pickle.dumps(value, protocol = -1))
else:
    value = buffer(pickle.dumps(value, protocol = -1))
```

Despite the discussion on the bug report, sqlite3.Binary seems to work. We shall see if this is portable to python3.

2.15.5 how to write new decorators

New placeholder class. E.g. for `@new_deco`

```
class new_deco(task_decorator):
    pass
```

Add to list of action names and ids:

```
action_names = ["unspecified",
                ...
                "task_new_deco",

action_task_new_deco     =  15
```

Add function:

```
def task_transform (self, orig_args):
```

Add documentation to:

- decorators/NEW_DECORATOR.rst
- decorators/decorators.rst
- _templates/layout.html
- manual

2.16 Implementation notes

N.B. Remember to cite Jake Biesinger and see if he is interested to be a co-author if we ever resubmit the drastically changed version... He contributed checkpointing, travis and tox etc.

2.16.1 `Ctrl-C` handling

Pressing `Ctrl-C` left dangling process in Ruffus 2.4 because `KeyboardInterrupt` does not play nice with python `multiprocessing.Pool` See http://stackoverflow.com/questions/1408356/keyboard-interrupts-with-pythons-multiprocessing-pool/1408476#1408476

http://bryceboe.com/2012/02/14/python-multiprocessing-pool-and-keyboardinterrupt-revisited/ provides a reimplementation of Pool which however only works when you have a fixed number of jobs which should then run in parallel to completion. Ruffus is considerably more complicated because we have a variable number of jobs completing and being submitted into the job queue at any one time. Think of tasks stalling waiting for the dependent tasks to complete and then all the jobs of the task being released onto the queue

The solution is

1. Use a `timeout` parameter when using `IMapIterator.next(timeout=None)` to iterate through `pool.imap_unordered` because only timed `condition` s can be interruptible by signals...!!
2. This involves rewriting the `for` loop manually as a `while` loop
3. We use a timeout of `99999999`, i.e. 3 years, which should be enough for any job to complete...
4. Googling after the fact, it looks like the galaxy guys (cool dudes or what) have written similar code
5. `next()` for normal iterators do not take `timeout` as an extra parameter so we have to wrap next in a conditional :-(. The galaxy guys do a shim around `next()` but that is as much obsfucation as a simple if...
6. After jobs are interrupted by a signal, we rethrow with our own exception because we want something that inherits from `Exception` unlike `KeyboardInterrupt`
7. When a signal happens, we need to immediately stop `feed_job_params_to_process_pool()` from sending more parameters into the job queue (`parameter_q`) We use a proxy to a `multiprocessing.Event` (via `syncmanager.Event()`). When `death_event` is set, all further processing stops...
8. We also signal that all jobs should finish by putting `all_tasks_complete()` into `parameter_q` but only `death_event` prevents jobs already in the queue from going through
9. Ater signalling, some of the child processes appear to be dead by the time we start cleaning up. `pool.terminate()` sometimes tries and fails to re-connect to the the `death_event` proxy via sockets and throws an exception. We should really figure out a better solution but in the meantime wrapping it in a `try / except` allows a clean exit.
10. If a vanilla exception is raised without multiprocessing running, we still need to first save the exception in `job_errors` (even if it is just one) before cleaning up, because the cleaning up process may lead to further (ignored) exceptions which would overwrite the current exception when we need to rethrow it

Exceptions thrown in the middle of a multiprocessing / multithreading job appear to be handled gracefully.

For drmaa jobs, `qdel` may still be necessary.

2.16.2 Python3 compatability

Required extensive changes especially in unit test code.

Changes:

1. `sort` in python3 does not order mixed types, i.e. `int()`, `list()` and `str()` are incommensurate
   - In `task.get_output_files (...)`, sort after conversion to string

     ```
     sorted(self.output_filenames, key = lambda x: str(x))
     ```

   - In `file_name_parameters.py`: `collate_param_factory (...)`, `sort` after conversion to string, then `groupby` without string conversion. This is because we can't guarantee that two different objects do not have the same string representation. But `groupby` requires that similar things are adjacent...

     In other words, `groupby` is a refinement of `sorted`

     ```
     for output_extra_params, grouped_params in groupby(sorted(io_params_iter, key = get_outp
         pass
     ```

2. `print()` is a function

   ```
   from __future__ import print_function
   ```

3. `items()` only returns a list in python2. Rewrite `dict.iteritems()` whenever this might cause a performance bottleneck

4. `zip` and `map` return iterators. Conditionally import in python2

   ```
   import sys
   if sys.hexversion < 0x03000000:
       from future_builtins import zip, map
   ```

5. `cPickle->pickle` `CStringIO->io` need to be conditionally imported

   ```
   try:
       import StringIO as io
   except:
       import io as io
   ```

6. `map` code can be changed to list comprehensions. Use `2to3` to do heavy lifting

7. All normal strings are unicode in python3. Have to use `bytes` to support 8-bit char arrays. Normally, this means that `str` "just works". However, to provide special handling of both 8-bit and unicode strings in python2, we often need to check for `isinstance(xxx, basestring)`.

   We need to conditionally define:

   ```
   if sys.hexversion >= 0x03000000:
       # everything is unicode in python3
       path_str_type = str
   else:
       path_str_type = basestring

   # further down...
   if isinstance(compiled_regex, path_str_type):
       pass
   ```

2.16.3 Refactoring: parameter handling

Though the code is still split in a not very sensible way between `ruffus_utility.py`, `file_name_parameters.py` some rationalisation has taken place, and comments added so further refactoring can be made more easily.

Common code for:

```
file_name_parameters.split_ex_param_factory()
file_name_parameters.transform_param_factory()
file_name_parameters.collate_param_factory()
```

has been moved to `file_name_parameters.py.yield_io_params_per_job()`

unit tests added to `test_file_name_parameters.py` and `test_ruffus_utility.py`

2.16.4 `formatter`

`get_all_paths_components(paths, regex_str)` in `ruffus_utility.py`

Input files names are first squished into a flat list of files. `get_all_paths_components()` returns both the regular expression matches and the break down of the path.

In case of name clashes, the classes with higher priority override:

1. Captures by name
2. Captures by index
3. **Path components:** 'ext' = extension with dot 'basename' = file name without extension 'path' = path before basename, not ending with slash 'subdir' = list of directories starting with the most nested and ending with the root (if normalised) 'subpath' = list of 'path' with successive directories removed starting with the most nested and ending with the root (if normalised)

E.g. `name = '/a/b/c/sample1.bam',formatter=r"(.*)(?P<id>\d+)\.(.+)")` returns:

```
0:          '/a/b/c/sample1.bam',          // Entire match captured by index
1:          '/a/b/c/sample',               // captured by index
2:          'bam',                         // captured by index
'id':       '1'                            // captured by name
'ext':      '.bam',
'subdir':   ['c', 'b', 'a', '/'],
'subpath':  ['/a/b/c', '/a/b', '/a', '/'],
'path':     '/a/b/c',
'basename': 'sample1',
```

The code is in `ruffus_utility.py`:

```
results = get_all_paths_components(paths, regex_str)
string.format(results[2])
```

All the magic is hidden inside black boxes `filename_transform` classes:

```
class t_suffix_filename_transform(t_filename_transform):
class t_regex_filename_transform(t_filename_transform):
class t_format_filename_transform(t_filename_transform):
```

formatter(): regex() and suffix()

The previous behaviour with regex() where mismatches fail even if no substitution is made is retained by the use of `re.subn()`. This is a corner case but I didn't want user code to break

```
# filter on ".txt"
input_filenames = ["a.wrong", "b.txt"]
regex("(.txt)$")

# fails, no substitution possible
r"\1"

# fails anyway even through regular expression matches not referenced...
r"output.filename"
```

2.16.5 @product()

- Use combinatoric generators from itertools and keep that naming scheme

- Put all new generators in an `combinatorics` submodule namespace to avoid breaking user code. (They can imported if necessary.)
- test code in test/test_combinatorics.py
- The `itertools.product(repeat)` parameter doesn't make sense for Ruffus and will not be used
- Flexible number of pairs of `task` / `glob` / file names + `formatter()`
- Only `formatter([OPTIONAl_REGEX])` provides the necessary flexibility to construct the output so we won't bother with suffix and regex
- Similar to `@transform` but with extra level of nested-ness

Retain same code for `@product` and `@transform` by adding an additional level of indirection:

- generator wrap around `get_strings_in_nested_sequence` to convert nested input parameters either to a single flat list of file names or to nested lists of file names

```
file_name_parameters.input_param_to_file_name_list (input_params)
file_name_parameters.list_input_param_to_file_name_list (input_params)
```

- `t_file_names_transform` class which stores a list of regular expressions, one for each `formatter()` object corresponding to a single set of input parameters

```
t_formatter_file_names_transform
t_nested_formatter_file_names_transform
```

- string substitution functions which will apply a list of `formatter` changes

```
ruffus.utility.t_formatter_replace()
ruffus.utility.t_nested_formatter_replace()
```

- `ruffus_uilility.swap_doubly_nested_order()` makes the syntax / implementation very orthogonal

2.16.6 `@permutations(...)`, `@combinations(...)`, `@combinations_with_replacement(`

Similar to `@product` extra level of nested-ness is self versus self

Retain same code for `@product`

- forward to a sinble `file_name_parameters.combinatorics_param_factory()`
- use `combinatorics_type` to dispatch to `combinatorics.permutations`, `combinatorics.combinations` and `combinatorics.combinations_with_replacement`
- use `list_input_param_to_file_name_list` from `file_name_parameters.product_param_factory()`

2.16.7 drmaa alternatives

Alternative, non-drmaa polling code at

https://github.com/bjpop/rubra/blob/master/rubra/cluster_job.py

2.16.8 Task completion monitoring

How easy is it to abstract out the database?

- **The database is Jacob Sondergaard's `dbdict` which is a nosql / key-value store wrapper around sqlite**

```
job_history = dbdict.open(RUFFUS_HISTORY_FILE, picklevalues=True)
```

- The key is the output file name, so it is important not to confuse Ruffus by having different tasks generate the same output file!
- Is it possible to abstract this so that **jobs** get timestamped as well?
- If we should ever want to abstract out `dbdict`, we need to have a similar key-value store class, and make sure that a single instance of `dbdict` is used through `pipeline_run` which is passed up and down the function call chain. `dbdict` would then be drop-in replaceable by our custom (e.g. flat-file-based) dbdict alternative.

To peek into the database:

```
$ sqlite3 .ruffus_history.sqlite
sqlite> .tables
data
sqlite> .schema data
CREATE TABLE data (key PRIMARY KEY,value);
sqlite> select key from data order by key;
```

Can we query the database, get Job history / stats?

Yes, if we write a function to read and dump the entire database but this is only useful with timestamps and task names. See below

What are the run time performance implications?

Should be fast: a single db connection is created and used inside `pipeline_run`, `pipeline_printout`, `pipeline_printout_graph`

Avoid pauses between tasks

Allows Ruffus to avoid adding an extra 1 second pause between tasks to guard against file systems with low timestamp granularity.

- If the local file time looks to be in sync with the underlying file system, saved system time is used instead of file timestamps

2.16.9 `@mkdir(...)`,

- `mkdir` continues to work seamlessly inside `@follows` but also as its own decorator `@mkdir` due to the original happy orthogonal design
- fixed bug in checking so that Ruffus does't blow up if non strings are in the output (number...)

- note: adding the decorator to a previously undecorated function might have unintended consequences. The undecorated function turns into a zombie.
- fixed ugly bug in `pipeline_printout` for printing single line output
- fixed description and printout indent

2.16.10 Parameter handling

Current design

Parameters in Ruffus v 2.x are obtained using a "pull" model.

Each task has its self.param_generator_func() This is an iterator function which yields `param` and `descriptive_param` per iteration:

```
for param, descriptive_param in self.param_generator_func(runtime_data):
    pass


``param`` and ``descriptive_param`` are basically the same except that globs are not expanded in
they are used for display.
```

The iterator functions have all the state they need to generate their input, output and extra parameters (only `runtime_data`) is added at run time. These closures are generated as nested functions inside "factory" functions defined in `file_name_parameters.py`

Each task type has its own factory function. For example:

```
args_param_factory (orig_args)
files_param_factory (input_files_task_globs, flatten_input, do_not_expand_single_job_tasks,
split_param_factory (input_files_task_globs, output_files_task_globs, *extra_params)
merge_param_factory (input_files_task_globs, output_param, *extra_params)
originate_param_factory (list_output_files_task_globs, extras)
```

The following factory files delegate most of their work to `yield_io_params_per_job`:

to support:

- `inputs()`, `add_inputs()` input parameter supplementing
- extra inputs, outputs, extra parameter replacement with `suffix()`, `regex()` and `formatter`

```
collate_param_factory       (input_files_task_globs,      flatten_input,
transform_param_factory     (input_files_task_globs,      flatten_input,
combinatorics_param_factory (input_files_task_globs,      flatten_input, combinatorics_type,
subdivide_param_factory     (input_files_task_globs,      flatten_input,
product_param_factory       (list_input_files_task_globs, flatten_input,


yield_io_params_per_job (input_params, file_names_transform, extra_input_files_task_globs, r
```

1. The first thing they do is to get a list of input parameters, either directly, or by expanding globs or by query upstream tasks:

   ```
   file_names_from_tasks_globs(files_task_globs, runtime_data, do_not_expand_single_job_
   ```

   Note: `True_if_split_or_merge` is a wierd parameter which directly

queries the upstream dependency for its output files if it is a single task...

This is legacy code. Probably should be refactored out of existence...

---

2. They then convert the input parameters to a flattened list of file names (passing through unchanged the original input parameters structure)

```
input_param_to_file_name_list()
# combinatorics and product call:
list_input_param_to_file_name_list()
```

This is done at the iterator level because the combinatorics decorators do not have just a list of input parameters (They have combinations, permutations, products of input parameters etc) but a list of lists of input parameters.

transform, collate, subdivide => list of strings. combinatorics / product => list of lists of strings

3. `yield_io_params_per_job` yields pairs of param sets by

   - Replacing or supplementing input parameters for the indicator objects `inputs()` and `add_inputs()`
   - Expanding extra parameters
   - Expanding output parameters (with or without expanding globs)

   In each case:

   - If these contains objects which look like strings, we do regular expression / file component substitution
   - If they contain tasks, these are queries for output files

---

Note: This should be changed:

If the flattened list of input file names is empty, ie. if the input parameters contain just other stuff, then the entire parameter is ignored.

Handling file names

All strings in input (or output parameters) are treated as file names unless they are wrapped with `output_from` in which case they are `Task`, `Pipeline` or function names.

A list of strings for ready for substitution to output parameters is obtained from the `ruffus_utility.get_strings_in_flattened_sequence()`

This is called from:

file_name_parameters

1. Either to check that input files exist: `check_input_files_exist()` `needs_update_check_directory_missing()` `needs_update_check_exist()` `needs_update_check_modify_time()`
2. Or to generate parameters from the various param factories

   `product_param_factory()` `transform_param_factory()` `collate_param_factory()` `combinatorics_param_factory()` `subdivide_param_factory()`

These first call `file_names_from_tasks_globs()` to get the input parameters, then pass a flattened list of strings to `yield_io_params_per_job()`

-> file_names_from_tasks_globs() -> yield_io_params_per_job(input_param_to_file_name_list() / list_input_param_to_file_name_list())

task

3. to obtain a list of file names to `touch`

   `job_wrapper_io_files`

4. to make directories

   `job_wrapper_mkdir`

5. update / remove files in `job_history` if job succeeded or failed

   `pipeline_run`

Refactor to handle input parameter objects with ruffus_params() functions

We want to expand objects with ruffus_params *only* when doing output parameter substitution, i.e. Case (2) above. They are not file names: cases (1), (3), (4), (5).

Therefore: Expand in `file_names_from_tasks_globs()` which also handles `inputs()` and `add_inputs` and `@split` outputs.

Refactor to handle formatter() replacement with "{EXTRAS[0][1][3]}" and "[INPUTS[1][2]]"

Non-recursive Substitution in all:

construct new list where each item is replaced referring to the original and then assign

extra_inputs() "[INPUTS[1][2]]" refers to the original input output / extras "[INPUTS[1][2]]" refers to substituted input

In addition to the flattened input paramters, we need to pass in the unflattened input and extra parameters

In `file_name_parameters.py.`: `yield_io_params_per_job`

From: .. code-block:: python

extra_inputs = extra_input_files_task_globs.file_names_transformed (filenames, file_names_transform) extra_params = tuple(file_names_transform.substitute(filenames, p) for p in extra_specs) output_pattern_transformed = output_pattern.file_names_transformed (filenames, file_names_transform) output_param = file_names_transform.substitute_output_files(filenames, output_pattern)

To: .. code-block:: python

extra_inputs = extra_input_files_task_globs.file_names_transformed (orig_input_param, extra_specs, filenames, file_names_transform) extra_params = tuple(file_names_transform.substitute(input_param, extra_specs, filenames, p) for p in extra_specs) output_pattern_transformed = output_pattern.file_names_transformed (input_param, extra_specs, filenames, file_names_transform) output_param = file_names_transform.substitute_output_files(input_param, extra_specs, filenames, output_pattern)

In other words, we need two extra parameters for inputs and extras

```
class t_file_names_transform(object):
    def substitute (self, input_param, extra_param, starting_file_names, pattern):
        pass
    def substitute_output_files (self, input_param, extra_param, starting_file_names, patter
        pass


class t_params_tasks_globs_run_time_data(object):
    def file_names_transformed (self, input_param, extra_param, filenames, file_names_transf
        pass
```

Refactor to handle alternative outputs with either_or(...,...)

- what happens to get_outputs or checkpointing when the job completes but the output files are not made?
- either_or matches
  - the only alternative to have all files existing
  - the alternative with the most recent file
- either_or behaves as `list()` in `file_name_parameters.py.` : `file_names_from_tasks_globs`
- Handled to check that input files exist:

  `check_input_files_exist()` `needs_update_check_directory_missing()`
  `needs_update_check_exist()` `needs_update_check_modify_time()`
- Handled to update / remove files in `job_history` if job succeeded or failed
- Only first either_or is used to obtain list of file names to `touch`

  `task.job_wrapper_io_files`
- Only first either_or is used to obtain list of file names to make directories

  `job_wrapper_mkdir`
- What happens in `task.get_output_files()`?

2.16.11 Add Object Orientated interface

Passed Unit tests

1. Refactored to remove unused "flattened" code paths / parameters
2. Prefix all attributes for Task into underscore so that help(Task) is not overloaded with details
3. **Named parameters**
   - parse named parameters in order filling in from unnamed
   - save parameters in `dict Task.parsed_args`
   - **call `setup_task_func()` afterwards which knows how to setup:**
     - poor man's OOP but
     - allows type to be changed after constructor: Because can't guarantee that `@transform` `@merge` is the first Ruffus decorator to be encountered.

- `setup_task_func()` is called for every task before pipeline_xxx()

4. Much more informative messages for errors when parsing decorator arguments
5. Pipeline decorator methods renamed to decorator_xxx as in `decorator_follows`
6. `Task.get_task_name()` * rename to `Task.get_display_name()` * distinguish between decorator and OO interface
7. Rename `_task` to `Task`
8. **Identifying tasks from t_job_result:**
    - job results do not contain references to `Task` so that it can be marshalled more easily
    - we need to look up task at job completion
    - use `_node_index` from `graph.py` so we have always a unique identifier for each `Task`
9. **Parse arguments using ruffus_utility.parse_task_arguments**
    - Reveals full hackiness and inconsistency between `add_inputs` and `inputs`. The latter only takes a single argument. Each of the elements of the former gets added along side the existing inputs.
10. Add `Pipeline` class * Create global called `"main"` (accessed by Pipeline.pipelines["main"])
11. **Task name lookup**
    - Task names are unique (Otherwise Ruffus will complain at Task creation)
    - Can also lookup by fully qualified or unqualified function name but these can be ambiguous
    - Ambiguous lookups give a list of tasks only so we can have nice diagnostic messages ... UI trumps clean design
12. Look up strings across pipelines #. Is pipeline name qualified? Check that #. Check default (current) pipeline #. Check if pipeline name. In which case returns all tail functions #. Check all pipelines
    - Will blow up at any instance of ambiguity in any particular pipeline
    - Will blow up at any instance of ambiguity across pipelines
    - Note that mis-spellings will cause problems but if this were c++, I would enforce stricter checking
13. Look up functions across pipelines * Try current pipeline first, then all pipelines * Will blow up at any instance of ambiguity in any particular pipeline * Will blow up at any instance of ambiguity across pipelines (if not in current pipeline)
14. @mkdir, @follows(mkdir)
15. `Pipeline.get_head_tasks(self)` (including tasks with mkdir())
16. `Pipeline.get_tail_tasks(self)`
17. `Pipeline._complete_task_setup()` which follows chain of dependencies for each task in a pipeline

Pipeline and Task creation

- Share code as far as possible between decorator and OOP syntax
- Cannot use textbook OOP inheritance hierarchy easily because @decorators are not necessarily given in order.

```
Pipeline.transform
    _do_create_task_by_OOP()

@transform
```

```
        Pipeline._create_task()
        task._decorator_transform

            task._prepare_transform()
                self.setup_task_func = self._transform_setup
                parse_task_arguments


    Pipeline.run
        pipeline._complete_task_setup()
            # walk up ancestors of all task and call setup_task_func
            unprocessed_tasks = Pipeline.tasks
            while len(unprocessed_tasks):
                ancestral_tasks = setup_task_func()
                if not already processed:
                    unprocessed_tasks.append(ancestral_tasks)

            Call _complete_task_setup() for all the pipelines of each task
```

Connecting Task into a DAG

```
    task._complete_setup()
        task._remove_all_parents()
        task._deferred_connect_parents()
        task._setup_task_func()
            task._handle_tasks_globs_in_inputs()
                task._connect_parents()
                    # re-lookup task from names in current pipeline so that pipeline.clone() works
```

- Task dependencies are normally deferred and saved to `Task.deferred_follow_params`
- If Task dependencies call for a new Task (`follows`/`follows(mkdir)`), this takes place immediately
- The parameters in `Task.deferred_follow_params` are updated with the created `Task` when this happens
- `Task._prepare_preceding_mkdir()` has a `defer` flag to prevent it from updating `Task.deferred_follow_params` when it is called to resolve deferred dependencies from `Task._connect_parents()`. Otherwise we will have two copies of each deferred dependency...
- `Task.deferred_follow_params` must be deep-copied otherwise cloned pipelines will interfere with each other when dependencies are resolved...

2.17 FAQ

2.17.1 Citations

Q. How should *Ruffus* be cited in academic publications?

The official publication describing the original version of *Ruffus* is:

> Leo Goodstadt (2010) : **Ruffus: a lightweight Python library for computational pipelines.** *Bioinformatics* 26(21): 2778-2779

2.17.2 Good practices

Q. What is the best way of keeping my data and workings separate?

It is good practice to run your pipeline in a temporary, "working" directory away from your original data.

The first step of your pipeline might be to make softlinks to your original data in your working directory. This is example (relatively paranoid) code to do just this:

```
def re_symlink (input_file, soft_link_name, logger, logging_mutex):
    """
    Helper function: relinks soft symbolic link if necessary
    """
    # Guard agains soft linking to oneself: Disastrous consequences of deleting the original
    if input_file == soft_link_name:
        logger.debug("Warning: No symbolic link made. You are using the original data direct
        return
    # Soft link already exists: delete for relink?
    if os.path.lexists(soft_link_name):
        # do not delete or overwrite real (non-soft link) file
        if not os.path.islink(soft_link_name):
            raise Exception("%s exists and is not a link" % soft_link_name)
        try:
            os.unlink(soft_link_name)
        except:
            with logging_mutex:
                logger.debug("Can't unlink %s" % (soft_link_name))
    with logging_mutex:
        logger.debug("os.symlink(%s, %s)" % (input_file, soft_link_name))
    #
    #   symbolic link relative to original directory so that the entire path
    #       can be moved around with breaking everything
    #
    os.symlink( os.path.relpath(os.path.abspath(input_file),
                os.path.abspath(os.path.dirname(soft_link_name))), soft_link_name)

#
#   First task should soft link data to working directory
#
@jobs_limit(1)
@mkdir(options.working_dir)
@transform( input_files,
            formatter(),
            # move to working directory
            os.path.join(options.working_dir, "{basename[0]}{ext[0]}"),
            logger, logging_mutex
           )
def soft_link_inputs_to_working_directory (input_file, soft_link_name, logger, logging_mutex
    """
    Make soft link in working directory
    """
    with logging_mutex:
        logger.info("Linking files %(input_file)s -> %(soft_link_name)s\n" % locals())
    re_symlink(input_file, soft_link_name, logger, logging_mutex)
```

Q. What is the best way of handling data in file pairs (or triplets etc.)

In Bioinformatics, DNA data often consists of only the nucleotide sequence at the two ends of larger fragments. The paired_end or mate pair data frequently consists of of file pairs with conveniently related names such as "*.R1.fastq" and* ".R2.fastq".

At some point in data pipeline, these file pairs or triplets must find each other and be analysed in the same job.

Provided these file pairs or triplets are named consistently, an easiest way to regroup them is to use the Ruffus *@collate* decorator. For example:

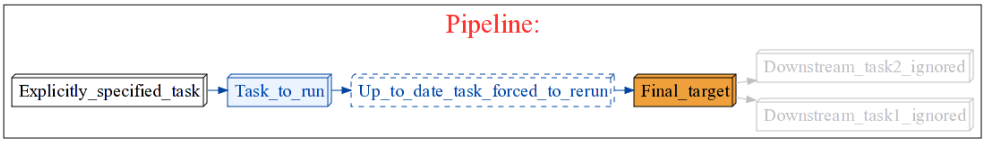
```
@collate(original_data_files,

            # match file name up to the "R1.fastq.gz"
            formatter("([^/]+)R[12].fastq.gz$"),

            # Create output parameter supplied to next task
            "{path[0]}/{1[0]}.sam",
            logger, logger_mutex)
def handle_paired_end(input_files, output_paired_files, logger, logger_mutex):
    # check that we really have a pair of two files not an orphaned singleton
    if len(input_files) != 2:
        raise Exception("One of read pairs %s missing" % (input_files,))

    # do stuff here
```

This (incomplete, untested) *example code* shows what this would look like *in vivo*.

2.17.3 General

Q. *Ruffus* won't create dependency graphs

A. You need to have installed `dot` from Graphviz to produce pretty flowcharts likes this:



Q. *Ruffus* seems to be hanging in the same place

A. If *ruffus* is interrupted, for example, by a Ctrl-C, you will often find the following lines of code highlighted:

```
File "build/bdist.linux-x86_64/egg/ruffus/task.py", line 1904, in pipeline_run
File "build/bdist.linux-x86_64/egg/ruffus/task.py", line 1380, in run_all_jobs_in_task
File "/xxxx/python2.6/multiprocessing/pool.py", line 507, in next
  self._cond.wait(timeout)
File "/xxxxx/python2.6/threading.py", line 237, in wait
  waiter.acquire()
```

This is *not* where *ruffus* is hanging but the boundary between the main programme process and the sub-processes which run *ruffus* jobs in parallel.

This is naturally where broken execution threads get washed up onto.

Q. Regular expression substitutions don't work

A. If you are using the special regular expression forms `"\1"`, `"\2"` etc. to refer to matching groups, remember to 'escape' the subsitution pattern string. The best option is to use 'raw' python strings. For example:

```
r"\1_substitutes\2correctly\3four\4times"
```

Ruffus will throw an exception if it sees an unescaped `"\1"` or `"\2"` in a file name.

Q. How to force a pipeline to appear up to date?

I have made a trivial modification to one of my data files and now Ruffus wants to rerun my month long pipeline. How can I convince Ruffus that everything is fine and to leave things as they are?

The standard way to do what you are trying to do is to touch all the files downstream... That way the modification times of your analysis files would postdate your existing files. You can do this manually but Ruffus also provides direct support:

```
pipeline_run (touch_files_only = True)
```

pipeline_run will run your script normally stepping over up-to-date tasks and starting with jobs which look out of date. However, after that, none of your pipeline task functions will be called, instead, each non-up-to-date file is touch-ed in turn so that the file modification dates follow on successively.

See the documentation for *pipeline_run()*

It is even simpler if you are using the new Ruffus.cmdline support from version 2.4. You can just type

```
your script --touch_files_only [--other_options_of_your_own_etc]
```

See *command line* documentation.

Q. How can I use my own decorators with Ruffus?

(Thanks to Radhouane Aniba for contributing to this answer.)

1. With care! If the following two points are observed:

1. Use @wraps from `functools` or Michele Simionato's decorator module

These will automatically forward attributes from the task function correctly:

- `__name__` and `__module__` is used to identify functions uniquely in a Ruffus pipeline, and
- `pipeline_task` is used to hold per task data

2. Always call Ruffus decorators first before your own decorators.

Otherwise, your decorator will be ignored.

So this works:

```
@follows(prev_task)
@custom_decorator(something)
def test():
    pass
```

This is a bit futile

```
# ignore @custom_decorator
@custom_decorator(something)
@follows(prev_task)
def test():
    pass
```

This order dependency is an unfortunate quirk of how python decorators work. The last (rather futile) piece of code is equivalent to:

```
test = custom_decorator(something)(ruffus.follows(prev_task)(test))
```

Unfortunately, Ruffus has no idea that someone else (`custom_decorator`) is also modifying the `test()` function after it (`ruffus.follows`) has had its go.

Example decorator:

Let us look at a decorator to time jobs:

```
import sys, time
def time_func_call(func, stream, *args, **kwargs):
    """prints elapsed time to standard out, or any other file-like object with a .write() methoc
    """
   start = time.time()
   # Run the decorated function.
   ret = func(*args, **kwargs)
   # Stop the timer.
   end = time.time()
   elapsed = end - start
   stream.write("{} took {} seconds\n".format(func.__name__, elapsed))
   return ret


from ruffus import *
import sys
import time

@time_job(sys.stderr)
def first_task():
    print "First task"


@follows(first_task)
@time_job(sys.stderr)
def second_task():
    print "Second task"


@follows(second_task)
@time_job(sys.stderr)
def final_task():
    print "Final task"
```

```
pipeline_run()
```

What would `@time_job` look like?

1. Using functools @wraps

```
import functools
def time_job(stream=sys.stdout):
    def actual_time_job(func):
        @functools.wraps(func)
        def wrapper(*args, **kwargs):
            return time_func_call(func, stream, *args, **kwargs)
        return wrapper
    return actual_time_job
```

2. Using Michele Simionato's decorator module

```
import decorator
def time_job(stream=sys.stdout):
    def time_job(func, *args, **kwargs):
        return time_func_call(func, stream, *args, **kwargs)
    return decorator.decorator(time_job)
```

2. By hand, using a callable object

```
class time_job(object):
    def __init__(self, stream=sys.stdout):
        self.stream = stream
    def __call__(self, func):
        def inner(*args, **kwargs):
            return time_func_call(func, self.stream, *args, **kwargs)
        # remember to forward __name__
        inner.__name__ = func.__name__
        inner.__module__ = func.__module__
        inner.__doc__ = func.__doc__
        if hasattr(func, "pipeline_task"):
            inner.pipeline_task = func.pipeline_task
        return inner
```

Q. Can a task function in a *Ruffus* pipeline be called normally outside of Ruffus?

A. Yes. Most python decorators wrap themselves around a function. However, *Ruffus* leaves the original function untouched and unwrapped. Instead, *Ruffus* adds a `pipeline_task` attribute to the task function to signal that this is a pipelined function.

This means the original task function can be called just like any other python function.

Q. My *Ruffus* tasks create two files at a time. Why is the second one ignored in successive stages of my pipeline?

This is my code:

```
from ruffus import *
import sys
@transform("start.input", regex(".+"), ("first_output.txt", "second_output.txt"))
def task1(i,o):
    pass

@transform(task1, suffix(".txt"), ".result")
def task2(i, o):
    pass

pipeline_printout(sys.stdout, [task2], verbose=3)
```

```
_____________________________________
Tasks which will be run:

Task = task1
       Job = [start.input
              ->[first_output.txt, second_output.txt]]

Task = task2
       Job = [[first_output.txt, second_output.txt]
              ->first_output.result]


_____________________________________
```

A: This code produces a single output of a tuple of 2 files. In fact, you want two outputs, each consisting of 1 file.

You want a single job (single input) to be produce multiple outputs (multiple jobs in downstream tasks). This is a one-to-many operation which calls for *@split*:

```
from ruffus import *
import sys
@split("start.input", ("first_output.txt", "second_output.txt"))
def task1(i,o):
    pass

@transform(task1, suffix(".txt"), ".result")
def task2(i, o):
    pass

pipeline_printout(sys.stdout, [task2], verbose=3)
```

```
_____________________________________
Tasks which will be run:

Task = task1
       Job = [start.input
              ->[first_output.txt, second_output.txt]]

Task = task2
       Job = [first_output.txt
              ->first_output.result]
       Job = [second_output.txt
              ->second_output.result]


_____________________________________
```

Q. How can a *Ruffus* task produce output which goes off in different directions?

A. As above, anytime there is a situation which requires a one-to-many operation, you should reach for *@subdivide*. The advanced form takes a regular expression, making it easier to produce multiple derivatives of the input file. The following example subdivides *2* jobs each into *3*, so that the subsequence task will run *2* x *3* = *6* jobs.

```
from ruffus import *
import sys
@subdivide(["1.input_file",
            "2.input_file"],
            regex(r"(.+).input_file"),      # match file prefix
           [r"\1.file_type1",
            r"\1.file_type2",
            r"\1.file_type3"])
def split_task(input, output):
   pass


@transform(split_task, regex("(.+)"), r"\1.test")
def test_split_output(i, o):
   pass

pipeline_printout(sys.stdout, [test_split_output], verbose = 3)
```

Each of the original 2 files have been split in three so that test_split_output will run 6 jobs simultaneously.

```
_____________________________________________
Tasks which will be run:

Task = split_task
       Job = [1.input_file ->[1.file_type1, 1.file_type2, 1.file_type3]]
       Job = [2.input_file ->[2.file_type1, 2.file_type2, 2.file_type3]]

Task = test_split_output
       Job = [1.file_type1 ->1.file_type1.test]
       Job = [1.file_type2 ->1.file_type2.test]
       Job = [1.file_type3 ->1.file_type3.test]
       Job = [2.file_type1 ->2.file_type1.test]
       Job = [2.file_type2 ->2.file_type2.test]
       Job = [2.file_type3 ->2.file_type3.test]
_____________________________________________
```

Q. Can I call extra code before each job?

A. This is easily accomplished by hijacking the process for checking if jobs are up to date or not (*@check_if_uptodate*):

```
from ruffus import *
import sys

def run_this_before_each_job (*args):
    print "Calling function before each job using these args", args
    # Remember to delegate to the default *Ruffus* code for checking if
    #   jobs need to run.
    return needs_update_check_modify_time(*args)
```

```
@check_if_uptodate(run_this_before_each_job)
@files([[None, "a.1"], [None, "b.1"]])
def task_func(input, output):
    pass

pipeline_printout(sys.stdout, [task_func])
```

This results in:

```
>>> pipeline_run([task_func])
Calling function before each job using these args (None, 'a.1')
Calling function before each job using these args (None, 'a.1')
Calling function before each job using these args (None, 'b.1')
    Job = [None -> a.1] completed
    Job = [None -> b.1] completed
Completed Task = task_func
```

Note: Because `run_this_before_each_job(...)` is called whenever *Ruffus* checks to see if a job is up to date or not, the function may be called twice for some jobs (e.g. `(None, 'a.1')` above).

Q. Does *Ruffus* allow checkpointing: to distinguish interrupted and completed results?

A. Use the builtin sqlite checkpointing

By default, `pipeline_run(...)` will save the timestamps for output files from successfully run jobs to an sqlite database file (`.ruffus_history.sqlite`) in the current directory .

- If you are using `Ruffus.cmdline`, you can change the checksum / timestamp database file name on the command line using `--checksum_file_name NNNN`
-

The level of timestamping / checksumming can be set via the `checksum_level` parameter:

```
pipeline_run(..., checksum_level = N, ...)
```

where the default is 1:

```
level 0 : Use only file timestamps
level 1 : above, plus timestamp of successful job completion
level 2 : above, plus a checksum of the pipeline function body
level 3 : above, plus a checksum of the pipeline function default arguments and the additional a
```

A. Use a flag file

When gmake is interrupted, it will delete the target file it is updating so that the target is remade from scratch when make is next run. Ruffus, by design, does not do this because, more often than not, the partial / incomplete file may be usefully if only to reveal, for example, what might have caused an interrupting error or exception. It also seems a bit too clever and underhand to go around the programmer's back to delete files...

A common *Ruffus* convention is create an empty checkpoint or "flag" file whose sole purpose is to record a modification-time and the successful completion of a job.

This would be task with a completion flag:

```
#
#   Assuming a pipelined task function named "stage1"
#
@transform(stage1, suffix(".stage1"), [".stage2", ".stage2_finished"] )
def stage2 (input_files, output_files):
    task_output_file, flag_file = output_files
    cmd = ("do_something2 %(input_file)s >| %(task_output_file)s ")
    cmd = cmd % {
                    "input_file":               input_files[0],
                    "task_output_file":         task_output_file
                }
    if not os.system( cmd ):
        #88888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888
        #
        #   It worked: Create completion flag_file
        #
        open(flag_file, "w")
        #
        #88888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888
```

The flag_files `xxx.stage2_finished` indicate that each job is finished. If this is missing, `xxx.stage2` is only a partial, interrupted result.

The only thing to be aware of is that the flag file will appear in the list of inputs of the downstream task, which should accordingly look like this:

```
@transform(stage2, suffix(".stage2"), [".stage3", ".stage3_finished"] )
def stage3 (input_files, output_files):

    #88888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888
    #
    #   Note that the first parameter is a LIST of input files, the last of which
    #       is the flag file from the previous task which we can ignore
    #
    input_file, previous_flag_file  = input_files
    #
    #88888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888
    task_output_file, flag_file     = output_files
    cmd = ("do_something3 %(input_file)s >| %(task_output_file)s ")
    cmd = cmd % {
                    "input_file":               input_file,
                    "task_output_file":         task_output_file
                }
    # completion flag file for this task
    if not os.system( cmd ):
        open(flag_file, "w")
```

The *Bioinformatics example* contains *code* for checkpointing.

A. Use a temp file

Thanks to Martin Goodson for suggesting this and providing an example. In his words:

"I normally use a decorator to create a temporary file which is only renamed after the task has completed without any problems. This seems a more elegant solution to the problem:"

```
def usetemp(task_func):
    """ Decorate a function to write to a tmp file and then rename it. So half finished task
    """
    @wraps(task_func)
    def wrapper_function(*args, **kwargs):
        args=list(args)
        outnames=args[1]
        if not isinstance(outnames, basestring) and  hasattr(outnames, '__getitem__'):
            tmpnames=[str(x)+".tmp" for x in outnames]
            args[1]=tmpnames
            task_func(*args, **kwargs)
            try:
                for tmp, name in zip(tmpnames, outnames):
                    if os.path.exists(tmp):
                        os.rename(tmp, str(name))
            except BaseException as e:
                for name in outnames:
                    if os.path.exists(name):
                        os.remove(name)
                raise (e)
        else:
            tmp=str(outnames)+'.tmp'
            args[1]=tmp
            task_func(*args, **kwargs)
            os.rename(tmp, str(outnames))
return wrapper_function
```

Use like this:

```
@files(None, 'client1.price')
@usetemp
def getusers(inputfile, outputname):
    #***********************************************
    # code goes here
    # outputname now refers to temporary file
    pass
```

2.17.4 Windows

Q. Windows seems to spawn *ruffus* processes recursively

A. It is necessary to protect the "entry point" of the program under windows. Otherwise, a new process will be started each time the main module is imported by a new Python interpreter as an unintended side effects. Causing a cascade of new processes.

See: http://docs.python.org/library/multiprocessing.html#multiprocessing-programming

This code works:

```
if __name__ == '__main__':
    try:
        pipeline_run([parallel_task], multiprocess = 5)
except Exception, e:
    print e.args
```

2.17.5 Sun Grid Engine / PBS / SLURM etc

Q. Can Ruffus be used to manage a cluster or grid based pipeline?

1. Some minimum modifications have to be made to your *Ruffus* script to allow it to submit jobs to a cluster

See *ruffus.drmaa_wrapper*

Thanks to Andreas Heger and others at CGAT and Bernie Pope for contributing ideas and code.

Q. When I submit lots of jobs via Sun Grid Engine (SGE), the head node occassionally freezes and dies

1. You need to use multithreading rather than multiprocessing. See *ruffus.drmaa_wrapper*

Q. Keeping Large intermediate files

Sometimes pipelines create a large number of intermediate files which might not be needed later.

Unfortunately, the current design of *Ruffus* requires these files to hang around otherwise the pipeline will not know that it ran successfully.

We have some tentative plans to get around this but in the meantime, Bernie Pope suggests truncating intermediate files in place, preserving timestamps:

```
# truncate a file to zero bytes, and preserve its original modification time
def zeroFile(file):
    if os.path.exists(file):
        # save the current time of the file
        timeInfo = os.stat(file)
        try:
            f = open(file,'w')
        except IOError:
            pass
        else:
            f.truncate(0)
            f.close()
            # change the time of the file back to what it was
            os.utime(file,(timeInfo.st_atime, timeInfo.st_mtime))
```

2.17.6 Sharing python objects between Ruffus processes running concurrently

The design of Ruffus envisages that much of the data flow in pipelines occurs in files but it is also possible to pass python objects in memory.

Ruffus uses the multiprocessing module and much of the following is a summary of what is covered in depth in the Python Standard Library Documentation.

Running Ruffus using `pipeline_run(..., multiprocess = NNN)` where `NNN` > 1 runs each job concurrently on up to `NNN` separate local processes. Each task function runs independently in a different python intepreter, possibly on a different CPU, in the most efficient way. However, this does mean we have to pay some attention to how data is sent across process boundaries (unlike the situation with `pipeline_run(..., multithread = NNN)`).

The python code and data which comprises your multitasking Ruffus job is sent to a separate process in three ways:

1. The python function code and data objects are pickled, i.e. converting into a byte stream, by the master process, sent to the remote process before being converted back into normal python (unpickling).
2. The parameters for your jobs, i.e. what Ruffus calls your task functions with, are separately pickled and sent to the remote process via multiprocessing.Queue
3. You can share and synchronise other data yourselves. The canonical example is the logger provided by `Ruffus.cmdline.setup_logging`

Note: Check that your function code and data can be pickled.

Only functions, built-in functions and classes defined at the top level of a module are picklable.

The following answers are a short "how-to" for sharing and synchronising data yourselves.

Can ordinary python objects be shared between processes?

1. Objects which can be pickled can be shared as is. These include
   - numbers
   - strings
   - tuples, lists, sets, and dictionaries containing only objects which can be pickled.
2. If these do not change during your pipeline, you can just use them without any further effort in your task.
3. If you need to use the value at the point when the task function is *called*, then you need to pass the python object as parameters to your task. For example:

```
# changing_list changes...
@transform(previous_task, suffix(".foo"), ".bar", changing_list)
def next_task(input_file, output_file, changing_list):
    pass
```

4. If you need to use the value when the task function is *run* then see *the following answer.*.

Why am I getting `PicklingError`?

What is happening? Didn't Joan of Arc solve this once and for all?

1. Some of the data or code in your function cannot be pickled and is being asked to be sent by python `mulitprocessing` across process boundaries.

   When you run your pipeline using multiprocess:

   ```
   pipeline_run([], verbose = 5, multiprocess = 5, logger = ruffusLoggerProxy)
   ```

   You will get the following errors:

   ```
   Exception in thread Thread-2:
   Traceback (most recent call last):
     File "/path/to/python/python2.7/threading.py", line 808, in __bootstrap_inner
       self.run()
     File "/path/to/python/python2.7/threading.py", line 761, in run
   ```

```
    self.__target(*self.__args, * *self.__kwargs)
  File "/path/to/python/python2.7/multiprocessing/pool.py", line 342, in _handle_task
    put(task)
PicklingError: Can't pickle <type 'function'>: attribute lookup __builtin__.function
```

which go away when you set `pipeline_run([], multiprocess = 1, ...)`

Unfortunately, pickling errors are particularly ill-served by standard python error messages. The only really good advice is to take the offending code and try and pickle it yourself and narrow down the errors. Check your objects against the list in the pickle module. Watch out especially for nested functions. These will have to be moved to file scope. Other objects may have to be passed in proxy (see below).

How about synchronising python objects in real time?

1. You can use managers and proxy objects from the multiprocessing module.

The underlying python object would be owned and managed by a (hidden) server process. Other processes can access the shared objects transparently by using proxies. This is how the logger provided by `Ruffus.cmdline.setup_logging` works:

```
#  optional logger which can be passed to ruffus tasks
logger, logger_mutex = cmdline.setup_logging (__name__, options.log_file, options.verbose)
```

`logger` is a proxy for the underlying python logger object, and it can be shared freely between processes.

The best course is to pass `logger` as a parameter to a *Ruffus* task.

The only caveat is that we should make sure multiple jobs are not writting to the log at the same time. To synchronise logging, we use proxy to a non-reentrant multiprocessing.lock.

```
logger, logger_mutex = cmdline.setup_logging (__name__, options.log_file, options.verbose)


@transform(previous_task, suffix(".foo"), ".bar", logger, logger_mutex)
def next_task(input_file, output_file, logger, logger_mutex):
    with logger_mutex:
        logger.info("We are in the middle of next_task: %s -> %s" % (input_file, output_file))
```

Can I share and synchronise my own python classes via proxies?

1. multiprocessing.managers.SyncManager provides out of the box support for lists, arrays and dicts etc.

   Most of the time, we can use a "vanilla" manager provided by multiprocessing.Manager():

   ```
   import multiprocessing
   manager = multiprocessing.Manager()

   list_proxy = manager.list()
   dict_proxy = manager.dict()
   lock_proxy           = manager.Lock()
   namespace_proxy      = manager.Namespace()
   queue_proxy          = manager.Queue([maxsize])
   rentrant_lock_proxy  = manager.RLock()
   semaphore_proxy      = manager.Semaphore([value])
   char_array_proxy     = manager.Array('c')
   integer_proxy        = manager.Value('i', 6)
   ```

```
@transform(previous_task, suffix(".foo"), ".bar", lock_proxy, dict_proxy, list_proxy)
def next_task(input_file, output_file, lock_proxy, dict_proxy, list_proxy):
    with lock_proxy:
        list_proxy.append(3)
        dict_proxy['a'] = 5
```

However, you can also create proxy custom classes for your own objects.

In this case you may need to derive from multiprocessing.managers.SyncManager and register proxy functions. See `Ruffus.proxy_logger` for an example of how to do this.

How do I send python objects back and forth without tangling myself in horrible synchronisation code?

1. Sharing python objects by passing messages is a much more modern and safer way to coordinate multitasking than using synchronization primitives like locks.

The python multiprocessing module provides support for passing python objects as messages between processes. You can either use pipes or queues. The idea is that one process pushes and object onto a pipe or queue and the other processes pops it out at the other end. Pipes are only two ended so queues are usually a better fit for sending data to multiple Ruffus jobs.

Proxies for queues can be passed between processes as in the previous section

How do I share large amounts of data efficiently across processes?

1. If it is really impractical to use data files on disk, you can put the data in shared memory.

It is possible to create shared objects using shared memory which can be inherited by child processes or passed as Ruffus parameters. This is probably most efficently done via the array interface. Again, it is easy to create locks and proxies for synchronised access:

```
from multiprocessing import Process, Lock
from multiprocessing.sharedctypes import Value, Array
from ctypes import Structure, c_double

manager = multiprocessing.Manager()

lock_proxy          = manager.Lock()
int_array_proxy     = manager.Array('i', [123] * 100)

@transform(previous_task, suffix(".foo"), ".bar", lock_proxy, int_array_proxy)
def next_task(input_file, output_file, lock_proxy, int_array_proxy):
    with lock_proxy:
        int_array_proxy[23] = 71
```

2.18 Glossary

task A stage in a computational pipeline.

Each **task** in *ruffus* is represented by a python function.

For example, a task might be to find the products of a sets of two numbers:

```
4 x 5 = 20
5 x 6 = 30
2 x 7 = 14
```

job Any number of operations which can be run in parallel and make up the work in a stage of a computional pipeline.

Each **task** in *ruffus* is a separate call to the **task** function.

For example, if a task is to find products of numbers, each of these will be a separate job.

Job1:

```
4 x 5 = 20
```

Job2:

```
5 x 6 = 30
```

Job3:

```
2 x 7 = 14
```

Jobs need not complete in order.

decorator Ruffus decorators allow functions to be incorporated into a computational pipeline, with automatic generation of parameters, dependency checking etc., without modifying any code within the function. Quoting from the python wiki:

> A Python decorator is a specific change to the Python syntax that allows us to more conveniently alter functions and methods.
>
> Decorators dynamically alter the functionality of a function, method, or class without having to directly use subclasses or change the source code of the function being decorated.

generator python generators are new to python 2.2 (see Charming Python: Iterators and simple generators). They allow iterable data to be generated on the fly.

Ruffus asks for generators when you want to generate **job** parameters dynamically.

Each set of job parameters is returned by the `yield` keyword for greater clarity. For example,:

```
def generate_job_parameters():

    for file_index, file_name in iterate(all_file_names):

        # parameter for each job
        yield file_index, file_name
```

Each job takes the parameters `file_index` and `file_name`

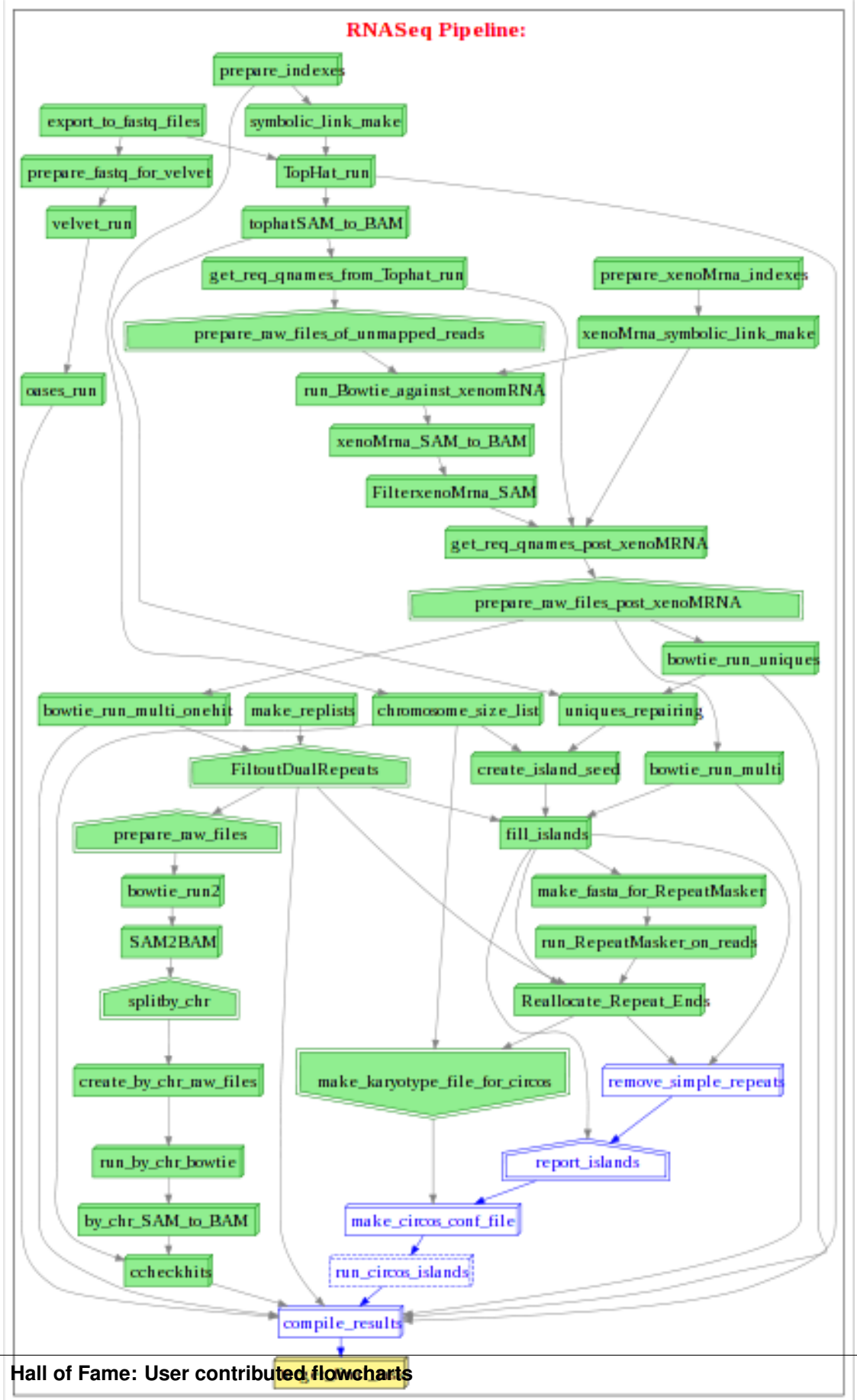
2.19 Hall of Fame: User contributed flowcharts

Please contribute your own work flows in your favourite colours with (an optional) short description to email: ruffus_lib at llew.org.uk

2.19.1 RNASeq pipeline

http://en.wikipedia.org/wiki/RNA-Seq

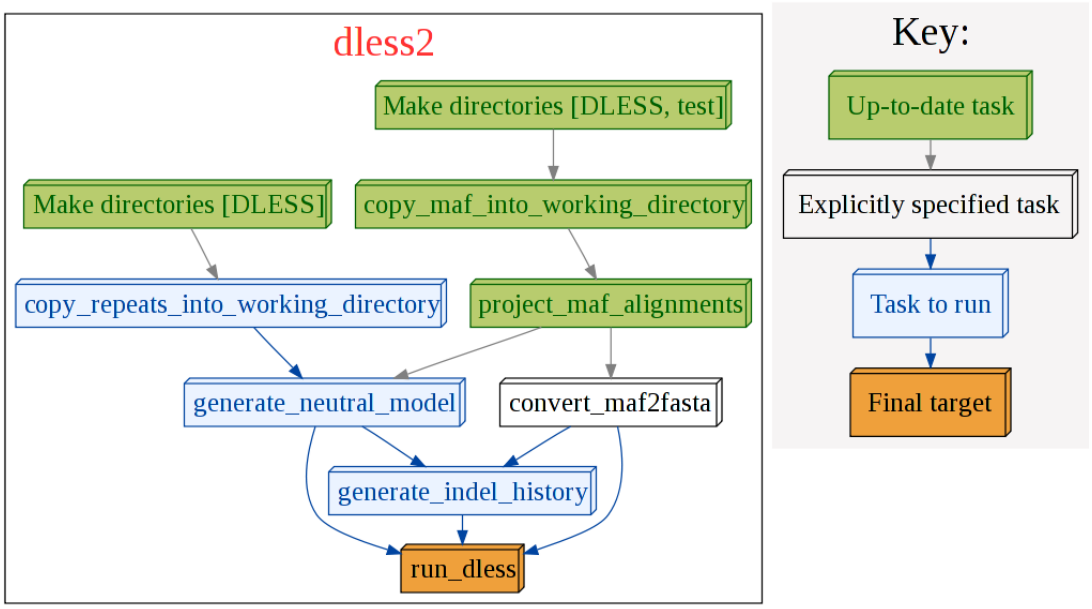
Mapping transcripts onto genomes using high-throughput sequencing technologies (`svg`).


RNASeq Pipeline:
prepare_indexes
export_to_fastq_files
symbolic_link_make
prepare_fastq_for_velvet
TopHat_run
velvet_run
tophatSAM_to_BAM
get_req_qnames_from_Tophat_run
prepare_xenoMrna_indexes
prepare_mw_files_of_unmapped_reads
xenoMrna_symbolic_link_make
oases_run
run_Bowtie_against_xenomRNA
xenoMrna_SAM_to_BAM
FilterxenoMrna_SAM
get_req_qnames_post_xenoMRNA
prepare_mw_files_post_xenoMRNA
bowtie_run_uniques
bowtie_run_multi_onehit
make_replists
chromosome_size_list
uniques_repairing
FiltoutDualRepeats
create_island_seed
bowtie_run_multi
prepare_mw_files
fill_islands
bowtie_run2
make_fasta_for_RepeatMasker
SAM2BAM
run_RepeatMasker_on_reads
splitby_chr
Reallocate_Repeat_Ends
create_by_chr_mw_files
make_karyotype_file_for_circos
remove_simple_repeats
run_by_chr_bowtie
report_islands
by_chr_SAM_to_BAM
make_circos_conf_file
ccheckhits
run_circos_islands
compile_results

2.19.2 non-coding evolutionary constraints

http://en.wikipedia.org/wiki/Noncoding_DNA

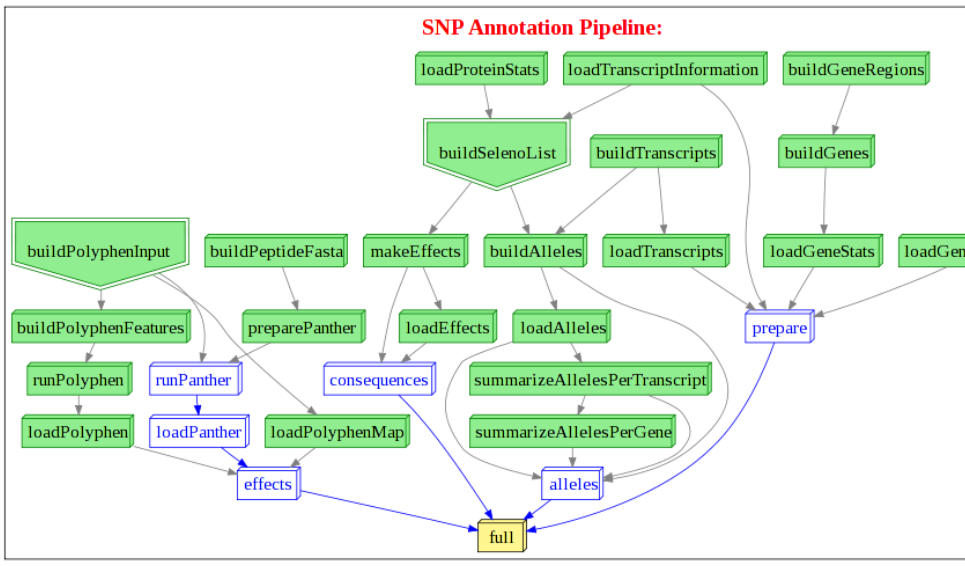
Non-protein coding evolutionary constraints in different species (`svg`).



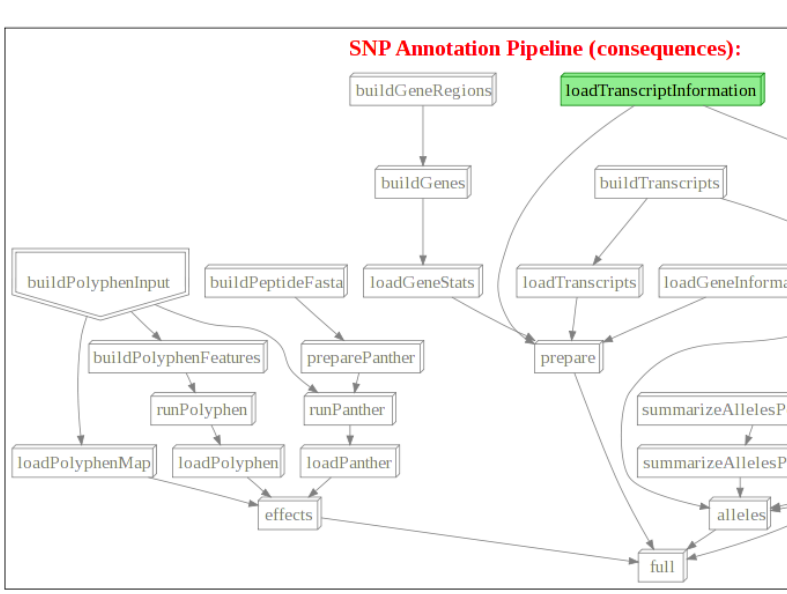
2.19.3 SNP annotation

Predicting impact of different Single Nucleotide Polymorphisms

http://en.wikipedia.org/wiki/Single-nucleotide_polymorphism



Population variation across genomes (`svg`).



Using "pseudo" targets to run only part of the pipeline (`svg`).

2.19.4 Chip-Seq analysis

Analysing DNA binding sites with Chip-Seq http://en.wikipedia.org/wiki/Chip-Sequencing

(`svg`)

2.20 Why *Ruffus*?

Cylindrophis ruffus is the name of the red-tailed pipe snake (bad python-y pun) which can be found in Hong Kong where the original author comes from.

Ruffus is a shy creature, and pretends to be a cobra or a banded krait by putting up its red tail and ducking its head in its coils when startled.

- Not venomous
- Mostly Harmless

- Deadly poisonous
- Seriously unfriendly

Be careful not to step on one when running down country park lanes at full speed in Hong Kong: this snake is a rare breed!

Ruffus does most of its work at night and sleeps during the day: typical of many (but alas not all) python programmers!

The original red-tail pipe and banded krait images are from wikimedia.

CHAPTER

THREE

EXAMPLES

3.1 Construction of a simple pipeline to run BLAST jobs

3.1.1 Overview

This is a simple example to illustrate the convenience **Ruffus** brings to simple tasks in bioinformatics.

1. **Split** a problem into multiple fragments that can be
2. **Run in parallel** giving partial solutions that can be
3. **Recombined** into the complete solution.

The example code runs a ncbi blast search for four sequences against the human refseq protein sequence database.

1. **Split** each of the four sequences into a separate file.
2. **Run in parallel** Blastall on each sequence file
3. **Recombine** the BLAST results by simple concatenation.

In real life,

- BLAST already provides support for multiprocessing
- Sequence files would be split in much larger chunks, with many sequences
- The jobs would be submitted to large computational farms (in our case, using the SunGrid Engine).
- The High Scoring Pairs (HSPs) would be parsed / filtered / stored in your own formats.

Note: This bioinformatics example is intended to showcase *some* of the features of Ruffus.

1. See the *manual* to learn about the various features in Ruffus.

3.1.2 Prerequisites

1. Ruffus

To install Ruffus on most systems with python installed:

```
easy_install -U ruffus
```

Otherwise, download Ruffus and run:

```
tar -xvzf ruffus-xxx.tar.gz
cd ruffus-xxx
./setup install
```

where xxx is the latest Ruffus version.

2. BLAST

This example assumes that the BLAST `blastall` and `formatdb` executables are installed and on the search path. Otherwise download from here.

3. human refseq sequence database

We also need to download the human refseq sequence file and format the ncbi database:

```
wget ftp://ftp.ncbi.nih.gov/refseq/H_sapiens/mRNA_Prot/human.protein.faa.gz
gunzip human.protein.faa.gz

formatdb -i human.protein.faa
```

4. test sequences

Query sequences in FASTA format can be found in original.fa

3.1.3 Code

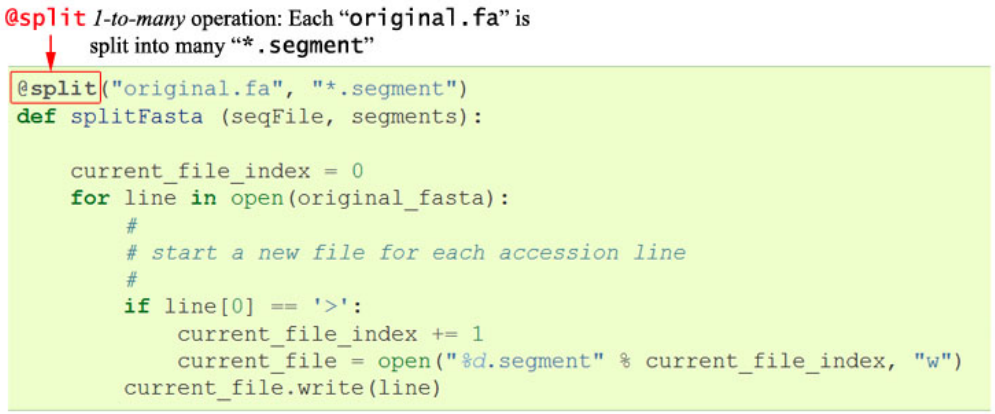
The code for this example can be found *here* and pasted into the python command shell.

3.1.4 Step 1. Splitting up the query sequences

We want each of our sequences in the query file original.fa to be placed in a separate files named `XXX.segment` where `XXX` = 1 -> the number of sequences.

```
current_file_index = 0
for line in open("original.fa"):
    # start a new file for each accession line
    if line[0] == '>':
        current_file_index += 1
        current_file = open("%d.segment" % current_file_index, "w")
    current_file.write(line)
```

To use this in a pipeline, we only need to wrap this in a function, "decorated" with the Ruffus keyword *@split*:



This indicates that we are splitting up the input file original.fa into however many `*.segment` files as it takes.

The pipelined function itself takes two arguments, for the input and output.

We shall see later this simple *@split* decorator already gives all the benefits of:

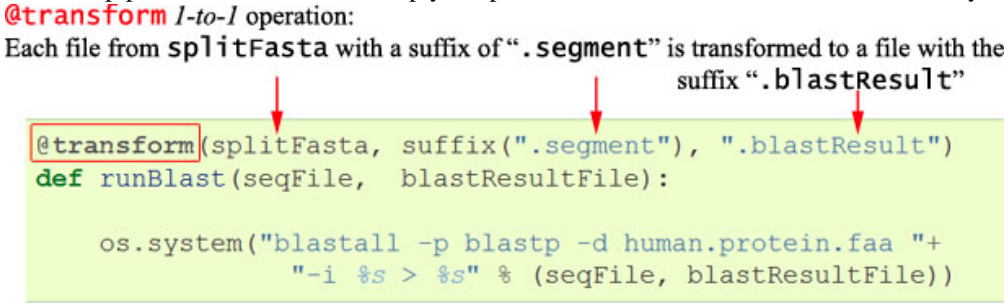
- Dependency checking
- Flowchart printing

3.1.5 Step 2. Run BLAST jobs in parallel

Assuming that blast is already installed, sequence matches can be found with this python code:

```
os.system("blastall -p blastp -d human.protein.faa -i 1.segment > 1.blastResult")
```

To pipeline this, we need to simply wrap in a function, decorated with the **Ruffus** keyword *@transform*.



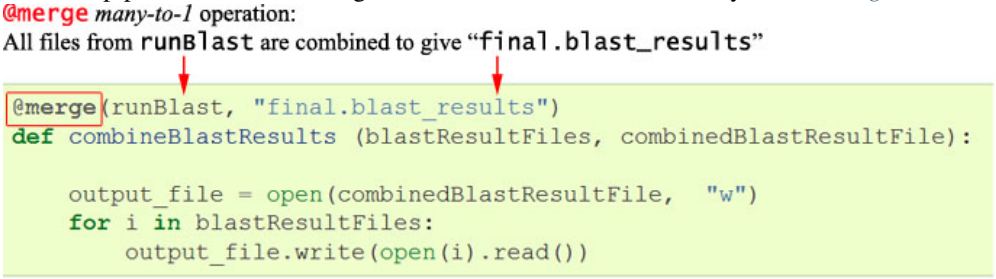
This indicates that we are taking all the output files from the previous `splitFasta` operation (`*.segment`) and *@transform*-ing each to a new file with the `.blastResult` suffix. Each of these transformation operations can run in parallel if specified.

3.1.6 Step 3. Combining BLAST results

The following python code will concatenate the results together

```
    output_file = open("final.blast_results",  "w")
    for i in glob("*.blastResults"):
        output_file.write(open(i).read())
```

To pipeline this, we need again to decorate with the **Ruffus** keyword *@merge*.



This indicates that we are taking all the output files from the previous `runBlast` operation (`*.blastResults`) and *@merge*-ing them to the new file `final.blast_results`.

3.1.7 Step 4. Running the pipeline

We can run the completed pipeline using a maximum of 4 parallel processes by calling *pipeline_run* :

```
pipeline_run([combineBlastResults], verbose = 2, multiprocess = 4)
```

Though we have only asked Ruffus to run `combineBlastResults`, it traces all the dependencies of this task and runs all the necessary parts of the pipeline.

Note: The full code for this example can be found *here* suitable for pasting into the python command shell.

The `verbose` parameter causes the following output to be printed to stderr as the pipeline runs:

```
>>> pipeline_run([combineBlastResults], verbose = 2, multiprocess = 4)
    Job = [original.fa -> *.segment] completed
Completed Task = splitFasta
    Job = [1.segment -> 1.blastResult] completed
    Job = [3.segment -> 3.blastResult] completed
    Job = [2.segment -> 2.blastResult] completed
    Job = [4.segment -> 4.blastResult] completed
Completed Task = runBlast
    Job = [[1.blastResult, 2.blastResult, 3.blastResult, 4.blastResult] -> final.blast_resul
Completed Task = combineBlastResults
```

3.1.8 Step 5. Testing dependencies

If we invoked *pipeline_run* again, nothing further would happen because the pipeline is now up-to-date. But what if the pipeline had not run to completion?

We can simulate the failure of one of the `blastall` jobs by deleting its results:

```
os.unlink("4.blastResult")
```

Let us use the *pipeline_printout* function to print out the dependencies of the pipeline at a high `verbose` level which will show both complete and incomplete jobs:

```
>>> import sys
>>> pipeline_printout(sys.stdout, [combineBlastResults], verbose = 4)

_____________________________________________
Tasks which are up-to-date:

Task = splitFasta
    "Split sequence file into as many fragments as appropriate depending on the size of
               original_fasta"



_____________________________________________
Tasks which will be run:

Task = runBlast
    "Run blast"
       Job = [4.segment
             ->4.blastResult]
         Job needs update: Missing file 4.blastResult

Task = combineBlastResults
    "Combine blast results"
       Job = [[1.blastResult, 2.blastResult, 3.blastResult, 4.blastResult]
             ->final.blast_results]
         Job needs update: Missing file 4.blastResult


_____________________________________________
```

Only the parts of the pipeline which involve the missing BLAST result will be rerun. We can confirm this by invoking the pipeline.

```
>>> pipeline_run([combineBlastResults], verbose = 2, multiprocess = 4)

    Job = [1.segment -> 1.blastResult] unnecessary: already up to date
    Job = [2.segment -> 2.blastResult] unnecessary: already up to date
    Job = [3.segment -> 3.blastResult] unnecessary: already up to date
    Job = [4.segment -> 4.blastResult] completed
Completed Task = runBlast
    Job = [[1.blastResult, 2.blastResult, 3.blastResult, 4.blastResult] -> final.blast_resul
Completed Task = combineBlastResults
```

3.1.9 What is next?

In the *next (short) part*, we shall add some standard (boilerplate) code to turn this BLAST pipeline into a (slightly more) useful python program.

3.2 Part 2: A slightly more practical pipeline to run blasts jobs

3.2.1 Overview

Previously, we had built a simple pipeline to split up a FASTA file of query sequences so that these can be matched against a sequence database in parallel.

We shall wrap this code so that

- It is more robust to interruptions
- We can specify the file names on the command line

3.2.2 Step 1. Cleaning up any leftover junk from previous pipeline runs

We split up each of our sequences in the query file original.fa into a separate files named `XXX.segment` where `XXX` is the number of sequences in the FASTA file.

However, if we start with 6 sequences (giving `1.segment` ... `6.segment`), and we then edited original.fa so that only 5 were left, the file `6.segment` would still be left hanging around as an unwanted, extraneous and confusing orphan.

As a general rule, it is a good idea to clean up the results of a previous run in a *@split* operation:

```
@split("original.fa", "*.segment")
def splitFasta (seqFile, segments):

    #
    #   Clean up any segment files from previous runs before creating new one
    #
    for i in glob.glob("*.segment"):
        os.unlink(i)

    # code as before...
```

3.2.3 Step 2. Adding a "flag" file to mark successful completion

When pipelined tasks are interrupted half way through an operation, the output may only contain part of the results in an incomplete or inconsistent state. There are three general options to deal with this:

1. Catch any interrupting conditions and delete the incomplete output
2. Tag successfully completed output with a special marker at the end of the file
3. Create an empty "flag" file whose only point is to signal success

Option (3) is the most reliable way and involves the least amount of work in Ruffus. We add flag files with the suffix `.blastSuccess` for our parallel BLAST jobs:

```
@transform(splitFasta, suffix(".segment"), [".blastResult", ".blastSuccess"])
def runBlast(seqFile,  output_files):

    blastResultFile, flag_file = output_files

    #
    #   Existing code unchanged
    #
    os.system("blastall -p blastp -d human.protein.faa "+
                "-i %s > %s" % (seqFile, blastResultFile))

    #
    #   "touch" flag file to indicate success
    #
    open(flag_file, "w")
```

3.2.4 Step 3. Allowing the script to be invoked on the command line

We allow the query sequence file, as well as the sequence database and end results to be specified at runtime using the standard python optparse module. We find this approach to run time arguments generally useful for many Ruffus scripts. The full code can be *viewed here* and downloaded from run_parallel_blast.py.

The different options can be inspected by running the script with the `--help` or `-h` argument.

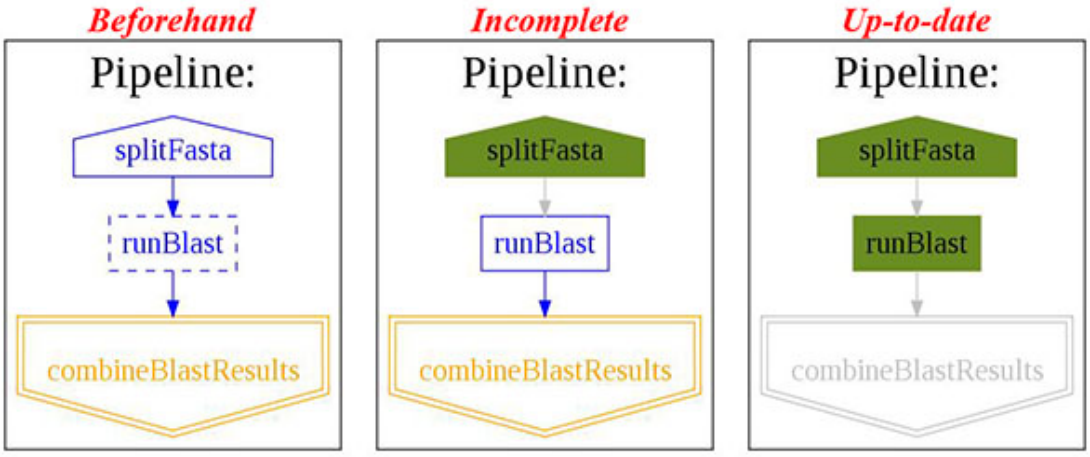
The following options are useful for developing Ruffus scripts:

```
--verbose | -v    :  Print more detailed messages for each additional verbose level.
                     E.g. run_parallel_blast --verbose --verbose --verbose ... (or -vvv)

--jobs | -j       :  Specifies the number of jobs (operations) to run in parallel.

--flowchart FILE  :  Print flowchart of the pipeline to FILE. Flowchart format
                     depends on extension. Alternatives include (".dot", ".jpg",
                     "*.svg", "*.png" etc). Formats other than ".dot" require
                     the dot program to be installed (http://www.graphviz.org/).

--just_print | -n    Only print a trace (description) of the pipeline.
                     The level of detail is set by --verbose.
```

3.2.5 Step 4. Printing out a flowchart for the pipeline

The `--flowchart` argument results in a call to `pipeline_printout_graph(...)` This prints out a flowchart of the pipeline. Valid formats include ".dot", ".jpg", ".svg", ".png" but all except for the first require the `dot` program to be installed (http://www.graphviz.org/).

The state of the pipeline is reflected in the flowchart:



3.2.6 Step 5. Errors

Because Ruffus scripts are just normal python functions, you can debug them using your usual tools, or jump to the offending line(s) even when the pipeline is running in parallel.

For example, these are the what the error messages would look like if we had mis-spelt `blastal`. In *run_parallel_blast.py*, python exceptions are raised if the `blastall` command fails.

Each of the exceptions for the parallel operations are printed out with the offending lines (line 204), and problems (`blastal` not found) highlighted in red.

```
Traceback (most recent call last):
  File "./run_parallel_blast.py", line 256, in <module>
    logger = logger, verbose=options.verbose)
  File "build/bdist.linux-i686/egg/ruffus/task.py", line 2655, in pipeline_run
ruffus.ruffus_exceptions.RethrownJobError:

    Exceptions running jobs for

   'def runBlast(...):'

   Original exceptions:
   Exception #1
   exceptions.Exception(Failed to run 'blastal -p blastp -d human.protein.faa
                                       -i tmp/1.segment > tmp/1.blastResult'
   /bin/sh: blastal: not found
   for __main__.runBlast.Job = [tmp/1.segment -> [tmp/1.blastResult,tmp/1.blastSuccess]]

   Traceback (most recent call last):
     [...]
     File "./run_parallel_blast.py", line 204, in runBlast
       run_cmd("blastal -p blastp -d human.protein.faa -i %s > %s" % (seqFile,
         blastResultFile))
     [...]

   Exception #2
   exceptions.Exception(Failed to run 'blastal -p blastp -d human.protein.faa
                                       -i tmp/1.segment > tmp/1.blastResult'
    /bin/sh: blastal: not found
   for __main__.runBlast.Job = [tmp/2.segment -> [tmp/2.blastResult, tmp/2.blastSuccess]]

   Traceback (most recent call last):
     [...]
     File "./run_parallel_blast.py", line 204, in runBlast
       run_cmd("blastal -p blastp -d human.protein.faa -i %s > %s" % (seqFile,
          blastResultFile))
     [...]

   Exception #3
   exceptions.Exception(Failed to run 'blastal -p blastp -d human.protein.faa
                                       -i tmp/1.segment > tmp/1.blastResult'
   /bin/sh: blastal: not found
   for __main__.runBlast.Job = [tmp/3.segment -> [tmp/3.blastResult, tmp/3.blastSuccess]]

   Traceback (most recent call last):
     [...]
     File "./run_parallel_blast.py", line 204, in runBlast
       run_cmd("blastal -p blastp -d human.protein.faa -i %s > %s" % (seqFile,
          blastResultFile))
     [...]
```

3.2.7 Step 6. Will it run?

The full code can be *viewed here* and downloaded from run_parallel_blast.py.

3.3 Ruffus code

```
import os, sys

exe_path = os.path.split(os.path.abspath(sys.argv[0]))[0]
sys.path.insert(0, os.path.abspath(os.path.join(exe_path,"..", "..","..")))

from ruffus import *


original_fasta = "original.fa"
database_file  = "human.protein.faa"

@split(original_fasta, "*.segment")
def splitFasta (seqFile, segments):
    """Split sequence file into
       as many fragments as appropriate
       depending on the size of original_fasta"""
    current_file_index = 0
    for line in open(original_fasta):
        #
        # start a new file for each accession line
        #
        if line[0] == '>':
            current_file_index += 1
            current_file = open("%d.segment" % current_file_index, "w")
        current_file.write(line)



@transform(splitFasta, suffix(".segment"), ".blastResult")
def runBlast(seqFile,  blastResultFile):
    """Run blast"""
    os.system("blastall -p blastp -d %s -i %s > %s" %
                (database_file, seqFile, blastResultFile))


@merge(runBlast, "final.blast_results")
def combineBlastResults (blastResultFiles, combinedBlastResultFile):
    """Combine blast results"""
    output_file = open(combinedBlastResultFile,  "w")
    for i in blastResultFiles:
        output_file.write(open(i).read())


pipeline_run([combineBlastResults], verbose = 2, multiprocess = 4)


#
#   Simulate interuption of the pipeline by
#        deleting the output of one of the BLAST jobs
#
os.unlink("4.blastResult")

pipeline_printout(sys.stdout, [combineBlastResults], verbose = 4)


#
```

```
#   Re-running the pipeline
#
pipeline_run([combineBlastResults], verbose = 2, multiprocess = 4)
```

3.4 Ruffus code

```
#!/usr/bin/env python
"""

    run_parallel_blast.py
    [--log_file PATH]
    [--quiet]

"""

################################################################################
#
#   run_parallel_blast
#
#
#   Copyright (c) 4/21/2010 Leo Goodstadt
#
#   Permission is hereby granted, free of charge, to any person obtaining a copy
#   of this software and associated documentation files (the "Software"), to deal
#   in the Software without restriction, including without limitation the rights
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#   copies of the Software, and to permit persons to whom the Software is
#   furnished to do so, subject to the following conditions:
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#
#   THE SOFTWARE IS PROVIDED "AS IS", WITHOUT WARRANTY OF ANY KIND, EXPRESS OR
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#   AUTHORS OR COPYRIGHT HOLDERS BE LIABLE FOR ANY CLAIM, DAMAGES OR OTHER
#   LIABILITY, WHETHER IN AN ACTION OF CONTRACT, TORT OR OTHERWISE, ARISING FROM,
#   OUT OF OR IN CONNECTION WITH THE SOFTWARE OR THE USE OR OTHER DEALINGS IN
#   THE SOFTWARE.
################################################################################
import os, sys
exe_path = os.path.split(os.path.abspath(sys.argv[0]))[0]
sys.path.insert(0,os.path.abspath(os.path.join(exe_path,"..", "..")))


#88888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888

#   options


#88888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888

from optparse import OptionParser
import sys, os

exe_path = os.path.split(os.path.abspath(sys.argv[0]))[0]
```

```
parser = OptionParser(version="%prog 1.0", usage = "\n\n    %prog --input_file QUERY_FASTA --database
parser.add_option("-i", "--input_file", dest="input_file",
                  metavar="FILE",
                  type="string",
                  help="Name and path of query sequence file in FASTA format. ")
parser.add_option("-d", "--database_file", dest="database_file",
                  metavar="FILE",
                  type="string",
                  help="Name and path of FASTA database to search. ")
parser.add_option("--result_file", dest="result_file",
                  metavar="FILE",
                  type="string",
                  default="final.blast_results",
                  help="Name and path of where the files should end up. ")
parser.add_option("-t", "--temp_directory", dest="temp_directory",
                  metavar="PATH",
                  type="string",
                  default="tmp",
                  help="Name and path of temporary directory where calculations "
                            "should take place. ")

#
#   general options: verbosity / logging
#
parser.add_option("-v", "--verbose", dest = "verbose",
                  action="count", default=0,
                  help="Print more detailed messages for each additional verbose level."
                       " E.g. run_parallel_blast --verbose --verbose --verbose ... (or -vvv)")

#
#   pipeline
#
parser.add_option("-j", "--jobs", dest="jobs",
                  default=1,
                  metavar="jobs",
                  type="int",
                  help="Specifies the number of jobs (operations) to run in parallel.")
parser.add_option("--flowchart", dest="flowchart",
                  metavar="FILE",
                  type="string",
                  help="Print flowchart of the pipeline to FILE. Flowchart format "
                       "depends on extension. Alternatives include ('.dot', '.jpg', "
                       "'*.svg', '*.png' etc). Formats other than '.dot' require "
                       "the dot program to be installed (http://www.graphviz.org/).")
parser.add_option("-n", "--just_print", dest="just_print",
                    action="store_true", default=False,
                    help="Only print a trace (description) of the pipeline. "
                         " The level of detail is set by --verbose.")

(options, remaining_args) = parser.parse_args()


if not options.flowchart:
    if not options.database_file:
        parser.error("\n\n\tMissing parameter --database_file FILE\n\n")
    if not options.input_file:
        parser.error("\n\n\tMissing parameter --input_file FILE\n\n")
```

```
#88888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888

#   imports

#88888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888

from ruffus import *
import subprocess



#88888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888

#   Functions


#88888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888
def run_cmd(cmd_str):
    """
    Throw exception if run command fails
    """
    process = subprocess.Popen(cmd_str, stdout = subprocess.PIPE,
                               stderr = subprocess.PIPE, shell = True)
    stdout_str, stderr_str = process.communicate()
    if process.returncode != 0:
        raise Exception("Failed to run '%s'\n%s%sNon-zero exit status %s" %
                        (cmd_str, stdout_str, stderr_str, process.returncode))


#88888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888

#   Logger


#88888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888

import logging
logger = logging.getLogger("run_parallel_blast")
#
# We are interesting in all messages
#
if options.verbose:
    logger.setLevel(logging.DEBUG)
    stderrhandler = logging.StreamHandler(sys.stderr)
    stderrhandler.setFormatter(logging.Formatter("    %(message)s"))
    stderrhandler.setLevel(logging.DEBUG)
    logger.addHandler(stderrhandler)



#88888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888

#   Pipeline tasks


#88888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888
original_fasta = options.input_file
```

```
database_file  = options.database_file
temp_directory = options.temp_directory
result_file    = options.result_file

@follows(mkdir(temp_directory))

@split(original_fasta, os.path.join(temp_directory, "*.segment"))
def splitFasta (seqFile, segments):
    """Split sequence file into
       as many fragments as appropriate
       depending on the size of original_fasta"""
    #
    #   Clean up any segment files from previous runs before creating new one
    #
    for i in segments:
        os.unlink(i)
    #
    current_file_index = 0
    for line in open(original_fasta):
        #
        # start a new file for each accession line
        #
        if line[0] == '>':
            current_file_index += 1
            file_name = "%d.segment" % current_file_index
            file_path = os.path.join(temp_directory, file_name)
            current_file = open(file_path, "w")
        current_file.write(line)


@transform(splitFasta, suffix(".segment"), [".blastResult", ".blastSuccess"])
def runBlast(seqFile,  output_files):
    #
    blastResultFile, flag_file = output_files
    #
    run_cmd("blastall -p blastp -d human.protein.faa -i %s > %s" % (seqFile, blastResultFile))
    #
    #   "touch" flag file to indicate success
    #
    open(flag_file, "w")


@merge(runBlast, result_file)
def combineBlastResults (blastResult_and_flag_Files, combinedBlastResultFile):
    """Combine blast results"""
    #
    output_file = open(combinedBlastResultFile,  "w")
    for blastResult_file, flag_file in blastResult_and_flag_Files:
        output_file.write(open(blastResult_file).read())
```

```
#88888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888

#   Print list of tasks

#88888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888
if options.just_print:
    pipeline_printout(sys.stdout, [combineBlastResults], verbose=options.verbose)


#88888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888

#   Print flowchart

#88888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888
elif options.flowchart:
    # use file extension for output format
    output_format = os.path.splitext(options.flowchart)[1][1:]
    pipeline_printout_graph (open(options.flowchart, "w"),
                             output_format,
                             [combineBlastResults],
                             no_key_legend = True)
#88888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888

#   Run Pipeline

#88888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888888
else:
    pipeline_run([combineBlastResults],  multiprocess = options.jobs,
                         logger = logger, verbose=options.verbose)
```

3.5 Example code for *FAQ Good practices: "What is the best way of handling data in file pairs (or triplets etc.)?"*

See also:

- *@collate*

```
#!/usr/bin/env python
import sys, os

from ruffus import *
import ruffus.cmdline as cmdline
from subprocess import check_call

parser = cmdline.get_argparse(description="Parimala's pipeline?")

#                                                                               .
#   Very flexible handling of input files                                       .
#                                                                               .
#      input files can be specified flexibly as:                                .
#                  --input a.fastq b.fastq                                      .
#                  --input a.fastq --input b.fastq                              .
#                  --input *.fastq --input other/*.fastq                        .
#                  --input "*.fastq"                                            .
#                                                                               .
#       The last form is expanded in the script and avoids limitations on command .
```

```
#           line lengths                                                        .
#                                                                               .
parser.add_argument('-i', '--input', nargs='+', metavar="FILE", action="append", help = "Fastq f

options = parser.parse_args()

#  standard python logger which can be synchronised across concurrent Ruffus tasks
logger, logger_mutex = cmdline.setup_logging ("PARIMALA", options.log_file, options.verbose)

#                                                                               .
#   Useful code to turn input files into a flat list                            .
#                                                                               .
from glob import glob
original_data_files = [fn for grouped in options.input for glob_spec in grouped for fn in glob(g
if not original_data_files:
    original_data_files = [["C1W1_R1.fastq.gz", "C1W1_R2.fastq.gz"]]
    #raise Exception ("No matching files specified with --input.")

#   <<<----  pipelined functions go here

#_______________________________________________________________________________
#                                                                               .
#   Group together file pairs                                                   .
#_______________________________________________________________________________
@collate(original_data_files,
            # match file name up to the "R1.fastq.gz"
            formatter("([^/]+)R[12].fastq.gz$"),
            # Create output parameter supplied to next task
            ["{path[0]}/{1[0]}paired.R1.fastq.gz",  # paired file 1
             "{path[0]}/{1[0]}paired.R2.fastq.gz"], # paired file 2
            # Extra parameters for our own convenience and use
            ["{path[0]}/{1[0]}unpaired.R1.fastq.gz",  # unpaired file 1
             "{path[0]}/{1[0]}unpaired.R2.fastq.gz"], # unpaired file 2
            logger, logger_mutex)
def trim_fastq(input_files, output_paired_files, discarded_unpaired_files, logger, logger_mutex)
    if len(input_files) != 2:
        raise Exception("One of read pairs %s missing" % (input_files,))
    cmd = ("java -jar ~/SPRING-SUMMER_2014/Softwares/Trimmomatic/Trimmomatic-0.32/trimmomatic-0.
           " PE -phred33  "
           " {input_files[0]} {input_files[1]} "
           " {output_paired_files[0]} {output_paired_files[1]} "
           " {discarded_unpaired_files[0]} {discarded_unpaired_files[1]} "
           " LEADING:30 TRAILING:30 SLIDINGWINDOW:4:15 MINLEN:50 "
        )

    check_call(cmd.format(**locals()))

    with logger_mutex:
            logger.debug("Hooray trim_fastq worked")

#_______________________________________________________________________________
#                                                                               .
#   Each file pair now makes its way down the rest of the pipeline as           .
#       a couple                                                                .
#_______________________________________________________________________________
@transform(trim_fastq,
            # regular expression match on first of pe files
            formatter("([^/]+)paired.R1.fastq.gz$"),
```

```
            # Output parameter supplied to next task
            "{path[0]}/{1[0]}.sam"

           # Extra parameters for our own convenience and use
            "{path[0]}/{1[0]}.pe_soap_pe",        # soap intermediate file
            "{path[0]}/{1[0]}.pe_soap_se",        # soap intermediate file
            logger, logger_mutex)
def align_seq(input_files, output_file, soap_pe_output_file, soap_se_output_file, logger, logger
    if len(input_files) != 2:
        raise Exception("One of read pairs %s missing" % (input_files,))
    cmd = ("~/SPRING-SUMMER_2014/Softwares/soap2.21release/soap "
            " -a {input_files[0]} "
            " -b {input_files[1]} "
            " -D Y55_genome.fa.index* "
            " -o {soap_pe_output_file} -2 {soap_se_output_file} -m 400 -x 600")

    check_call(cmd.format(**locals()))


    #Soap_to_sam
    cmd = " perl ~/SPRING-SUMMER_2014/Softwares/soap2sam.pl -p {soap_pe_output_file} > {output_f

    check_call(cmd.format(**locals()))


    with logger_mutex:
            logger.debug("Hooray align_seq worked")


cmdline.run (options)
```

CHAPTER

FOUR

REFERENCE:

4.1 Decorators

4.1.1 Ruffus Decorators

See also:

Indicator objects

Core

Decorator	Examples	
@originate (*Summary* / *Manual*) • Creates (originates) a set of starting file without dependencies from scratch (*ex nihilo*!) • Only called to create files which do not exist. • Invoked onces (a job created) per item in the `output_files` list.	• *@originate* (**output_files, [extra_parameters,...]**)	
@split (*Summary* / *Manual*) • Splits a single input into multiple output • Globs in `output` can specify an indeterminate number of files.	• *@split* (**tasks_or_file_names, output_files, [extra_parameters,...]**)	
@transform (*Summary* / *Manual*) • Applies the task function to transform input data to output.	• *@transform* (**tasks_or_file_names,** *suffix*(**suffix_string**)**, output_pat** • *@transform* (**tasks_or_file_names,** *regex*(**regex_pattern**)**, output_pat** • *@transform* (**tasks_or_file_names,** *formatter*(**regex_pattern**)**, output_**	
@merge (*Summary* / *Manual*) • Merges multiple input files into a single output.	• *@merge* (**tasks_or_file_names, output, [extra_parameters,...]**)	

Combinatorics

Decorator	Examples	
@product (*Summary* / *Manual*) • Generates the **product**, i.e. all vs all comparisons, between sets of input files.	• *@product* (`tasks_or_file_names`, *formatter* (*[* `regex_pattern` *])* ,*[* `* task`	
@permutations (*Summary* / *Manual*) • Generates the **permutations**, between all the elements of a set of **Input** • Analogous to the python itertools.permutations • permutations('ABCD', 2) –> AB AC AD BA BC BD CA CB CD DA DB DC	• *@permutations* (`tasks_or_file_names`, *formatter* (*[* `regex_pattern` *]*), `tup`	
@combinations (*Summary* / *Manual*) • Generates the **permutations**, between all the elements of a set of **Input** • Analogous to the python itertools.combinations • combinations('ABCD', 3) –> ABC ABD ACD BCD • Generates the **combinations**, between all the elements of a set of **Input**: i.e. r-length tuples of *input* elements with no repeated elements (**A A**) and where order of the tuples is irrelevant (either **A B** or **B A**, not both).	• *@combinations* (`tasks_or_file_names`, *formatter* (*[* `regex_pattern` *]*), `tup`	
@combinations_with_replacement (*Summary* / *Manual*) • Generates the **permutations**, between all the elements of a set of **Input** • Analogous to the python itertools.permutations • combinations('ABCD', 3) –> ABC ABD ACD BCD • Generates the **combinations_with_replacement**, between all the elements of a set of **Input**: i.e. r-length tuples of *input* elements with no repeated elements (**A A**) and where order of the tuples is irrelevant (either **A B** or **B A**, not both).	• *@combinations_with_replacement* (`tasks_or_file_names`, *formatter* (*[* `regex`	

Advanced

Decorator	Examples
@subdivide (*Summary* / *Manual*) - Subdivides a set of *Inputs* each further into multiple *Outputs*. - The number of files in each *Output* can be set at runtime by the use of globs. - **Many to Even More** operator. - The use of **split** is a synonym for subdivide is deprecated.	• *@subdivide* (`tasks_or_file_names`, *regex*(`regex_pattern`), [*inputs* | *add_* • *@subdivide* (`tasks_or_file_names`, *formatter*([`regex_pattern`]), [*inputs*
@transform (*Summary* / *Manual*) • Infers input as well as output from regular expression substitutions • Useful for adding additional file dependencies	• *@transform* (`tasks_or_file_names`, *regex*(`regex_pattern`), [*inputs* | *add* • *@transform* (`tasks_or_file_names`, *formatter*(`regex_pattern`), [*inputs* |
@collate (*Summary* / *Manual*) • Groups multiple input files using regular expression matching • Input resulting in the same output after substitution will be collated together.	• *@collate* (`tasks_or_file_names`, *regex*(`regex_pattern`), `output_patte` • *@collate* (`tasks_or_file_names`, *regex*(`regex_pattern`), *inputs* | *add_inpu* • *@collate* (`tasks_or_file_names`, *formatter*(`formatter_pattern`), `outpu` • *@collate* (`tasks_or_file_names`, *formatter*(`formatter_pattern`), *inputs* |
@follows (*Summary* / *Manual*) • Indicates task dependency • optional *mkdir* prerequisite (*see Manual*)	• *@follows* (`task1`, `'task2'`)) • *@follows* (`task1`, *mkdir*(`'my/directory/'`))
@posttask (*Summary* / *Manual*) • Calls function after task completes • Optional *touch_file* indicator (*Manual*)	• *@posttask* (`signal_task_completion_function`) • *@posttask* (*touch_file*(`'task1.completed'`))
@active_if (*Summary* / *Manual*) • Switches tasks on and off at run time depending on its parameters • Evaluated each time *pipeline_run(...)*, *pipeline_printout(...)* or *pipeline_printout_graph(...)* is called. • Dormant tasks behave as if they are up to date and have no output.	• *@active_if* (`on_or_off1, [on_or_off2, ...]`)
@jobs_limit (*Summary* / *Manual*) • Limits the amount of multiprocessing for the specified task • Ensures that fewer than N	• *@jobs_limit* (`NUMBER_OF_JOBS_RUNNING_CONCURRENTLY`)

Esoteric!

Decorator	Examples	
@files (*Summary* / *Manual*) • I/O parameters • skips up-to-date jobs • Should use *@transform* etc instead	• *@files*(**parameter_list**) • *@files*(**parameter_generating_function**) • *@files* (**input_file, output_file, other_params, ...**)	
@parallel (*Summary* / *Manual*) • By default, does not check if jobs are up to date • Best used in conjuction with *@check_if_uptodate*	• *@parallel* (**parameter_list**) (*see Manual*) • *@parallel* (**parameter_generating_function**) (*see Manual*)	
@check_if_uptodate (*Summary* / *Manual*) • Custom function to determine if jobs need to be run	• *@check_if_uptodate* (**is_task_up_to_date_function**)	
Tip: **The use of this overly complicated function is discouraged.** **@files_re** (*Summary*) • I/O file names via regular expressions • start from lists of file names or *glob* results • skips up-to-date jobs	• *@files_re* (**tasks_or_file_names, matching_regex, [input_pattern,]** `input_pattern/output_pattern` are regex patterns used to create input/output file names from the starting list of either glob_str or file names	

See also:

- *Decorators*
- *suffix(...)* in the **Ruffus** Manual
- *regex(...)* in the **Ruffus** Manual
- *formatter(...)* in the **Ruffus** Manual

4.1.2 Indicator Objects

How *ruffus* disambiguates certain parameters to decorators.

They are like keyword arguments in python, a little more verbose but they make the syntax much simpler.

Indicator objects are also "self-documenting" so you can see exactly what is happening clearly.

formatter

formatter([`regex | None` **, regex | None...])**

- The optional enclosed parameters are a python regular expression strings

- Each regular expression matches a corresponding *Input* file name string
- *formatter* parses each file name string into path and regular expression components
- Parsing fails altogether if the regular expression is not matched

Path components include:

- `basename`: The base name *excluding* extension, `"file.name"`
- `ext` : The extension, `".ext"`
- `path` : The dirname, `"/directory/to/a"`
- `subdir` : A list of sub-directories in the `path` in reverse order, `["a", "to", "directory", "/"]`
- `subpath` : A list of descending sub-paths in reverse order, `["/directory/to/a", "/directory/to", "/directory", "/"]`

The replacement string refers to these components using python string.format style curly braces. `{NAME}`

We refer to an element from the Nth input string by index, for example:

- `"{ext[0]}"` is the extension of the first input string.
- `"{basename[1]}"` is the basename of the second input string.
- `"{basename[1][0:3]}"` are the first three letters from the basename of the second input string.

Used by:

- *@split*
- *@transform*
- *@merge*
- *@subdivide*
- *@collate*
- *@product*
- *@permutations*
- *@combinations*
- *@combinations_with_replacement*

@transform example:

```
from ruffus import *

#   create initial file pairs
@originate([    ['job1.a.start', 'job1.b.start'],
                ['job2.a.start', 'job2.b.start'],
                ['job3.a.start', 'job3.c.start']    ])
def create_initial_file_pairs(output_files):
    for output_file in output_files:
        with open(output_file, "w") as oo: pass


#---------------------------------------------------------------
#
#   formatter
#
```

```
@transform(create_initial_file_pairs,                                   # Input

           formatter(".+/job(?P<JOBNUMBER>\d+).a.start",                # Extract job number
                     ".+/job[123].b.start"),                            # Match only "b" files

           ["{path[0]}/jobs{JOBNUMBER[0]}.output.a.1",                  # Replacement list
            "{path[1]}/jobs{JOBNUMBER[0]}.output.b.1"])
def first_task(input_files, output_parameters):
    print "input_parameters = ", input_files
    print "output_parameters = ", output_parameters


#
#       Run
#
pipeline_run(verbose=0)
```

This produces:

```
input_parameters  =  ['job1.a.start',
                      'job1.b.start']
output_parameters =  ['/home/lg/src/temp/jobs1.output.a.1',
                      '/home/lg/src/temp/jobs1.output.b.1', 45]

input_parameters  =  ['job2.a.start',
                      'job2.b.start']
output_parameters =  ['/home/lg/src/temp/jobs2.output.a.1',
                      '/home/lg/src/temp/jobs2.output.b.1', 45]
```

@permutations example:

Combinatoric decorators such as *@product* or *@product* behave much like nested for loops in enumerating, combining, and permutating the original sets of inputs.

The replacement strings require an extra level of indirection to refer to parsed components:

```
from ruffus import *
from ruffus.combinatorics import *

#   create initial files
@originate([ 'a.start', 'b.start', 'c.start'])
def create_initial_files(output_file):
    with open(output_file, "w") as oo: pass


#---------------------------------------------------------------
#
#   formatter
#
@permutations(create_initial_files,                                     # Input

              formatter("(.start)$"),                                   # match input
              2,

              "{path[0][0]}/{basename[0][0]}_vs_{basename[1][0]}.product",    # Output Replace
              "{path[0][0]}",                                           # path for 1st s
              ["{basename[0][0]}",                                      # basename for 1
               "{basename[1][0]}"])                                     # basename for 2
def product_task(input_file, output_parameter, shared_path, basenames):
```

```
    print "input_parameter  = ", input_file
    print "output_parameter = ", output_parameter
    print "shared_path      = ", shared_path
    print "basenames        = ", basenames


#
#       Run
#
pipeline_run(verbose=0)
```

This produces:

```
>>> pipeline_run(verbose=0)
input_parameter  =  ('a.start', 'b.start')
output_parameter =  /home/lg/src/oss/ruffus/a_vs_b.product
shared_path      =  /home/lg/src/oss/ruffus
basenames        =  ['a', 'b']

input_parameter  =  ('a.start', 'c.start')
output_parameter =  /home/lg/src/oss/ruffus/a_vs_c.product
shared_path      =  /home/lg/src/oss/ruffus
basenames        =  ['a', 'c']

input_parameter  =  ('b.start', 'a.start')
output_parameter =  /home/lg/src/oss/ruffus/b_vs_a.product
shared_path      =  /home/lg/src/oss/ruffus
basenames        =  ['b', 'a']

input_parameter  =  ('b.start', 'c.start')
output_parameter =  /home/lg/src/oss/ruffus/b_vs_c.product
shared_path      =  /home/lg/src/oss/ruffus
basenames        =  ['b', 'c']

input_parameter  =  ('c.start', 'a.start')
output_parameter =  /home/lg/src/oss/ruffus/c_vs_a.product
shared_path      =  /home/lg/src/oss/ruffus
basenames        =  ['c', 'a']

input_parameter  =  ('c.start', 'b.start')
output_parameter =  /home/lg/src/oss/ruffus/c_vs_b.product
shared_path      =  /home/lg/src/oss/ruffus
basenames        =  ['c', 'b']
```

suffix

suffix(`string` **)**

The enclosed parameter is a string which must match *exactly* to the end of a file name.

Used by:

- *@transform*

Example:

```
#
#   Transforms ``*.c`` to ``*.o``::
#
```

```
@transform(previous_task, suffix(".c"), ".o")
def compile(infile, outfile):
    pass
```

regex

regex(`regular_expression` **)**

The enclosed parameter is a python regular expression string, which must be wrapped in a `regex` indicator object.

See python regular expression (re) documentation for details of regular expression syntax

Used by:

- *@transform*
- *@subdivide*
- *@collate*
- The deprecated *@files_re*

Example:

```
@transform(previous_task, regex(r".c$"), ".o")
def compile(infile, outfile):
    pass
```

add_inputs

add_inputs(`input_file_pattern` **)**

The enclosed parameter(s) are pattern strings or a nested structure which is added to the input for each job.

Used by:

- *@transform*
- *@collate*
- *@subdivide*

Example @transform with suffix(...)

A common task in compiling C code is to include the corresponding header file for the source.
To compile `*.c` to `*.o`, adding `*.h` and the common header `universal.h`:

```
@transform(["1.c", "2.c"], suffix(".c"), add_inputs([r"\1.h", "universal.h"]),  ".o")
def compile(infile, outfile):
    # do something here
    pass
```

The starting files names are `1.c` and `2.c`.
`suffix(".c")` matches ".c" so `\1` stands for the unmatched prefices `"1"` and `"2"`

This will result in the following functional calls:

```
compile(["1.c", "1.h", "universal.h"], "1.o")
compile(["2.c", "2.h", "universal.h"], "2.o")
```

A string like `universal.h` in `add_inputs` will added *as is*. `r"\1.h"`, however, performs suffix substitution, with the special form `r"\1"` matching everything up to the suffix. Remember to 'escape' `r"\1"` otherwise Ruffus will complain and throw an `Exception` to remind you. The most convenient way is to use a python "raw" string.

Example of add_inputs(...) with regex(...)

The suffix match (`suffix(...)`) is exactly equivalent to the following code using regular expression (`regex(...)`

```
@transform(["1.c", "2.c"], regex(r"^(.+)\.c$"), add_inputs([r"\1.h", "universal.h"]),  r
def compile(infile, outfile):
    # do something here
    pass
```

The `suffix(..)` code is much simpler but the regular expression allows more complex substitutions.

add_inputs(...) preserves original inputs

`add_inputs` nests the the original input parameters in a list before adding additional dependencies.

This can be seen in the following example:

```
@transform([    ["1.c", "A.c", 2]
                ["2.c", "B.c", "C.c", 3]],
               suffix(".c"), add_inputs([r"\1.h", "universal.h"]),  ".o")
def compile(infile, outfile):
    # do something here
    pass
```

This will result in the following functional calls:

```
compile([["1.c", "A.c", 2],        "1.h", "universal.h"], "1.o")
compile([["3.c", "B.c", "C.c", 3], "2.h", "universal.h"], "2.o")
```

The original parameters are retained unchanged as the first item in a list

inputs

inputs(`input_file_pattern` **)**

Used by:

- *@transform*
- *@collate*
- *@subdivide*

The enclosed single parameter is a pattern string or a nested structure which is used to construct the input for each job.

If more than one argument is supplied to inputs, an exception will be raised.

Use a tuple or list (as in the following example) to send multiple input arguments to each job.

Used by:

- The advanced form of *@transform*

inputs(...) replaces original inputs

`inputs(...)` allows the original input parameters to be replaced wholescale.

This can be seen in the following example:

```
@transform([    ["1.c", "A.c", 2]
                ["2.c", "B.c", "C.c", 3]],
               suffix(".c"), inputs([r"\1.py", "docs.rst"]),  ".pyc")
def compile(infile, outfile):
    # do something here
    pass
```

This will result in the following functional calls:

```
compile(["1.py", "docs.rst"], "1.pyc")
compile(["2.py", "docs.rst"], "2.pyc")
```

In this example, the corresponding python files have been sneakily substituted without trace in the place of the C source files.

mkdir

mkdir(`directory_name1` **, [** `directory_name2` **, ...])**

The enclosed parameter is a directory name or a sequence of directory names. These directories will be created as part of the prerequisites of running a task.

Used by:

- *@follows*

Example:

```
@follows(mkdir("/output/directory"))
def task():
    pass
```

touch_file

touch_file(`file_name` **)**

The enclosed parameter is a file name. This file will be `touch`-ed after a task is executed.

This will change the date/time stamp of the `file_name` to the current date/time. If the file does not exist, an empty file will be created.

Used by:

- *@posttask*

Example:

```
@posttask(touch_file("task_completed.flag"))
@files(None, "a.1")
def do_task(input_file, output_file):
    pass
```

output_from

output_from (`file_name_string1` **[,** `file_name_string1` **, ...])**

Indicates that any enclosed strings are not file names but refer to task functions.

Used by:

- *@split*
- *@transform*
- *@merge*
- *@collate*
- *@subdivide*
- *@product*
- *@permutations*
- *@combinations*
- *@combinations_with_replacement*
- *@files*

Example:

```
@split(["a.file", ("b.file", output_from("task1", 76, "task2"))], "*.split")
def task2(input, output):
    pass
```

is equivalent to:

```
@split(["a.file", ("b.file", (task1, 76, task2))], "*.split")
def task2(input, output):
    pass
```

combine

combine(`arguments` **)**

> **Warning:** This is deprecated syntax.
> Please do not use!
> *@merge* and *@collate* are more powerful and have straightforward syntax.

Indicates that the *inputs* of *@files_re* will be collated or summarised into *outputs* by category. See the *Manual* or :ref:‘ @collate <new_manual.collate>‘ for examples.

Used by:

- *@files_re*

Example:

```
@files_re('*.animals',                          # inputs = all *.animal files
          r'mammals.([^.]+)',                   # regular expression
          combine(r'\1/animals.in_my_zoo'),     # single output file per species
          r'\1' )                               # species name
def capture_mammals(infiles, outfile, species):
```

```
            # summarise all animals of this species
            ""
```

Core

See also:

- *@originate* in the **Ruffus** Manual
- *Decorators* for more decorators

4.1.3 @originate (output, [extras,...])

Purpose:

- Creates (originates) a set of starting file without dependencies from scratch (*ex nihilo*!)
- Only called to create files which do not exist.
- Invoked onces (a job created) per item in the *output* list.

Note: The first argument for the task function is the *output*. There is by definition no *input* for `@originate`

Example:

```
from ruffus import *
@originate(["a", "b", "c", "d"], "extra")
def test(output_file, extra):
    open(output_file, "w")

pipeline_run()
```

```
>>> pipeline_run()
    Job  = [None -> a, extra] completed
    Job  = [None -> b, extra] completed
    Job  = [None -> c, extra] completed
    Job  = [None -> d, extra] completed
Completed Task = test

>>> # all files exist: nothing to do
>>> pipeline_run()

>>> # delete 'a' so that it is missing
>>> import os
>>> os.unlink("a")

>>> pipeline_run()
    Job  = [None -> a, extra] completed
Completed Task = test
```

Parameters:

- **output = *output***
  - Can be a single file name or a list of files
  - Each item in the list is treated as the *output* of a separate job
- **extras = *extras*** Any extra parameters are passed verbatim to the task function
  If you are using named parameters, these can be passed as a list, i.e. `extras= [...]`
  Any extra parameters are consumed by the task function and not forwarded further down the pipeline.

See also:

- *@split* in the **Ruffus** Manual
- *Decorators* for more decorators

4.1.4 @split (input, output, [extras,...])

Purpose:

Splits a single set of *input* into multiple *output*, where the number of *output* may not be known beforehand.

Only out of date tasks (comparing *input* and *output* files) will be run

Example:

```
@split("big_file", '*.little_files')
def split_big_to_small(input_file, output_files):
```

For advanced users

See also:

- *@subdivide* in the **Ruffus** Manual
- *Decorators* for more decorators

4.1.7 @subdivide

@subdivide (input, regex(matching_regex) | formatter(matching_formatter), [inputs (input_pattern_or_glob) | add_inputs (input_pattern_or_glob)], output, [extras,...])

Purpose:

- Subdivides a set of *Inputs* each further into multiple *Outputs*.
- **Many to Even More** operator
- The number of files in each *Output* can be set at runtime by the use of globs
- Output file names are specified using the *formatter* or *regex* indicators from *input*, i.e. from the output of specified tasks, or a list of file names, or a *glob* matching pattern.
- **Additional inputs or dependencies can be added dynamically to the task:**
  add_inputs nests the the original input parameters in a list before adding additional dependencies.
  inputs replaces the original input parameters wholescale.
- Only out of date tasks (comparing input and output files) will be run.

Note: The use of **split** is a synonym for subdivide is deprecated.

Example:

```
from ruffus import *
from random import randint
from random import os

@originate(['0.start', '1.start', '2.start'])
def create_files(output_file):
    with open(output_file, "w"):
        pass


#
#   Subdivide each of 3 start files further into [NNN1, NNN2, NNN3] number of files
#      where NNN1, NNN2, NNN3 are determined at run time
#
@subdivide(create_files, formatter(),
            "{path[0]}/{basename[0]}.*.step1",  # Output parameter: Glob matches any number
            "{path[0]}/{basename[0]}")          # Extra parameter:  Append to this for outp
def subdivide_files(input_file, output_files, output_file_name_root):
    #
    #   IMPORTANT: cleanup rubbish from previous run first
    #
    for oo in output_files:
        os.unlink(oo)
    #   The number of output files is decided at run time
    number_of_output_files = randint(2,4)
    for ii in range(number_of_output_files):
        output_file_name = "{output_file_name_root}.{ii}.step1".format(**locals())
        with open(output_file_name, "w"):
            pass


#
#   Each output of subdivide_files results in a separate job for downstream tasks
#
@transform(subdivide_files, suffix(".step1"), ".step2")
def analyse_files(input_file, output_file_name):
    with open(output_file_name, "w"):
```

Combinatorics

See also:

- *@product* in the **Ruffus** Manual
- *Decorators* for more decorators

4.1.17 @product(*input*, *filter*, [*input2*, *filter2*, ...], *output*, [*extras*,...])

Purpose:

Generates the Cartesian **product**, i.e. all vs all comparisons, between multiple sets of *input* (e.g. **A B C D**, and **X Y Z**),
The effect is analogous to the python itertools function of the same name, i.e. a nested for loop.

```
>>> from itertools import product
>>> # product('ABC', 'XYZ') --> AX AY AZ BX BY BZ CX CY CZ
>>> [ "".join(a) for a in product('ABC', 'XYZ')]
['AX', 'AY', 'AZ', 'BX', 'BY', 'BZ', 'CX', 'CY', 'CZ']
```

Only out of date tasks (comparing input and output files) will be run
output file names and strings in the extra parameters are generated by string replacement via the *formatter()* filter from the *input*. This can be, for example, a list of file names or the *output* of up stream tasks. . The replacement strings require an extra level of nesting to refer to parsed components.

1. The first level refers to which *set* in each tuple of *input*.
2. The second level refers to which *input* file in any particular *set* of *input*.

This will be clear in the following example:

Example:

Calculates the **@product** of **A,B** and **P,Q** and **X, Y** files
If *input* is three *sets* of file names

```
set1 = [ 'a.start',                          # 0
         'b.start'])

set2 = [ 'p.start',                          # 1
         'q.start'])

set3 = [ ['x.1_start', 'x.2_start'],         # 2
         ['y.1_start', 'y.2_start'] ]
```

The first job of:

```
@product( input  = set1, filter  = formatter(),
          input2 = set2, filter2 = formatter(),
          input3 = set2, filter3 = formatter(),
          ...)
```

Will be

```
# One from each set
['a.start']
# versus
['p.start']
# versus
['x.1_start', 'x.2_start'],
```

First level of nesting (one list of files from each set):

```
['a.start']                  # [0]
['p.start']                  # [1]
['x.1_start', 'x.2_start'], # [2]
```

Second level of nesting (one file):

```
a.start'                     # [0][0]
'p.start'                    # [1][0]
'x.1_start'                  # [2][0]
```

Parse filename without suffix

Esoteric

See also:

- *@files* in the **Ruffus** Manual
- *Decorators* for more decorators

4.1.21 Generating parameters on the fly for @files

@files (*custom_function*)

Purpose:

Uses a custom function to generate sets of parameters to separate jobs which can run in parallel.
The first two parameters in each set represent the input and output which are used to see if the job is out of date and needs to be (re-)run.
By default, out of date checking uses input/output file timestamps. (On some file systems, timestamps have a resolution in seconds.) See *@check_if_uptodate()* for alternatives.

Example:

```
from ruffus import *
def generate_parameters_on_the_fly():
    parameters = [
                          ['input_file1', 'output_file1', 1, 2], # 1st job
                          ['input_file2', 'output_file2', 3, 4], # 2nd job
                          ['input_file3', 'output_file3', 5, 6], # 3rd job
                 ]
    for job_parameters in parameters:
        yield job_parameters

@files(generate_parameters_on_the_fly)
def parallel_io_task(input_file, output_file, param1, param2):
    pass

pipeline_run([parallel_task])
```

is the equivalent of calling:

```
parallel_io_task('input_file1', 'output_file1', 1, 2)
parallel_io_task('input_file2', 'output_file2', 3, 4)
parallel_io_task('input_file3', 'output_file3', 5, 6)
```

Parameters:

- ***custom_function*:** Generator function which yields each time a complete set of parameters for one job

Checking if jobs are up to date: Strings in `input` and `output` (including in nested sequences) are interpreted as file names and used to check if jobs are up-to-date.
See *above* for more details

See also:

- *@check_if_uptodate* in the **Ruffus** Manual
- *Decorators* for more decorators

4.1.22 @check_if_uptodate

@check_if_uptodate (*dependency_checking_function*)

Purpose: Checks to see if a job is up to date, and needs to be run.
Usually used in conjunction with *@parallel()*

Example:

```
from ruffus import *
import os
def check_file_exists(input_file, output_file):
    if not os.path.exists(output_file):
        return True, "Missing file %s" % output_file
    else:
        return False, "File %s exists" % output_file
```

Deprecated

See also:
- *@files (deprecated)* in the **Ruffus** Manual
- *Decorators* for more decorators

4.1.24 @files

@files (*input1*, *output1*, [*extra_parameters1*, ...])

@files for single jobs

Purpose: Provides parameters to run a task.
The first two parameters in each set represent the input and output which are used to see if the job is out of date and needs to be (re-)run.
By default, out of date checking uses input/output file timestamps. (On some file systems, timestamps have a resolution in seconds.) See *@check_if_uptodate()* for alternatives.

Example:

```
from ruffus import *
@files('a.1', 'a.2', 'A file')
def transform_files(infile, outfile, text):
    pass
pipeline_run([transform_files])
```

If `a.2` is missing or was created before `a.1`, then the following will be called:

```
transform_files('a.1', 'a.2', 'A file')
```

Parameters:
- ***input*** Input file names
- ***output*** Output file names
  - ***extra_parameters*** optional `extra_parameters` are passed verbatim to each job.

Checking if jobs are up to date: Strings in `input` and `output` (including in nested sequences) are interpreted as file names and used to check if jobs are up-to-date.
See *above* for more details

@files (*((input, output, [extra_parameters,...]), (...), ...)*)

@files in parallel

Purpose:
Passes each set of parameters to separate jobs which can run in parallel
The first two parameters in each set represent the input and output which are used to see if the job is out of date and needs to be (re-)run.
By default, out of date checking uses input/output file timestamps. (On some file systems, timestamps have a resolution in seconds.) See *@check_if_uptodate()* for alternatives.

Example:

```
from ruffus import *
parameters = [
                    [ 'a.1', 'a.2', 'A file'], # 1st job
                    [ 'b.1', 'b.2', 'B file'], # 2nd job
              ]

@files(parameters)
def parallel_io_task(infile, outfile, text):
    pass
pipeline_run([parallel_io_task])
```

is the equivalent of calling:

```
parallel_io_task('a.1', 'a.2', 'A file')
parallel_io_task('b.1', 'b.2', 'B file')
```

Parameters:
- ***input*** Input file names

4.2 Modules:

4.2.1 ruffus.Task

Decorators

Basic Task decorators are:

@follows()

and

@files()

Task decorators include:

@split()

@transform()

@merge()

@posttask()

More advanced users may require:

@transform()

@collate()

@parallel()

@check_if_uptodate()

@files_re()

Pipeline functions

pipeline_run

ruffus.task.**pipeline_run**(*target_tasks*, *forcedtorun_tasks=[]*, *multiprocess=1*, *logger=stderr_logger*, *gnu_make_maximal_rebuild_mode=True*)

Run pipelines.

Parameters

- **target_tasks** – targets task functions which will be run if they are out-of-date
- **forcedtorun_tasks** – task functions which will be run whether or not they are out-of-date
- **multiprocess** – The number of concurrent jobs running on different processes.
- **multithread** – The number of concurrent jobs running as different threads. If > 1, ruffus will use multithreading *instead of* multiprocessing (and ignore the multiprocess parameter). Using multi threading is particularly useful to manage high performance clusters which otherwise are prone to "processor storms" when large number of cores finish jobs at the same time. (Thanks Andreas Heger)
- **logger** (logging objects) – Where progress will be logged. Defaults to stderr output.
- **verbose** –
  - level 0 : nothing

  - level 1 : Out-of-date Task names
  - level 2 : All Tasks (including any task function docstrings)
  - level 3 : Out-of-date Jobs in Out-of-date Tasks, no explanation
  - level 4 : Out-of-date Jobs in Out-of-date Tasks, with explanations and warnings
  - level 5 : All Jobs in Out-of-date Tasks, (include only list of up-to-date tasks)
  - level 6 : All jobs in All Tasks whether out of date or not
  - level 10: logs messages useful only for debugging ruffus pipeline code
- **touch_files_only** – Create or update input/output files only to simulate running the pipeline. Do not run jobs. If set to CHECKSUM_REGENERATE, will regenerate the checksum history file to reflect the existing i/o files on disk.
- **exceptions_terminate_immediately** – Exceptions cause immediate termination rather than waiting for N jobs to finish where N = multiprocess
- **log_exceptions** – Print exceptions to logger as soon as they occur.
- **checksum_level** – Several options for checking up-to-dateness are available: Default is level 1.
  - level 0 : Use only file timestamps
  - level 1 : above, plus timestamp of successful job completion
  - level 2 : above, plus a checksum of the pipeline function body
  - level 3 : above, plus a checksum of the pipeline function default arguments and the additional arguments passed in by task decorators
- **one_second_per_job** – To work around poor file timepstamp resolution for some file systems. Defaults to True if checksum_level is 0 forcing Tasks to take a minimum of 1 second to complete.
- **runtime_data** – Experimental feature: pass data to tasks at run time
- **gnu_make_maximal_rebuild_mode** – Defaults to re-running *all* out-of-date tasks. Runs minimal set to build targets if set to `True`. Use with caution.
- **history_file** – Database file storing checksums and file timestamps for input/output files.
- **verbose_abbreviated_path** – whether input and output paths are abbreviated.
  - level 0: The full (expanded, abspath) input or output path
  - level > 1: The number of subdirectories to include. Abbreviated paths are prefixed with `[,,,]/`
  - level < 0: Input / Output parameters are truncated to `MMM` letters where `verbose_abbreviated_path ==-MMM`. Subdirectories are first removed to see if this allows the paths to fit in the specified limit. Otherwise abbreviated paths are prefixed by `<???>`

pipeline_printout

ruffus.task.**pipeline_printout**(*output_stream=None*, *target_tasks=[]*, *forcedtorun_tasks=[]*, *verbose=None*, *indent=4*, *gnu_make_maximal_rebuild_mode=True*, *wrap_width=100*, *runtime_data=None*, *checksum_level=None*, *history_file=None*, *verbose_abbreviated_path=None*, *pipeline=None*)

Printouts the parts of the pipeline which will be run

Because the parameters of some jobs depend on the results of previous tasks, this function produces only the current snap-shot of task jobs. In particular, tasks which generate variable number of inputs into following tasks will not produce the full range of jobs.

:: verbose = 0 : Nothing verbose = 1 : Out-of-date Task names verbose = 2 : All Tasks (including any task function docstrings) verbose = 3 : Out-of-date Jobs in Out-of-date Tasks, no explanation verbose = 4 : Out-of-date Jobs in Out-of-date Tasks, with explanations and warnings verbose = 5 : All Jobs in Out-of-date Tasks, (include only list of up-to-date tasks) verbose = 6 : All jobs in All Tasks whether out of date or not

Parameters

- **output_stream** (file-like object with `write()` function) – where to print to
- **target_tasks** – targets task functions which will be run if they are out-of-date
- **forcedtorun_tasks** – task functions which will be run whether or not they are out-of-date
- **verbose** – level 0 : nothing level 1 : Out-of-date Task names level 2 : All Tasks (including any task function docstrings) level 3 : Out-of-date Jobs in Out-of-date Tasks, no explanation level 4 : Out-of-date Jobs in Out-of-date Tasks, with explanations and warnings level 5 : All Jobs in Out-of-date Tasks, (include only list of up-to-date tasks) level 6 : All jobs in All Tasks whether out of date or not level 10: logs messages useful only for debugging ruffus pipeline code
- **indent** – How much indentation for pretty format.
- **gnu_make_maximal_rebuild_mode** – Defaults to re-running *all* out-of-date tasks. Runs minimal set to build targets if set to `True`. Use with caution.
- **wrap_width** – The maximum length of each line
- **runtime_data** – Experimental feature: pass data to tasks at run time
- **checksum_level** – Several options for checking up-to-dateness are available: Default is level 1. level 0 : Use only file timestamps level 1 : above, plus timestamp of successful job completion level 2 : above, plus a checksum of the pipeline function body level 3 : above, plus a checksum of the pipeline function default arguments and the additional arguments passed in by task decorators
- **history_file** – Database file storing checksums and file timestamps for input/output files.
- **verbose_abbreviated_path** – whether input and output paths are abbreviated. level 0: The full (expanded, abspath) input or output path level > 1: The number of subdirectories to include. Abbreviated paths are prefixed with `[,,,]` / level < 0: Input / Output parameters are truncated to `MMM` letters where `verbose_abbreviated_path ==-MMM`. Subdirectories are first removed to see if this allows the paths to fit in the specified limit. Otherwise abbreviated paths are prefixed by `<???>`

pipeline_printout_graph

ruffus.task.**pipeline_printout_graph**(*stream*, *output_format=None*, *target_tasks=[]*, *forcedtorun_tasks=[]*, *draw_vertically=True*, *ignore_upstream_of_target=False*, *skip_uptodate_tasks=False*, *gnu_make_maximal_rebuild_mode=True*, *test_all_task_for_update=True*, *no_key_legend=False*, *minimal_key_legend=True*, *user_colour_scheme=None*, *pipeline_name='Pipeline:'*, *size=(11, 8)*, *dpi=120*, *runtime_data=None*, *checksum_level=None*, *history_file=None*, *pipeline=None*)

print out pipeline dependencies in various formats

Parameters

- **stream** (file-like object with `write()` function) – where to print to
- **output_format** – ["dot", "jpg", "svg", "ps", "png"]. All but the first depends on the dot program.
- **target_tasks** – targets task functions which will be run if they are out-of-date.
- **forcedtorun_tasks** – task functions which will be run whether or not they are out-of-date.
- **draw_vertically** – Top to bottom instead of left to right.
- **ignore_upstream_of_target** – Don't draw upstream tasks of targets.
- **skip_uptodate_tasks** – Don't draw up-to-date tasks if possible.
- **gnu_make_maximal_rebuild_mode** – Defaults to re-running *all* out-of-date tasks. Runs minimal set to build targets if set to `True`. Use with caution.
- **test_all_task_for_update** – Ask all task functions if they are up-to-date.
- **no_key_legend** – Don't draw key/legend for graph.
- **minimal_key_legend** – Only legend entries for used task types
- **user_colour_scheme** – Dictionary specifying flowchart colour scheme
- **pipeline_name** – Pipeline Title
- **size** – tuple of x and y dimensions
- **dpi** – print resolution
- **runtime_data** – Experimental feature: pass data to tasks at run time
- **history_file** – Database file storing checksums and file timestamps for input/output files.
- **checksum_level** – Several options for checking up-to-dateness are available: Default is level 1. level 0 : Use only file timestamps level 1 : above, plus timestamp of successful job completion level 2 : above, plus a checksum of the pipeline function body level 3 : above, plus a checksum of the pipeline function default arguments and the additional arguments passed in by task decorators

Logging

class ruffus.task.**t_black_hole_logger**

Does nothing!

class ruffus.task.**t_stderr_logger**
Everything to stderr

Implementation:

Parameter factories:

ruffus.task.**merge_param_factory**(*input_files_task_globs*, *output_param*, **extra_params*)
Factory for task_merge

ruffus.task.**collate_param_factory**(*input_files_task_globs*, *file_names_transform*, *extra_input_files_task_globs*, *replace_inputs*, *output_pattern*, **extra_specs*)
Factory for task_collate

Looks exactly like @transform except that all [input] which lead to the same [output / extra] are combined together

ruffus.task.**transform_param_factory**(*input_files_task_globs*, *file_names_transform*, *extra_input_files_task_globs*, *replace_inputs*, *output_pattern*, **extra_specs*)
Factory for task_transform

ruffus.task.**files_param_factory**(*input_files_task_globs*, *do_not_expand_single_job_tasks*, *output_extras*)

Factory for functions which yield tuples of inputs, outputs / extras

..Note:

```
1. Each job requires input/output file names
2. Input/output file names can be a string, an arbitrarily nested sequence
3. Non-string types are ignored
3. Either Input or output file name must contain at least one string
```

ruffus.task.**args_param_factory**(*orig_args*)

Factory for functions which yield tuples of inputs, outputs / extras

..Note:

```
1. Each job requires input/output file names
2. Input/output file names can be a string, an arbitrarily nested sequence
3. Non-string types are ignored
3. Either Input or output file name must contain at least one string
```

ruffus.task.**split_param_factory**(*input_files_task_globs*, *output_files_task_globs*, **extra_params*)
Factory for task_split

Wrappers around jobs:

ruffus.task.**job_wrapper_generic**(*params*, *user_defined_work_func*, *register_cleanup*, *touch_files_only*)
run func

ruffus.task.**job_wrapper_io_files**(*params*, *user_defined_work_func*, *register_cleanup*, *touch_files_only*, *output_files_only=False*)
run func on any i/o if not up to date

ruffus.task.**job_wrapper_mkdir**(*params*, *user_defined_work_func*, *register_cleanup*, *touch_files_only*)

Make missing directories including any intermediate directories on the specified path(s)

Checking if job is update:

ruffus.task.**needs_update_check_modify_time**(**params*, ***kwargs*)

Given input and output files, see if all exist and whether output files are later than input files Each can be

1.string: assumed to be a filename "file1"

2.any other type

3.arbitrary nested sequence of (1) and (2)

ruffus.task.**needs_update_check_directory_missing**(**params*, ***kwargs*)

Called per directory: Does it exist? Is it an ordinary file not a directory? (throw exception

Exceptions and Errors

4.2.2 ruffus.proxy_logger

Create proxy for logging for use with multiprocessing

These can be safely sent (marshalled) across process boundaries

Example 1

Set up logger from config file:

```
from proxy_logger import *
args={}
args["config_file"] = "/my/config/file"

(logger_proxy,
 logging_mutex) = make_shared_logger_and_proxy (setup_std_shared_logger,
                                                "my_logger", args)
```

Example 2

Log to file `"/my/lg.log"` in the specified format (Time / Log name / Event type / Message).

Delay file creation until first log.

Only log `Debug` messages

Other alternatives for the logging threshold (`args["level"]`) include

- `logging.DEBUG`
- `logging.INFO`
- `logging.WARNING`
- `logging.ERROR`

- logging.CRITICAL

```
from proxy_logger import *
args={}
args["file_name"] = "/my/lg.log"
args["formatter"] = "%(asctime)s - %(name)s - %(levelname)6s - %(message)s"
args["delay"]     = True
args["level"]     = logging.DEBUG

(logger_proxy,
 logging_mutex) = make_shared_logger_and_proxy (setup_std_shared_logger,
                                                "my_logger", args)
```

Example 3

Rotate log files every 20 Kb, with up to 10 backups.

```
from proxy_logger import *
args={}
args["file_name"] = "/my/lg.log"
args["rotating"] = True
args["maxBytes"]=20000
args["backupCount"]=10
(logger_proxy,
 logging_mutex) = make_shared_logger_and_proxy (setup_std_shared_logger,
                                                "my_logger", args)
```

To use:

```
(logger_proxy,
 logging_mutex) = make_shared_logger_and_proxy (setup_std_shared_logger,
                                                "my_logger", args)

with logging_mutex:
    my_log.debug('This is a debug message')
    my_log.info('This is an info message')
    my_log.warning('This is a warning message')
    my_log.error('This is an error message')
    my_log.critical('This is a critical error message')
    my_log.log(logging.DEBUG, 'This is a debug message')
```

Note that the logging function `exception()` is not included because python stack trace information is not well-marshalled (pickled) across processes.

Proxies for a log:

ruffus.proxy_logger.**make_shared_logger_and_proxy**(*logger_factory*, *logger_name*, *args*)

Make a logging object called "`logger_name`" by calling `logger_factory(args)`

This function will return a proxy to the shared logger which can be copied to jobs in other processes, as well as a mutex which can be used to prevent simultaneous logging from happening.

Parameters

- **logger_factory** – functions which creates and returns an object with the logging interface. `setup_std_shared_logger()` is one example of a logger factory.

- **logger_name** – name of log
- **args** – parameters passed (as a single argument) to `logger_factory`

Returns a proxy to the shared logger which can be copied to jobs in other processes

Returns a mutex which can be used to prevent simultaneous logging from happening

Create a logging object

`ruffus.proxy_logger.`**`setup_std_shared_logger`**(*logger_name*, *args*)

This function is a simple around wrapper around the python logging module.

This *logger_factory* example creates logging objects which can then be managed by proxy via `ruffus.proxy_logger.make_shared_logger_and_proxy()`

This can be:

•a disk log file

•a automatically backed-up (rotating) log.

•any log specified in a configuration file

These are specified in the `args` dictionary forwarded by `make_shared_logger_and_proxy()`

Parameters

- **logger_name** – name of log
- **args** – a dictionary of parameters forwarded from `make_shared_logger_and_proxy()`

  Valid entries include:

  `"level"`
  Sets the threshold for the logger.

  `"config_file"`
  The logging object is configured from this configuration file.

  `"file_name"`
  Sets disk log file name.

  `"rotating"`
  Chooses a (rotating) log.

  `"maxBytes"`
  Allows the file to rollover at a predetermined size

  `"backupCount"`
  If backupCount is non-zero, the system will save old log files by appending the extensions `.1`, `.2`, `.3` etc., to the filename.

  `"delay"`
  Defer file creation until the log is written to.

  `"formatter"`
  Converts the message to a logged entry string. For example,

  ```
  "%(asctime)s - %(name)s - %(levelname)6s - %(message)s"
  ```

CHAPTER

FIVE

INDICES AND TABLES

- *genindex*
- *modindex*
- *search*

r