



# Snakemake for reproducible research

Decorating and optimising a Snakemake workflow



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# What could we improve? (again)

- Avoiding hard-coded parameters
- Processing list of files
- (Optimising resource usage)
- (Using non-conventional **outputs**)

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- Avoiding hard-coded parameters → config file
- Processing list of files → expand() syntax
- (Optimising resource usage) → (Directives resources and threads)
- (Using non-conventional outputs) → (temp(), directory()...)

# Avoiding hard-coded parameters: config file

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- Imported file with **configfile** keyword in Snakefile
  - `configfile: 'path/to/config.yaml'` (relative to working directory)
- 2 possible formats: JSON and YAML
  - Personal opinion: YAML is easier to write, understand and can be commented

```
{  
  "retries": 5,  
  "samples": [  
    "file1",  
    "file2"  
  ],  
  "resources": {  
    "threads": 8,  
    "memory": "500M"  
  }  
}
```

JSON

```
retries: 5 # Single value  
samples: # Multiple values  
- file1  
- file2  
resources: # Nested parameters  
threads: 8  
memory: 500M
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YAML

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  - Change config instead of code!
- Imported file with **configfile** keyword in Snakefile
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- 2 possible formats: JSON and YAML
  - Personal opinion: YAML is easier to write, understand and can be commented
- Accessed via global variable `config`
  - Imported as a Python dictionary (use keys to access values):  
`config['samples']`

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YAML

# Config file?

- Question 5

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- Ideally, everything that should not be hard-coded:
  - File locations
  - Sample names and associated information
  - Rule computing resources
  - Etc...



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- Ideally, everything that should not be hard-coded:
  - File locations
  - Sample names and associated information
  - Rule computing resources
  - Etc...
- But it is preferable to use paths to other smaller config files
  - Same as Snakefile and snakefiles
  - Example:
    - Table containing the sample names and information: `config/samples_info.tsv`
      - Tab-separated format is easy to write, read and parse
    - In the config file: `samples: 'config/samples_info.tsv'`
    - Add a function in a Snakefile to parse the table

# What should **NOT** appear in a config file?

- Credentials: access tokens, passwords...
- Use environment variables (**envvars**)

# Processing list of files: the expand syntax

- `expand()`: Snakemake function to expand a wildcard expression to several values
  - Useful to define multiple `inputs` or `outputs` with a common pattern

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- `expand()`: Snakemake function to expand a wildcard expression to several values
  - Useful to define multiple **inputs** or **outputs** with a common pattern
  - Syntax: `expand('{wildcard_name}', wildcard_name=<values>)`
    - <values>: iterable (*i.e.* list, tuple, set) containing the wildcard values

```
rule merge_files:
    input:
        'data/test_1.txt',
        'data/test_2.txt',
        'data/test_3.txt'
    output:
        'results/total.tsv'
    shell:
        'cat {input} > {output}'
```

```
rule merge_files:
    input:
        expand('data/test_{file}.txt', file=[1, 2, 3])
    output:
        'results/total.tsv'
    shell:
        'cat {input} > {output}'
```

- The **rule** `merge_files` uses all three **input** files to generate a single **output** file
  - `expand()` does not apply the **rule** three times, once per **input**!

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```
files = ['test_A', 'test_B']
nbs = [1, 2]

rule merge_files:
    input:
        expand('data/{file}_{nb}.tsv', file=files, nb=nbs)
    output:
        'results/total.tsv'
    shell:
        'cat {input} > {output}'
```



```
input:
    ['data/test_A_1.tsv', 'data/test_A_2.tsv',
     'data/test_B_1.tsv', 'data/test_B_2.tsv']
```

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rule merge_files:
    input:
        expand('data/{file}_{nb}.tsv', file=files, nb=nbs)
    output:
        'results/{file}.tsv'
    shell:
        'cat {input} > {output}'
```

- Here, `{file}` value will NOT be propagated to the `input`



# Optimising resource usage: threads

- 'threads' is a **directive**; its value is the number of threads to allocate to each job spawned by a **rule**
  - New type of value: numeric (integer)
  - When executed locally, '`--cores`' controls the total number of threads allocated to Snakemake; **threads** is automatically decreased if it's lower than '`--cores`'
  - **Check whether software can actually multithread!**

```
rule example:
    input:
        'data/test.txt'
    output:
        'results/modified_test.txt'
    threadsh: 4
    shell:
        'command --threads {threads} {input} > {output}'
```

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- 'resources' is a **directive**; its values set the resources available for a job
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- 'resources' is a **directive**; its values set the resources available for a job
  - New kind of directive value: pair of <key>=<value>
- **mem\_<unit>**
  - Amount of memory needed by the job
  - <unit>: mb, gb, tb...
- **runtime\_<unit>**
  - Amount of wall clock time a job needs to run
  - <unit>: s, m, h, d...

```
rule example:
    input:
        'data/test.txt'
    output:
        'results/modified_test.txt'
    resources:
        mem_gb = 1,
        runtime_h = 1
    shell:
        'command {input} > {output}'
```

# Using non-conventional outputs

- Snakemake has built-in utilities to assign properties to 'special' outputs

Property	Syntax	Function
Temporary	<code>temp('path/to/file.txt')</code>	File is deleted as soon as it is not required by any future jobs
Protected	<code>protected('path/to/file.txt')</code>	File cannot be overwritten after the job ends (useful to prevent erasing a file by mistake, for example files requiring heavy computation)
Ancient	<code>ancient('path/to/file.txt')</code>	Ignore file timestamp and assume file is older than any outputs: file will not be re-created when re-running the workflow, except when <code>--force</code> parameters are used
Directory	<code>directory('path/to/directory')</code>	Output is a directory instead of a file (better to use 'touch' instead if possible)
Touch	<code>touch('path/to/file.txt')</code>	Create an empty flag file 'file.txt' regardless of the shell command (if the command finished without errors)

# Exercises

- Through the day:
  - Develop a simple RNAseq analysis workflow, from reads (fastq files) to Differentially Expressed Genes (DEG)
- For this session:
  - Use a config file
  - Process list of inputs
  - Modularise a workflow
  - Aggregate outputs
  - (Optimise resource usage)
  - (Manage non-conventional outputs)

