



Snakemake for reproducible research

Making Snakemake even more reproducible

What could we improve? (again)

- Being reproducible
- Using scripts from other languages
- Using unknown number of **inputs/outputs**

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Being reproducible with Snakemake and Conda

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 - **Conda/mamba**: open-source, cross-platform, language-agnostic package manager and environment management system
 - **Channels**: field-specific repositories of software
 - [Conda-forge](#): general computation
 - [Bioconda](#): bioinformatics

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 - **Channels**: field-specific repositories of software
 - [Conda-forge](#): general computation
 - [Bioconda](#): bioinformatics
 - Environments defined in YAML files

```
name: python_env
channels:
  - conda-forge
  - bioconda
dependencies:
  - python >= 3.12
  - pandas == 2.2.3
```

py.yaml

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rule rename_file:
    input:
        'data/test.txt'
    output:
        'results/renamed_file.txt'
    conda:
        '../envs/py.yaml'
    shell:
        'mv {input} {output}'
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- Execution parameter:

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```

- v7 and before: `--use-conda`

```
snakemake --cores 1 --use-conda results/rename_file.txt
```

- v8+: `--software-deployment-method` or `--sdm` (shorthand version)

```
snakemake --cores 1 --sdm conda
results/rename_file.txt
```

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 - Handles Docker and Apptainer images
 - **Global** OR **rule-specific**

```
container:
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```

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snakemake -c 1 --use-singularity
            results/renamed_file.txt
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```
snakemake -c 1 --sdm apptainer
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Being reproducible with Snakemake and Docker

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 - Handles Docker and Apptainer images
 - **Global OR rule-specific**
 - Execution parameter
 - v7 and before: `--use-singularity`
 - V8+: `--sdm apptainer`
 - Can be combined with conda `--sdm conda apptainer`
 - Pull the image
 - Create the conda env from **within the container**
 - Containerisation of Conda-based workflows

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snakemake -c 1 --sdm apptainer
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```
snakemake -c 1 --sdm conda apptainer
results/renamed_file.txt
```

```
snakemake -c 1 --containerize > Dockerfile
```

Snakemake environments

- Question 10

What is the best setting for Snakemake environments?

- Use package and container managers!
- Same as Snakefile and config files: split things reasonably
 - 1 .smk file \approx 1 'thematic' module \approx 1 environment
- Always check for version conflicts

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    input:
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    params:
        lines = 5
    run:
        input_file = open(input[0])
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        for i in range(params.lines):
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- Replaces **shell/run**
- Access to directive values and variables, like in **shell**
- Value = path to the script relative to the rule's snakefile
- Advantages:
 - Great for long code
 - Can use **conda/container** directive!!!

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```

```
# Retrieve information from Snakemake
input_file = open(snakemake.input[0])
output_file = open(snakemake.output[0], 'w')
n_lines = snakemake.params.lines

# Process file
for i in range(n_lines):
    output_file.write(input_file.readline())
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first_step.py

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```
library(readr)

# Retrieve information from Snakemake
input_path <- snakemake@input[[1]]
output_path <- snakemake@output[[1]]
n_lines <- snakemake@params$lines[1]

# Process file
data <- read_delim(input_path, '\t',
```

first_step.R

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 - No parentheses, no argument

```
def seq_input(wildcards):  
    type = wildcards.type  
    if type == 'SE':  
        return 'data/file1.fq'  
    else:  
        return ['data/file1.fq', 'data/file2.fq']  
  
rule merge_files:  
    input:  
        seq_input  
    output:  
        'results/{type}.txt'  
    shell:  
        'cat {input} > {output}'
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- Input functions = Python functions
 - Single argument: **wildcards**
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 - Can also return a dictionary with **input** names as keys
 - Use `input: unpack(<function_name>)` to obtain named inputs

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- Functions are evaluated before workflow execution ⇒ can't list **output** files
 - **No output functions!**

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```

```
snakemake --cores 1 results/not_SE.txt
```



```
{type} = "NotSE"
```



```
input:  
    ['data/file1.fq', 'data/file2.fq']
```

Working after an unknown number of inputs/outputs

- *aka* 'Data-dependent conditional execution' *aka* **checkpoint** (instead of **rule**)
- When:
 - An unknown number of files is generated by a rule
 - **Output** files are unknown before execution
- Conditional reevaluation of the DAG of jobs based on the outputs content
 - Since DAG is re-evaluated midway □ you can't see the whole workflow at the start
- **Very complicated!**

Exercises

- Through the day:
 - Develop a simple RNAseq analysis workflow, from reads (fastq files) to Differentially Expressed Genes (DEG)
- For this session:
 - Use an input function
 - Use R and Python scripts
 - Run a rule inside a conda environment
 - Run a rule inside a Docker/Singularity container

