

What could we improve?

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rule hello_world:
    output:
        'results/hello.txt'
    shell:
        'echo "Hello world!" > results/hello.txt'

rule copy_file:
    input:
        rules.hello_world.output
    output:
        'results/copied_file.txt'
    shell:
        'cp results/hello.txt results/copied_file.txt'
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- Using hard-coded file paths
- Having multiple **inputs/outputs** per rule
- (Checking Snakemake behaviour)

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- Using hard-coded file paths —————→ Placeholders and wildcards
- Having multiple **inputs/outputs** per rule —————→ Numbered/named inputs/outputs
- (Checking Snakemake behaviour) —————→ (Log files)

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Avoiding hard-coded filepaths: placeholders

- Placeholder:
 - A person or thing that occupies the position or place of another person or thing
 - A symbol in a mathematical or logical expression that may be replaced by the name of any element of a set

(From the Merriam-Webster dictionary)

Avoiding hard-coded filepaths: placeholders

```
rule rename_file:  
    input:  
        'data/test.txt'  
    output:  
        'results/renamed_test.txt'  
    shell:  
        'mv data/test.txt results/renamed test.txt'
```

Avoiding hard-coded filepaths: placeholders

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    input:  
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    output:  
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    shell:  
        'mv data/test.txt results/renamed test.txt'
```

```
rule rename_file:  
    input:  
        'data/test.txt'  
    output:  
        'results/renamed_test.txt'  
    shell:  
        'mv {input} {output}'
```


Avoiding hard-coded filepaths: placeholders

- `{input}` and `{output}` are placeholders
- Used in `shell` directive
- Similar to python f-string
- Snakemake will replace them with appropriate values before running the command
- Many directives can use placeholders: `{log}`, `{benchmark}`, `{params}`...

```
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    output:
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    shell:
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    input:
        rules.hello_world.output
    output:
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    shell:
        'cp {input} {output}'
```

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Making more general-purpose rules: wildcards

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} Defined paths

Making more general-purpose rules: wildcards

- **Wildcards** ≈ "variables" automatically inferred by Snakemake

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rule rename_file:
    input:
        'data/test.txt'
    output:
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    shell:
        'mv {input} {output}'
```

} Defined paths



```
rule rename_file:
    input:
        'data/{file}.txt'
    output:
        'results/{file}.txt'
    shell:
        'mv {input} {output}'
```

} Adaptable paths
with **wildcards**

Making more general-purpose rules: wildcards

- **Wildcards** ≈ "variables" automatically inferred by Snakemake
- Enclose wildcard name with curly brackets `{ }`

```
rule rename_file:
    input:
        'data/test.txt'
    output:
        'results/renamed_test.txt'
    shell:
        'mv {input} {output}'
```

} Defined paths



```
rule rename_file:
    input:
        'data/{file}.tsv'
    output:
        'results/{file}.txt'
    shell:
        'mv {input} {output}'
```

} Adaptable paths
with **wildcards**



Making more general-purpose rules: wildcards

- **Wildcards** are "resolved" from the target and propagated to other **directives**
 - Regular expression matching: `.+`
 - "1 or more occurrences of any character except newline"
 - Can be constrained
- Using **wildcards** forces to ask for **output(s)**: Snakemake doesn't guess!
 - **Target rules cannot contain wildcards**

```
rule rename_file:
    input:
        'data/{file}.txt'
    output:
        'results/renamed_{file}.txt'
    shell:
        'mv {input} {output}'
```

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



`{file} = "test"`



```
input: 'data/test.txt'
```

Making more general-purpose rules: wildcards

- **Wildcards** are "resolved" from the target and propagated to other **directives**
 - Regular expression matching: `.*`
- Both a workflow and a **rule** can use multiple **wildcards**

```
rule rename_file:
    input:
        'data/{file}_{nb}.txt'
    output:
        'results/renamed_{file}_{nb}.txt'
    shell:
        'mv {input} {output}'
```

```
snakemake --cores 1 results/renamed_test_1.txt
```



```
{file} = "test"; {nb} = "1"
```



```
input: 'data/test_1.txt'
```


Making more general-purpose rules: wildcards

- **Wildcards** are "resolved" from the target and propagated to other **directives**
 - Regular expression matching: `.*`
- Both a workflow and a **rule** can use multiple **wildcards**
- **Input** and **output** files do not need to share the same **wildcards**
- **All outputs, logs... created by a rule must have the same wildcards!**

```
rule rename_file:
    input:
        'data/{file}.txt'
    output:
        'results/renamed_{file}_{nb}.txt'
    shell:
        'mv {input} {output}'
```

```
snakemake --cores 1 results/renamed_test_1.txt
```



```
{file} = "test"; {nb} = "1"
```



```
input: 'data/test.txt'
```

Building a Directed Acyclic Graph (DAG)

- Rule can appear more than once, with different wildcards
 - 1 rule + 1 wildcard values = 1 job



What could we improve?

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rule hello_world:
    output:
        'results/hello.txt'
    shell:
        'echo "Hello world!" > {output}'

rule copy_file:
    input:
        rules.hello_world.output
    output:
        'results/copied_file.txt'
    shell:
        'cp {input} {output}'
```

- Using hard-coded file paths → Placeholders and wildcards
- Having multiple **inputs/outputs** per rule → **Numbered/named inputs/outputs**
- (Checking Snakemake behaviour) → (Log files)

Creating rules with multiple inputs/outputs

- Rules can use multiple inputs/outputs

Creating rules with multiple inputs/outputs

- **Rules** can use multiple **inputs/outputs**
 - Separated by a comma
 - Input values are **unpacked** (replaced by a space-separated list)

```
rule gather_files:  
    input:  
        'data/test1.txt',  
        'data/test2.txt'  
    output:  
        'results/merged_test.txt'  
    shell:  
        'cat {input} > {output}'
```



```
shell:  
    'cat data/test1.txt data/test2.txt > results/merged_test.txt'
```

Creating rules with multiple inputs/outputs

- **Rules** can use multiple **inputs/outputs**
 - Separated by a comma
 - Input values are **unpacked** (replaced by a space-separated list)
- **Shell** can have multiple commands
 - Separated by a semicolon
 - Commands are concatenated

```
rule gather_files:
    input:
        'data/test1.txt'
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    output:
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    shell:
        'cat {input} > {output}'
        'cat {input} >> {output}'
```

Creating rules with multiple inputs/outputs

- **Rules** can use multiple **inputs/outputs**
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 - Input values are **unpacked** (replaced by a space-separated list)
- **Shell** can have multiple commands
 - ~~○ Separated by a semicolon~~
 - Commands are concatenated

```
rule gather_files:
    input:
        'data/test1.txt'
        'data/test2.txt'
    output:
        'results/merged_test.txt'
    shell:
        '''
        cat {input} > {output}
        cat {input} >> {output}
        '''
```

Creating rules with multiple inputs/outputs

- **Rules** can use multiple **inputs/outputs**
 - Separated by a comma
 - Input values are **unpacked** (replaced by a space-separated list)
- **Shell** can have multiple commands
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 - Commands are concatenated
- **Inputs** can be accessed by their positional index: `input[n]`
 - Numbering starts at 0

```
rule gather_files:
    input:
        'data/test1.txt'
        'data/test2.txt'
    output:
        'results/merged_test.txt'
    shell:
        '''
        cat {input[0]} > {output}
        cat {input[1]} >> {output}
        '''
```


Creating rules with multiple inputs/outputs

- **Rules** can use multiple **inputs/outputs**
 - Separated by a comma
 - Input values are **unpacked** (replaced by a space-separated list)
- **Shell** can have multiple commands
 - ~~○ Separated by a semicolon~~
 - Commands are concatenated
- **Inputs** can be accessed by their positional index: `input[n]`
 - Numbering starts at 0
- Named **inputs** can be accessed by their names: `input.input_name`

```
rule gather_files:
    input:
        file_1='data/test1.txt',
        file_2='data/test2.txt'
    output:
        'results/merged_test.txt'
    shell:
        '''
        cat {input.file_1} > {output}
        cat {input.file_2} >> {output}
        '''
```

Creating rules with multiple inputs/outputs

- **Outputs** work like **inputs**
 - Separated by ','
 - Can be named
 - Can be accessed by positional index or by name
- All **outputs** need to be created or the job will fail

```
rule gather_files:
    input:
        file_1='data/test1.tsv'
        file_2='data/test2.tsv'
    output:
        copy_1='results/copied_test1.txt'
        copy_2='results/copied_test2.txt'
    shell:
        '''
        cat {input.file_1} > {output.copy_1}
        cat {input.file_2} > {output.copy_2}
        '''
```

```
snakemake --cores 1 results/first_step_1.txt
```



```
'results/first_step_1.txt', 'results/first_step_2.txt'
```

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    output:
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    shell:
        'echo "Hello world!" > {output}'

rule copy_file:
    input:
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- Using hard-coded file paths → Placeholders and wildcards
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Checking Snakemake behaviour: log files

- 'log' is a **directive**; its value is a path to a log file for one **rule**
 - Can be accessed with a placeholder in **shell**:
`{log}`

```
rule rename_file:
    input:
        'data/test.txt'
    output:
        'results/renamed_file.txt'
    log:
        'logs/renaming.log'
    shell:
        'mv {input} {output} 2> {log}'
```

Checking Snakemake behaviour: log files

- 'log' is a **directive**; its value is a path to a log file for one **rule**
 - Can be accessed with a placeholder in **shell**:
`{log}`
- You need to **manually redirect messages to logs**, but Snakemake automatically creates the folder path

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 - Can be accessed with a placeholder in **shell**:
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- You need to **manually redirect messages to logs**, but Snakemake automatically creates the folder path
- Log files must have the **same wildcards as the output!**
- Good practice: put all logs in same folder

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    output:
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    log:
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```

Exercises

- Through the day:
 - Develop a simple RNAseq analysis workflow, from reads (fastq files) to Differentially Expressed Genes (DEG)
- For this session:
 - Use placeholders and wildcards
 - Use multiple inputs and outputs
 - (Check workflow behaviour)
 - Visualise a DAG

