Snakemake

Making High-Performance Computing a bit easier

Snakemake

The Snakemake **workflow management system** is a **tool** to create reproducible and scalable data analyses.

Easy use of multiple threads without the dangers of multithreading.

Snakemake pipeline structure

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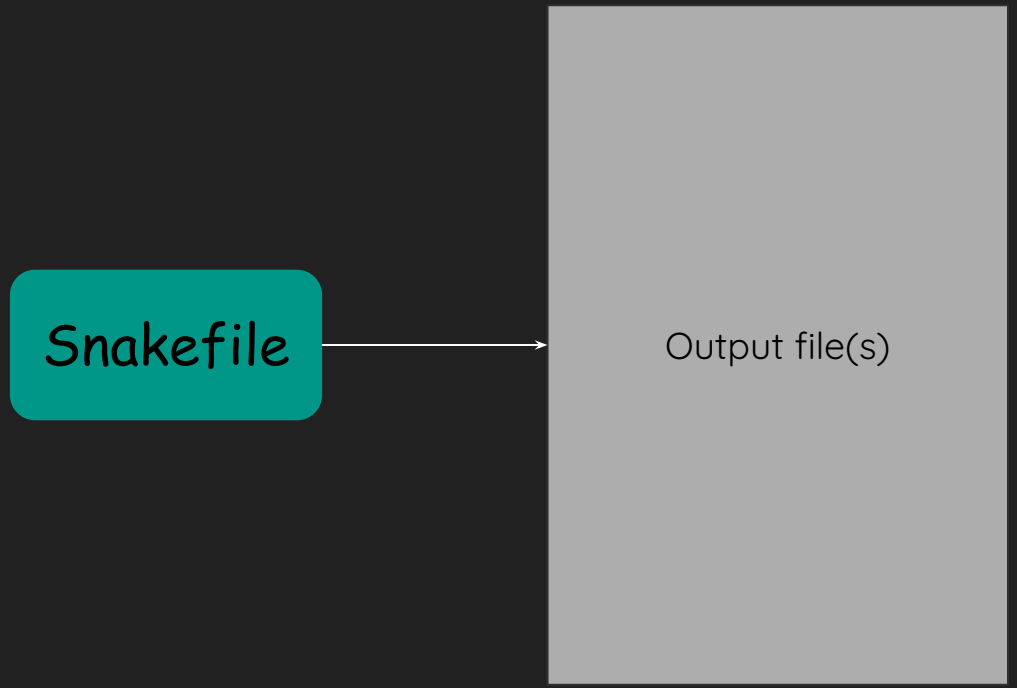

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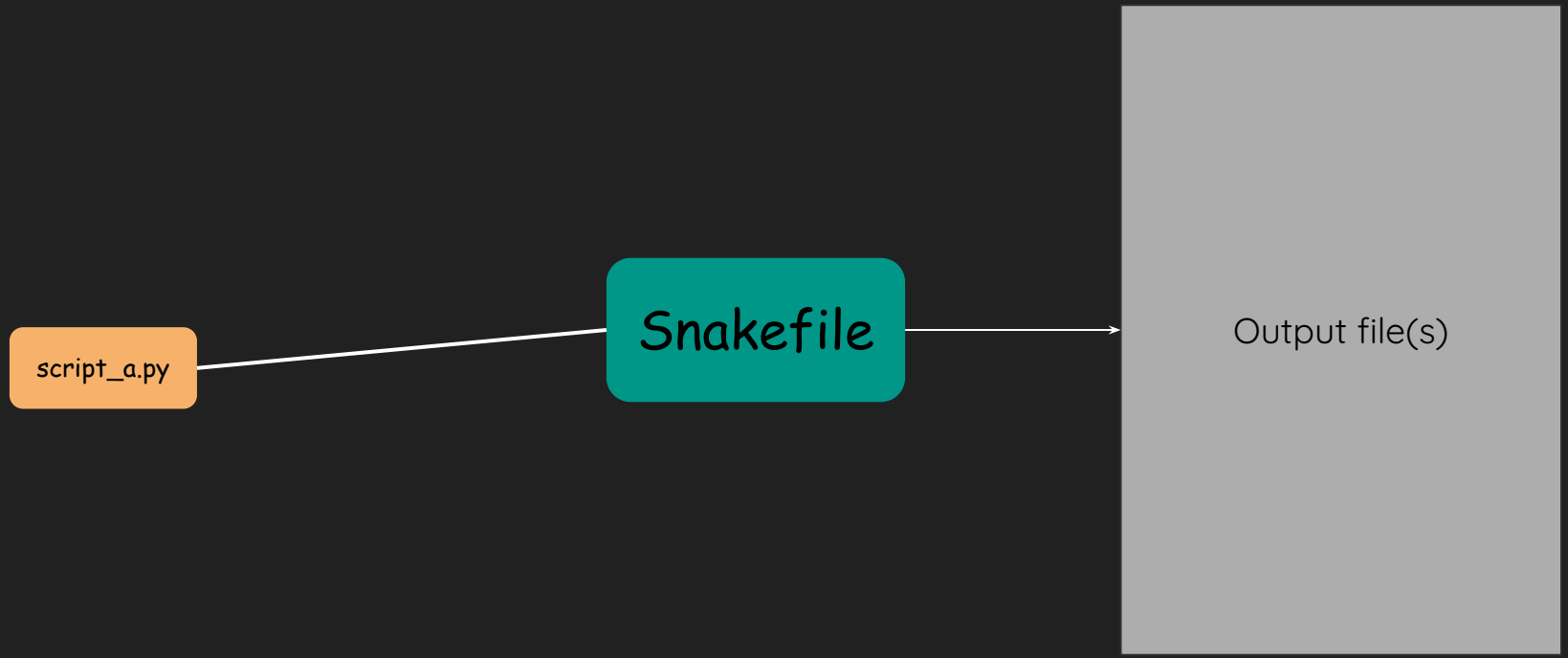

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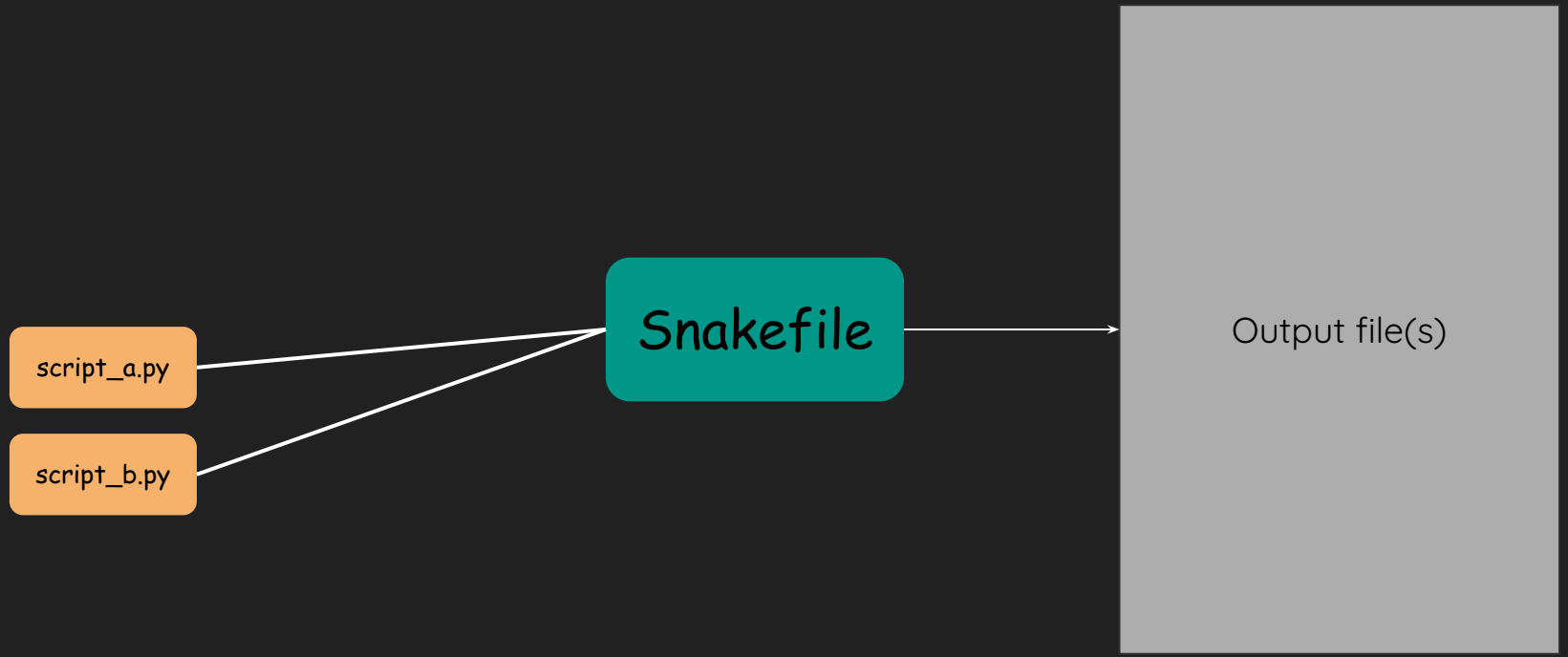

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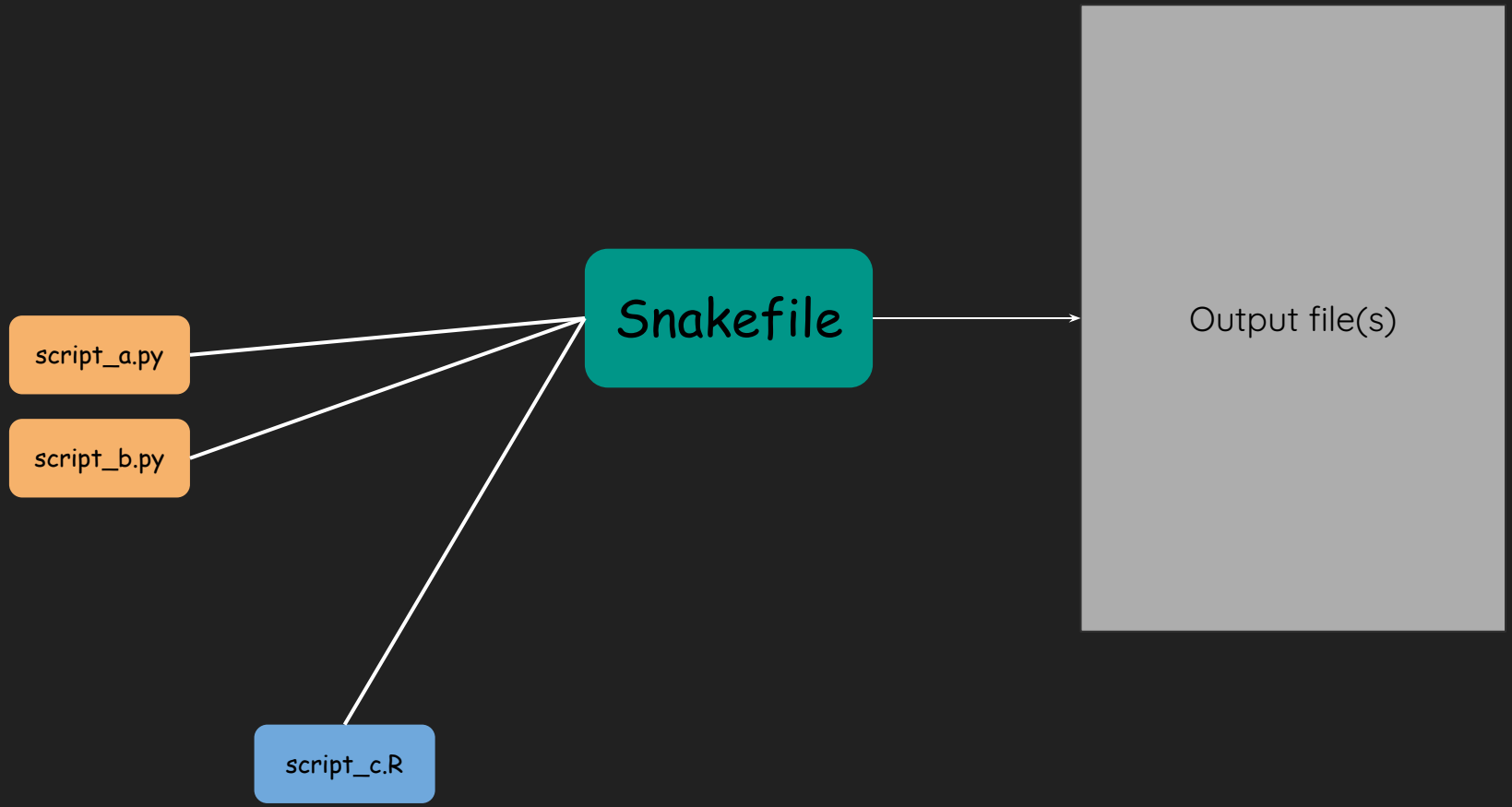

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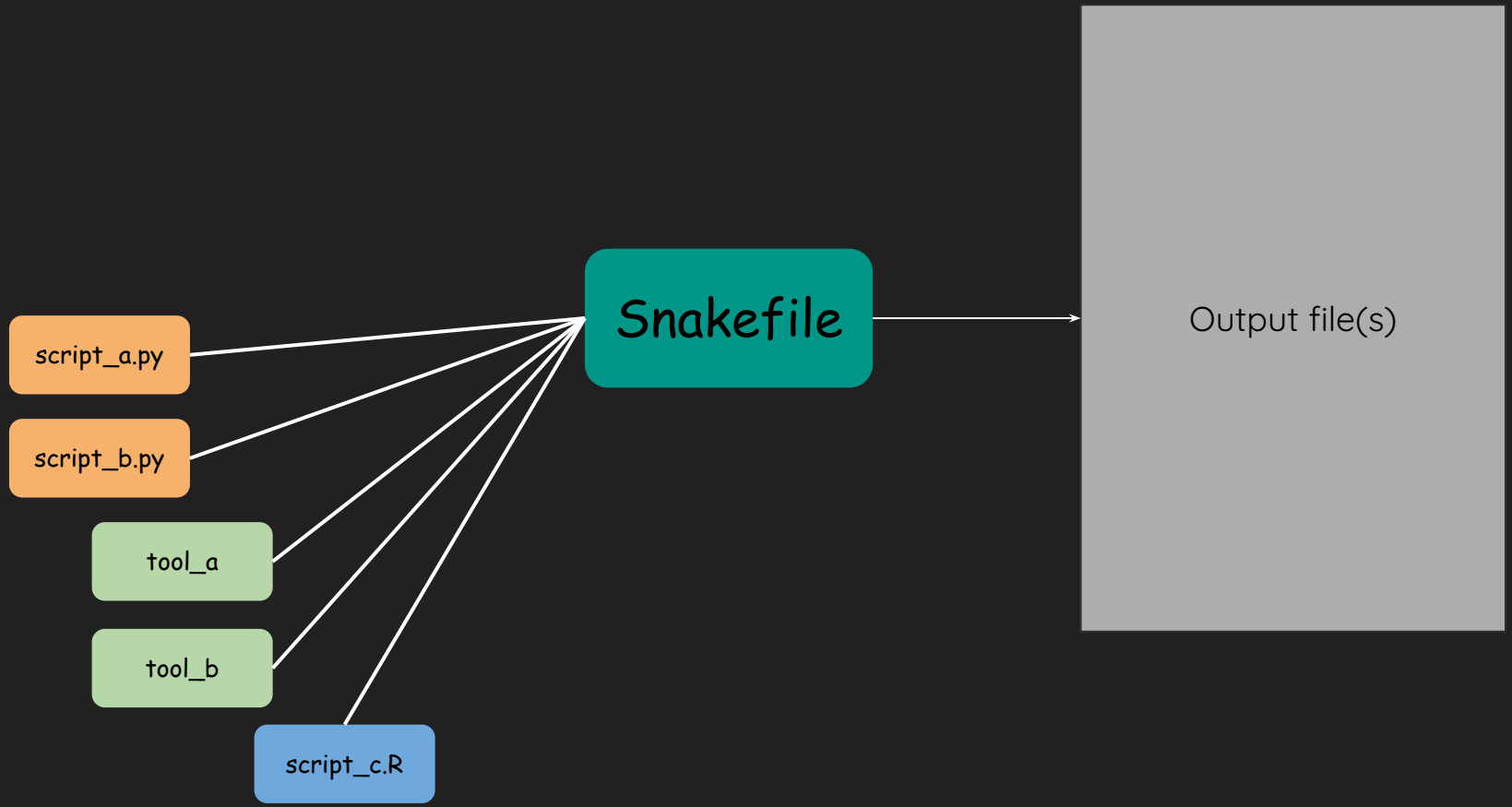

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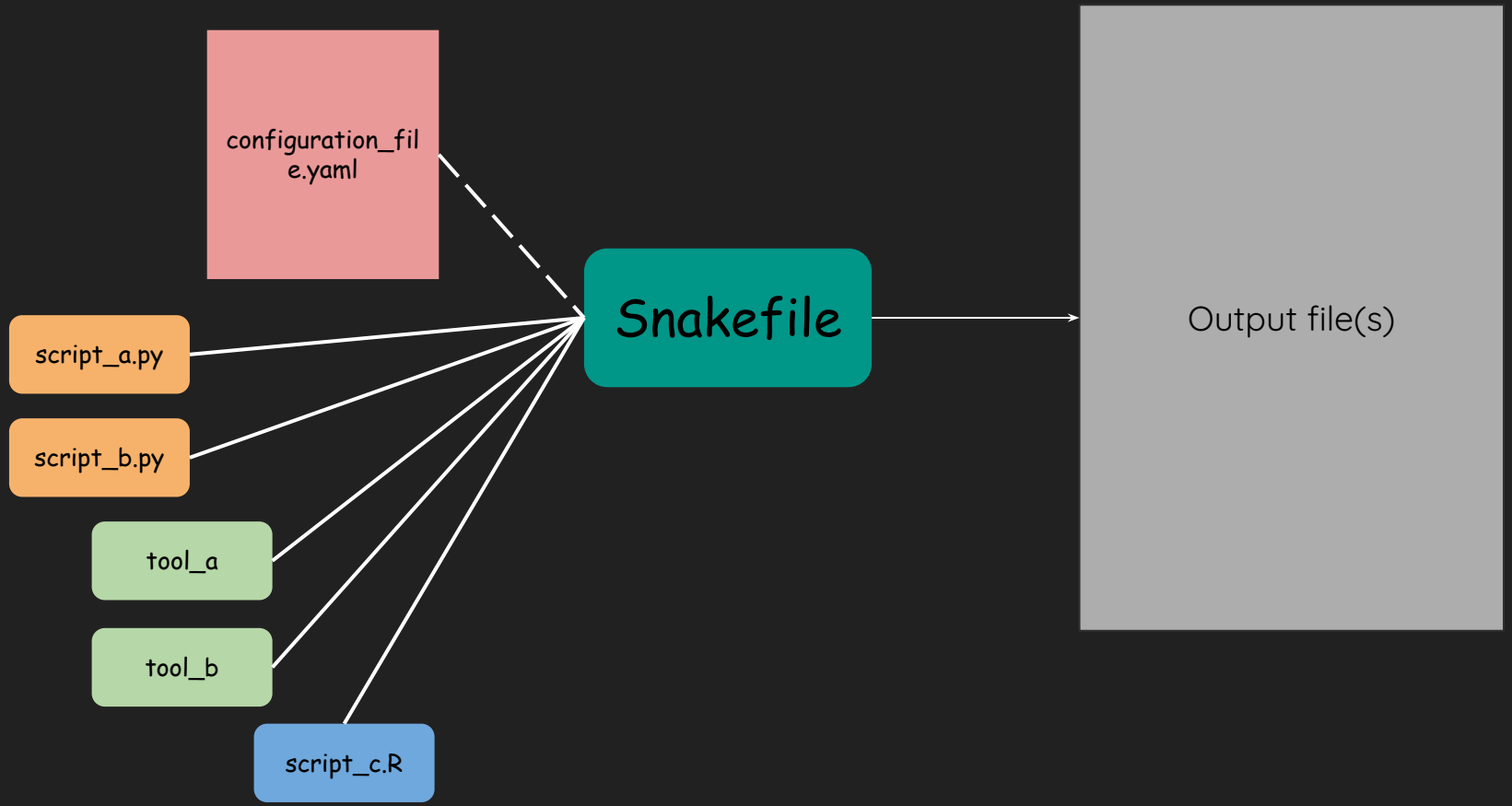

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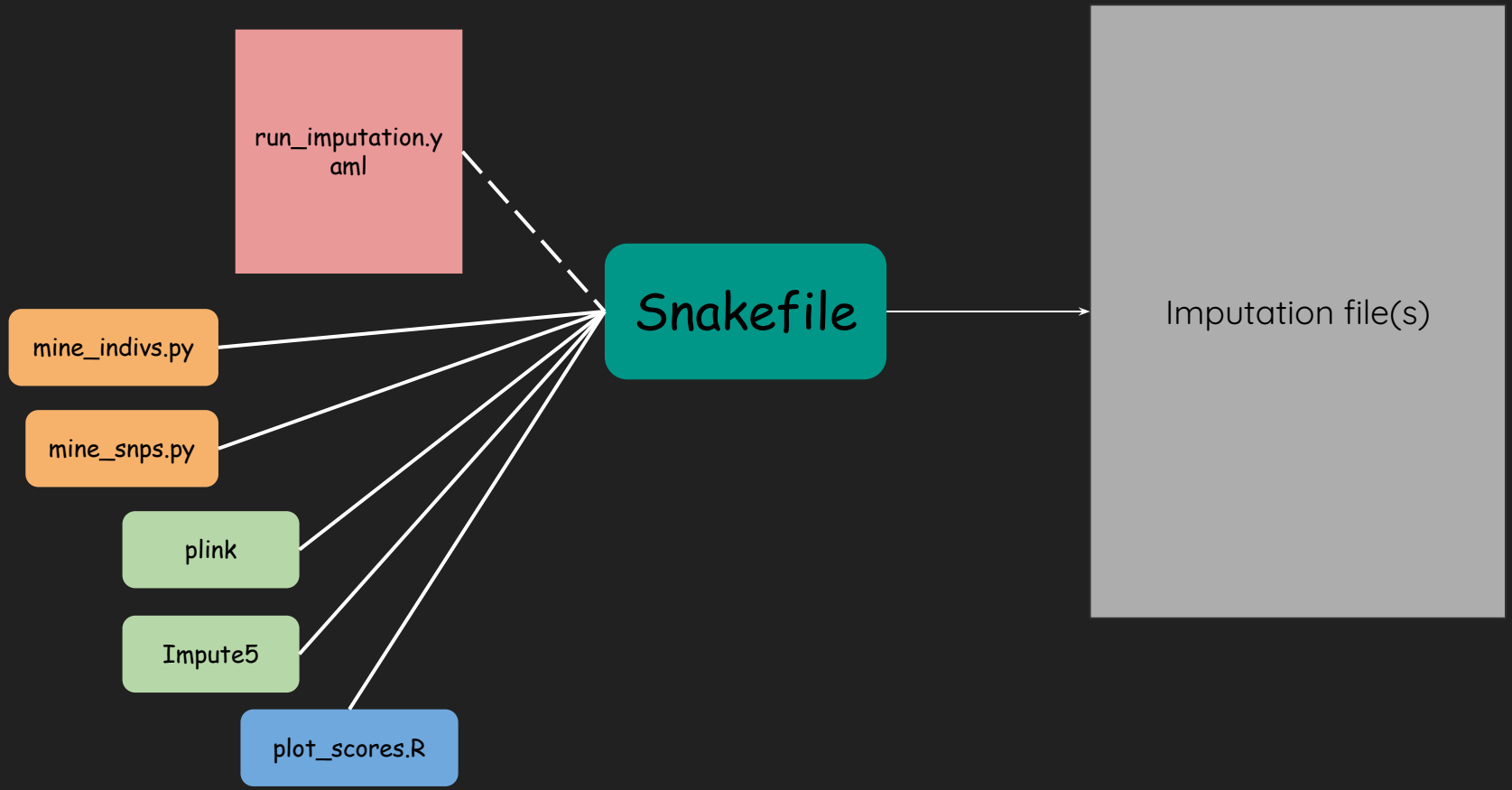
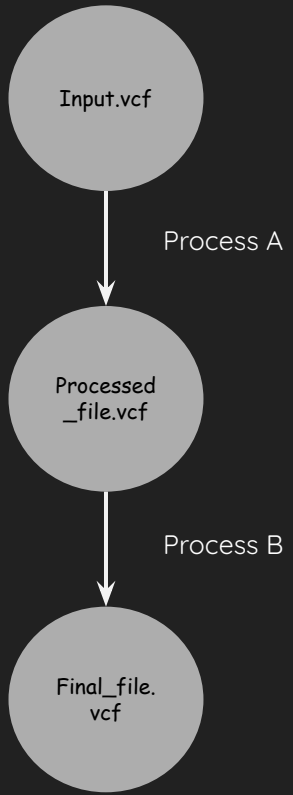


The process

[Directed Acyclic Graph]



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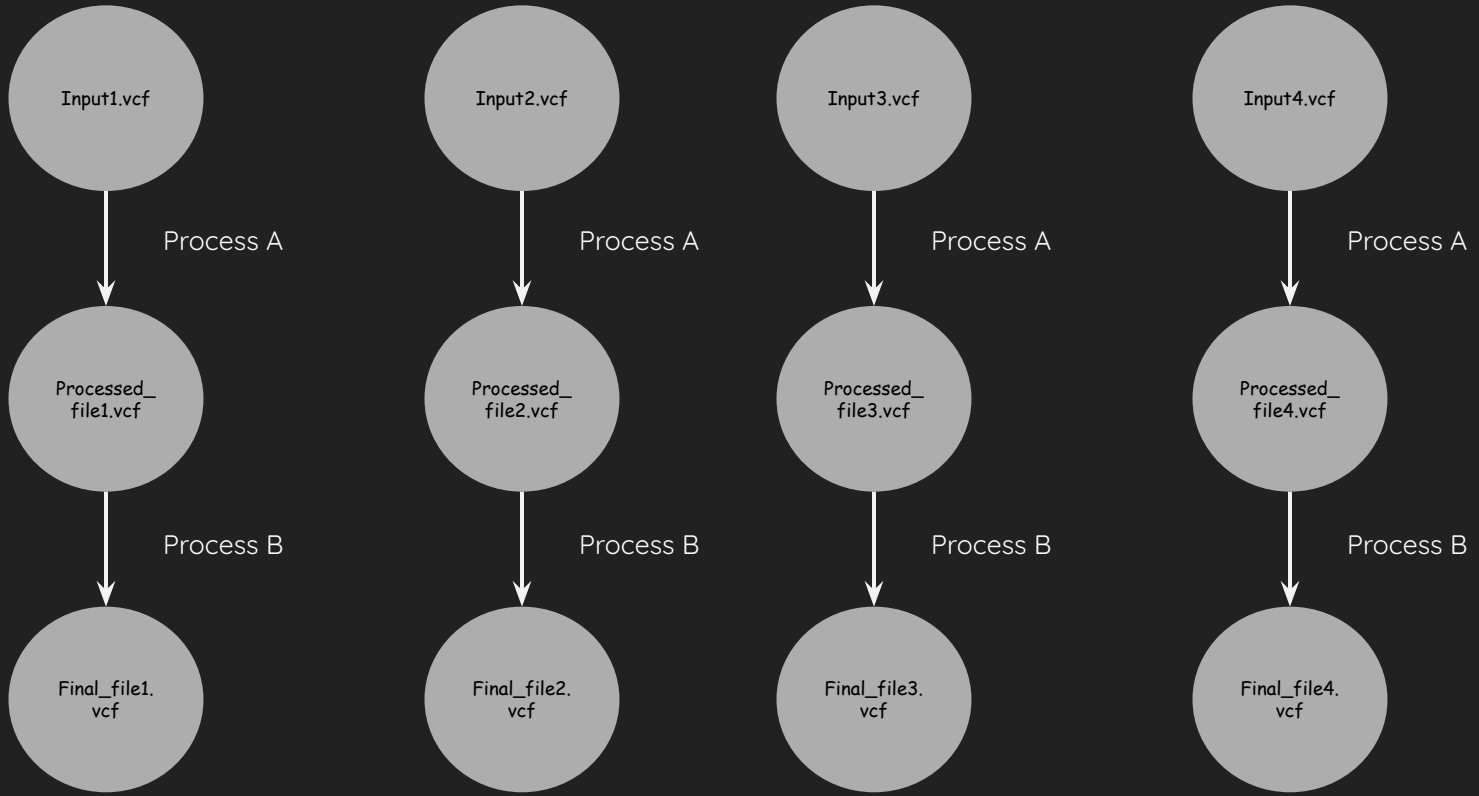

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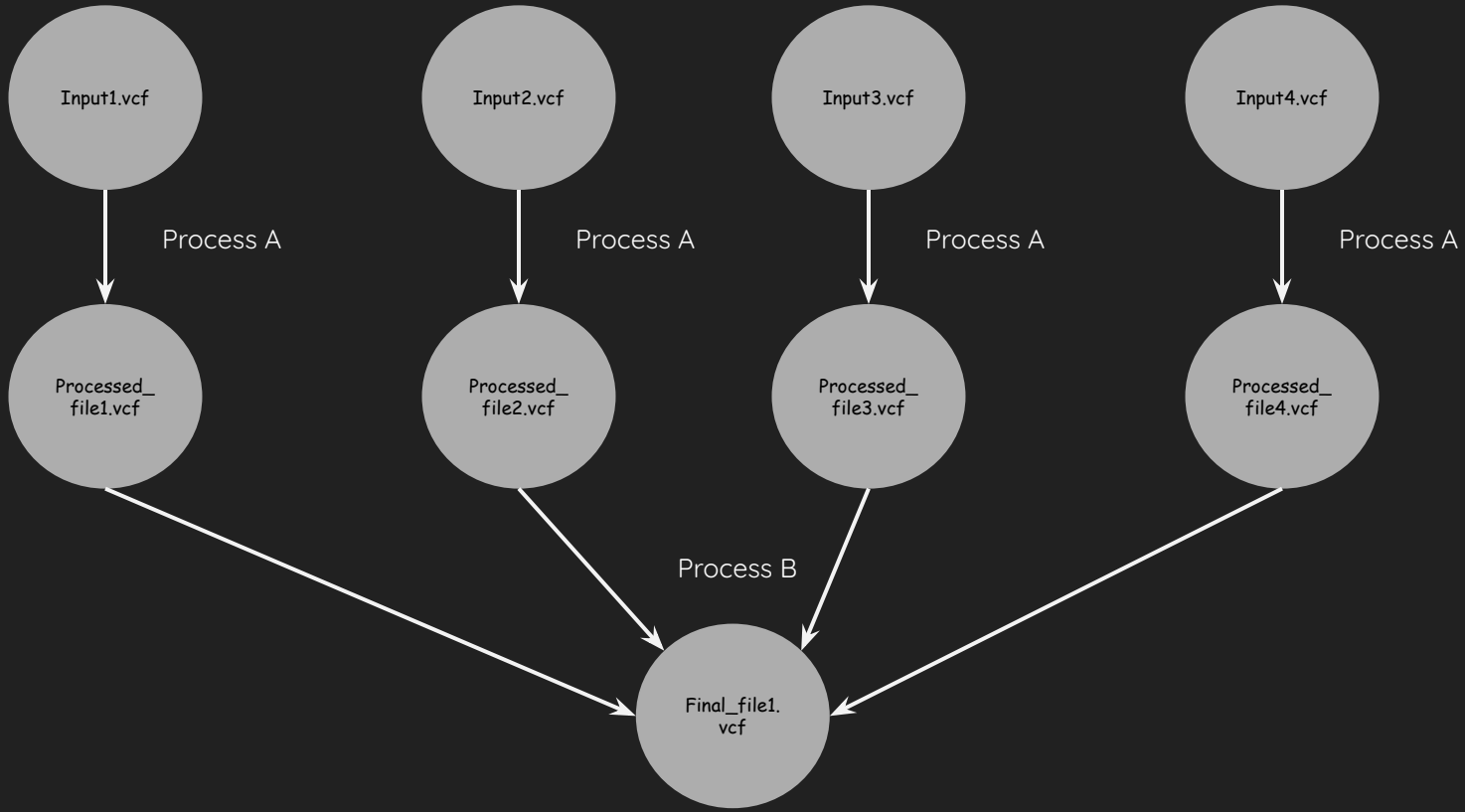

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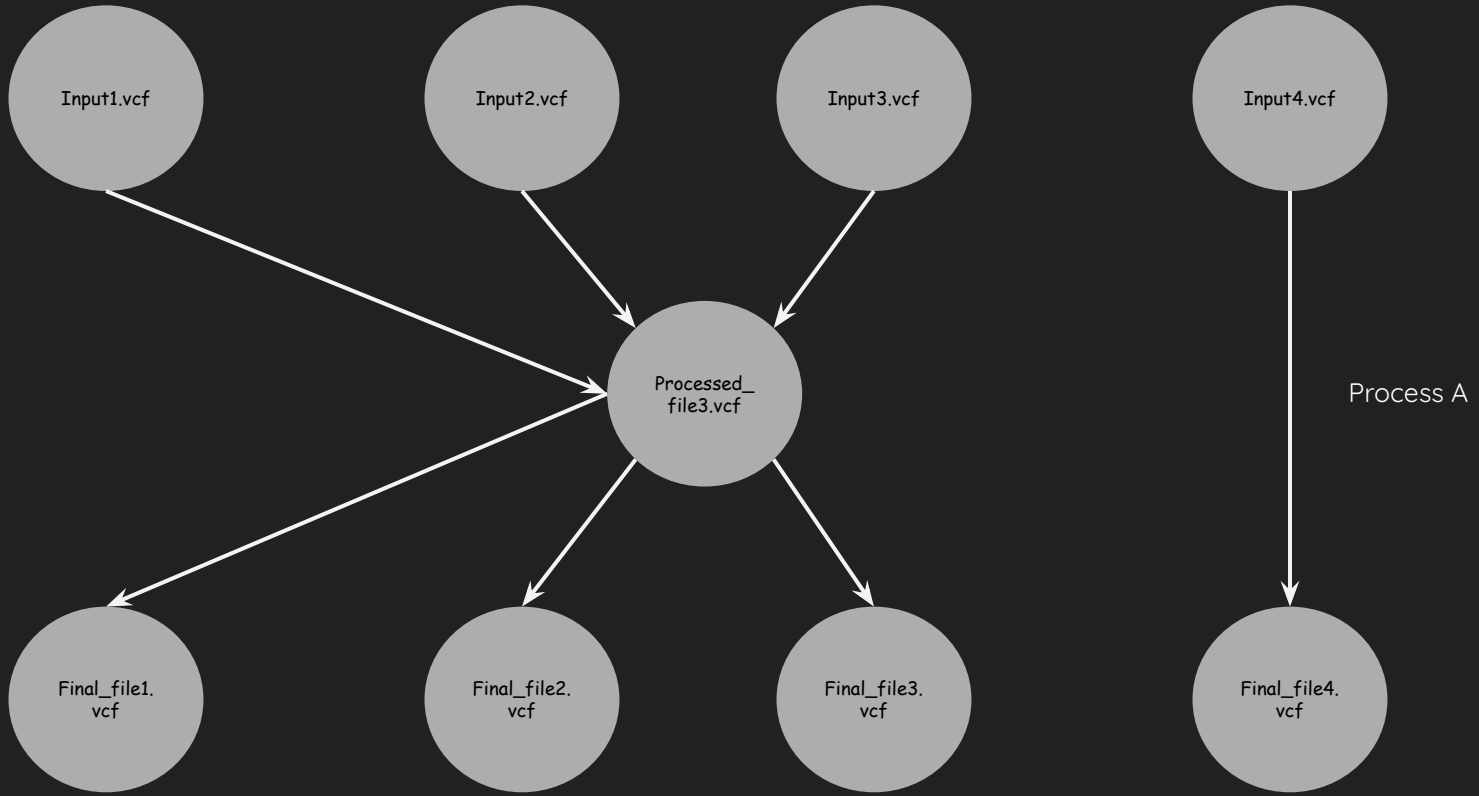
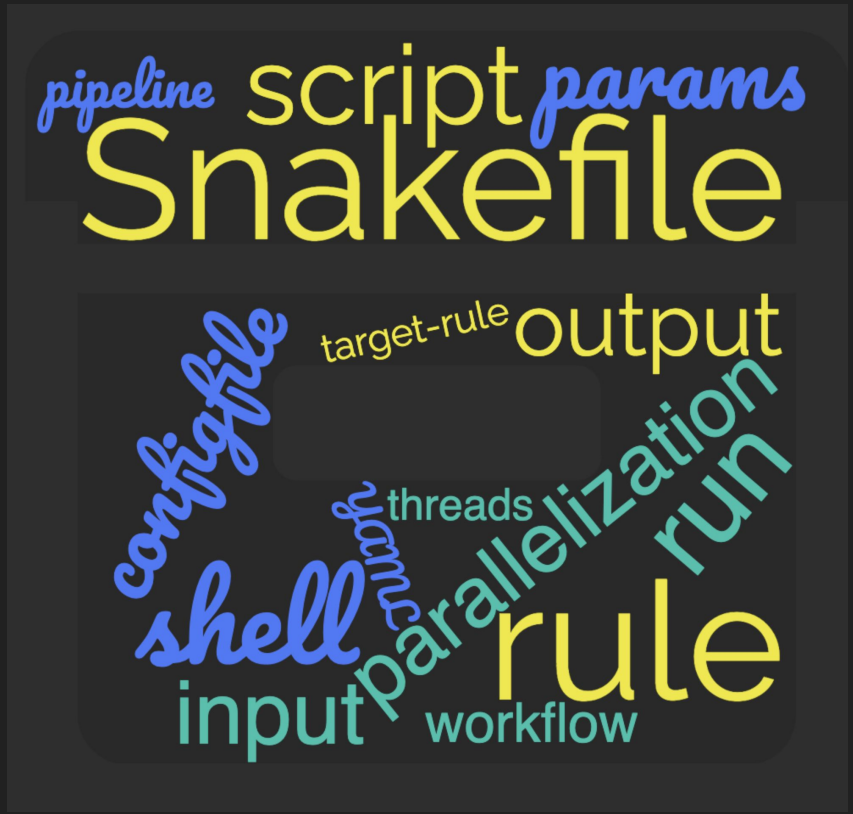
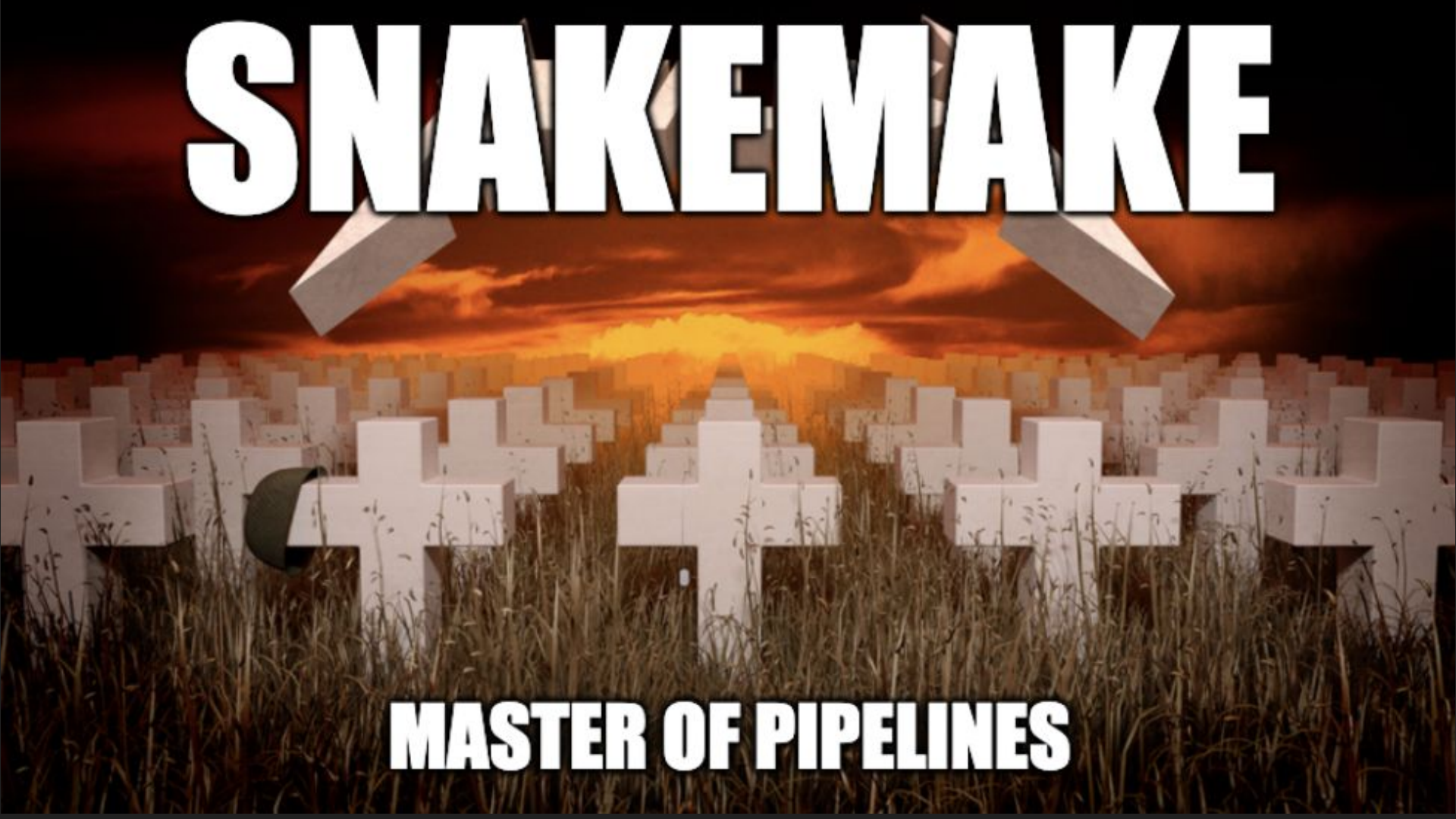


Important terms/Keywords




SNAKEMAKE
MASTER OF PIPELINES

Exam

Exercise 1

- Create a **schematic** of the imputation process.

- **No explanation** of the process.
- Be a minimalist but show the important things:
  - **Steps** (e.g. filtering)
  - **Logic** (step order)
  - **Files** necessary (use names that reflect the file contents)

- Max 3 slides
- Submit a PDF

Exercise 2

- Provide explanation for the schematic
  - Why this step?
  - **Why** this tool?
  - **What** is in this file?
  - **Which** arguments should be used? (for tools)

- Short answers will be appreciated.

- Submit a PDF (one page)
  - Font: Times New Roman
  - Size: 12

Exercise 3

- Download files.
- Build a pipeline for genotype imputation.

- You should edit the **Snakefile** only.
  - Use arguments when using tools.
  - Target file:
    - All_chromosomes.vcf
  - Make sure to keep the file structure.
  - It is **pseudo-code** no need to run it.

- Submit the Snakefile only!

Thank you