Building reproducible bioinformatics workflows using Snakemake

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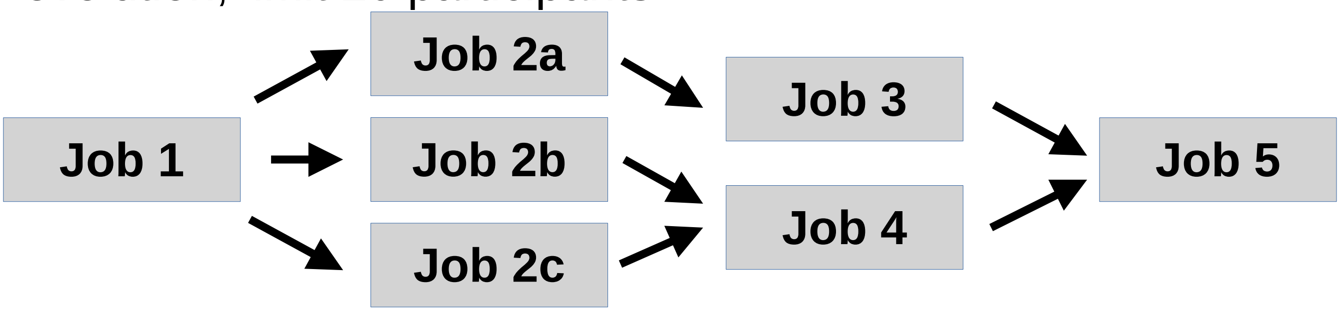
Do you want to learn how to **simplify and streamline complex bioinformatic tasks** by building **automated and reproducible bioinformatics workflows**? This workshop will show you how to build your own workflows for any type of multi step bioinformatics applications where the output generated by one or multiple jobs will be the input of other jobs (like in the example below) using the **Snakemake** framework.

- Automate your bioinformatics analyses by building your own Snakemake workflows and run them on an **HPC cluster** like MetaCentrum
- **Requirements:** Experience with using the command line. Also some basic knowledge of Python would be advantageous
- **Duration:** 3 days with 6 h each
- **Sign-up**: MB120P12 - Current approaches in plant ecology and evolution, limit 20 participants



For an overview of Snakemake go to https://snakemake.github.io/