

Introduction to Snakemake

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Lesson 3

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3. Priorities
4. Script files (Python, R, and Julia)
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Assignment 2

When Things Go Wrong

Locked Working Directories

- Snakemake locks its working directory when running
 - Prevents other snakemake instances from running in the same place
- Snakemake removes the lock when it completes (success *or* failure)
- Lockfile may not be removed when if snakemake crashes or is killed by slurm
 - `scancel --user your_username`

```
Unable to lock working directory.
```

Unlocking a Stale Lock

The Correct Way: `--unlock`

```
sbatch -c 1 --mem 2G --wrap "snakemake --unlock -s path/to/your/workflow.smk -j 1"
```

💀💀💀 Nuclear Option 💀💀💀

```
rm -r ./snakemake
```

When Things Go Wrong

It Should Have Worked But It Didn't!

- Sometimes a job finishes successfully but snakemake doesn't detect the outputs
- Filesystem latency *especially* on a cluster like Waffles can be a factor
 - It takes some non-zero amount of time to write results to disk
- Consider setting `--latency-wait` with larger number (default: 5 seconds)

Priorities

- Rule priorities may be set
- These **are not** the same as slurm partitions
- Only determine the priority of execution *within* the workflow
- Rules default to priority 0
- Bigger numbers are higher priority

```
rule my_example:  
  input: ...  
  output: ...  
  priority: 50  
  shell: ...
```


Script Files

- Not to be confuse with an external command
- Like a `run` block, but stored in another file
 - Path is specified relative to the workflow
- Available languages:
 - Python
 - R
 - Julia
- Snakemake will use special variables in the script
 - These scripts won't be general purpose!
 - Tied to snakemake

Script Files

```
# workflow.smk
rule scriptfile_example:
    input:
        "path/to/inputfile",
        "path/to/other/inputfile"
    output:
        "path/to/outputfile",
        "path/to/another/outputfile"
    script:
        "scripts/script.py"
```

```
# scripts/script.py
def do_something(data_path, out_path, threads, myparam):
    # python code here

do_something(snakemake.input[0], snakemake.output[0],
             snakemake.threads, snakemake.config["myparam"])
```

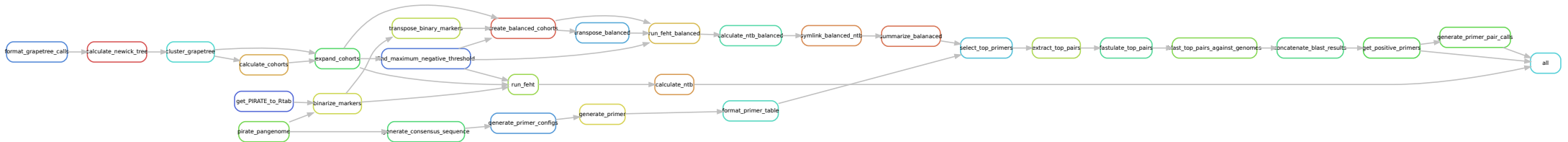
Including Workflows

- Existing workflows can be included with `include`
- Allows more modular design of workflows
- Like copy/pasting another workflow in

```
rule all:  
    input: "summary_report.txt"  
  
include: "summary_report.smk"  
include: "determine_amr.smk"  
include: "assemble_genomes.smk"
```

Visualizing Workflows

```
# Shows just the abstract graph of rules
snakemake -s your/workflow.smk --rulegraph | dot -Tpng > workflow.png
# OR
# Show every sample's journey through the workflow
snakemake -s your/workflow.smk --dag | dot -Tpng > workflow.png
```



Clinic

Please feel free to ask any questions!