
Snakemake-RNASeq-Workflows Documentation

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Sangram Keshari Sahu

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Workflows may contain modified parameters, Please look at `snakemake` files before use.

CHAPTER 1

Current workflows

- STAR-Cufflinks
- Salmon

2.1 1. Prepare samples directory properly

Before you run `write_sample_to_json.py`, **samples** directory arrangement and it's naming needs to be proper such that it can be read by the script and call further in `snakemake` files.

Something like this:

2.2 2. Generate `samples.json` file

This will be used to automatic detect samples names and call them in `snakemake` files.

2.3 3. Run Workflows

First Edit the `config.yml` files inside workflow directory with required full paths.

Then simply call `snakemake` from workflow directory (With additional parameters if required)

2.4 Additional

For checking workflow and debug

Visualise the workflow

CHAPTER 3

Indices and tables

- `genindex`
- `modindex`
- `search`