Snakemake-RNASeq-Workflows Documentation

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

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CURRCT WORKFLOWS

- STAR-Cufflinks
- Salmon

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QUICK START

2.1 1. Prepare samples directory properly

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

Something like this:

```
samples
├── SET1_dummy
│   ├── SET1_dummy_R1.fastq.gz
│   └── SET1_dummy_R2.fastq.gz
└── SET3_dummy
    ├── SET3_dummy_R1.fastq.gz
    └── SET3_dummy_R2.fastq.gz
```

2.2 2. Generate `samples.json` file

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

```
python3 write_sample_to_json.py --fastq_dir full_path_to_samples_directory
```

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)

```
snakemake --cores 12
```

2.4 Additional

For checking workflow and debug

```
snakemake -np
```

Visualise the workflow

```
snakemake --forceall --dag | dot -Tpng | display
```

CHAPTER

THREE

INDICES AND TABLES

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