NextFlow pipeline for SARS-CoV-2 Illumina data

Table of contents

Quickstart

Installation and usage

1. Install NextFlow

```
curl -s https://get.nextflow.io | bash
mv nextflow ~/bin
```

2. Build two containers:

```
docker build --target production -f Dockerfile-main -t
nf_illumina_sars-3.0-main .
docker build --target prodcution -f Dockerfile-manta -t
nf_illumina_sars-3.0-manta .
```

3. Install `pangolin-data` package locally in `data/pangolin` directory:

```
pip install \
    --target data/pangolin \
    --upgrade \
    git+https://github.com/cov-lineages/pangolin-data.git@<VERSION>
```

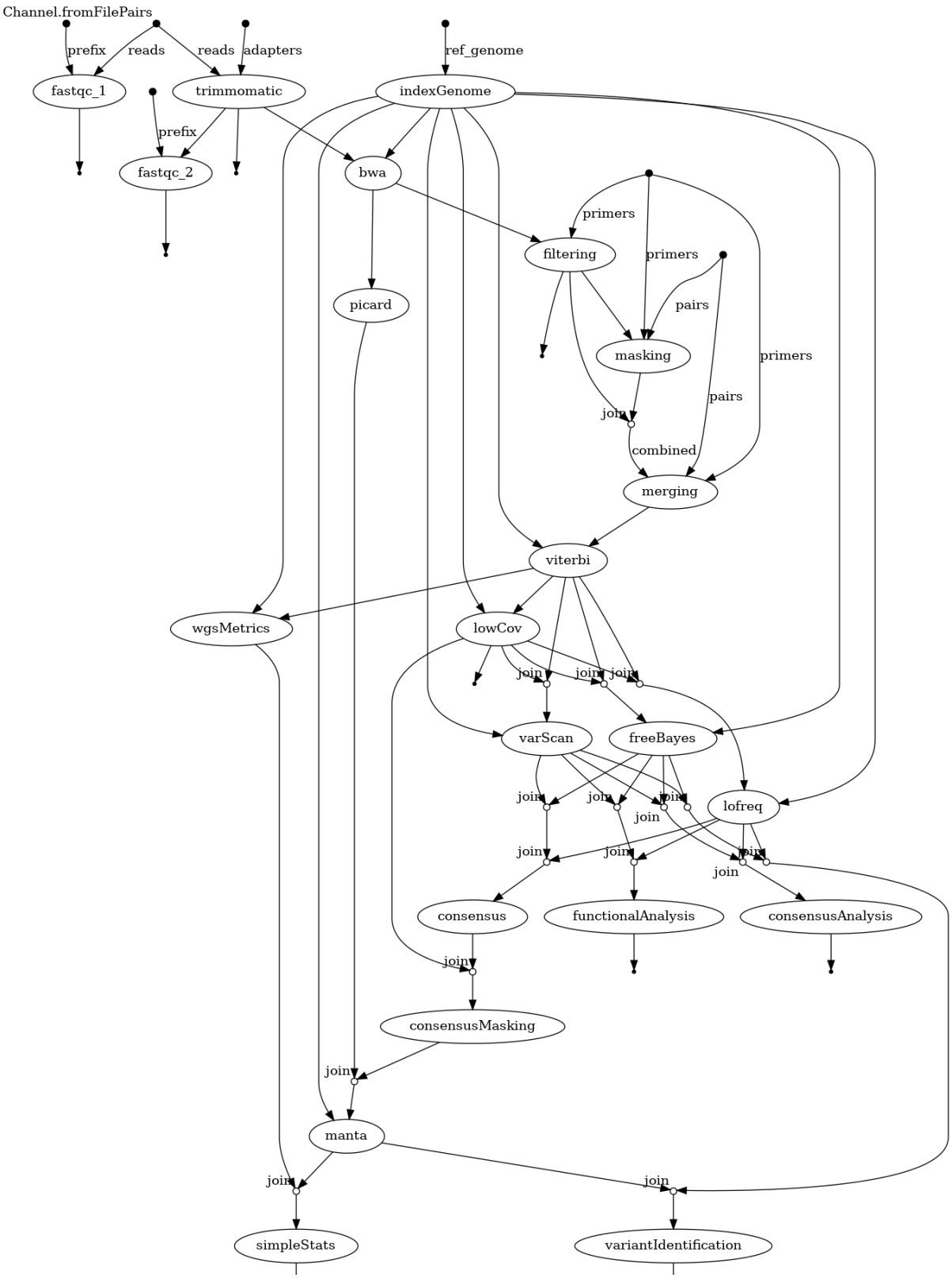
Substitute `<VERSION>` with desired tag name from git repository. List of tags is available here (https://github.com/cov-lineages/pangolin-data/tags).

4. Copy `run_nf_pipeline.sh.template` to `run_nf_pipeline.sh` and fill in the paths to the reads and output directory.

5. Run the pipeline:

```
./run_nf_pipeline.sh
```

Pipeline overview



Updates

Pangolin

Pangolin (https://github.com/cov-lineages/pangolin) (**P**hylogenetic **A**ssignment of **N**amed **G**lobal **O**utbreak **LIN**eages) is software for assigning evolutionary lineage to SARS-Cov2.

To make it work properly, it requires a database that is stored in the Git repository pangolin-data (https://github.com/cov-lineages/pangolin-data).

Pangolin-data is actually a regular python package. Normal update procedure is via command: `pangolin --update-data`. It also can be installed by `pip` command. Keeping it inside container is slightly tricky. We don't want to rebuild entire container just to update the database. We also don't want to keep the database inside the container, because it would force us to run the update before every pipeline run, which is stupid. The best solution is to mount the database from the host.

To achive this we install the package externally to the container in designated path using host native `pip`.

```
pip install \
    --target data/pangolin \
    --upgrade \
    git+https://github.com/cov-lineages/pangolin-data.git@v1.25.1
```

> Make sure you entered proper version in the end of git url. The version number is also git tag. List of available tags with their release dates is here (https://github.com/cov-lineages/pangolin-data/tags).

Then that dir is mounted as docker volume inside the container (which is done automagically in the Nextflow module file):

```
process variantIdentification {
    containerOptions "--volume
${params.pangolin_db_absolute_path_on_host}:/home/SARS-CoV2/pangolin"
    (...)
```

During container build the `$PYTHONPATH` environment variable is set to indicate proper dir.

```
(...)
ENV PYTHONPATH="/home/SARS-CoV2/pangolin"
(...)
```

So the user have to do two things:

1. Install the desired version of `pangolin-data` package in `data/pangolin` directory.
2. Provide absolute path to that dir during starting pipeline

   `--pangolin_db_absolute_path_on_host /absolute/path/to/data/pangolin`