

Pipeline quick-start notes

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Assume Project-Library(es)-Lane(s) hierarchy.

Make working folder for the project in own user's area on scratch

e.g. /scratch/medgen/user/project

It will be used to launch the jobs on cluster, keep intermediate data during calculations on cluster and (possibly) keep logs after calculations.

Copy job description templates folder to the project folder

The start_job script will be used to launch the jobs: no need for sbatch

Rename the job description templates. Modify the templates to set location of source data and results. Check default analysis options, tool and resources: modify if necessary.

Make / check / modify the samples file in the source data folder

Samples file for initial step should be prepared manually. Example of the samples file for initial step is given in the templates folder. Its tab-separated, POSIX-compliant (EOL at the end of last line!) text file with unix encoded EOLs. To ensure the PISX-compliance keep one empty line at the end. Use MobaTextEditor to check field separator and EOLs.

Samples files for later steps are created by the pipeline. They can be edited if only a subset of samples need to be taken to the next step.

Run the job

e.g. /scratch/medgen/user/project/jobs/start_job.sh lib1_lane1_alignment.job