
IggyTools Documentation

Release

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To setup IggyTools, use: `source /n/informatics/iggy/setup.sh`

SeqPrep

Use the command **seqprep** to demultiplex runs. To see usage, type: `seqprep -h`

The following are a few example calls to **seqprep**: `seqprep 150305_D00365_0435_BH2LLNBCXX`
`--suffix '_test1' --verbose --lanes 2`

`seqprep 150305_NS500422_0094_AH57JTBGXX --verbose --mismatches 1`
`--suppressAdapterTrimming --suffix '_test1'`

To run an hourly cron job which runs **seqprep** on new runs, add the following line to your crontab file: `0 *`

`* * * /n/informatics/iggy/IggyTools/iggytools/bin/cron_seqprep.sh`

Once a run has begun processing, `seqprep_seen.txt` will be written to the run folder. If you want the cron job to process a run again, delete this file from the run's `primray_data` folder.

To see current state of a processing run, look at `log.txt` in its log folder:

`/n/informatics_external/seq/seqprep_log/<run_name>`

If you started processing with the **seqprep**, be sure to add the suffix that you passed to **seqprep** to the log folder name.

Notes

A note on the NextSeq bcl2fastq2 parameter `--minimum-trimmed-read-length` (which corresponds to seqprep parameter `--minTrimmedReadLength`): When using the `--use-bases-mask` option, this option must be manually set to be less than or equal to the minimum read length. Otherwise, bcl2fastq 2.15.0 will N-pad the reads to the default minimum trimmed read length of 32 basepairs.

More information about this bug is in the bcl2fastq release notes: http://support.illumina.com/content/dam/illumina-support/documents/documentation/software_documentation/bcl2fastq/bcl2fastq2-v2.15.0-customer-release-notes-15053886-b.pdf

As a workaround, SeqPrep passes a value of 0 to bcl2fastq2 for the minimum trimmed read length.