

Mg-traits2.1.bash

- 0 - Parse parameters
- 1 - Database connection
- 2 - Download file from MG URL
- 3 - Validate file
- 4 - Create job directory
- 5 - Check for utilities and directories
- 6 - Download data files from SVN (pfam, tfile, SLV)
- 7 - Check for duplicates
- 8 - Calculate sequence statistics

.config.bash

vars.tmp

commands_db2.1.bash

- 0 - write JobID and Hostname to database
- 1 - Database connection error comm.
- 2 - Download file from MG_URL error comm.
- 3 - Validate file error comm.
- 4 - Create job directory check error comm.
- 5 - Utilities and directories error comm.
- 6 - Download files from SVN error comm.
- 7 - Check for duplicates error comm.
- 8 - Calculate sequence statistics error comm.

preprocessed fasta file

preprocessed fasta file

mg_traits_jobs

Mg-traits2.2.bash

- 1 - run fgs
- 2 - run sortmerna
- 3 - run sina
- 4 - run finish

vars.tmp

commands_db2.2.bash

- 1 - run fgs error comm.
- 2 - run sortmerna error comm.
- 3 - run sina error comm.

commands_db2.3.bash

mg_traits_results

