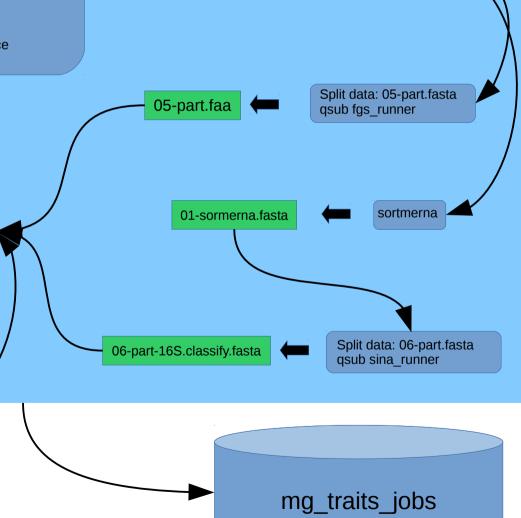
Mg-traits.bash

- 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, tffile, SLV)
- 7 Check for duplicates
- 8 Calculate sequence statistics: Number of bases, GC content, GC variance

gsub finish runner

- 1-3. Check number of sub-jobs, genes and 16S sequences
- 4. Functional annotation: UProC and Pfam
- 5. Create functional table
- 6. Compute codon usage
- 7. Create codon and amino acid usage table
- 8-9. Compute nucleotide and dinucleotide composition
- 10. Create dinucleotide table
- 11-13. Get taxonomic annotation from SINA
- 14-18. Insert aa, codon, dinuc, taxnonmy, pfam to mg_traits_jobs table
- 19. Insert simple traits mg_traits_jobs table
- 20. PCAs for aa, codon, dinuc, function and taxonomy
- 21. Load PCA data in the DB



01-environment

01-raw.fasta

.config.finish.bash