

FUNNELING

RAW FILES

Each finished job will produce 50,000 files at the individual level and 2 files at the model level.

Values of all individuals/generation
Fixed Mutations files
SLiM Full Output files

STATS_ONE.R

Reads in the raw files and averages all values across the individuals. Smallest unit is now the model seed (replicate ID). Reads in the mutation + output file and calculates allelic frequencies.

Graphs for one model run (seed level)
BigPopa_onerun files (collated data)
Tetris_onerun files (mean values + μ)

TANK.PBS TANK.PS1

Stats_one.R needs to be run for each node folder of each modeltype and optima combination; this script collects the final output and transfers it into a folder called tank for the next script to work on. Tank is situated in Modeltype/Optima.

STATS-REPS.R

Reads in the files in the tank folder (BigPopa and Tetris files) and averages all values across the seeds. Smallest unit is now the unique parameter combination, given by the combination of modelindex and node number.

Graphs for one param combination (multiple seeds)
PogNoodle files (collated data)
PogNoodled files (mean across seeds)

AQUARIUM.PBS AQUARIUM.PS1

Stats_model.R needs to be run for each model type and optima combination, so the PogNoodle and PogNoodled files are moved to a common folder at the root of the optima branch. Move from node level organization to optima level organization.

STATS_MODEL.R

Reads in the files in the aquarium folder (PogNoodle and PogNoodled) and averages all values across combinations. The resulting output contains the mean adaptive walk, mean allelic frequencies and final data on a model (optima x modeltype) level.

Graphs for a model (type x optima)
Shelldon files (collated data)
Richard files (mean across combos)

OCEAN.PBS OCEAN.PS1

Unlike previous pbs/ps1 scripts, this script copies required files for stats-types.r, as this last step breaks the linear flow and can call in any of the previous data sets

STATS-TYPES.R

Final piece in the pipeline for tests and more sophisticated analysis utilizing any of the previous data sets. Key function is comparison of ADD and ODE models.

Zephyr files