

README

LocusByLocus *LocusByLocus will elaborate the box plots showing the distributions of similarity values to the reference genome.*

Recruit2Cloud *Given a series of genome reads, a reference genome, and a blast of the reference genome generate a "cloud" of pseudo-random genomes similar to the reads.*

TaxonomySearch *Given a .csv formatted file containing GI values of each genome, retrieve the corresponding taxonomy name from NCBI database.*

MCLSyntenyPlotting *Given an MCL output file, parse and format a synteny .csv file for GNU plotting*

MRPlot *Given a BLAST or CAMERA csv output, creates an output .csv file, recruitment plot file, and GNU plot file.*

LatticeHist *Creates a lattice of histograms using data from a specific csv file.*

Runhist *Uses histogram function in R to output histogram plots for every paired combination of samples*

Combiner *Takes two .fastq files containing first and second paired end reads and output in an interweaved .fastq format*

TrimPipe *Given .fastq files, trims them with DynamicTrim.pl and uses FastQC to perform quality analyses.*

Read2Genome *Takes a blast formatted as tab delimited outputs part of a gnuplot script.*