

Chapter 1

Perl Scripts

1.1 3_indiv_minimal.pl

1.1.1 Overview

Usage ./3_individual.pl ;individual columns; ;fileName;

Purpose Make sure all individuals are different using a minimal set of information from the genotyped individuals. Practically, this means extracting additional lines from an input file until every individual appears different (or the total input file, whichever comes first)

Lines of Code 88

File size 2 KiB

1.1.2 Command Line Options

This script has no additional command line options.

[Additional Comments]

1.2 5_pop_minimal.pl

1.2.1 Overview

Usage ./5_pop_minimal.pl p;P1 name; ;P1 ids; p;P2 name; ;P2 ids; ...

Purpose Make sure all populations are different using a minimal set of information from the genotyped individuals practically, this means extracting additional lines from an input file until every individual within a population appears different to every individual from the other population(s) (or the total input file, whichever comes first)

Lines of Code 151

File size 4 KiB

1.2.2 Command Line Options

This script has no additional command line options.

[Additional Comments]

1.3 8_modelfit.pl

1.3.1 Overview

Usage ./8_modelfit.pl ;reference model; ;iteration set; ;PW file;

Purpose scans a marker pairwise comparison file (output like 2_maximal.pl) for the next marker that, in conjunction with previously discovered markers, best fits a reference model

Lines of Code 76

File size 2 KiB

1.3.2 Command Line Options

This script has no additional command line options.

[Additional Comments]

1.4 9_predictive_power.pl

1.4.1 Overview

Usage /9_predictive_power.pl p1P1 name¿ p1P1 cols¿ p1P2 name¿ p1P2 cols¿

Purpose Determine the predictive power of each marker, including power to distinguish between two populations outputs a list of markers, and probabilities associated with the distinguishing power of each marker

Lines of Code 167

File size 4 KiB

1.4.2 Command Line Options

-summarise Only create summary statistics (mean values)

[Additional Comments]

1.5 addpops2structure.pl

1.5.1 Overview

Usage ./addpops2structure.pl ipop1Name¿ipop1Count¿ipop2Name¿ipop2Count¿...
i file¿

Purpose adds population identifier IDs to a structure file

Lines of Code 29

File size 850 B

1.5.2 Command Line Options

This script has no additional command line options.

[Additional Comments]

1.6 affy2simplegt.pl

1.6.1 Overview

Usage ./affy2simplegt.pl ;file name;

Purpose Converts data from the affymetrix chip format (marker, individual, genotype, QC) to simplegt format.

Lines of Code 26

File size 843 B

1.6.2 Command Line Options

This script has no additional command line options.

[Additional Comments]

1.7 calc_gtcounts.pl

1.7.1 Overview

Usage ./calc_gtcounts.pl ;file name;

Purpose determines per-marker genotype counts for a simplegt formatted text file.

Lines of Code 44

File size 1 KiB

1.7.2 Command Line Options

This script has no additional command line options.

[Additional Comments]

1.8 calc_gtfreq.pl

1.8.1 Overview

Usage ./calc_gtfreq.pl ;file name;

Purpose determines per-marker genotype frequencies for a simplegt formatted text file.

Lines of Code 60

File size 1 KiB

1.8.2 Command Line Options

This script has no additional command line options.

[Additional Comments]

1.9 coladd.pl

1.9.1 Overview

Usage ./coladd.pl ;file name;

Purpose adds the columns of an input file (second column onwards, starting from the second line)

Lines of Code 29

File size 936 B

1.9.2 Command Line Options

This script has no additional command line options.

[Additional Comments]

1.10 colmean.pl

1.10.1 Overview

Usage ./colmean.pl ;file name;

Purpose averages the columns of an input file (second column onwards, starting from the second line). By default this groups by the first column in the file

Lines of Code 64

File size 1 KiB

1.10.2 Command Line Options

This script has no additional command line options.

[Additional Comments]

1.11 coriell2snpcchip.pl

1.11.1 Overview

Usage ./coriell2snpcchip.pl i.pre File_i i.map File_i

Purpose read in (3+N)xM array (coriell .pre data file notation). Presumed file format is istudy_i [-]ipersonID_i 1 iGT1/1_i iGT1/2_i iGT2/1_i iGT2/2_i ...

Lines of Code 51

File size 1 KiB

1.11.2 Command Line Options

This script has no additional command line options.

[Additional Comments]

1.12 delta_stats.pl

1.12.1 Overview

Usage /delta_stats.pl pP1 name_i iP1 cols_i pP2 name_i iP2 cols_i

Purpose just produces delta for each marker

Lines of Code 134

File size 3 KiB

1.12.2 Command Line Options

This script has no additional command line options.

[Additional Comments]

1.13 emp_fst.pl

1.13.1 Overview

Usage ./emp_fst.pl pP1 name_i iP1 cols_i pP2 name_i iP2 cols_i i file_i

Purpose Calculates Fst values using pairwise comparisons calculations are carried out for between and within populations, with the resultant statistic being the following: $F_{st} = (\text{mean}(\text{between}) - \text{mean}(\text{mean}(\text{within1}), \text{mean}(\text{within2}))) / \text{mean}(\text{between})$

Lines of Code 96

File size 3 KiB

1.13.2 Command Line Options

This script has no additional command line options.

[Additional Comments]

1.14 fieldrm.pl

1.14.1 Overview

Usage ./fieldrm.pl [f1 f2 f3... fn] [options] ;file;

Purpose removes specified fields from a file

Lines of Code 33

File size 1 KiB

1.14.2 Command Line Options

-startat [n] Start removing fields from this field onwards

[Additional Comments]

1.15 filterdiff.pl

1.15.1 Overview

Usage ./filterdiff.pl [options]

Purpose Filters out similar genotype lines from a file.

Lines of Code 148

File size 6 KiB

1.15.2 Command Line Options

-help Only display this help message

-v ;float; Threshold value for inclusion (Default: 0.5)

[Additional Comments]

1.16 firstn.pl

1.16.1 Overview

Usage ./firstn.pl [options] ;filename;

Purpose extracts the first n lines with a given field repeated

Lines of Code 46

File size 1 KiB

1.16.2 Command Line Options

-t ;string; Define field separator

-f ;integer; Field to consider for repetitions

-n ;integer; Maximum count per identical field

[Additional Comments]

1.17 flatten_tex.pl

1.17.1 Overview

Usage ./flatten_tex.pl ;file name;

Purpose flattens a .tex file structure to remove include / input statements.

Lines of Code 36

File size 981 B

1.17.2 Command Line Options

This script has no additional command line options.

[Additional Comments]

1.18 ged2linkage.pl

1.18.1 Overview

Usage ./ged2linkage.pl ;file name;

Purpose creates a linkage formatted pedigree file based on family definitions in a GEDCOM file.

Lines of Code 138

File size 4 KiB

1.18.2 Command Line Options

This script has no additional command line options.

[Additional Comments]

1.19 gt2bayes.pl

1.19.1 Overview

Usage ./bayes.pl ;simplegt file_i p_iP1 name_i iP1 ids_i p_iP2 name_i iP2 ids_i

Purpose calculate bayesian probability for group assignment, assuming marker independence. Also calculates $\log(p(\text{max})/p(\text{min}))$ to determine reliability of group assignment

Lines of Code 136

File size 4 KiB

1.19.2 Command Line Options

This script has no additional command line options.

[Additional Comments]

1.20 gt2phase.pl

1.20.1 Overview

Usage ./gt2phase.pl i ;file name_i

Purpose convert from simplegt formatted text file input file formatted for PHASE or fastPHASE.

Lines of Code 77

File size 2 KiB

1.20.2 Command Line Options

-nocombine Don't combine complementary genotypes

[Additional Comments]

1.21 gt2plink.pl

1.21.1 Overview

Usage ./gt2plink.pl ;input file; ;map file; [options]

Purpose Convert from simplegt-formatted file to plink rotated input files

Lines of Code 329

File size 13 KiB

1.21.2 Command Line Options

-help Only display this help message

-output output base file name

-t ;character; map file separator character

[Additional Comments]

1.22 gtminimal.pl

1.22.1 Overview

Usage ./gtminimal.pl -(individual—population) [options] ; ;input file;

Purpose Determine minimal set sizes for an input data set. Data is processed in a linear fashion, taking successive lines and finding out how large an untrained selection of markers needs to be in order to distinguish populations

Lines of Code 128

File size 4 KiB

1.22.2 Command Line Options

-help Only display this help message

-population Calculate population-based sizes

-individual Calculate individual-based sizes

-verbose Print out generated hash values during run

[Additional Comments]

1.23 gtshuffle.pl

1.23.1 Overview

Usage ./gtshuffle.pl *input file* [*options*]

Purpose Shuffles a simplegt input file, producing output files containing random splits of the population

Lines of Code 224

File size 9 KiB

1.23.2 Command Line Options

-help Only display this help message

-output output base file name

-r *float* Proportion of individuals in the first group (Default: 0.5)

-n *integer* Number of individuals in the first group (overrides ratio)

[Additional Comments]

1.24 hardyweinberg.pl

1.24.1 Overview

Usage ./hardyweinberg.pl *p1P1 name* *p1P1 cols* *p1P2 name* *p1P2 cols*

Purpose Determines genotype frequencies for each marker, as well as expected frequencies under HW equilibrium. The calculations are done on a per-population basis.

Lines of Code 152

File size 4 KiB

1.24.2 Command Line Options

-summarise Only generate mean summary statistics

[Additional Comments]

1.25 linecount.pl

1.25.1 Overview

Usage ./linecount.pl *sorted, ranked file* *linecount_output.txt*

Purpose print out the line at which a marker has been seen a particular number of times. The marker is assumed to be in the first field of each line.

Lines of Code 17

File size 859 B

1.25.2 Command Line Options

This script has no additional command line options.

[Additional Comments]

1.26 maf_stats.pl

1.26.1 Overview

Usage ./maf_stats.pl *p1P1 name cols p1P2 name cols ...*

Purpose calculates allele frequencies, based on MAF of first population (derived from delta_stats.pl).

Lines of Code 103

File size 2 KiB

1.26.2 Command Line Options

This script has no additional command line options.

[Additional Comments]

1.27 make_documentation.pl

1.27.1 Overview

Usage ./make_documentation.pl *file name*

Purpose creates LaTeX documentation for script files.

Lines of Code 206

File size 7 KiB

1.27.2 Command Line Options

This script has no additional command line options.

[Additional Comments]

1.28 makemdrcfg.pl

1.28.1 Overview

Usage

Purpose generates a configuration file for the MDR/pMDR programs

Lines of Code 158

File size 7 KiB

1.28.2 Command Line Options

This script has no additional command line options.

[Additional Comments]

1.29 mdr2markerstats.pl

1.29.1 Overview

Usage ./mdr2markerstats.pl [MDR output file]

Purpose retrieves marker values from MDR formatted file (as produced by running MDR from the command line), and produces a list of SNPs with mean association values

Lines of Code 53

File size 2 KiB

1.29.2 Command Line Options

-nosearch disable searching for Landscape string

[Additional Comments]

1.30 mdrpermute.pl

1.30.1 Overview

Usage ./mdrpermute.pl [input file] [number of permutations]

Purpose permutes the case (last) column of a MDR formatted text file

Lines of Code 91

File size 2 KiB

1.30.2 Command Line Options

This script has no additional command line options.

[Additional Comments]

1.31 nwayfilter.pl

1.31.1 Overview

Usage ./nwayfilter.pl [options] ;marker statistics file;

Purpose Does an n-way comparison of SNPs, assuming a given 1-way complexity

Lines of Code 80

File size 3 KiB

1.31.2 Command Line Options

-c ;integer; equivalent complexity to this many one-way interactions

-n ;integer; number of interactions to consider

-v be verbose about what is being done

[Additional Comments]

1.32 plink2gt.pl

1.32.1 Overview

Usage ./plink2gt.pl ;.tped file name;

Purpose Convert from plink rotated input files to simplegt-formatted files

Lines of Code 66

File size 2 KiB

1.32.2 Command Line Options

This script has no additional command line options.

[Additional Comments]

1.33 resort.pl

1.33.1 Overview

Usage ./resort.pl ;file name;

Purpose sorts fields from a file, based on provided column numbers in arguments

Lines of Code 24

File size 1 KiB

1.33.2 Command Line Options

This script has no additional command line options.

[Additional Comments]

1.34 rsfilter.pl

1.34.1 Overview

Usage ./rsfilter.pl ;marker1; ;marker2; ... [options] ;file name;

Purpose hunts (quickly) for a set of markers in one pass of a file.

Lines of Code 91

File size 3 KiB

1.34.2 Command Line Options

-r invert filter (i.e. select markers to exclude)

-o order by selection

[Additional Comments]

1.35 snpchip2linkage.pl

1.35.1 Overview

Usage ./snpchip2linkage.pl ;marker location file; ;genotype file;

Purpose converts from a simplegt formatted file into a linkage formatted file.

Lines of Code 84

File size 2 KiB

1.35.2 Command Line Options

This script has no additional command line options.

[Additional Comments]

1.36 snpchip2mdr.pl

1.36.1 Overview

Usage ./snpchip2mdr.pl [options] ;file name;

Purpose convert from simplegt formatted text file to MDR formatted text file.

Lines of Code 74

File size 2 KiB

1.36.2 Command Line Options

-pMDR format for pMDR instead of MDR

[Additional Comments]

1.37 snpchip2structure.pl

1.37.1 Overview

Usage ./snpchip2structure.pl ;file name;

Purpose convert from simplegt formatted text file input file formatted for structure.

Lines of Code 73

File size 2 KiB

1.37.2 Command Line Options

-nocombine Don't combine complementary genotypes

[Additional Comments]

1.38 snpimpute.pl

1.38.1 Overview

Usage ./snpimpute.pl [options] i jfile namej

Purpose infers unknown genotypes using a bayesian approach

Lines of Code 475

File size 20 KiB

1.38.2 Command Line Options

-nohet don't do heterozygote calculations

-probs print prior/conditional probabilities

-inferall infer all genotypes, rather than just unknown ones

[Additional Comments]

1.39 snplookup.pl

1.39.1 Overview

Usage ./snplookup.pl i jfile namej

Purpose retrieves chromosome location information from Entrez

Lines of Code 27

File size 1 KiB

1.39.2 Command Line Options

This script has no additional command line options.

[Additional Comments]

1.40 snprank.pl

1.40.1 Overview

Usage ./snprank.pl jbootstrap-sorted filej j output_ranked.txt

Purpose ranks markers in a bootstrap-sorted file. Expected input is the output of bootstrap.r, sorted first by bootstrap, then by marker information statistic.

Lines of Code 18

File size 871 B

1.40.2 Command Line Options

This script has no additional command line options.

[Additional Comments]

1.41 sorted_affy2simplegt.pl

1.41.1 Overview

Usage ./sorted_affy2simplegt.pl ;file name;

Purpose converts from affymetrix formatted file to simplegt formatted file.

Lines of Code 34

File size 1 KiB

1.41.2 Command Line Options

This script has no additional command line options.

[Additional Comments]

1.42 tfam_gender.pl

1.42.1 Overview

Usage ./tfam_gender.pl ;sample file; [options] ; input file;

Purpose modify gender data using sample data file

Lines of Code 136

File size 4 KiB

1.42.2 Command Line Options

-help Only display this help message

-nowarn Don't warn about missing individuals in tfam file

-phenomarker ;file; Produce phenotypes as simplegt format

[Additional Comments]

1.43 wdb2svg.pl

1.43.1 Overview

Usage ./worldmap2svg.pl [input file(s)] [options]

Purpose convert vector information formatted in plain-text world databank format into an SVG file. Details of this format can be found at <http://www.evl.uic.edu/pape/data/WDB/>

Lines of Code 459

File size 20 KiB

1.43.2 Command Line Options

-help Only display this help message

-lat ;float; Set central latitude

-long ;float; Set central longitude

-res ;float; Resolution of line nodes, in degrees

-mark ;float; ;float; Mark a point on the map (E/W, N/S)

-projection ;name; Change projection function, $(x,y) = f(lat,long)$

[Additional Comments]

Chapter 2

R Scripts

2.1 agrf2simplegt.r

2.1.1 Overview

Usage ./agrf2simplegt.r *input file*

Purpose Convert a three-column Excel file from AGRF into a simplegenotype file (similar to those used in the HapMap samples)

Lines of Code 42

File size 2 KiB

2.1.2 Command Line Options

This script has no additional command line options.

[Additional Comments]

2.2 bootstrap.r

2.2.1 Overview

Usage ./bootstrap.r *case/control column file* [*options*]

Purpose runs a bootstrap process across a genotype file

Lines of Code 482

File size 21 KiB

2.2.2 Command Line Options

-help Only display this help message

-input File containing genotype data

-controlfile File containing column data for cases/controls

-repfiles *f1* *f2* Files containing replicate columns (for repeat experiments)

-controlsfirst case/control file has controls as first line

-count Number of bootstraps to carry out

-casereps case subpopulation size for bootstraps (overrides proportion)

-controlreps control subpopulation size for bootstraps (overrides proportion)

-proportion proportion of individuals for bootstraps (currently ", replicates.proportion,")

-sort sort bootstrap results by value

-strictGT Keep complementary alleles separate (don't combine)

-strictChi Respect zero counts in χ^2 table, creates null results

-output output file for results

-method method to use for calculating results

[Additional Comments]

2.3 bs2meancalc.r

2.3.1 Overview

Usage ./bs2meanvar.r |file| [options]

Purpose calculates mean / SD from bootstrap summary results

Lines of Code 95

File size 3 KiB

2.3.2 Command Line Options

-help Only display this help message

[Additional Comments]

2.4 contour-MA.r

2.4.1 Overview

Usage ./contour_MA.r |file|

Purpose converts a delta summary file into a Minor Allele Frequency contour graph.

Lines of Code 81

File size 4 KiB

2.4.2 Command Line Options

This script has no additional command line options.

[Additional Comments]

2.5 csplot.r

2.5.1 Overview

Usage ./csplot.r [file] [options]

Purpose generates a chromosome "manhattan" plot for a genome-wide statistic

Lines of Code 224

File size 10 KiB

2.5.2 Command Line Options

-help Only display this help message

-threshold [value] Only display data greater than [value]

-pointsize [value] Multiplier for size of points in graph

-invert Invert values (lowest value at top of graph)

-normlimit Limit value display to a reasonable normal distribution

-limit [value] Trim values greater than [limit]

-keep [value] Keep a proportion of values below the cutoff value

-label [string] Label for Y axis

[Additional Comments]

2.6 data2plot.r

2.6.1 Overview

Usage cat [file] — ./data2plot.r(p[fname] [range from] [range to])*

Purpose takes as input a space-separated text file, converts it into a plot

Lines of Code 26

File size 1 KiB

2.6.2 Command Line Options

This script has no additional command line options.

[Additional Comments]

2.7 distvals.r

2.7.1 Overview

Usage ./distvals.r ;file;

Purpose generates a genotype distance matrix from genotype data

Lines of Code 22

File size 1 KiB

2.7.2 Command Line Options

This script has no additional command line options.

[Additional Comments]

2.8 error.r

2.8.1 Overview

Usage ./error.r;file; ;Case/Control Split location; [-flip]]

Purpose generates error plot (false/true positive/negative) for a diagnostic test

Lines of Code 156

File size 7 KiB

2.8.2 Command Line Options

-help show only this screen

-flip invert positive/negative classification

-vline ;float; place a vertical line at ;location;

-hline ;float; place a horizontal line at ;location;

-batch batch mode output

-header display batch mode header

-roc ROC analysis, with AUC calculation

[Additional Comments]

2.9 gt2plink.r

2.9.1 Overview

Usage `./gt2plink.r`input file_i ;map file_i [options]

Purpose Convert from simplegt-formatted file to plink rotated input files

Lines of Code 186

File size 7 KiB

2.9.2 Command Line Options

-help Only display this help message

-output output base file name

-t ;character_i map file separator character

[Additional Comments]

2.10 gt2pw.r

2.10.1 Overview

Usage `./gt2pw.r` ;simplegt file_i [options]

Purpose Calculate allele sharing values across all markers for all individuals in the input file

Lines of Code 224

File size 9 KiB

2.10.2 Command Line Options

-help Only display this help message

-clustersize Number of parallel processes

-usempi Use MPI for parallel cluster

-makeimage Create an image after calculating matrix

-dendrogram Create a sorted dendrogram after matrix

[Additional Comments]

2.11 icdiff.r

2.11.1 Overview

Usage ./icdiff.r

Purpose Calculate information content difference for fastphase-formatted genotype file

Lines of Code 205

File size 8 KiB

2.11.2 Command Line Options

-help Only display this help message

-hapmap3 Hapmap phase 3 formatted Files

[Additional Comments]

2.12 infocred.r

2.12.1 Overview

Usage ./infocred.r[file] [split point] [options]

Purpose carries out a difference-of-means test for difference between two populations

Lines of Code 255

File size 10 KiB

2.12.2 Command Line Options

-help Only display this help message

[Additional Comments]

2.13 markercount2pdf.r

2.13.1 Overview

Usage ./markercount2pdf.r [file]

Purpose generates plot of marker counts versus number of bootstraps

Lines of Code 19

File size 1 KiB

2.13.2 Command Line Options

This script has no additional command line options.

[Additional Comments]

2.14 njfilter.r

2.14.1 Overview

Usage ./njfilter.r iGenotype filei -s isplit pointi [iSNP ranking filei] [options]

Purpose iteratively adds SNPs that don't have a genotype profile similar to SNPs already added to a set of informative SNPs

Lines of Code 188

File size 8 KiB

2.14.2 Command Line Options

This script has no additional command line options.

[Additional Comments]

2.15 poscounts.r

2.15.1 Overview

Usage ./poscounts.r istructure qfilei -s isplit pointi [options]

Purpose determine clinical parameters for structure file outputs TP: True positive (count of "positive" results that are clinically positive) FN: False negative (count of "negative" results that are clinically positive) TN: True negative (count of "negative" results that are clinically negative) FP: False positive (count of "positive" results that are clinically negative)

Lines of Code 95

File size 3 KiB

2.15.2 Command Line Options

This script has no additional command line options.

[Additional Comments]

2.16 pwmatrix2pdf.r

2.16.1 Overview

Usage ./pwmatrix2pdf.r [top/right file] [bottom/left file]

Purpose Converts a pairwise matrix (such as that generated from gt2pw.r) into a heatmap PDF file.

Lines of Code 422

File size 17 KiB

2.16.2 Command Line Options

- help** Only display this help message
- ignore (value)*** Ignore particular individuals
- svg** Output to an SVG file
- bitmap** Output to a bitmap (XPM) file
- image** Create a more customisable image
- invert [value]** Create a similarity matrix (value is no. of alleles)
- nolabels** Don't output population labels
- norects** Don't draw squares around populations
- dendrogram** Sort, and draw a dendrogram / tree
- heatmap** Use the built-in heatmap function
- noscale** Don't scale bottom half to range of top half
- outliers [value]** Ignore values outside specified probability
- size [value]** Change label size

[Additional Comments]

2.17 pwsummary2pdf.r

2.17.1 Overview

Usage ./pwsummary2pdf.r [top/right file] [bottom/left file]

Purpose Converts a pairwise summary (such as that generated from pwsummary.txt in 2_maximal.pl) into a heatmap PDF file

Lines of Code 317

File size 12 KiB

2.17.2 Command Line Options

This script has no additional command line options.

[Additional Comments]

2.18 recombine.r

2.18.1 Overview

Usage ./recombine.r

Purpose carries out a simulated recombination of chromosomes

Lines of Code 254

File size 9 KiB

2.18.2 Command Line Options

-help Only display this help message

[Additional Comments]

2.19 snpblaster.r

2.19.1 Overview

Usage ./snpblaster.r ;file; [-size ;windowSize;]

Expects a CSV file with headings: [Marker],Delta,Mutation,Chromosome,Location

Purpose Calculates location differences to determine which markers can be removed without much loss

Lines of Code 52

File size 2 KiB

2.19.2 Command Line Options

This script has no additional command line options.

[Additional Comments]

2.20 snpchip2fst.r

2.20.1 Overview

Usage ./snpchip2fst.r;file; (p;name; ;range from; ;range to;)+ [options]

Purpose calculates F statistics from a simplegt file

Lines of Code 153

File size 6 KiB

2.20.2 Command Line Options

This script has no additional command line options.

[Additional Comments]

2.21 snpchip2gtmap.r

2.21.1 Overview

Usage ./snpchip2gtmap.r |genotype file| |SNP location file|

Purpose Creates a chromosome location diagram for a sequence of SNPs, with a genotype summary below

Lines of Code 141

File size 5 KiB

2.21.2 Command Line Options

This script has no additional command line options.

[Additional Comments]

2.22 stats2contour.r

2.22.1 Overview

Usage ./stats2contour.r |file|

Purpose converts a delta summary file into a Minor Allele Frequency contour graph

Lines of Code 33

File size 2 KiB

2.22.2 Command Line Options

This script has no additional command line options.

[Additional Comments]

2.23 structure2pdf.r

2.23.1 Overview

Usage ./structure2pdf.r {file} ({pname} {range from} {range to}) * [options]

Purpose generates box/dot plot for results from structure

Lines of Code 500

File size 18 KiB

2.23.2 Command Line Options

- help** Only display this help message
- gdionly** [**K=2**] Only calculate Genome Diagnostic Index
- line** {value} Draw a horizontal line at {value}
- sort** Sort individuals by Q values
- basicsort** Sort individuals strictly by Q values
- barplot** [**K=2**] Always do a barplot (rather than scatterplot)
- error** [**k=2**] Show error bars from "ffile"
- mean** [**K=2**] Draw mean and SE lines for each popualtion
- noshade** [**K=2**] Don't draw background coloured stripes
- nostack** [**K,2**] Don't put highest Q on the bottom
- stacksort** [**K,2**] Sort each individual's bar vertically
- halfheight** Output a PDF file half the usual height
- svg** Output to an SVG file (instead of PDF)
- pointsize** {value} Scaling factor for point size
- flip** [**K=2**] swap Q values for first and second clusters
- rotatelabels** Make population labels display vertically
- labelaxis** Place population labels on the axis

[Additional Comments]