LINKDATAGEN Cheatsheet

Last updated on 3rd February 2016

Options, or values within curly brackets ({}), separated by a:

- spaced-comma (,) are mutually exclusive.
- pipe (|) may be mixed, but at least one should be specified.

Mandatory:

Option	Values	Summary
-annotFile , -chip	< filename > { 1 , 2 , 3 , 4 , 5 , 6 , 7 , 8} [note: must also use –annotDir]	File containing SNP annotation data. Chip (or HapMap) number.
-callDir , -callFile	< path to directory > < filename >	Directory containing genotype data file(s). File containing genotype data.
-data	{ a , i , m }	Affymetrix or Illumina SNP chip, or MPS data.
-pedfile	< filename >	File containing pedigree information (pedfile).
-freq | -prog | -popHetTest , -bestPopTest	NO VALUE { all | me | al | mo | pl | pr | cp | be | fe | re | fp } { summary , verbose , perChr , perChrVerbose } NO VALUE [note: mutually exclusive to the other 3 options]	Output allele frequencies of founders. Format to output data in. Goodness-of-fit test of specified allele frequencies. Identifies best population using allele frequencies.
-whichSamplesFile , -whichSamplesList	< filename > < filename >	File linking pedfile to genotype data file. File linking pedfile to genotype data file(s).

Others:

Option	Values	Summary
-annotDir	< path to directory > [note: **mandatory** if using –chip]	Directory containing SNP annotation data file.
-binsize	{ real number >= 0.0 } [default = 0.3]	Non-overlapping bin size (in cM) to divide SNPs.
-crlmm	NO VALUE	Declare that data is in CRLMM format.
-fileKeepSNPs	< filename >	File containing SNPs to keep for selection.
-fileRemoveSNPs	< filename >	File containing SNPs to exclude from selection.
-help	NO VALUE	Print help to screen.
-minDist	{ real number >= 0.0 } [default = min { 0.2 , 0.5 * binsize }]	Minimum distance (cM) between selected SNPs.
-noX	NO VALUE	Declare that chr X data to be exclude from output.
-outputDir	< prefix > [note: will be created or overwritten]	Prefix to output directory created.
-pop , -popCol	{ ASW , CEU , CHB , CHD , GIH , JPT , LWK , MEX , MKK , TSI , YRI } { integer >= 1 }	Specify population allele frequencies (AF). Specify column number of AF in annotation file.
-randomSNP	NO VALUE	Declare selection of a random SNP from each bin.
-regions	{ #,chr#,#:######-######,chr#:######-######,… }	Specify regions of genome to analyse.
-regionsFile	< filename >	File containing regions of genome to analyse.
-removeWFHBS	{ i , u }	Declare removal of SNPs with within-family HBS.
-keepME	NO VALUE	Declare keeping of SNPs with Mendelian errors.

-seed	{ integer } [default = 12345]	Seed to change “random” SNP selection.