**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:

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| --- | --- | --- |
| 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:

|  |  |  |
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| Option | Values | Summary |
| -actg | **Not functioning.** | Output data in ACTG format. **Not functioning.** |
| -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. |