**Description how to use the program “SNPrune”**

The program SNPrune requires a command file, called “SNPrune.inp” that provides all information required by the program.

SNPrune.inp looks for instance as follows to analyse the pig data:

52843

genotypes

../genotypes3.txt

../genotypes3\_purged.txt

dense

high\_LD

1

0.99

0

1

The explanation for each of the lines in SNPrune.inp is as follows:

|  |  |
| --- | --- |
| **Line** | **Explanation** |
| 1 | Number of SNP on input |
| 2 | Defines whether on input “genotypes” (0,1,2; default), or “alleles” are provided |
| 3 | Name of genotype file on input |
| 4 | If pruned data need to be written to file, then provide the name of the file here. Otherwise: put “no” |
| 5 | Format of the genotype file: either with (“sparse”) or without spaces (“dense”) between columns with genotypes |
| 6 | Prune for SNP pairs with LD above a predefine R2-threshold (“high\_LD”; default), or for SNP pairs in complete LD (“identical”) |
| 7 | Number of threads to be used by the program |
| 8 | R2-threshold; choose “1.0” when using the option “identical” on line 6 |
| 9 | When using “alleles”: lowest allele code used. When using “genotypes”: put “0” |
| 10 | When using “alleles”: highest allele code used. When using “genotypes”: put “1” |