

Input File Format

The input data file contains pedigree relationship, genotype, and phenotype information, one row for each individual. The first 5 columns give the pedigree id, individual id, father id (0 if founder), mother id (0 if founder), and sex (1=male, 2=female), in that order. Note that these fields need to be numeric. The sixth column gives the affection status (1=unaffected; 2=affected; 0=unknown). The remaining columns code for marker genotypes (2 column per SNP), with the two alleles for each marker represented by two consecutive numbers (0=missing). The following shows the first 5 individuals in the first family (out of 100) in the sample pedigree file:

```
1 1 0 0 1 2 0 0 0 0
1 2 0 0 2 1 2 1 2 1
1 3 1 2 1 1 1 1 2 1
1 4 1 2 1 2 1 1 2 1
1 5 0 0 2 1 0 0 0 0
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In this example, we can see that individual 1, 2, and 5 are founders; individual 1 and 4 are affected by the trait. There are two SNPs coded in the last 4 columns. Individual 1 and 5's genotypes are missing. Individual 2 has genotype 1/2 and 1/2 at both loci, while individual 3 is homozygous at the first SNP (1/1 genotype) and heterozygous at the second SNP (1/2 genotype).