

Last Update: 5/27/2014

MMAP Genotype File

MMAP has commands to manipulate the binary genotype file

To transpose the file from marker-by-subject (MxS) to subject-by-marker (SxM) or subject-by-marker (SxM) to marker-by-subject (MxS)

--transpose_binary_genotype_file --binary_input_filename <infile> --binary_output_filename <outfile>

If you transpose twice then you will get the original file.

MxS format is useful for GWA, computation of LD matrices and allele frequency calculations.

SxM format is useful for computation of genetic covariance matrices and haplotype analysis.

Creating a marker and/or subject reduced binary genotype file. Same command applies to MxS and SxM formats.

--write_reduced_genotype_binary --binary_input_filename <infile> --binary_output_filename <outfile> [marker and subject options]

The outfile is the new binary genotype file

Example options

--autosome

Extract the autosomal SNPs

--chromosome <numbers>

Extract SNP on chromosomes in <numbers>

--genomic_region <chr> <start bp> <stop bp>

Extract SNPs in the genomic region(s) specified.

--marker_set <file>

Extract markers in <file>

--subject_set <file>

Extract subjects in <file>

Extracting Genotypes as csv file

--marker_by_subject_binary2csv --binary_input_filename <infile> --csv_output_filename <outfile>

The infile must be MxS format. The outfile has the results. The options above are valid with this command.

Allele frequency calculations

--write_binary_allele_frequency_file --binary_input_filename <MxS file> --binary_output_filename <filename> --csv_output_filename <filename>

The allele frequency for each SNP will be in the csv file.