Recode Genotypes with X Chromosome Adjustment

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Overview

This script recodes genotypes based on an additive model with major/minor allele classification. Markers within the selected chromosomes are adjusted for male samples.

This script requires a marker mapped spreadsheet with several genotypic columns and a binary or categorical Sex column. If the Sex column is binary, 0 represents Males and 1 represents Females. The first letter of the value in a categorical column is used, i.e. both male and M could represent a male sample.

Recommended Directory Location

Save the script to the following directory:
*..\Application Data\Golden Helix SVS\UserScripts\Spreadsheet\Edit\Recode\n
Note: The Application Data folder is a hidden folder on Windows operating systems and its location varies between XP and Vista. The easiest way to locate this directory on your computer is to open SVS and select Tools >Open Folder > UserScripts Folder. If saved to the proper folder, this script will be accessible from the spreadsheet’s Edit >Recode submenu.

Using the Script

1. Open a spreadsheet containing several mapped genotypic columns and a sex column.
2. Choose Edit >Recode >Recode Genotypes with X Chromosome Adjustment. Choose a binary or categorical Sex column and specify any additional chromosomes (default X) that should be adjusted. Click OK.

The resulting spreadsheet is created as a child node of the original spreadsheet and contains the same active dimensions. Genotypic columns are converted to integer columns with possible values 0, 1, 2 and missing. Multi-Allelic columns are not converted and are still available as genotypic columns.

Columns within the designated chromosomes are adjusted in the following manner for male samples:
- Homozygous minor calls are adjusted from 2 ->1.
- Heterozygous calls are adjusted from 1->Missing.

Female samples are not adjusted. Missing calls remain missing.