

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\`

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.