Activate Variants by Sample Genotypes
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Overview

This tool examines variant data and inactivates genotypic columns that do follow the specified genotypic patterns for the selected samples. The spreadsheet must contain mapped genotypic columns and the marker map must contain a reference allele field.

An example use case could be filtering related individuals, such as a trio or small family, so that only variants that follow the specified inheritance pattern remain active.

Recommended Directory Location

Save the script to the following directory:
*..**\Application Data\Golden Helix SVS\UserScripts\Spreadsheet\Select**

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 go to **Tools > Open Folder > User Scripts Folder**. If saved to the proper folder, this script will be accessible from the spreadsheet **Select** menu.

Using the Script

1. From a spreadsheet containing mapped genotypic data, choose **Select >Activate Variants by Sample Genotypes**.
2. The dialog will display options for all samples (rows) found in the spreadsheet. Check the appropriate genotypes under the samples you wish to include.
    a. **Note**: Not checking any boxes for a sample results in that sample not being examined (and thus all genotypes are allowed). This is equivalent to checking all boxes for a sample.

The only active mapped genotypic columns in the spreadsheet now contain sample genotypes specified.

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