Genetic Distance between Samples

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Overview

This script takes genotypic data (either marker mapped or not) and outputs genetic distances between markers for all pairs of samples.

Recommended Directory Location

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

Note: The **Application Data** folder is a hidden folder on Windows operating systems and its location varies between operating systems. The easiest way to locate this directory on your computer is to open SVS and go to **Tools > Open UserScripts Folder** and save the script in the **\Spreadsheet\Genotype\Quality_Assurance** folder. If saved to the proper folder, this script will be accessible from the spreadsheet **Genotype > Quality Assurance** submenu.

Using the Script

1. From a spreadsheet that contains genotypic data, go to **Genotype > Quality Assurance > Genetic Distance between Samples**

The script will calculate genetic distance based on all active markers and samples and returns a lower triangular sample matrix where for n samples there are n rows and n-1 columns (a column isn't created for the last sample).

The formula used is: distance = 1 – (total number of shared alleles/(total number of informative SNP loci*2)).