Import BEAGLE Files

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Overview

This script will import .gz files containing genotype data (.phased, .unphased, and .bgl) as output from running the BEAGLE and BEAGLECALL software.
http://www.stat.auckland.ac.nz/~bbrowning/beagle/beagle.html

Recommended Directory Location

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

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 the **Tools >Open Folder > UserScripts Folder** menu option.   If saved to the proper folder, this script will be accessible from the project navigator **Import** menu.

Using the Script

1. From an open project select **Import** > **Import BEAGLE**

2. Select the Beagle output file or files to import. Change the file extension filter to select the GZ version of files, if available.

    NOTE: If multiple files are selected, it is assumed that the samples are identical and in the same order in all of the files. The expected use case would be if there was one file per chromosome.

Three spreadsheets are created on import, a phenotype spreadsheet, a genotype spreadsheet and the phenotypes joined to the genotype spreadsheet. A marker map will need to be created separately and applied to the spreadsheets containing genotype data.