

Import BEAGLE

Author: Greta Linse Peterson, Golden Helix, Inc.

Overview

This script will import .gz files containing genotype data (.phased, .unphased, and .bgl) as outputted 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 to import.

The resulting spreadsheet has samples in rows and markers in columns.