Export BEAGLECALL Genotype Probabalities

Author: Christophe Lambert, Golden Helix, Inc.

Overview

You can use this script on a marker mapped spreadsheet that has rows as samples and genotype columns. Upon completion, 23 separate .gprobs files will be created, one for each active chromosome in the marker mapped spreadsheet.

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\Spreadsheet\File**

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 spreadsheet **File** menu.

Using the Script

1. Open the marker mapped spreadsheet that matches the previous description.

Your spreadsheet should look similar to **Error! Reference source not found.**.

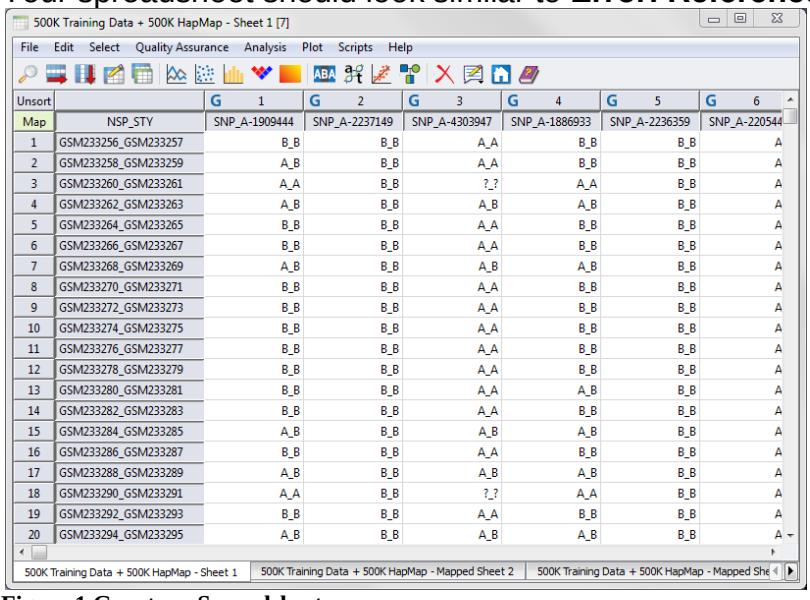

Figure 1 Genotype Spreadsheet

2. To run the script, choose **File >Export BEAGLECALL Allele Signals**.
3. Give the file a name, browse to a folder where you want the file saved, and click **Save**.

Upon completion, a separate .gprobs file for each active chromosome is saved in the specified folder.