Export BEAGLE by Chromosome

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Overview

From a spreadsheet containing genotype data and optionally phenotype and pedigree information, this script saves the spreadsheet in a series of BEAGLE files with the chromosome name appended to each file. If there is no marker map, it will write everything to one file. If the user selects a Population Stratum column, separate files for each unique strata can be created.

This script differs from Export Beagle File because it needs less memory, as individual files are created for each chromosome rather than one large file for the entire genome.

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 versions. The easiest way to locate this directory on your computer is to open SVS and select **Tools >Open Folder > User Scripts Folder.** If saved to the proper folder, this script will be accessible from the spreadsheet **File** menu.

Using the Script

1. Open a spreadsheet that contains genotype information in columns.
2. Select **File >Export BEAGLE by Chromosome**.
3. Choose the directory in which you want the files saved and choose a base name for the files.
4. Optionally choose additional phenotype and pedigree columns. Click **OK**.
5. If a population stratum column is selected a prompt will appear asking if one file should be created per strata. Select either **Yes** or **No**.

   NOTE: Selecting **Yes** will create one file per strata per chromosome. If there are 10 strata and 22 chromosomes, this will create 220 files (strata x chromosome).

Upon completion, a separate .bgl file is saved for each chromosome (and population strata if that option was selected) with data in the folder you indicated.