Export MACH PED_DAT Files

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Requires: SVS 7.4.x or higher

Overview

This script exports MACH/Merlin PED and DAT formatted files. Run this script from a pedigree spreadsheet that can contain as many phenotypes as desired.

The user will be provided with the option to create one file per chromosome if a marker map is applied to the pedigree spreadsheet. This option is recommended as MACH can crash if run on a dataset with too many markers.

Note: This script assumes that genetic data contains only allele encodings accepted by MACH (1, 2, 3, 4, A, G, C, T). Also, for AGCT encoded genotypes, it is assumed that the genotypic data is represented by the same strand.

Recommended Directory Location

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

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\File\Save As** folder. If saved to the proper folder, this script will be accessible from the spreadsheet **File > Save As…** menu.

Using the Script

1. Open the pedigree spreadsheet, with or without a marker map applied.

2. Go to **File > Save As…**. The script will prompt the user to choose to partition the output files by chromosome (if a map is applied) and the file base name and save location.

The data will be output in PED and DAT files in the specified location. Inactive data will be ignored in the output process.