

Import Transposed

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Overview

This script will import a comma-delimited text file into HelixTree where the rows are SNPs and the columns are observations.

Note: The CSV file must contain only genetic data to be imported with this script.

Recommended Directory Location

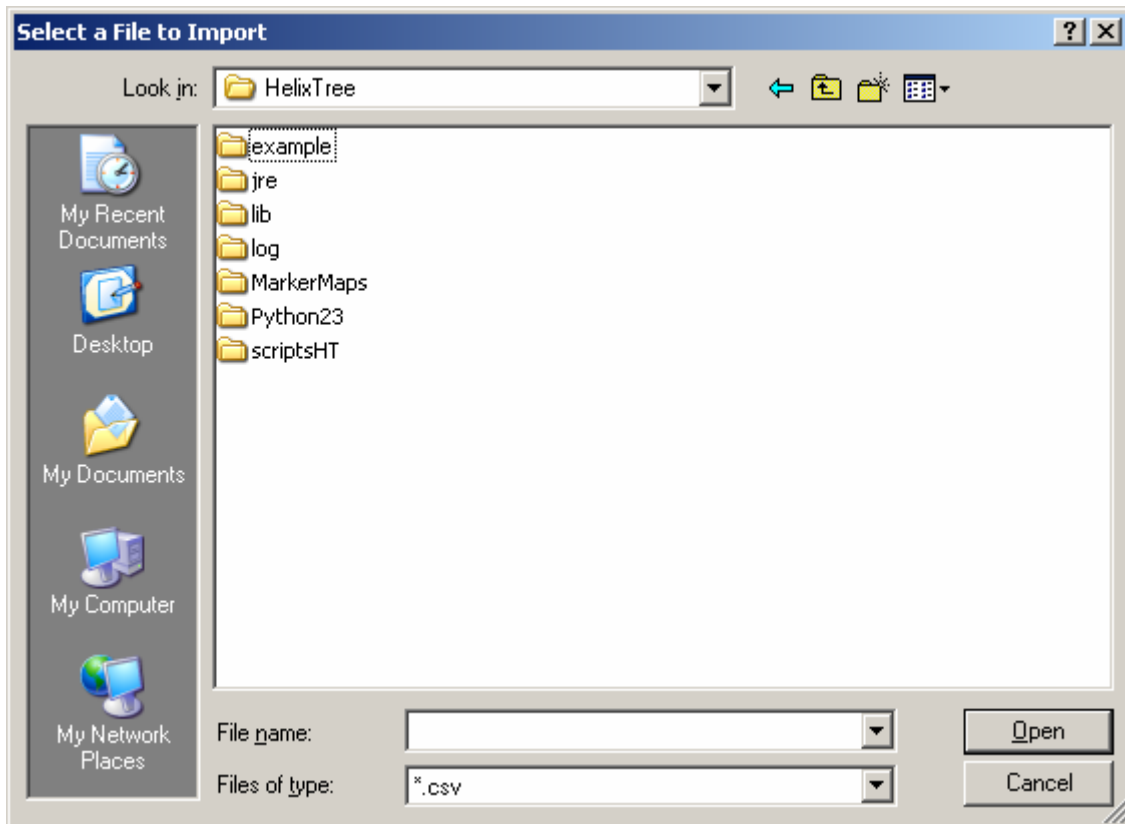
A good directory location for saving this script would be:

C:/HelixTree/scriptsHT/user/HelixTree/File/.

When saved to this folder, the script will be accessible from the File menu of the Project Viewer.

Using the Script

To run this script, you must have opened a project in HelixTree. Select the Import Transposed script from the project viewer menu location where it was stored, or from the select **Tools->Run Script** to open a dialog to browse for the script location. A file browser will open for you to search for the comma-delimited text file you wish to import.



After you have selected your file, click **Open**. The file you selected will open when the import is complete.

	Labels	G 1	G 2	G 3	G 4	G 5
1	g1m1	0_1	0_0	1_1	0_1	0_
2	g1m2	0_0	0_1	0_1	0_0	0_
3	g1m3	0_1	0_1	0_1	0_0	0_
4	g1m4	1_1	0_1	0_0	0_1	0_
5	g1m5	1_1	0_1	??	0_0	0_
6	g1m6	0_1	0_0	??	0_0	0_
7	g1m7	1_1	1_1	0_1	1_1	1_
8	g1m8	0_0	0_0	0_1	0_0	0_
9	g1m9	0_0	0_1	0_0	0_1	0_
10	g1m10	0_1	1_1	1_1	??	1_
11	g2m1					