LD Pairwise Analysis

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Overview

LD Analysis is performed on all pairs within a chromosome (if a marker map is applied) or within a haplotype block. The resulting spreadsheet contain values for both the EM and CHM methods and both R^2 and D' values.

This script can be run on a spreadsheet that includes both genotype and phenotype data, with or without a marker map. It can also be run on a subset spreadsheet created from an LD plot by selecting **Subset Markers**. You can also run this script on markers in haplotype blocks as specified in a Haplotype Block Spreadsheet.

It is not recommended to run this script on a whole genome dataset as the computations are very time-intensive. Rather it would be best to subset or active only a few hundred markers that are of interest.

Recommended Directory Location

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

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 **Analysis** menu.
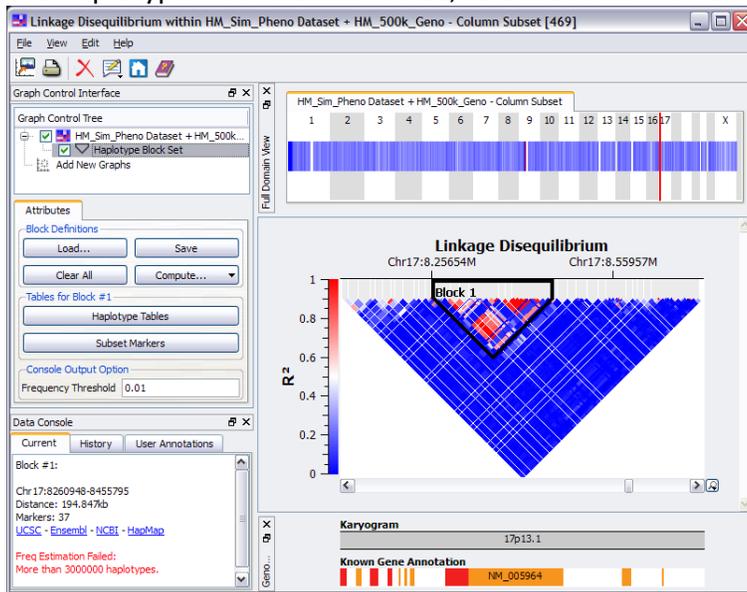
Using the Script

1) Method One:
   a) Open a spreadsheet containing genotype data (possibly including phenotype data and may or may not be marker mapped).

b) Activate at most 75 markers from each chromosome, including unmapped markers. Phenotype data does not have to be inactivated.

c) Select **Analysis > LD Pairwise Analysis.**

d) Select **No** when asked if using a haplotype block spreadsheet.

2) Method Two:

a) Open a Plot viewer containing an LD plot. Select a block of markers, and under the Haplotype Block Set attributes, select Subset Markers.

b) This creates a subset spreadsheet with these markers.

c) Select **Analysis > LD Pairwise Analysis.**
d) Select **No** when asked if using a haplotype block spreadsheet.

3) Method Three:
   a) Open a spreadsheet containing genotype data (possibly including phenotype data and may or may not be marker mapped).

   b) Select **Analysis > LD Pairwise Analysis.**

   c) Select **Yes** when asked if using a haplotype block spreadsheet.

   d) Select the haplotype block spreadsheet.

The result is a new spreadsheet with the first two columns listing the markers that were compared (all pair-wise comparisons, only listing one occurrence of the pair), the distance in markers, the distance in kb (if the genotype spreadsheet was marker mapped), both R^2 and D' values for the EM method and the CHM method.