LD Adjacent Pairs Analysis

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Overview

LD Analysis is performed on all adjacent pairs within a chromosome (if a marker map is applied) or within a haplotype block. The results 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.

Recommended Directory Location

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

   ![Spreadsheet Image]

   b) Select Analysis > LD Adjacent pairs Analysis.
c) 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**.

   ![Image of a Plot viewer]

   b) This creates a subset spreadsheet with these markers.

   ![Subset spreadsheet image]

   c) Select **Analysis > LD Adjacent pairs 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).

   ![Spreadsheet image]

   b) Select **Analysis > LD Adjacent pairs 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 row labels and first column listing the markers that were compared (all adjacent pairs 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.