LD Pairwise Analysis within Gene Regions

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Overview

LD Analysis is performed on all pairs within a gene region, specified by a user-selected annotation track. The resulting spreadsheet contain values for both the EM and CHM methods and both $R^2$ and $D'$ values.

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

   ![Spreadsheet Image]

   a) Select Analysis > LD Pairwise Analysis within Gene Regions.
   b) Select a gene track that defines the desired gene regions. Click Select Track, then navigate to the appropriate track.
NOTE: To enhance the speed of the function, we recommend using a local track. If you have not yet downloaded the track to your machine, you can do this from the Annotation Track Manager.

The result is a new spreadsheet with the first two columns listing the markers that were compared (all pair-wise (within gene) comparisons, only listing one occurrence of the pair), the gene, 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.