

Recombinant DNA Techniques

We will be looking at the microarray data and starting the analyses of the yeast project.

Using MagicSpot to analyze data

Tutorial

1. In the Genomics CD, double click on the MagicTool icon.
2. Double click on the MAGIC_Users_Guide icon.
3. Go to Getting Started (page 4).
4. To start the MagicSpot program, select MagicTool.bat.
5. Go through the tutorial. The following files are the ones mentioned in the tutorial:
 - a. When you start a new project, enter any name that you can remember.
 - b. The files listed below are located on the CD in the RecomMicroarrayData directory.
 - c. The control R and G files are green1.tif and red1.tif (for the single grid).
 - d. The gene list file is Y01godlist1grid.txt. (for the single grid).
 - e. Go through step 25. This will give you a basic understanding of how to compile the data for the microarray.

On your own

1. There are Magic spot tutorials for common tasks at <http://www.bio.davidson.edu/projects/magic/tutorials/MTUG.htm>.
2. Repeat the steps in the tutorial for the 4 grid microarray. Use the same file names as in the tutorial, except that the 1's are changed to 4's (e.g. red4.tif instead of red1.tif).