

Due Thursday, Jan 31 (via email)
Go to the Stanford Microarray Database:
website: <http://genome-www5.stanford.edu/>

1 Instructions

1. Click on **Publications**
2. Select organism (or not), and click on **Re-list**
3. Click on the **SMD** book icon
4. Click on the yellow box: **Raw Data**
5. Save the zip file to your hard drive (flash drive!!)
6. Open each zipped file in Excel, and save each file as a tab delimited file (you may want to re-name them array1.txt, array2.txt,...)

2 Criteria

- You should download the *raw* data
- The data cannot be Affymetrix data
- The dataset should have at least 20 samples
- I would prefer the data are not a timecourse dataset
- More recent data is probably better
- Make sure to retrieve the entire published manuscript that corresponds to the dataset

3 Assignment

- The full citation & abstract of the corresponding manuscript
- The following information:
 - organism
 - experimental conditions
 - number of samples
 - number of genes