Sebida – Sex Bias Database

For this exercise, you should use the Sebida database at:

http://www.sebida.de

1. Click on the "search" link at the left. This will allow you to search the database for a specific gene. The male/female (M/F) or testes/ovaries expression ratio from several different microarray or RNA-seq experiments are provided, as well as other molecular evolution statistics.

a) Search for the *D. melanogaster* gene CG10252.

On which chromosome arm is it located?

Does it show sex-biased expression? If so, which sex has higher expression?

How does the M/F ratio of whole flies (or testes vs. ovaries) compare to the M/F of gonadectomized flies? What does this suggest about the expression of CG10252? Does other Sebida information support this conclusion?

According to FlyAtlas, which tissues show enriched expression of CG10252?

Is this consistent with the modENCODE expression data for this gene available through FlyBase (www.flybase.org)?

What is the dN/dS between *D. melanogaster* and *D. simulans*? Between *D. melanogaster* and *D. yakuba*? What does this suggest?

2. Go to the "analysis" section of Sebida.

What are some general patterns that have been observed concerning male-biased genes in Drosophila?

What is the "meta-analysis" used to classify sex-biased genes in *D. melanogaster*? How many expression datasets were used for the meta-analysis? How were they weighted?

What does "False Discovery Rate (FDR)" mean? Using a FDR of 10%, how many genes are classified as male-biased? Female-biased? Unbiased?

What does "2-fold cutoff" mean? Using the 2-fold cutoff, how many how many genes are classified as male-biased? Female-biased? Unbiased?

How do the FDR and 2-fold classifications compare to each other?

3. Go to the "download" section of Sebida and download "Sebida 3.2" for *D. melanogaster*. Be sure to read the download instructions. It is in tab-delimited-text format. You should be able to open this in Excel or other spreadsheet software.

Using meta-analysis FDR<5% to classify sex-biased genes, what is the average dN/dS between *D. melanogaster* and *D. simulans* for male-biased genes? For female-biased genes?

Using a meta-analysis 2-fold cutoff to classify sex-biased genes, what is the average dN/dS between *D. melanogaster* and *D. simulans* for male-biased genes? For female-biased genes? Compare these values with those above for FDR<5%. What does this suggest?

Bonus:

1. What type of microarrays were used by Ayroles et al. (2009)?

2. What p-value corresponds to a FDR of 10% in the *D. melanogaster* meta-analysis (v. 3.0)?

3. Use the "browse" function to find:
The gene with the greatest male-biased expression.

The gene with the greatest female-biased expression.

The gene with the least sex-bias in its expression.