1   Instructions

1. The goal for this part of the project is to obtain the "M" values that we'll be working with for the rest of the more analysis parts of the course/project.

2. Note, you probably want to link to this assignment so that your front page doesn't get to cluttered.

3. Using the R function `normalizeWithinArrays`, play around with the verb;method; and `weights` arguments to get the normalization that you think is best for your data. Also, feel free to adjust the other arguments (`span`, `d`, `bc.method`, etc.). Use `?normalizeWithinArrays` to learn about the function and its arguments.

2   Things to put on your web site (next)

- A summary of the normalization procedures applied to your data. Your summary should include the following figures (listed below) as well as a description of what you did and why. You should walk the reader through the main points using the figures to clarify your ideas.

    - At least two pairs of loess plots:
        * Within each pair, a loess plot on the raw data *and* on the transformed data
        * Try to find one pair where normalization made a small difference and one pair where normalization made a huge difference.
    - Boxplots of the raw data and the normalized data.
    - Boxplots of the background data for each array.

- A test of whether or not your "normalization" actually "normalized." Using at least 10 randomly selected genes (it's easy to do more if you use a loop) test whether your data are normally distributed. Both tests are of the form:

$$H_0 : X \sim F = \text{N(0,1)}$$
$$H_1 : X \sim G \neq \text{N(0,1)}$$

where X represents a randomly selected gene (that is, row in your M data matrix).

- Kolmogorov-Smirnov test of normality

- Looney & Gulledge test for normality using the correlation of a qq-plot of normal quantiles.