Installing SAM (or really, `siggenes`)

The siggenes package may or may not be easily available on your computer. You can try installing the package from the pull down menu, but that didn't work for me (the package wasn't available). Instead, you'll need to copy the package onto your desk top and install the .zip file (try starting at step 3 below). It's possible that first you need to make sure both R (you should be running R 2.6.2) and Bioconductor are updated:

1. `www.r-project.org` (click on Download on the right panel)

2. `www.bioconductor.org` (run the R code from the Download page)

3. `http://bioconductor.org/packages/2.1/bioc/html/siggenes.html`

4. copy the appropriate (either Windows or Mac) zipped version of siggenes 1.12.0 onto your computer.

5. In R, go to `Packages` then `Install package(s) from local zip files...` It should be very similar on a Mac.

6. `library(siggenes)`

Running SAM

- The function we'll be using is called `sam`. Try `?sam`.

- `sam` doesn't take weights like `limma`. If you really want to use weighted data, then try the following (ask me if the command doesn't make sense, or try `?ifelse`):
  `ymsn.wtM <- ifelse(ymsn.norm4$weights == 0, NA, ymsn.norm4$M)`

- I am comparing 5 groups, so I need to tell `sam` which arrays are in which group. `sam` is particular about how the groups are labeled, it wants them as integers with the reference group as "1". Below the first option is with weights. The second option is without weights. Don't do both.
  ```
  ymsn.sam <- sam(ymsn.wtM,c(rep(1,7),rep(2,7),rep(3,4),
                  rep(4,7),rep(5,7)),gene.names=ymsn.norm4$genes[,3])
  ymsn.sam <- sam(ymsn.norm4$M,c(rep(1,7),rep(2,7),rep(3,4),
                  rep(4,7),rep(5,7)),gene.names=ymsn.norm4$genes[,3])
  ```

- Note that you can use method=d.stat for t-tests or F-test (2 or 3+ samples, respectively), or you can use method = wilc.stat if you want to use ranked data (and you only have two groups).

- `ymsn.sam`   # gives various FDR and delta values
  `plot(ymsn.sam)`   # FDR vs. delta values plotted
  `summary(ymsn.sam,1.47)`   # info & list of genes for delta=1.47
  `plot(ymsn.sam, 1.47)`