

Observations by Jenny right after STAT 540 poster session April 2012.

Overall, nice work! Pleasant to engage with and easy to evaluate.

5 posters / group felt great. I think last year we had more and evaluation fatigue was a risk. But this year, w/ 5 posters to assess, I was able to spend quality time and attention at each.

Common shortcomings that I'd like to see future students address (change rubric?):

Only one group, I think, "showed me the data" (see Jerry Maguire). I would love each poster to show some actual data relevant to their primary question of interest and the primary method they use to address it. Typical example: gene expression for one gene on y axis, a quantitative predictor on the x axis, and a categorical predictor conveyed via the color of the points. Or just a stripplot of gene expression for two groups, like I showed at nauseum in the two group comparison lectures. Show me this for a "typical" randomly selected gene and/or for a "hit", i.e. one of the genes you're excited about and/or of a non hit, i.e. one of the genes you find least interesting. There were lots of high level figures and facts, e.g. about how many genes were found to be differentially expressed, but very little concrete plain graphical info on what a "hit" looks like.

limma was used quite a bit but the reporting of *how* it was used and the total result "package" was often very sketchy. Exactly what was the model? Did you rank based on the t statistic for a specific coefficient or on the overall F test? How much borrowing strength did limma decide to do, i.e. report something about that degrees of freedom parameter that conveys how direct evidence and indirect evidence are weighted when moderating variance estimates. What was the estimated proportion of null genes?

Results about the number of genes being studied were often not given, were spread out in weird places, had gaps etc. There really should be a central place to track the following type of info:

- # probes or genes or whatever
- # passing first filter (usually on data quality) --> # kept for stat analysis
- # passing the statistical filter (for differential expression or what have you)

Heatmap conventions and aesthetic choices could have been better. More care re: sorting of rows and coloring of cells. For example, if depicting a z-score, use a color scheme that goes from one vivid color to a distinct vivid color, passing through white or black for values at and near zero. Consider sorting on signed stat significance, so interesting things are at very top and very bottom, corresponding to two differential directions of being interesting.

I noted a real hesitancy to build models that include two or more predictors. Tendency to study with two different models and then do post hoc overlap / synthesis. Related: hesitancy to use a larger model to attack a large dataset all at once (groups elected to

divide dataset into pieces based on one covariate, do analysis on pieces, then try to patch back together).