* Search gene name – autofill
* On main page also show pca biplot or tsne labelled by class, list of most highly associated genes (~10) with fold change and pvalue
* Results: avg, std expression in control and affected, fold change, stacked histogram, violinplot or boxplot of control vs affected expression, t-test result p-value
* Also list 5-10 highly correlated genes with correlation values, just store these not all of them
* Also show gene’s GO terms-is there a module for this in python? If not store them in advance (ugh)
* In this list have options to view scatterplot of 2 genes colored by class, also be able to go that that gene’s page
* Maybe be able to search by go term or go to other genes which have the same go term
* Always have the search bar at the top or a return to search page
* Maybe have links to external sample page/genecards/affymetrixetc page as well?
* Schema:
* Sample: sample\_id, class
* Expression: sample\_id, probe\_id, value
* Gene: probe\_id, p\_value, fold\_change,gene\_symbol, gene\_name
* Correlation: probe\_id\_1,probe\_id\_2,corr