# Stat 215A - Week 9a

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#### **Lab 3 Introduction**

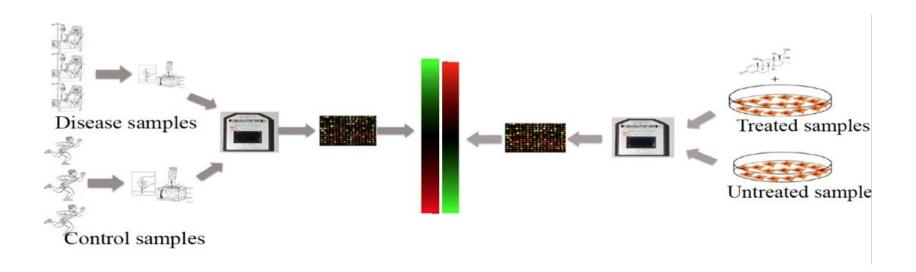
### Lab 3 (extension of lab 2)

In this lab you will use the binary encoded data from lab 2.

You are asked to study the stability of k-means by randoming subsampling the data numerous times.

In this lab you will use parallelization and source C++ code to speed up the computations.

# I use this stuff in my own research!



#### **Our solution**

Count number of decreasing subsequences of length k in windows of length l (each window computes in  $O(k \ l \log(l))$  time)

gene	rank in drug signature	rank in disease signature	
555	1	1000	
2	2	850	
300	3	989	
:	:	:	
•	•	•	
690	998	100	
690	999	10	
700	1000	2	•

## **Running simulations**

When I ran our method on to count these decreasing subsequences in a real dataset of 66,000 compounds it took ~22 days (with parallelization)

Running it on the same data but using Rcpp means it now only takes ~48 minutes