Stat 215A - Week 9a

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Lab 3 Introduction

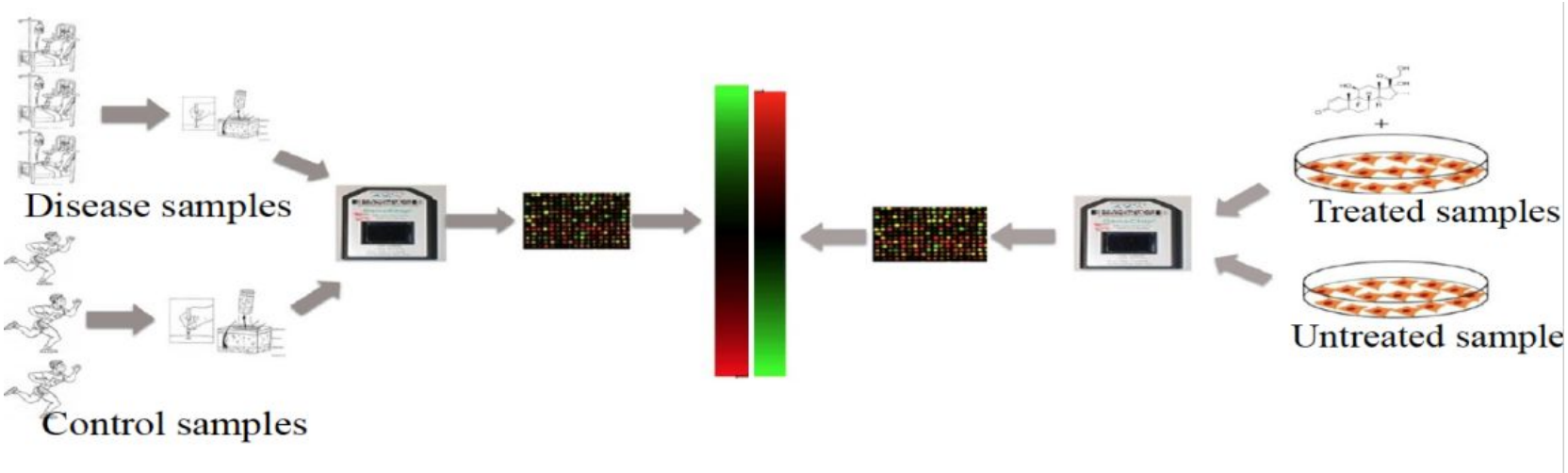
Lab 3 (extension of lab 2)

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.

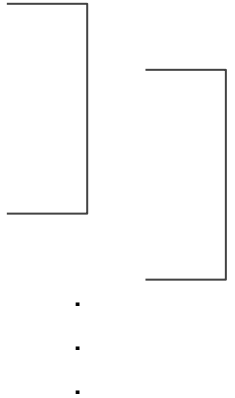
I use this stuff in my own research!



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



Counting number of decreasing subsequences

Consider: **51432**

- There are 3 decreasing subsequences of length 3
  - **543**, **542**, **432**

Algorithm: let `dp[i, m]` be the number of decreasing subsequences of length `m` ending at `i`. Then update the matrix as follows

```
Initialize dp[i, m] = 0; dp[i, 1] = 1
for i = 2 to n
    for j = 1 to i - 1
        if z[i] > z[j]
            for m = 2 to k
                dp[i, m] += dp[j, m - 1]
```

Running simulations

When I ran our method on to count these decreasing subsequences on 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