Final Exam

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- 1. What is PCA? Why would it be used?
- 2. Use the following to do a Bonferoni Correction on the data (Hint: Use p.adjust())

How many pass a threshold of $\alpha = 0.01$ before and after?

3. For this problem we are going to use the gene expression data set found here: $http://www-bcf.usc.edu/\sim gareth/ISL/Ch10Ex11.csv$

This data is gene expression from 40 tissue samples with measurements on 1000 genes. The first 20 samples are from healthy patients while the second 20 are from a diseased group.

- A) Load data into R. Remember to set **header=F**.
- B) Apply hierarchial clustering to the samples using correlation-based distance, and plot the dendrogram. Do the genes seperate the samples into the two groups? Do your results depend on the type of linkage used?
- C) Your collaborator wants to know which genes differ the most across the two groups. Suggest a way to answer the question. For a bonus, apply it here.
- 4. Using the genetics package, run:

```
install.packages("genetics", repos="http://cran.rstudio.com/")
library(genetics)
```

Then use the **genotype()** method and the **LD()** method to compute the r^2 pairwise linkage disequilibrium on the following arrays. What does this tell us?

```
v1<- c('A/A','A/C','C/C','C/A',NA,'A/A','A/C','A/C')
v2<- c('A/A','C/C','C/A','C/A',NA,'A/A','A/C','A/C')
```

Bonus: For the following haplotype frequencies

The downloaded binary packages are in

/var/folders/tj/8dxhxfns3fb0fx5kswwdvjbr0000gp/T//Rtmpxto0r9/downloaded_packages

Haplotype	Frequency
A_1B_1	x_{11}
A_1B_2	<i>x</i> ₁₂
A_2B_1	<i>x</i> ₂₁
A_2B_2	x ₂₂

And for the following allele frequencies

Allele	Frequency
A_1	$p_1 = x_{11} + x_{12}$
A_2	$p_2 = x_{21} + x_{22}$
\boldsymbol{B}_1	$q_1 = x_{11} + x_{21}$
B_2	$q_2 = x_{12} = x_{22}$

Which can be rewritten

	A_1	A_2	Total
\boldsymbol{B}_1	$x_{11} = p_1 q_1 + D$	$x_{21} = p_2 q_1 - D$	q_1
B2	$x_{12}=p_1q_2-D$	$x_{22} = p_2 q_2 + D$	q_2
Total	p_1	p_2	

Prove that the Linkage Disequilibrium D is $D=(x_{11})(x_{22})\check{\ }(x_{12})(x_{21})$