

Khan Inan hw 4

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```
#STEP 1
GSE124548.raw.fixed <- read.delim("C:/Users/khani/Downloads/GSE124548.raw.fixed.txt", header=FALSE)
#Specifying columns with HC or CF base
readcount <- GSE124548.raw.fixed[, c(1,4,5,7,8,10,11,13,14,15,16,18,19,21,22,24,26,27,28,29,30,
                                     32,33,35,36,37,38,39,40,41,42,43,45,47,49)]

#Setting row names and column names
rownames(readcount) <- readcount[,1]
readcount <- readcount[,-1]
colnames(readcount) = readcount[1,]
readcount <- readcount[-1,]
readcount = data.matrix(readcount)
head(readcount)
```

```
##          Raw_10_HC_Auto_066_237 Raw_11_Orkambi_006_Base Raw_13_HC_Auto_068_239
## 1                3482                2013                2281
## 503538            2712                1720                1468
## 144571            3348                 114                2310
## 8086              767                3146                3230
## 65985            1149                 352                 238
## 195827            1018                 164                1137
##          Raw_14_Orkambi_007_Base Raw_16_HC_Auto_072_243 Raw_17_Orkambi_009_Base
## 1                3105                 405                 702
## 503538            2266                3923                4164
## 144571            2404                 92                 3120
## 8086              238                1686                 637
## 65985            787                1452                1840
## 195827            1063                1666                2174
##          Raw_19_HC_Auto_074_245 Raw_1_Orkambi_001_Base Raw_20_Orkambi_010_Base
## 1                 71                3242                 94
## 503538            2908                2105                3143
## 144571            1167                 625                 693
## 8086              630                3225                 522
## 65985            670                 381                1276
## 195827            1582                 254                1535
##          Raw_21_HC_Immune_004 Raw_23_HC_Auto_076_247 Raw_24_Orkambi_012_Base
## 1                 275                3450                 60
## 503538            3799                3474                3236
## 144571            4051                3814                 513
## 8086              1220                1349                 465
## 65985            1329                1010                1454
## 195827            1982                1757                1790
##          Raw_26_HC_Auto_078_249 Raw_27_Orkambi_013_Base Raw_29_HC_Auto_080_251
## 1                 3039                3620                 667
## 503538            2548                2655                3931
```

##	144571	3364	2774	163
##	8086	304	1039	1479
##	65985	581	897	1252
##	195827	697	1287	1773
##	Raw_30_Orkambi_014_Base	Raw_3_HC_Auto_062_233	Raw_42_HC_Auto_089_261	
##	1	2955	3198	3549
##	503538	1967	2484	2953
##	144571	2010	2103	3757
##	8086	161	655	601
##	65985	311	357	778
##	195827	760	792	1173
##	Raw_4_HC_Immune_002	Raw_5_Orkambi_002_Base	Raw_7_HC_Auto_064_235	
##	1	2560	2163	3626
##	503538	2166	2006	3421
##	144571	3247	3217	3544
##	8086	339	424	1064
##	65985	493	902	813
##	195827	600	891	1107
##	Raw_8_Orkambi_004_Base	Raw_HC_Auto_082_253	Raw_HC_Auto_084_255	
##	1	2867	452	2981
##	503538	2548	3191	2047
##	144571	520	3324	2276
##	8086	3108	939	34
##	65985	3364	1063	518
##	195827	3	1857	558
##	Raw_HC_Auto_088_259	Raw_HC_Auto_091_263	Raw_HC_Auto_093_265	
##	1	3699	2	177
##	503538	3080	3059	4457
##	144571	713	3790	1008
##	8086	42	3755	1388
##	65985	1058	926	2094
##	195827	1401	1967	2779
##	Raw_HC_Auto_095_267	Raw_HC_Immune_006	Raw_HC_Immune_008	
##	1	3886	3786	430
##	503538	2704	2728	2816
##	144571	282	3583	2466
##	8086	256	186	3665
##	65985	1115	1320	778
##	195827	1642	1571	1794
##	Raw_Orkambi_015_Base	Raw_Orkambi_016_Base	Raw_Orkambi_017_Base	
##	1	3899	1854	262
##	503538	3498	1970	3153
##	144571	3104	966	3946
##	8086	1255	2518	4142
##	65985	1377	458	1606
##	195827	1357	499	1799
##	Raw_Orkambi_018_Base			
##	1	244		
##	503538	2981		
##	144571	133		
##	8086	2		
##	65985	1705		
##	195827	2058		

```

#STEP 2
#Creating data frame with condition column
expgroup <- data.frame(condition = c("HC", "CF", "HC", "CF", "HC", "CF", "HC", "CF", "CF", "HC",
                                     "HC", "CF", "HC", "CF", "HC", "CF", "HC", "HC", "HC", "CF",
                                     "HC", "CF", "HC", "HC", "HC", "HC", "HC", "HC", "HC", "HC",
                                     "CF", "CF", "CF", "CF"), row.names = colnames(readcount))

```

```
head(expgroup)
```

```

##              condition
## Raw_10_HC_Auto_066_237      HC
## Raw_11_Orkambi_006_Base      CF
## Raw_13_HC_Auto_068_239      HC
## Raw_14_Orkambi_007_Base      CF
## Raw_16_HC_Auto_072_243      HC
## Raw_17_Orkambi_009_Base      CF

```

```

#STEP 3
#creating the matrix for the counts dataset
cds <- DESeqDataSetFromMatrix(countData = readcount, colData = expgroup, design = ~ condition)

```

```

## Warning in DESeqDataSet(se, design = design, ignoreRank): some variables in
## design formula are characters, converting to factors

```

```
head(cds)
```

```

## class: DESeqDataSet
## dim: 6 34
## metadata(1): version
## assays(1): counts
## rownames(6): 1 503538 ... 65985 195827
## rowData names(0):
## colnames(34): Raw_10_HC_Auto_066_237 Raw_11_Orkambi_006_Base ...
##   Raw_Orkambi_017_Base Raw_Orkambi_018_Base
## colData names(1): condition

```

```

#STEP 4
#correcting the size
cds <- estimateSizeFactors(cds)
cds <- estimateDispersions(cds)

```

```
## gene-wise dispersion estimates
```

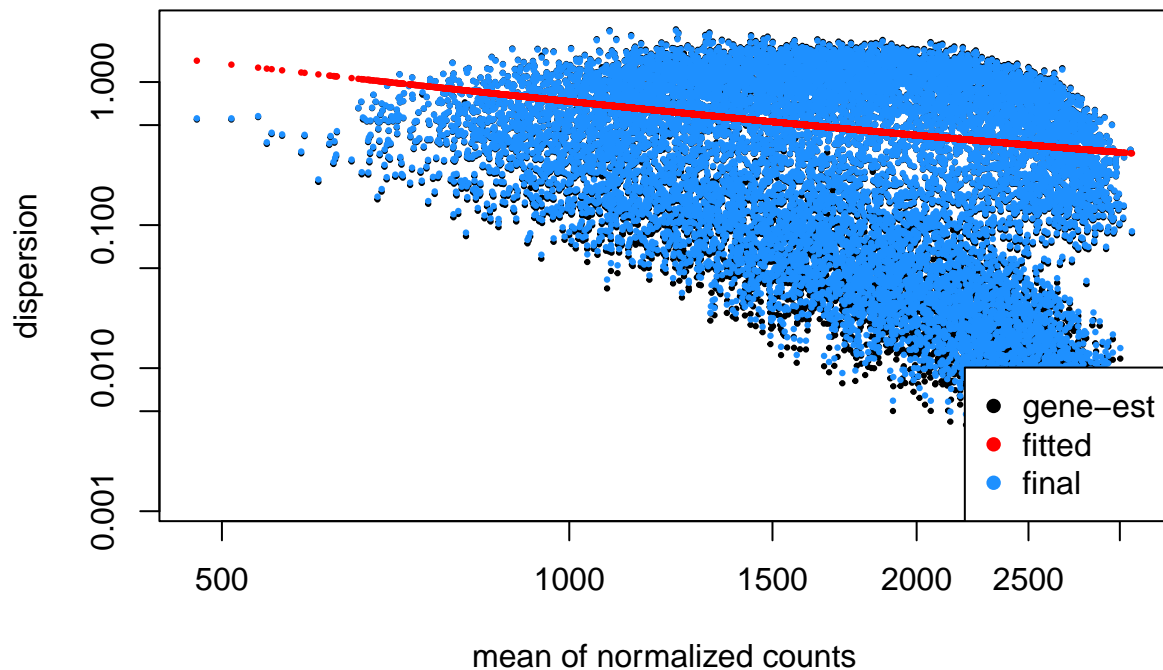
```
## mean-dispersion relationship
```

```
## final dispersion estimates
```

```

#plotting
plotDispEsts(cds)

```



The graph essentially tells me the about how the dispersion related to the normalized counts. The red dotted line represents the fitted line for the estimates of the dispersion. The graph itself shows me that the dispersion level increased along with the means. The dispersion cluster does not and should not show any kind of bending or skew

```
#STEP 5
#doing the differential analysis
cds <- DESeq(cds)

## using pre-existing size factors

## estimating dispersions

## found already estimated dispersions, replacing these

## gene-wise dispersion estimates

## mean-dispersion relationship

## final dispersion estimates

## fitting model and testing

## -- replacing outliers and refitting for 18 genes
## -- DESeq argument 'minReplicatesForReplace' = 7
## -- original counts are preserved in counts(dds)
```

```
## estimating dispersions
```

```
## fitting model and testing
```

```
#getting the results
```

```
results <- results(cds)
```

```
#STEP 6
```

```
#subsetting the genes with specific parameters such as p-value and log2foldchange values
```

```
diffexpgenes <- subset(results, padj < 0.05 & abs(log2FoldChange) > 1)
```

```
#counting the genes in this subset
```

```
nrow(diffexpgenes)
```

```
## [1] 78
```

```
#STEP 7
```

```
#normalizing the data from the counts
```

```
normvalues <- counts(cds, normalized = TRUE)
```

```
head(normvalues)
```

```
##      Raw_10_HC_Auto_066_237 Raw_11_Orkambi_006_Base Raw_13_HC_Auto_068_239
## 1      3190.7881      2602.4327      2955.8028
## 503538      2485.1859      2223.6385      1902.2878
## 144571      3067.9950      147.3807      2993.3820
## 8086      702.8531      4067.1899      4185.5515
## 65985      1052.9051      455.0702      308.4091
## 195827      932.8611      212.0213      1473.3660
##      Raw_14_Orkambi_007_Base Raw_16_HC_Auto_072_243 Raw_17_Orkambi_009_Base
## 1      3153.7934      289.74110      450.5253
## 503538      2301.6090      2806.55390      2672.3467
## 144571      2441.7776      65.81773      2002.3347
## 8086      241.7400      1206.18146      408.8100
## 65985      799.3673      1038.77549      1180.8641
## 195827      1079.7045      1191.87326      1395.2166
##      Raw_19_HC_Auto_074_245 Raw_1_Orkambi_001_Base Raw_20_Orkambi_010_Base
## 1      65.8643      3780.5536      77.8705
## 503538      2697.6534      2454.6778      2603.6914
## 144571      1082.5865      728.8236      574.0879
## 8086      584.4297      3760.7296      432.4298
## 65985      621.5364      444.2908      1057.0507
## 195827      1467.5680      296.1939      1271.6088
##      Raw_21_HC_Immune_004 Raw_23_HC_Auto_076_247 Raw_24_Orkambi_012_Base
## 1      209.8622      2673.7707      51.7377
## 503538      2899.1506      2692.3709      2790.3868
## 144571      3091.4607      2955.8729      442.3574
## 8086      931.0249      1045.4831      400.9672
## 65985      1014.2067      782.7561      1253.7770
## 195827      1512.5340      1361.6856      1543.5081
##      Raw_26_HC_Auto_078_249 Raw_27_Orkambi_013_Base Raw_29_HC_Auto_080_251
## 1      3642.2150      3040.6218      504.9728
## 503538      3053.7558      2230.0693      2976.0840
## 144571      4031.7247      2330.0235      123.4041
```

##	8086	364.3414	872.7089	1119.7223
##	65985	696.3234	753.4359	947.8650
##	195827	835.3484	1081.0167	1342.3040
##	Raw_30_Orkambi_014_Base	Raw_3_HC_Auto_062_233	Raw_42_HC_Auto_089_261	
##	1	3568.6726	3452.0078	2893.6901
##	503538	2375.4920	2681.2968	2407.7394
##	144571	2427.4220	2270.0351	3063.2837
##	8086	194.4353	707.0247	490.0275
##	65985	375.5862	385.3555	634.3451
##	195827	917.8312	854.9062	956.4098
##	Raw_4_HC_Immune_002	Raw_5_Orkambi_002_Base	Raw_7_HC_Auto_064_235	
##	1	2947.2962	2170.0541	3277.2420
##	503538	2493.6889	2012.5421	3091.9595
##	144571	3738.2308	3227.4915	3203.1290
##	8086	390.2865	425.3828	961.6618
##	65985	567.5848	904.9417	734.8036
##	195827	690.7726	893.9058	1000.5259
##	Raw_8_Orkambi_004_Base	Raw_HC_Auto_082_253	Raw_HC_Auto_084_255	
##	1	3053.687271	391.7258	3400.75818
##	503538	2713.915301	2765.4804	2335.24052
##	144571	553.860265	2880.7449	2596.48629
##	8086	3310.380202	813.7844	38.78758
##	65985	3583.049871	921.2490	590.94020
##	195827	3.195348	1609.3692	636.57265
##	Raw_HC_Auto_088_259	Raw_HC_Auto_091_263	Raw_HC_Auto_093_265	
##	1	2815.73516	1.660216	110.2262
##	503538	2344.54293	2539.300047	2775.5831
##	144571	542.74646	3146.108917	627.7289
##	8086	31.97104	3117.055141	864.3728
##	65985	805.36572	768.679910	1304.0321
##	195827	1066.46255	1632.822227	1730.6138
##	Raw_HC_Auto_095_267	Raw_HC_Immune_006	Raw_HC_Immune_008	
##	1	3514.3460	3126.4690	399.8607
##	503538	2445.3916	2252.7754	2618.6226
##	144571	255.0297	2958.8322	2293.1545
##	8086	231.5164	153.5983	3408.1149
##	65985	1008.3623	1090.0526	723.4689
##	195827	1484.9604	1297.3278	1668.2560
##	Raw_Orkambi_015_Base	Raw_Orkambi_016_Base	Raw_Orkambi_017_Base	
##	1	2897.0026	2366.9243	201.9968
##	503538	2599.0549	2515.0167	2430.9002
##	144571	2306.3083	1233.2518	3042.2874
##	8086	932.4797	3214.6254	3193.3995
##	65985	1023.1271	584.7095	1238.1940
##	195827	1008.2669	637.0524	1386.9932
##	Raw_Orkambi_018_Base			
##	1	186.850617		
##	503538	2282.793810		
##	144571	101.848902		
##	8086	1.531562		
##	65985	1305.656976		
##	195827	1575.977746		

```
#STEP 8
#creating the matrix for the genes that are differentially expressed
diffexpvalues <- normvalues[rownames(diffexpgenes), ]
```

```
#STEP 9
#doing the hierarchical clustering
hc <- hclust(dist(diffexpvalues), method = "complete")
#splitting the tree into 8 groups
groups <- cutree(hc, k = 8)
#counting the number of genes in each of the groups
table(groups)
```

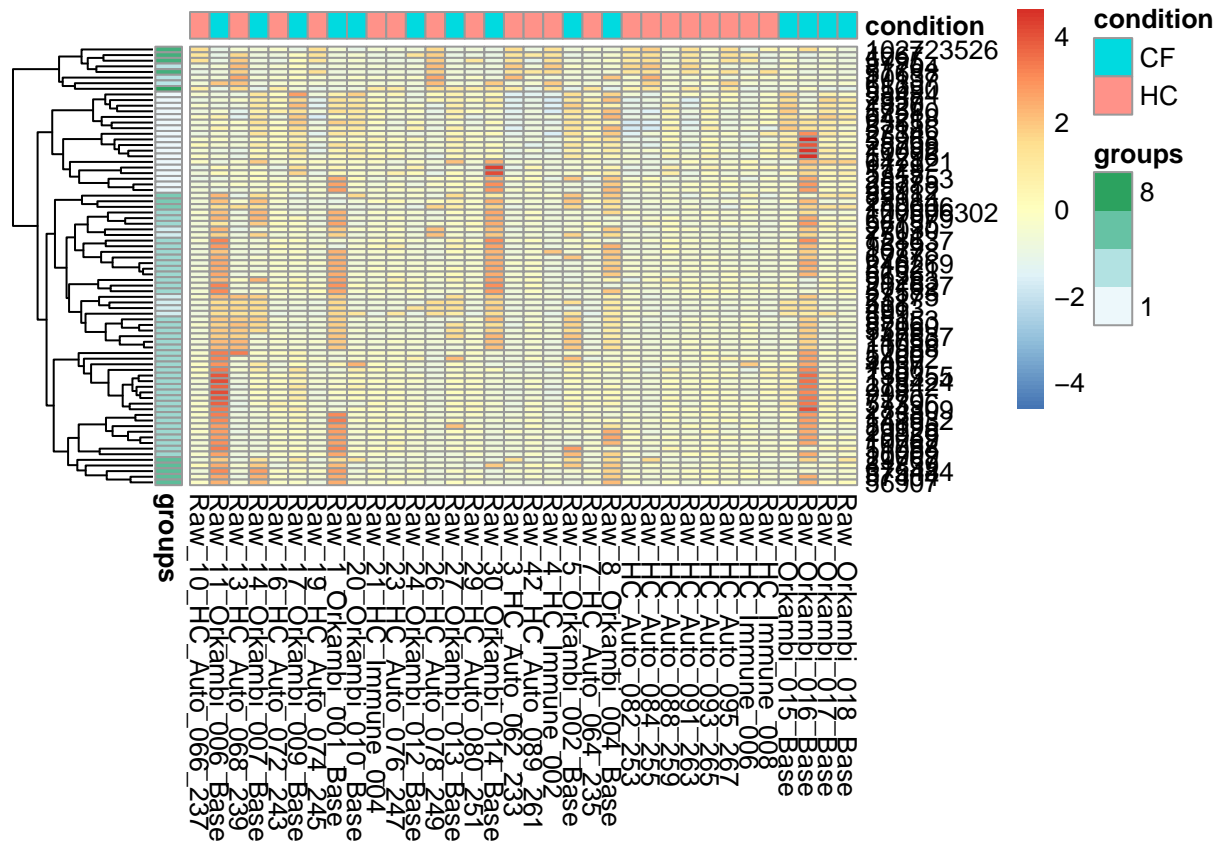
```
## groups
##  1  2  3  4  5  6  7  8
## 18  6  3 38  3  5  4  1
```

The number of genes in each group are shown in the table above

```
#STEP 10
#creating the heatmap. I had some difficulty incorporating annotation_row at first
library(pheatmap)
```

```
## Warning: package 'pheatmap' was built under R version 4.2.3
```

```
groups <- data.frame(groups)
pheatmap(diffexpvalues, scale = "row", cluster_cols = F, shown_rownames = F,
         annotation_col = expgroup, annotation_row = groups)
```



```
#STEP 11
params <- new("GOHyperGParams", geneIds = rownames(diffexpgenes),
  universeGeneIds = rownames(readcount),
  annotation = "org.Hs.eg.db", ontology = "BP",
  pvalueCutoff = 0.001, testDirection = "over")
```

#STEP 12

Based on my analysis throughout this process I have found genes that are differentially expressed between the CF patients before the treatment as well as the healthy patients. In reference to GO terms and GO stats, the genes do show signs of being impacted in CF. The heatmap shows patterns of differential expression as well because some genes show higher expression than others. The hierarchical clustering was useful for grouping the genes based on the patterns they portray during expression. In conclusion, I would say that there is definitely a difference between healthy and CF patients. The next steps would be to find out what are the roles of these genes in terms of vital biological functions, and then we can better understand the effects of CF and what it can target