Alzheimers Disease Brain Blood Samples

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This analysis is done using the NCBI gene expression samples taken from a study that used the middle temporal gyrus side of the brain of frozen samples taken from Alzheimer's patients that totalled 78 samples of control and repeat microarray gene expression results. The file was able to be downloaded and unzipped complete with the platform gene symbol ID already attached. A separate file of the meta information that includes the age, gender, tissue type and disease as Alzheimer's Disease (AD) or control was made from the Series information for each sample. The age range for these samples of healthy and AD patients is from 70-95 years of age.

This study can be linked to with all the sample and meta information at: https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE109887 The link to the 41 mb text file of series of samples with ID that is too large for github, or my github account type is: ftp://ftp.ncbi.nlm.nih.gov/geo/series/GSE109nnn/GSE109887/matrix/GSE109887_series_matrix.txt.gz

Open the original Sample ID values text file and write out as a csv file.

```
alz <- read.delim('GSE109887_series_matrix.txt', sep='\t', header=TRUE, na.strings=c('',' '), comment.cl

write.csv(alz,'alzheimerSamples.csv', row.names=FALSE)
```

```
head(alz)
```

```
##   ID_REF GSM2973262 GSM2973263 GSM2973264 GSM2973265 GSM2973266 GSM2973267
## 1    7A5   6.436441   6.500922   6.513507   6.480839   6.478978   6.509372
## 2   A1BG   6.736136   6.649034   6.612224   6.559642   6.574546   6.471425
## 3   A1CF   6.545395   6.479783   6.588104   6.482503   6.466453   6.442931
## 4  A26C3   6.529725   6.504956   6.531813   6.549229   6.458589   6.602654
## 5  A2BP1   6.773307   7.675723   7.159857   7.334894   7.928057   7.427863
## 6    A2M  11.253437  10.758069  10.790378  11.280206  10.550165  11.015546
##   GSM2973268 GSM2973269 GSM2973270 GSM2973271 GSM2973272 GSM2973273 GSM2973274
## 1   6.558079   6.539648   6.476178   6.384209   6.474428   6.506147   6.547314
## 2   6.601043   6.680376   6.619720   6.695035   6.636312   6.549436   6.631196
## 3   6.448482   6.511453   6.537003   6.485914   6.481272   6.470623   6.556559
## 4   6.551262   6.618060   6.473897   6.475091   6.494137   6.539573   6.504725
## 5   7.753590   7.542770   6.962004   7.844319   7.045881   8.032980   7.021767
## 6  10.374510  10.232084  11.219453  10.558733  11.928947  10.029828  11.261613
##   GSM2973275 GSM2973276 GSM2973277 GSM2973278 GSM2973279 GSM2973280 GSM2973281
## 1   6.482653   6.431043   6.467538   6.496945   6.455699   6.533167   6.502415
## 2   6.637651   6.610124   6.629145   6.633296   6.574900   6.686115   6.594453
## 3   6.500758   6.521914   6.561131   6.483240   6.495440   6.545356   6.540573
## 4   6.574710   6.434496   6.499997   6.456096   6.506443   6.601116   6.455450
## 5   7.237758   7.626402   7.702040   7.108037   8.086046   7.320380   7.262326
## 6  10.869890  10.028131  10.710539  10.902636  10.507890  10.889177  10.479438
```

```
##   GSM2973282 GSM2973283 GSM2973284 GSM2973285 GSM2973286 GSM2973287 GSM2973288
## 1   6.444786   6.501353   6.477281   6.544612   6.400074   6.520184   6.539472
## 2   6.571460   6.662062   6.610356   6.586472   6.590251   6.587090   6.597562
## 3   6.462481   6.499808   6.487859   6.539648   6.521903   6.523406   6.469701
## 4   6.449598   6.531614   6.493402   6.426615   6.542165   6.577142   6.421726
## 5   7.229908   7.817468   7.986829   8.202127   7.727549   7.299809   8.396471
## 6  10.736578  10.754942   9.644938  10.630864   9.750951  11.035407  10.141873
##   GSM2973289 GSM2973290 GSM2973291 GSM2973292 GSM2973293 GSM2973294 GSM2973295
## 1   6.424923   6.474643   6.589264   6.445287   6.529792   6.537969   6.459321
## 2   6.680176   6.550771   6.679956   6.569058   6.675714   6.579930   6.559305
## 3   6.530320   6.473031   6.517640   6.506745   6.516516   6.464695   6.556136
## 4   6.533016   6.370309   6.488512   6.445287   6.455889   6.412834   6.477753
## 5   8.017758   8.169229   8.477709   7.172333   7.303684   8.116424   8.008762
## 6  10.213843  10.347774  10.304462   9.771581  11.610263  10.145408   9.672881
##   GSM2973296 GSM2973297 GSM2973298 GSM2973299 GSM2973300 GSM2973301 GSM2973302
## 1   6.418835   6.503889   6.485979   6.485081   6.530189   6.450836   6.489789
## 2   6.616573   6.893967   6.556532   6.569898   6.896213   6.618346   6.637531
## 3   6.481994   6.476141   6.525448   6.504118   6.471415   6.439531   6.522903
## 4   6.443488   6.490153   6.502554   6.540274   6.610700   6.443019   6.483445
## 5   7.650064   7.083986   7.212323   7.138866   6.818649   7.580220   6.876141
## 6  11.445590  10.917707  10.639809  10.877692  11.223275   9.632867  10.446053
##   GSM2973303 GSM2973304 GSM2973305 GSM2973306 GSM2973307 GSM2973308 GSM2973309
## 1   6.450708   6.461540   6.470023   6.446682   6.580688   6.506489   6.335251
## 2   6.593549   6.678117   6.591719   6.636234   6.648021   6.622491   6.577416
## 3   6.503260   6.528314   6.487072   6.525948   6.540932   6.499622   6.479403
## 4   6.592281   6.483814   6.582309   6.535979   6.521488   6.538749   6.492057
## 5   7.380896   6.899655   8.136078   7.597110   7.000424   8.066728   6.978048
## 6  11.354353  10.837673   9.561554  10.928431  10.706460  10.236279  10.857606
##   GSM2973310 GSM2973311 GSM2973312 GSM2973313 GSM2973314 GSM2973315 GSM2973316
## 1   6.435910   6.383139   6.504311   6.442846   6.495440   6.423849   6.439607
## 2   6.715207   6.776508   6.606429   6.632080   6.614676   6.610304   6.641509
## 3   6.589606   6.485514   6.522903   6.514882   6.493620   6.504014   6.494156
## 4   6.473449   6.466644   6.498143   6.367646   6.512105   6.483955   6.578028
## 5   6.770394   8.196010   8.175675   8.239208   7.745435   7.878781   8.135434
## 6  11.231447  10.371160   9.715824   9.869439  10.131814  10.695212  10.372269
##   GSM2973317 GSM2973318 GSM2973319 GSM2973320 GSM2973321 GSM2973322 GSM2973323
## 1   6.476767   6.432943   6.567727   6.590029   6.518445   6.402109   6.462368
## 2   6.647461   6.583375   6.641342   6.559408   6.603364   6.667564   6.643683
## 3   6.522168   6.490471   6.612509   6.502178   6.495266   6.483240   6.539573
## 4   6.577480   6.422356   6.485102   6.515997   6.489093   6.380886   6.519553
## 5   7.967045   7.416130   7.679170   8.173208   7.996740   7.893309   8.566021
## 6  10.452866  10.354096  10.449631   9.839133   9.939212  10.397824  10.141047
##   GSM2973324 GSM2973325 GSM2973326 GSM2973327 GSM2973328 GSM2973329 GSM2973330
## 1   6.429510   6.461409   6.404062   6.527984   6.519651   6.447827   6.462642
## 2   6.610161   6.570311   6.587222   6.672783   6.565616   6.645337   6.667337
## 3   6.473020   6.468053   6.550716   6.533538   6.514122   6.499146   6.540705
## 4   6.397061   6.451695   6.484181   6.441520   6.464654   6.473196   6.557970
## 5   8.215478   8.026517   7.850848   8.178894   7.749528   8.342166   8.141308
## 6   9.837524  10.109630  11.115016   9.570170  11.066659   9.929106   9.642897
##   GSM2973331 GSM2973332 GSM2973333 GSM2973334 GSM2973335 GSM2973336 GSM2973337
## 1   6.536339   6.506450   6.429433   6.427672   6.488852   6.503583   6.508713
## 2   6.551605   6.557762   6.600702   6.648831   6.660864   6.617121   6.541810
## 3   6.491767   6.479403   6.535446   6.487697   6.515856   6.546361   6.457605
## 4   6.505190   6.585256   6.594342   6.523304   6.526753   6.492019   6.623703
```

```
## 5   8.334120   8.201316   7.891050   8.061283   7.794727   7.156839   6.903667
## 6  10.061636  11.116617  10.779104  10.415084  10.889901  11.026483  10.926880
##   GSM2973338 GSM2973339
## 1   6.442999   6.465497
## 2   6.547078   6.611912
## 3   6.469584   6.521874
## 4   6.467831   6.453058
## 5   8.187274   7.777883
## 6   9.636975  10.613131
```

Lets read in the meta information for age, gender, and disease type as AD or control.

```
meta <- read.csv('AlzheimerAgeGenderTissueSamplesMeta.csv', sep=',',
                 header=TRUE, na.strings=c('',' '))
```

```
head(meta)
```

```
##   sampleID                          GSM2973262
## 1   gender                                   M
## 2      age                                  91
## 3  disease                                  AD
## 4   tissue brain, middle temporal gyrus blood
##                            GSM2973263                          GSM2973264
## 1                                   M                                   F
## 2                                  87                                  82
## 3                                  AD                                  AD
## 4 brain, middle temporal gyrus blood brain, middle temporal gyrus blood
##                            GSM2973265                          GSM2973266
## 1                                   F                                   M
## 2                                  73                                  94
## 3                                  AD                                  AD
## 4 brain, middle temporal gyrus blood brain, middle temporal gyrus blood
##                            GSM2973267                          GSM2973268
## 1                                   M                                   F
## 2                                  72                                  90
## 3                                  AD                                  AD
## 4 brain, middle temporal gyrus blood brain, middle temporal gyrus blood
##                            GSM2973269                          GSM2973270
## 1                                   F                                   F
## 2                                  86                                  87
## 3                             control                                  AD
## 4 brain, middle temporal gyrus blood brain, middle temporal gyrus blood
##                            GSM2973271                          GSM2973272
## 1                                   M                                   M
## 2                                  92                                  81
## 3                             control                                  AD
## 4 brain, middle temporal gyrus blood brain, middle temporal gyrus blood
##                            GSM2973273                          GSM2973274
## 1                                   M                                   F
## 2                                  87                                  92
## 3                             control                                  AD
## 4 brain, middle temporal gyrus blood brain, middle temporal gyrus blood
##                            GSM2973275                          GSM2973276
```

```
## 1                                  F                                  M
## 2                                 95                                 75
## 3                                 AD                                 AD
## 4 brain, middle temporal gyrus blood brain, middle temporal gyrus blood
##                           GSM2973277                         GSM2973278
## 1                                  F                                  M
## 2                                 87                                 95
## 3                                 AD                                 AD
## 4 brain, middle temporal gyrus blood brain, middle temporal gyrus blood
##                           GSM2973279                         GSM2973280
## 1                                  M                                  F
## 2                                 90                                 77
## 3                            control                                 AD
## 4 brain, middle temporal gyrus blood brain, middle temporal gyrus blood
##                           GSM2973281                         GSM2973282
## 1                                  F                                  M
## 2                                 84                                 85
## 3                                 AD                                 AD
## 4 brain, middle temporal gyrus blood brain, middle temporal gyrus blood
##                           GSM2973283                         GSM2973284
## 1                                  M                                  F
## 2                                 89                                 89
## 3                            control                            control
## 4 brain, middle temporal gyrus blood brain, middle temporal gyrus blood
##                           GSM2973285                         GSM2973286
## 1                                  F                                  F
## 2                                 82                                 78
## 3                            control                            control
## 4 brain, middle temporal gyrus blood brain, middle temporal gyrus blood
##                           GSM2973287                         GSM2973288
## 1                                  M                                  F
## 2                                 70                                 86
## 3                                 AD                            control
## 4 brain, middle temporal gyrus blood brain, middle temporal gyrus blood
##                           GSM2973289                         GSM2973290
## 1                                  F                                  F
## 2                                 75                                 94
## 3                                 AD                                 AD
## 4 brain, middle temporal gyrus blood brain, middle temporal gyrus blood
##                           GSM2973291                         GSM2973292
## 1                                  M                                  M
## 2                                 82                                 82
## 3                            control                                 AD
## 4 brain, middle temporal gyrus blood brain, middle temporal gyrus blood
##                           GSM2973293                         GSM2973294
## 1                                  M                                  F
## 2                                 73                                 77
## 3                            control                            control
## 4 brain, middle temporal gyrus blood brain, middle temporal gyrus blood
##                           GSM2973295                         GSM2973296
## 1                                  M                                  M
## 2                                 85                                 92
## 3                                 AD                            control
## 4 brain, middle temporal gyrus blood brain, middle temporal gyrus blood
```

```
##                            GSM2973297                            GSM2973298
## 1                                   F                                     F
## 2                                  84                                    87
## 3                             control                                    AD
## 4 brain, middle temporal gyrus blood brain, middle temporal gyrus blood
##                            GSM2973299                            GSM2973300
## 1                                   M                                     F
## 2                                  86                                    92
## 3                             control                                    AD
## 4 brain, middle temporal gyrus blood brain, middle temporal gyrus blood
##                            GSM2973301                            GSM2973302
## 1                                   M                                     F
## 2                                  92                                    90
## 3                                  AD                                    AD
## 4 brain, middle temporal gyrus blood brain, middle temporal gyrus blood
##                            GSM2973303                            GSM2973304
## 1                                   F                                     F
## 2                                  82                                    82
## 3                                  AD                                    AD
## 4 brain, middle temporal gyrus blood brain, middle temporal gyrus blood
##                            GSM2973305                            GSM2973306
## 1                                   F                                     M
## 2                                  89                                    90
## 3                                  AD                                    AD
## 4 brain, middle temporal gyrus blood brain, middle temporal gyrus blood
##                            GSM2973307                            GSM2973308
## 1                                   M                                     M
## 2                                  87                                    78
## 3                                  AD                                    AD
## 4 brain, middle temporal gyrus blood brain, middle temporal gyrus blood
##                            GSM2973309                            GSM2973310
## 1                                   F                                     F
## 2                                  88                                    86
## 3                                  AD                                    AD
## 4 brain, middle temporal gyrus blood brain, middle temporal gyrus blood
##                            GSM2973311                            GSM2973312
## 1                                   F                                     M
## 2                                  88                                    86
## 3                             control                                    AD
## 4 brain, middle temporal gyrus blood brain, middle temporal gyrus blood
##                            GSM2973313                            GSM2973314
## 1                                   F                                     F
## 2                                  92                                    81
## 3                             control                                    AD
## 4 brain, middle temporal gyrus blood brain, middle temporal gyrus blood
##                            GSM2973315                            GSM2973316
## 1                                   M                                     F
## 2                                  82                                    92
## 3                                  AD                               control
## 4 brain, middle temporal gyrus blood brain, middle temporal gyrus blood
##                            GSM2973317                            GSM2973318
## 1                                   F                                     M
## 2                                  81                                    89
## 3                             control                                    AD
```

```
## 4 brain, middle temporal gyrus blood brain, middle temporal gyrus blood
##                            GSM2973319                            GSM2973320
## 1                                   F                                     M
## 2                                  85                                    94
## 3                                  AD                               control
## 4 brain, middle temporal gyrus blood brain, middle temporal gyrus blood
##                            GSM2973321                            GSM2973322
## 1                                   F                                     F
## 2                                  85                                    82
## 3                             control                               control
## 4 brain, middle temporal gyrus blood brain, middle temporal gyrus blood
##                            GSM2973323                            GSM2973324
## 1                                   M                                     F
## 2                                  81                                    77
## 3                             control                               control
## 4 brain, middle temporal gyrus blood brain, middle temporal gyrus blood
##                            GSM2973325                            GSM2973326
## 1                                   F                                     M
## 2                                  81                                    79
## 3                             control                               control
## 4 brain, middle temporal gyrus blood brain, middle temporal gyrus blood
##                            GSM2973327                            GSM2973328
## 1                                   M                                     F
## 2                                  78                                    78
## 3                             control                                    AD
## 4 brain, middle temporal gyrus blood brain, middle temporal gyrus blood
##                            GSM2973329                            GSM2973330
## 1                                   M                                     M
## 2                                  79                                    86
## 3                             control                               control
## 4 brain, middle temporal gyrus blood brain, middle temporal gyrus blood
##                            GSM2973331                            GSM2973332
## 1                                   M                                     M
## 2                                  91                                    82
## 3                             control                                    AD
## 4 brain, middle temporal gyrus blood brain, middle temporal gyrus blood
##                            GSM2973333                            GSM2973334
## 1                                   M                                     F
## 2                                  84                                    91
## 3                                  AD                                    AD
## 4 brain, middle temporal gyrus blood brain, middle temporal gyrus blood
##                            GSM2973335                            GSM2973336
## 1                                   F                                     M
## 2                                  87                                    86
## 3                             control                                    AD
## 4 brain, middle temporal gyrus blood brain, middle temporal gyrus blood
##                            GSM2973337                            GSM2973338
## 1                                   M                                     M
## 2                                  88                                    81
## 3                                  AD                               control
## 4 brain, middle temporal gyrus blood brain, middle temporal gyrus blood
##                            GSM2973339
## 1                                   F
## 2                                  85
```

```
## 3                                  AD
## 4 brain, middle temporal gyrus blood
```

Transpose the meta to fields instead of rows

```
meta1 <- as.data.frame(t(meta))
names <- as.character(meta$sampleID)
colnames(meta1) <- names
meta2 <- meta1[-1,]
head(meta2)
```

```
##            gender age disease                              tissue
## GSM2973262      M  91      AD brain, middle temporal gyrus blood
## GSM2973263      M  87      AD brain, middle temporal gyrus blood
## GSM2973264      F  82      AD brain, middle temporal gyrus blood
## GSM2973265      F  73      AD brain, middle temporal gyrus blood
## GSM2973266      M  94      AD brain, middle temporal gyrus blood
## GSM2973267      M  72      AD brain, middle temporal gyrus blood
```

Separate the data into gender and control or AD data sets respectively in each gender and for both genders.

Data tables of males and females for meta only:

```
row.names(alz) <- alz$ID_REF
alz1 <- alz[,-1]

row.names(meta) <- meta$sampleID
Meta <- meta[,-1]

names <- row.names(Meta)
Meta1 <- as.data.frame(t(Meta))
colnames(Meta1) <- names

fem <- grep('F', Meta1$gender)
mal <- grep('M', Meta1$gender)

Fem <- Meta1[fem,]
Mal <- Meta1[mal,]

Fem$sampleID <- as.factor(row.names(Fem))
Mal$sampleID <- as.factor(row.names(Mal))
```

Display the fields of these gender specific tables by meta information:

```
colnames(Fem)
```

```
## [1] "gender"   "age"      "disease"  "tissue"   "sampleID"
```

```
colnames(Mal)
```

```
## [1] "gender"   "age"      "disease"  "tissue"   "sampleID"
```

The same indices of each row name is the same as the alz1, alzheimer table colnames indices. So, use those same female and male indices values from the regex commands to separate the alzheimer table into male and female tables.

```
Females <- alz1[,fem]
Males <- alz1[,mal]
```

Data tables of control or AD for males and for females for meta only:

```
femControl <- grep('control', Fem$disease)
malControl <- grep('control', Mal$disease)

femAD <- grep('AD', Fem$disease)
malAD <- grep('AD', Mal$disease)

FemCtrl <- Fem[femControl,]
MalCtrl <- Mal[malControl,]

FemAD <- Fem[femAD,]
MalAD <- Mal[malAD,]
```

Display the AD or Control tables by gender for meta information:

```
colnames(FemCtrl)
```

```
## [1] "gender"   "age"      "disease"  "tissue"   "sampleID"
```

```
colnames(FemAD)
```

```
## [1] "gender"   "age"      "disease"  "tissue"   "sampleID"
```

```
colnames(FemAD)
```

```
## [1] "gender"   "age"      "disease"  "tissue"   "sampleID"
```

```
colnames(MalAD)
```

```
## [1] "gender"   "age"      "disease"  "tissue"   "sampleID"
```

Now use that same index information within each gender table derived from the alzheimer gene expression data:

```
Females_AD <- Females[,femAD]
Females_control <- Females[,femControl]

males_AD <- Males[,malAD]
males_control <- Males[, malControl]
```

Write these last tables to csv file:

```
write.csv(Females_AD, 'females_Alzheimers.csv', row.names=TRUE)
write.csv(Females_control, 'females_healthy_control.csv', row.names=TRUE)
write.csv(males_AD, 'males_Alzheimers.csv', row.names=TRUE)
write.csv(males_control, 'males_healthy_control.csv', row.names=TRUE)
```

What is the age range on these samples of healthy controls and AD patients?

```
age1 <- range(as.numeric(as.character(FemAD$age)))
age2 <- range(as.numeric(as.character(FemCtrl$age)))
age3 <- range(as.numeric(as.character(MalAD$age)))
age4 <- range(as.numeric(as.character(MalCtrl$age)))

char <- c('The minimum age: ', 'The maximum age: ')

AD_fem <- paste0(char,age1, sep='')
AD_mal <- paste0(char,age3, sep='')
ctrl_fem <- paste0(char,age2, sep='')
ctrl_mal <- paste0(char, age4, sep='')

adf <- c('Alzheimer females: ')
adm <- c('Alzheimer males: ')
cf <- c('healthy females: ')
cm <- c('healthy males: ')

ranges <- c(adf,AD_fem, adm, AD_mal, cf, ctrl_fem, cm, ctrl_mal)
ranges
```

```
##  [1] "Alzheimer females: " "The minimum age: 73" "The maximum age: 95"
##  [4] "Alzheimer males: "   "The minimum age: 70" "The maximum age: 95"
##  [7] "healthy females: "   "The minimum age: 77" "The maximum age: 92"
## [10] "healthy males: "     "The minimum age: 73" "The maximum age: 94"
```

The age range in all of this data for these healthy and AD patients is age 70 to age 95 years of age.Just useful to know when cross comparing blood microarray samples across the females from our overweight females using epigallocatechin (EGCG) in their 40s, the males from Russia who are also in their 40s with or without myocardial infarction (MI), the hemochromatosis (iron toxicity) males and females averaging their 40s in years of age with or without iron toxicity, and the flu vaccinated blood samples of males and females also in their 40s with or without antibiotic treatment combined with flu vaccination.

Lets do some data analysis of the means and fold change between the groups to create some additional statistical information on these Alzheimers blood samples and healthy controls of elderly patients. We will use dplyr for this and plot with ggplot2 later.

```
library(dplyr)
```

First lets look at the control and the AD tables within the gender specific tables: Females_AD, Females_control, males_AD, males_control. Get the means of each gene and compare into one table. This and these tables of data were already cleaned to only have one gene per row, due to not having to merge the platform fields to the series table and duplicate genes for missing data in the additional rows like previous studies mentioned earlier required.

Get the row means of each table and add to each table.

```
names <- row.names(Females_AD)
Females_AD1 <- rowMeans(Females_AD)
#colnames(Females_AD1) <- 'fem_AD_Mean'

Females_control1 <- rowMeans(Females_control)
#colnames(Females_control1) <- 'fem_ctrl_Mean'

males_AD1 <- rowMeans(males_AD)
#colnames(males_AD1) <- 'mal_AD_Mean'

males_control1 <- rowMeans(males_control)
#colnames(males_control1) <- 'mal_ctrl_Mean'
```

```
means <- cbind(Females_AD1, Females_control1, males_AD1, males_control1)
Means <- as.data.frame(means)
colnames(Means) <- paste(colnames(Means),'_Mean',sep='')
str(Means)
```

```
## 'data.frame':    31700 obs. of  4 variables:
##  $ Females_AD1_Mean     : num  6.48 6.63 6.52 6.51 7.42 ...
##  $ Females_control1_Mean: num  6.47 6.65 6.5 6.48 7.97 ...
##  $ males_AD1_Mean       : num  6.48 6.6 6.5 6.51 7.51 ...
##  $ males_control1_Mean  : num  6.48 6.62 6.51 6.5 8.01 ...
```

Now for the fold change values between the Means of the female control and AD patients, then for the male control and AD patients.

```
names <- row.names(Means)
FC_females <- Means %>% mutate(FC_fem_ctrl_AD =
                                 Females_AD1_Mean/Females_control1_Mean)
str(FC_females)
```

```
## 'data.frame':    31700 obs. of  5 variables:
##  $ Females_AD1_Mean     : num  6.48 6.63 6.52 6.51 7.42 ...
##  $ Females_control1_Mean: num  6.47 6.65 6.5 6.48 7.97 ...
##  $ males_AD1_Mean       : num  6.48 6.6 6.5 6.51 7.51 ...
##  $ males_control1_Mean  : num  6.48 6.62 6.51 6.5 8.01 ...
##  $ FC_fem_ctrl_AD       : num  1.001 0.998 1.004 1.005 0.931 ...
```

```
row.names(FC_females) <- names
```

```
names <- row.names(FC_females)
FC_both <- FC_females %>% mutate(FC_male_ctrl_AD =
                                   males_AD1_Mean/males_control1_Mean)
row.names(FC_both) <- names
str(FC_both)
```

```
## 'data.frame':    31700 obs. of  6 variables:
##  $ Females_AD1_Mean     : num  6.48 6.63 6.52 6.51 7.42 ...
##  $ Females_control1_Mean: num  6.47 6.65 6.5 6.48 7.97 ...
##  $ males_AD1_Mean       : num  6.48 6.6 6.5 6.51 7.51 ...
```

```
##  $ males_control1_Mean  : num  6.48 6.62 6.51 6.5 8.01 ...
##  $ FC_fem_ctrl_AD       : num  1.001 0.998 1.004 1.005 0.931 ...
##  $ FC_male_ctrl_AD      : num  0.999 0.997 0.999 1.002 0.938 ...
```

```
write.csv(FC_both, 'FC_both.csv', row.names=TRUE)
```

Combine the data of the samples with IDs in the alz1 table with the stats.

```
both <- cbind(FC_both, alz1)

Both <- round(both, 3)

write.csv(Both, 'Both.csv', row.names=TRUE)
```

Top 100 genes Most expressed in fold change for females with AD:

```
top100_fem <- Both[order(Both$FC_fem_ctrl_AD, decreasing=TRUE)[0:100],]
a <- row.names(top100_fem)
a
```

```
##   [1] "SLC5A3"       "LOC339879"    "DDIT4L"       "SLC6A12"      "SLC7A2"
##   [6] "SFMBT2"       "LOC727908"    "CHST6"        "TEAD2"        "GPER"
##  [11] "FLJ38717"     "FCGBP"        "HEY2"         "ITPRIPL2"     "SIPA1"
##  [16] "DDX27"        "RAPGEF3"      "C15ORF52"     "CALD1"        "ITSN1"
##  [21] "AEBP1"        "PLXNB1"       "HS.37648"     "LOC100129828" "NBPF8"
##  [26] "GSDMD"        "ITPKB"        "PTH1R"        "SYTL4"        "MYOT"
##  [31] "TMEM137"      "FAM65C"       "FZD9"         "VCAN"         "ZCCHC24"
##  [36] "HS.505676"    "HS.534061"    "LOC100133019" "LRRC32"       "AHNAK"
##  [41] "LYL1"         "NOTCH1"       "APLNR"        "HS.379253"    "PTRF"
##  [46] "RPPH1"        "C1ORF110"     "INPPL1"       "LOC649841"    "DLC1"
##  [51] "ITGB5"        "RASL12"       "AKR1C3"       "FOXC1"        "LOC100132532"
##  [56] "RAB13"        "WSCD1"        "LOC643287"    "ACACB"        "CUEDC1"
##  [61] "INPP5D"       "LOC100129681" "LOC642031"    "TNFRSF1B"     "CFLAR"
##  [66] "FXYD5"        "LOC100131541" "PDGFRB"       "RAXL1"        "ANGPT2"
##  [71] "LOC100131277" "SLC15A3"      "FLNC"         "LOC648921"    "NACC2"
##  [76] "RUNDC2C"      "UBXN2A"       "VIL2"         "ZNF786"       "DCLRE1C"
##  [81] "FLJ46906"     "HS.143018"    "LOC727948"    "HS.193767"    "LRCH4"
##  [86] "MT1H"         "SCRIB"        "KIF1C"        "LASS1"        "LOC100130598"
##  [91] "NDE1"         "RN7SK"        "ZNF621"       "C9ORF130"     "CAPS"
##  [96] "EML3"         "HS.576072"    "KCNJ10"       "LOC100131096" "LOC653158"
```

Top 100 genes most expressed in fold change for males with AD:

```
top100_male <- Both[order(Both$FC_male_ctrl_AD, decreasing=TRUE)[0:100],]
b <- row.names(top100_male)
b
```

```
##   [1] "RGS1"         "SLC5A3"       "LOC649362"    "TTR"          "CD44"
##   [6] "FCGBP"        "SLC7A2"       "C10ORF10"     "EMP1"         "ITPRIP"
##  [11] "DDIT4"        "PLXNB1"       "ITPKB"        "S100A8"       "SERPINA3"
##  [16] "TEAD2"        "ADAMTS1"      "CCL2"         "ZFP36"        "HEY2"
##  [21] "PTH1R"        "CHST6"        "GFAP"         "HLA-DRA"      "SLC6A12"
```

```
##  [26] "ACACB"        "GPR4"         "SRGN"         "CD14"         "CDKN1A"
##  [31] "LRRC32"       "FOS"          "HLA-DMB"      "KIAA1881"     "TNFRSF1B"
##  [36] "HLA-DMA"      "MS4A6A"       "RAB13"        "CALD1"        "RASL12"
##  [41] "MT2A"         "SYTL4"        "AHNAK"        "CEBPD"        "FAM65C"
##  [46] "TGFBI"        "TMC6"         "CAPS"         "DDIT4L"       "ID3"
##  [51] "ITGB2"        "LCP1"         "RNU1G2"       "S1PR3"        "SIPA1"
##  [56] "GADD45G"      "GSDMD"        "NUPR1"        "ANLN"         "GEM"
##  [61] "PDGFRB"       "VCAN"         "AEBP1"        "CD163"        "KIF1C"
##  [66] "LOC387763"    "RUNDC2C"      "ZFP36L1"      "CFLAR"        "CTGF"
##  [71] "IL8"          "PDK4"         "PLIN2"        "SLC16A9"      "CSF1R"
##  [76] "IL17RB"       "LOC100133692" "LOC643287"    "SCIN"         "TAGLN"
##  [81] "TMEM106A"     "ADM"          "EDN1"         "FOXC1"        "GADD45B"
##  [86] "HSPA1A"       "MT1M"         "APLNR"        "APOLD1"       "C7"
##  [91] "HS.37648"     "IGFBP5"       "MYOT"         "RN7SK"        "C15ORF52"
##  [96] "GJA4"         "GPER"         "ITGB5"        "LEP"          "PLXDC2"
```

Bottom 100 genes that are least expressed in fold change in females with AD:

```
bottom100_fem <- Both[order(Both$FC_fem_ctrl_AD, decreasing=FALSE)[0:100],]
c <-row.names(bottom100_fem)
c
```

```
##   [1] "SYT1"         "CHGB"         "PCSK1"        "VGF"          "MAL2"
##   [6] "RGS4"         "GABRA1"       "NPTX2"        "SST"          "STAT4"
##  [11] "C1ORF173"     "CBLN4"        "DYNC1I1"      "STXBP1"       "GNG2"
##  [16] "RGS7"         "TSPAN13"      "EFCBP1"       "NELL2"        "HPRT1"
##  [21] "TAGLN3"       "DCLK1"        "ST6GALNAC5"   "GLRB"         "BEX5"
##  [26] "DIRAS2"       "SYP"          "KIAA1107"     "PAK1"         "PTPRN"
##  [31] "SERPINI1"     "ZCCHC12"      "NELL1"        "DACH2"        "ELMOD1"
##  [36] "NECAB1"       "NEFM"         "PARM1"        "RTN1"         "VAMP2"
##  [41] "ENC1"         "TMEM16C"      "CREG2"        "STX1A"        "SVOP"
##  [46] "CAP2"         "SCG2"         "UCHL1"        "CALY"         "KIAA0748"
##  [51] "NAP1L3"       "RIMBP2"       "YWHAG"        "GABRG2"       "LOC100128403"
##  [56] "NAP1L2"       "NAP1L5"       "STMN2"        "ADCYAP1"      "SCN3B"
##  [61] "GAD1"         "HS.390250"    "INA"          "SCN2B"        "GPRASP2"
##  [66] "ITFG1"        "SNX10"        "SV2B"         "ATP6V1G2"     "GABBR2"
##  [71] "GAD2"         "HPCA"         "NUDT11"       "LPPR4"        "TMEM155"
##  [76] "CAMK1G"       "EPHA4"        "GABRA5"       "MYT1L"        "HS.553187"
##  [81] "CDH13"        "VSNL1"        "XK"           "CKMT1A"       "HS.31961"
##  [86] "PCSK1N"       "PRKCG"        "SYT13"        "NPY"          "PRKCB"
##  [91] "RASL11B"      "SYN2"         "CADPS"        "TSPYL1"       "C12ORF53"
##  [96] "HSPB3"        "MKL2"         "PPP3R1"       "SNCA"         "C2ORF80"
```

Bottom 100 genes that are least expressed in fold change in males with AD:

```
bottom100_male <- Both[order(Both$FC_male_ctrl_AD, decreasing=FALSE)[0:100],]
d <- row.names(bottom100_male)
d
```

```
##   [1] "VGF"          "PCSK1"        "RGS4"         "CHGB"         "STAT4"
##   [6] "GABRA1"       "ST6GALNAC5"   "ADCYAP1"      "MAL2"         "SYT1"
##  [11] "CREG2"        "NPTX2"        "TMEM16C"      "CBLN4"        "SVOP"
##  [16] "KIAA1107"     "RGS7"         "BEX5"         "C1ORF173"     "NELL1"
```

```
##  [21] "SST"          "PARM1"        "DYNC1I1"      "NAP1L5"       "NEFM"
##  [26] "VAMP2"        "HS.390250"    "PTPRN"        "HSPB3"        "LOC100128403"
##  [31] "STXBP1"       "ENC1"         "GAD2"         "PAK1"         "ANO3"
##  [36] "INA"          "LOC387856"    "SLC30A3"      "STX1A"        "ZCCHC12"
##  [41] "SCN2B"        "C2ORF80"      "CRYM"         "EPHA4"        "GLRB"
##  [46] "HPRT1"        "KIAA0748"     "STMN2"        "C11ORF87"     "CAP2"
##  [51] "GAD1"         "SNX10"        "EFCBP1"       "RPH3A"        "SERPINI1"
##  [56] "DACH2"        "DCLK1"        "GPRASP2"      "SYP"          "TSPAN13"
##  [61] "VIP"          "C12ORF53"     "CALY"         "OLFM3"        "SV2B"
##  [66] "COPG2IT1"     "DIRAS2"       "ELMOD1"       "NELL2"        "SCG2"
##  [71] "SLC39A10"     "GABRG2"       "SLITRK4"      "TAGLN3"       "TMEM155"
##  [76] "CKMT1B"       "CYP26B1"      "GABBR2"       "CPNE4"        "HS.553187"
##  [81] "MFF"          "PRKCG"        "TUBB2A"       "ELAVL4"       "LRFN5"
##  [86] "NCALD"        "RIMBP2"       "RTN1"         "SLC6A17"      "SYT13"
##  [91] "YWHAE"        "CCKBR"        "FGF12"        "G3BP2"        "HOPX"
##  [96] "NAP1L3"       "NMNAT2"       "ZNF365"       "C20ORF103"    "CADPS"
```

```
ab <- c(a,b)
topBoth <- unique(ab)

cd <- c(c,d)
bottomBoth <- unique(cd)
```

The unique top genes are:

```
topBoth
```

```
##   [1] "SLC5A3"        "LOC339879"    "DDIT4L"       "SLC6A12"      "SLC7A2"
##   [6] "SFMBT2"        "LOC727908"    "CHST6"        "TEAD2"        "GPER"
##  [11] "FLJ38717"      "FCGBP"        "HEY2"         "ITPRIPL2"     "SIPA1"
##  [16] "DDX27"         "RAPGEF3"      "C15ORF52"     "CALD1"        "ITSN1"
##  [21] "AEBP1"         "PLXNB1"       "HS.37648"     "LOC100129828" "NBPF8"
##  [26] "GSDMD"         "ITPKB"        "PTH1R"        "SYTL4"        "MYOT"
##  [31] "TMEM137"       "FAM65C"       "FZD9"         "VCAN"         "ZCCHC24"
##  [36] "HS.505676"     "HS.534061"    "LOC100133019" "LRRC32"       "AHNAK"
##  [41] "LYL1"          "NOTCH1"       "APLNR"        "HS.379253"    "PTRF"
##  [46] "RPPH1"         "C1ORF110"     "INPPL1"       "LOC649841"    "DLC1"
##  [51] "ITGB5"         "RASL12"       "AKR1C3"       "FOXC1"        "LOC100132532"
##  [56] "RAB13"         "WSCD1"        "LOC643287"    "ACACB"        "CUEDC1"
##  [61] "INPP5D"        "LOC100129681" "LOC642031"    "TNFRSF1B"     "CFLAR"
##  [66] "FXYD5"         "LOC100131541" "PDGFRB"       "RAXL1"        "ANGPT2"
##  [71] "LOC100131277"  "SLC15A3"      "FLNC"         "LOC648921"    "NACC2"
##  [76] "RUNDC2C"       "UBXN2A"       "VIL2"         "ZNF786"       "DCLRE1C"
##  [81] "FLJ46906"      "HS.143018"    "LOC727948"    "HS.193767"    "LRCH4"
##  [86] "MT1H"          "SCRIB"        "KIF1C"        "LASS1"        "LOC100130598"
##  [91] "NDE1"          "RN7SK"        "ZNF621"       "C9ORF130"     "CAPS"
##  [96] "EML3"          "HS.576072"    "KCNJ10"       "LOC100131096" "LOC653158"
## [101] "RGS1"          "LOC649362"    "TTR"          "CD44"         "C10ORF10"
## [106] "EMP1"          "ITPRIP"       "DDIT4"        "S100A8"       "SERPINA3"
## [111] "ADAMTS1"       "CCL2"         "ZFP36"        "GFAP"         "HLA-DRA"
## [116] "GPR4"          "SRGN"         "CD14"         "CDKN1A"       "FOS"
## [121] "HLA-DMB"       "KIAA1881"     "HLA-DMA"      "MS4A6A"       "MT2A"
## [126] "CEBPD"         "TGFBI"        "TMC6"         "ID3"          "ITGB2"
```

```
## [131] "LCP1"         "RNU1G2"       "S1PR3"        "GADD45G"      "NUPR1"
## [136] "ANLN"         "GEM"          "CD163"        "LOC387763"    "ZFP36L1"
## [141] "CTGF"         "IL8"          "PDK4"         "PLIN2"        "SLC16A9"
## [146] "CSF1R"        "IL17RB"       "LOC100133692" "SCIN"         "TAGLN"
## [151] "TMEM106A"     "ADM"          "EDN1"         "GADD45B"      "HSPA1A"
## [156] "MT1M"         "APOLD1"       "C7"           "IGFBP5"       "GJA4"
## [161] "LEP"          "PLXDC2"
```

The unique bottom genes are:

```
bottomBoth
```

```
##   [1] "SYT1"         "CHGB"         "PCSK1"        "VGF"          "MAL2"
##   [6] "RGS4"         "GABRA1"       "NPTX2"        "SST"          "STAT4"
##  [11] "C1ORF173"     "CBLN4"        "DYNC1I1"      "STXBP1"       "GNG2"
##  [16] "RGS7"         "TSPAN13"      "EFCBP1"       "NELL2"        "HPRT1"
##  [21] "TAGLN3"       "DCLK1"        "ST6GALNAC5"   "GLRB"         "BEX5"
##  [26] "DIRAS2"       "SYP"          "KIAA1107"     "PAK1"         "PTPRN"
##  [31] "SERPINI1"     "ZCCHC12"      "NELL1"        "DACH2"        "ELMOD1"
##  [36] "NECAB1"       "NEFM"         "PARM1"        "RTN1"         "VAMP2"
##  [41] "ENC1"         "TMEM16C"      "CREG2"        "STX1A"        "SVOP"
##  [46] "CAP2"         "SCG2"         "UCHL1"        "CALY"         "KIAA0748"
##  [51] "NAP1L3"       "RIMBP2"       "YWHAG"        "GABRG2"       "LOC100128403"
##  [56] "NAP1L2"       "NAP1L5"       "STMN2"        "ADCYAP1"      "SCN3B"
##  [61] "GAD1"         "HS.390250"    "INA"          "SCN2B"        "GPRASP2"
##  [66] "ITFG1"        "SNX10"        "SV2B"         "ATP6V1G2"     "GABBR2"
##  [71] "GAD2"         "HPCA"         "NUDT11"       "LPPR4"        "TMEM155"
##  [76] "CAMK1G"       "EPHA4"        "GABRA5"       "MYT1L"        "HS.553187"
##  [81] "CDH13"        "VSNL1"        "XK"           "CKMT1A"       "HS.31961"
##  [86] "PCSK1N"       "PRKCG"        "SYT13"        "NPY"          "PRKCB"
##  [91] "RASL11B"      "SYN2"         "CADPS"        "TSPYL1"       "C12ORF53"
##  [96] "HSPB3"        "MKL2"         "PPP3R1"       "SNCA"         "C2ORF80"
## [101] "ANO3"         "LOC387856"    "SLC30A3"      "CRYM"         "C11ORF87"
## [106] "RPH3A"        "VIP"          "OLFM3"        "COPG2IT1"     "SLC39A10"
## [111] "SLITRK4"      "CKMT1B"       "CYP26B1"      "CPNE4"        "MFF"
## [116] "TUBB2A"       "ELAVL4"       "LRFN5"        "NCALD"        "SLC6A17"
## [121] "YWHAE"        "CCKBR"        "FGF12"        "G3BP2"        "HOPX"
## [126] "NMNAT2"       "ZNF365"       "C20ORF103"
```

The top genes in common are those genes most expressed in fold change in females AND males who have Alzheimer:

```
A <- as.data.frame(a)
B <- as.data.frame(b)

topBoth <- merge(A,B,by.x='a', by.y='b')
topBoth$a
```

```
##  [1] ACACB     AEBP1     AHNAK     APLNR     C15ORF52  CALD1     CAPS
##  [8] CFLAR     CHST6     DDIT4L    FAM65C    FCGBP     FOXC1     GPER
## [15] GSDMD     HEY2      HS.37648  ITGB5     ITPKB     KIF1C     LOC643287
## [22] LRRC32    MYOT      PDGFRB    PLXNB1    PTH1R     RAB13     RASL12
## [29] RN7SK     RUNDC2C   SIPA1     SLC5A3    SLC6A12   SLC7A2    SYTL4
```

```
## [36] TEAD2     TNFRSF1B  VCAN
## 100 Levels: ACACB AEBP1 AHNAK AKR1C3 ANGPT2 APLNR C15ORF52 C1ORF110 ... ZNF786
```

The bottom genes in common are the least expressed genes in females AND males who have Alzheimer:

```
C <- as.data.frame(c)
D <- as.data.frame(d)

bottomBoth <- merge(C,D, by.x='c', by.y='d')
bottomBoth$c
```

```
##  [1] ADCYAP1      BEX5         C12ORF53     C1ORF173     C2ORF80
##  [6] CADPS        CALY         CAP2         CBLN4        CHGB
## [11] CREG2        DACH2        DCLK1        DIRAS2       DYNC1I1
## [16] EFCBP1       ELMOD1       ENC1         EPHA4        GABBR2
## [21] GABRA1       GABRG2       GAD1         GAD2         GLRB
## [26] GPRASP2      HPRT1        HS.390250    HS.553187    HSPB3
## [31] INA          KIAA0748     KIAA1107     LOC100128403 MAL2
## [36] NAP1L3       NAP1L5       NEFM         NELL1        NELL2
## [41] NPTX2        PAK1         PARM1        PCSK1        PRKCG
## [46] PTPRN        RGS4         RGS7         RIMBP2       RTN1
## [51] SCG2         SCN2B        SERPINI1     SNX10        SST
## [56] ST6GALNAC5   STAT4        STMN2        STX1A        STXBP1
## [61] SV2B         SVOP         SYP          SYT1         SYT13
## [66] TAGLN3       TMEM155      TMEM16C      TSPAN13      VAMP2
## [71] VGF          ZCCHC12
## 100 Levels: ADCYAP1 ATP6V1G2 BEX5 C12ORF53 C1ORF173 C2ORF80 CADPS ... ZCCHC12
```

Lets look at three top expressed and three least expressed genes in common for females and males:

```
b3 <- as.character(bottomBoth$c[1:3])
t3 <- as.character(topBoth$a[1:3])

mix <- c(b3,t3)
mix
```

```
## [1] "ADCYAP1"  "BEX5"     "C12ORF53" "ACACB"    "AEBP1"    "AHNAK"
```

```
Mix <- as.data.frame(mix)
mBoth <- Both
mBoth$gene <- row.names(mBoth)
MixBoth <- merge(Mix, mBoth, by.x='mix', by.y='gene')

toPlot <- MixBoth[,c(1,6,7)]
colnames(toPlot)[1] <- 'gene'
toPlot
```

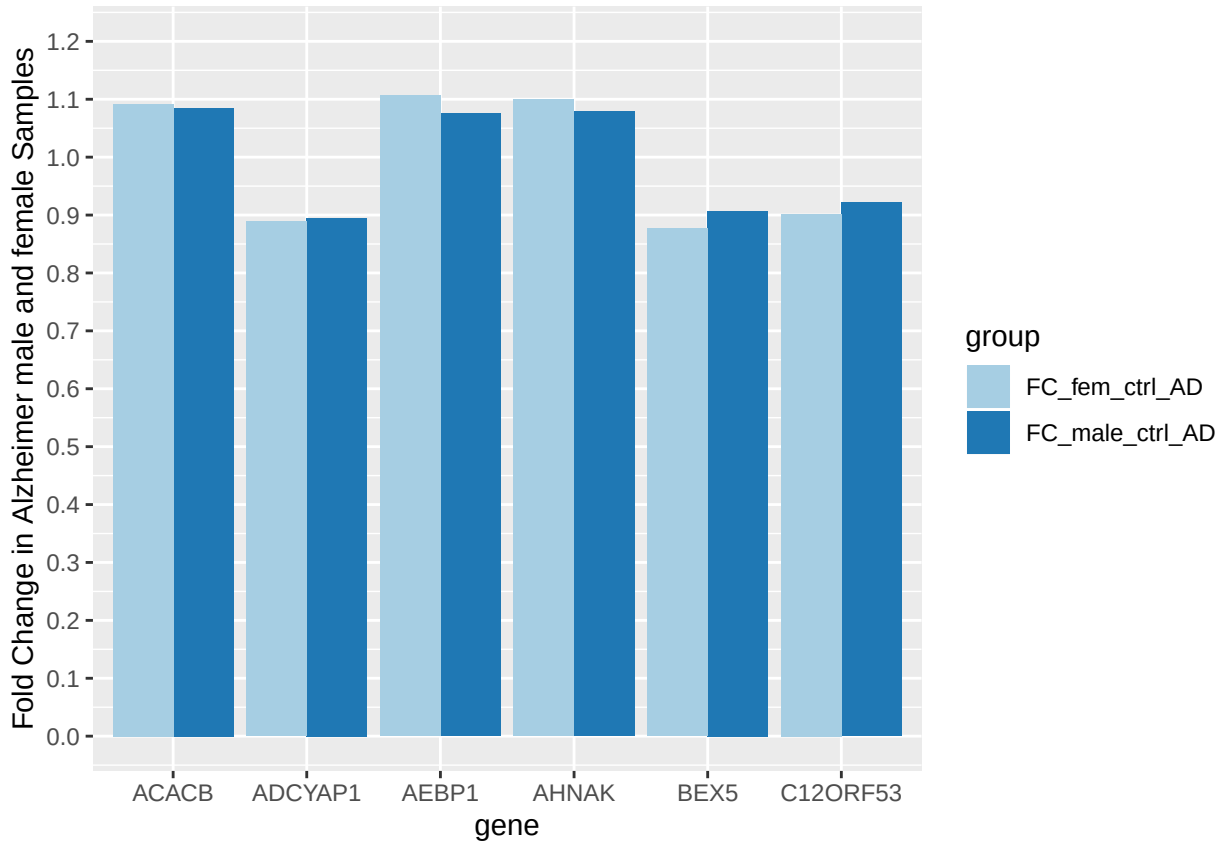
```
##       gene FC_fem_ctrl_AD FC_male_ctrl_AD
## 1    ACACB          1.092           1.085
## 2  ADCYAP1          0.889           0.895
## 3    AEBP1          1.107           1.075
## 4    AHNAK          1.099           1.079
## 5     BEX5          0.877           0.907
## 6 C12ORF53          0.902           0.922
```

```
library(ggplot2)
library(tidyr)
```

```
to_plot <- gather(toPlot, 'group','foldChange',2:3)
to_plot
```

```
##         gene           group foldChange
## 1      ACACB  FC_fem_ctrl_AD      1.092
## 2    ADCYAP1  FC_fem_ctrl_AD      0.889
## 3      AEBP1  FC_fem_ctrl_AD      1.107
## 4      AHNAK  FC_fem_ctrl_AD      1.099
## 5       BEX5  FC_fem_ctrl_AD      0.877
## 6   C12ORF53  FC_fem_ctrl_AD      0.902
## 7      ACACB FC_male_ctrl_AD      1.085
## 8    ADCYAP1 FC_male_ctrl_AD      0.895
## 9      AEBP1 FC_male_ctrl_AD      1.075
## 10     AHNAK FC_male_ctrl_AD      1.079
## 11      BEX5 FC_male_ctrl_AD      0.907
## 12 C12ORF53 FC_male_ctrl_AD      0.922
```

```
ggplot(data = to_plot, aes(x=gene, y=foldChange, fill=group)) +
  geom_bar(stat='identity', position=position_dodge())+
  scale_y_continuous(breaks = seq(0, 1.2, by=.1), limits=c(0,1.2))+
  scale_fill_brewer(palette='Paired') +
  ylab('Fold Change in Alzheimer male and female Samples')
```



Some other data sets on diseases would be interesting to compare to this data on Alzheimer patients. The other data sets to compare this blood tissue type of microarray gene expression profiles are the: hemochromatosis (iron toxicity) from https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE121620, epigallocatechin EGCG (green tea extract) use by overweight females in 40s found at https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE74560, myocardial infarction MI (heart disease) in Russian males in 40s found at https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE141512, antibiotic treatment in flu vaccinated patients of males and females between 18-45 years of age found at https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE120717 and https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE120719, and an immunization blood sample data set that only has healthy donors blood six days after receiving the tetanis-diphtheria toxoids and acellular pertussis found at https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE59697.

Those data sets are needed for their stats with Fold Change values for each study respectively, except the tetanis shot because it is only healthy donor samples analyzing the tetanis-diptheria toxoids as an antigen to test the B lymphocytes route in the plasma cells.

The females in the overweight study, the females in the flu study, and the females in the iron toxicity study could be cross compared to the females in this study on Alzheimer female patients. The males in the heart disease study, iron toxicity study, and flu study could be compared to the males in this Alzheimer study. And both genders from those studies could also be compared to both genders in this study.

The plan is to get the genes these studies all have in common and compare between the genders on fold change stats of those genes. That being iron toxicity fold change, and flu vaccinated fold change compared to added antibiotics (not compared to healthy non vaccinated patients) for comparison with Alzheimer patients. Overweight females using EGCG for weight loss is exclusive to the female comparisons, and the heart disease study was exclusive to male patients.

This study's data on fold change, means, and sample values is the **both.csv** file. The flu study had days 0,3,7, and 21 comparisons and both genders in the **FoldChange_All.csv** file for that study. The iron toxicity fold change stats is in the **all-fc-grops.csv** file for the hemochromatosis study on both genders. The overweight females using EGCG to diet with the included fold change values for those using EGCG or EGCG+vitamin C+fish oil is in the **foldChange_EGCG.csv** file. And the males who have heart disease of type MI is in the file **foldChange_MI_males.csv**. The tetanis immunization samples don't have the fold change because they are all healthy donors with no age data or gender data and taken 6 days after the tetanis shot, but it is useful to compare genes with healthy females and males in the healthy and control groups **tetanisImmunizationBlood.csv** is that file.

Lets read in those files with their respective and appropriately described names.

```
Alzheimer <- read.csv('both.csv', sep=',', header=T, na.strings=c('',' '))
Heart_Disease_Males <- read.csv('foldChange_MI_males.csv', sep=',',
                                header=T, na.strings=c('',' '))
TetanisImmunity <- read.csv('tetanisImmunizationBlood.csv', sep=',',
                            header=T, na.strings=c('',' '))
Overweight_Females_EGCG <- read.csv('foldChange_EGCG.csv', sep=',',
                                    header=T, na.strings=c('',' '))
flu_Vaccinated <- read.csv('FoldChange_All.csv', sep=',', header=T,
                           na.strings=c('',' '))
iron_toxicity <- read.csv('all-fc-grops.csv', sep=',', header=T,
                          na.strings=c('', ' '))
```

Look at the column names and select the ones needed or that have fold change values to cross compare, or to compare means across samples as with the tetanis data set.

The Alzheimer column names are:

```r
colnames(Alzheimer)
```

```
##  [1] "X"                    "Females_AD1_Mean"     "Females_control1_Mean"
##  [4] "males_AD1_Mean"       "males_control1_Mean"  "FC_fem_ctrl_AD"
##  [7] "FC_male_ctrl_AD"      "GSM2973262"           "GSM2973263"
## [10] "GSM2973264"           "GSM2973265"           "GSM2973266"
## [13] "GSM2973267"           "GSM2973268"           "GSM2973269"
## [16] "GSM2973270"           "GSM2973271"           "GSM2973272"
## [19] "GSM2973273"           "GSM2973274"           "GSM2973275"
## [22] "GSM2973276"           "GSM2973277"           "GSM2973278"
## [25] "GSM2973279"           "GSM2973280"           "GSM2973281"
## [28] "GSM2973282"           "GSM2973283"           "GSM2973284"
## [31] "GSM2973285"           "GSM2973286"           "GSM2973287"
## [34] "GSM2973288"           "GSM2973289"           "GSM2973290"
## [37] "GSM2973291"           "GSM2973292"           "GSM2973293"
## [40] "GSM2973294"           "GSM2973295"           "GSM2973296"
## [43] "GSM2973297"           "GSM2973298"           "GSM2973299"
## [46] "GSM2973300"           "GSM2973301"           "GSM2973302"
## [49] "GSM2973303"           "GSM2973304"           "GSM2973305"
## [52] "GSM2973306"           "GSM2973307"           "GSM2973308"
## [55] "GSM2973309"           "GSM2973310"           "GSM2973311"
## [58] "GSM2973312"           "GSM2973313"           "GSM2973314"
## [61] "GSM2973315"           "GSM2973316"           "GSM2973317"
## [64] "GSM2973318"           "GSM2973319"           "GSM2973320"
## [67] "GSM2973321"           "GSM2973322"           "GSM2973323"
## [70] "GSM2973324"           "GSM2973325"           "GSM2973326"
## [73] "GSM2973327"           "GSM2973328"           "GSM2973329"
## [76] "GSM2973330"           "GSM2973331"           "GSM2973332"
## [79] "GSM2973333"           "GSM2973334"           "GSM2973335"
## [82] "GSM2973336"           "GSM2973337"           "GSM2973338"
## [85] "GSM2973339"
```

The heart disease column names are:

```r
colnames(Heart_Disease_Males)
```

```
##  [1] "X"                          "Symbol"
##  [3] "FC_MI_males"                "HealthyMale_Means"
##  [5] "MI_Male_Means"              "healthy_Males_GSM4205364"
##  [7] "healthy_Males_GSM4205363"   "healthy_Males_GSM4205362"
##  [9] "healthy_Males_GSM4205361"   "healthy_Males_GSM4205360"
## [11] "healthy_Males_GSM4205359"   "MI_Males_GSM4205358"
## [13] "MI_Males_GSM4205357"        "MI_Males_GSM4205356"
## [15] "MI_Males_GSM4205355"        "MI_Males_GSM4205354"
## [17] "MI_Males_GSM4205353"
```

The tetanis immunization column names are:

```r
colnames(TetanisImmunity)
```

```
## [1] "X"             "GENE_SYMBOL"   "GSM1443061"    "GSM1443062"
## [5] "GSM1443063"    "GSM1443064"    "GSM1443065"    "GSM1443066"
## [9] "Tetanis_Means"
```

The EGCG overweight females column names are:

```
colnames(Overweight_Females_EGCG)
```

```
##  [1] "X"                          "FC_egcg_quer"
##  [3] "FC_egcg"                    "DE_EGCG"
##  [5] "DE_Quercentin"              "Pre_Means"
##  [7] "Post_EGCG_Means"            "Post_EGCG_Quercentin_Means"
##  [9] "pre_GSM1923000"             "pre_GSM1923004"
## [11] "pre_GSM1923010"             "pre_GSM1923012"
## [13] "pre_GSM1923007"             "pre_GSM1923020"
## [15] "pre_GSM192998"              "pre_GSM1922995"
## [17] "pre_GSM1923002"             "pre_GSM1923008"
## [19] "pre_GSM1923015"             "pre_GSM1923018"
## [21] "pre_GSM1923022"             "pre_GSM1923017"
## [23] "post_EG_GSM1923001"         "post_EG_GSM1923005"
## [25] "post_EG_GSM1923011"         "post_EG_GSM1923013"
## [27] "post_EG_GSM1923021"         "post_EG_GSM1923006"
## [29] "post_EG_GSM1923014"         "post_EQ_GSM192996"
## [31] "post_EQ_GSM1923003"         "post_EQ_GSM1923009"
## [33] "post_EQ_GSM1923016"         "post_EQ_GSM1923019"
## [35] "post_EQ_GSM1923023"         "post_EQ_GSM192997"
```

The flu vaccinated with antibiotics treatment or not column names are:

```
colnames(flu_Vaccinated)
```

```
##  [1] "Gene"                                "FC_t1"
##  [3] "FC_t3"                               "FC_t7"
##  [5] "FC_t21"                              "FC_nt1"
##  [7] "FC_nt3"                              "FC_nt7"
##  [9] "FC_nt21"                             "FCB_1"
## [11] "FCB_3"                               "FCB_7"
## [13] "FCB_21"                              "T0_Mean"
## [15] "T1_Mean"                             "T3_Mean"
## [17] "T7_Mean"                             "T21_Mean"
## [19] "NT0_Mean"                            "NT1_Mean"
## [21] "NT3_Mean"                            "NT7_Mean"
## [23] "NT21_Mean"                           "GSM3409106_29_day_0"
## [25] "GSM3409107_29_day_1"                 "GSM3409108_29_day_3"
## [27] "GSM3409004_29_day_7"                 "GSM3409105_29_day_21_screening"
## [29] "GSM3409006_30._day_0"                "GSM3409007_30_day_1"
## [31] "GSM3409008_30_day_3"                 "GSM3409009_30_day_7"
## [33] "GSM3409005_30_day_21_screening"      "GSM3409013_05_.day_0"
## [35] "GSM3409014_05_day_1"                 "GSM3409015_05_day_3"
## [37] "GSM3409016_05_day_7"                 "GSM3409012_05_day_21_screening"
## [39] "GSM3409161_33_day_0_no"              "GSM3409162_33_day_1_no"
## [41] "GSM3409163_33_day_3_no"              "GSM3409111_33._day_7_no"
## [43] "GSM3409160_33_day_21_screening_no"   "GSM3409124_36_day_0_no"
## [45] "GSM3409125_36_day_1_no"              "GSM3409126_36_day_3_no"
## [47] "GSM3409127_36_day_7_no"              "GSM3409123_36_day_21_screening_no"
## [49] "GSM3409135_38_day_0_no"              "GSM3409136_38_day_1_no"
## [51] "GSM3409137_38_day_3_no"              "GSM3409138_38_day_7_no"
## [53] "GSM3409134_38_day_21_screening_no"
```

The iron toxicity column names are:

```
colnames(iron_toxicity)
```

```
##  [1] "X"                  "G1M_Mean"           "G2M_Mean"
##  [4] "G3M_Mean"           "G1F_Mean"           "G2F_Mean"
##  [7] "G3F_Mean"           "healthyFemale_Mean" "healthyMale_Mean"
## [10] "hemoFemale_Mean"    "hemoMale_Mean"      "FC_1m"
## [13] "FC_2m"              "FC_3m"              "FC_1F"
## [16] "FC_2F"              "FC_3F"              "FC_malesOverall"
## [19] "FC_femalesOverall"  "GSM3440208"         "GSM3440209"
## [22] "GSM3440210"         "GSM3440211"         "GSM3440212"
## [25] "GSM3440213"         "GSM3440214"         "GSM3440215"
## [28] "GSM3440216"         "GSM3440217"         "GSM3440218"
## [31] "GSM3440219"         "GSM3440220"         "GSM3440221"
## [34] "GSM3440222"         "GSM3440223"         "GSM3440224"
## [37] "GSM3440225"         "GSM3440226"         "GSM3440227"
## [40] "GSM3440228"         "GSM3440229"         "GSM3440230"
## [43] "GSM3440231"
```