Homework 5

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Exercise 1

a)

```
#read in the dataset
genes <- data.frame(read.table(file = "http://maitra.public.iastate.edu/stat579/datasets/diurnaldata.csv", sep = ",", header = TRUE))

dim(genes)
```

```
## [1] 22810    23
```

```
names(genes) <- c("Probe", "0h", "1h", "2h", "4h", "8h", "12h", "13h","14h", "16h", "20h", "24h",
                  "0h.", "1h.", "2h.", "4h.", "8h.", "12h.", "13h.", "14h.", "16h.", "20h.", "24h.")
```

b)

```
#Create an array
trial1 <- as.matrix(cbind(genes[,2:12]), nrow = 22810, ncol = 11, byrow = T)
trial2 <- as.matrix(cbind(genes[,13:23]),nrow = 22810, ncol = 11, byrow = T)
genearray <- array( data = c(trial1, trial2), dim = c(22810, 11, 2))

#means for each probe across the 2 measurements
means <- as.matrix(x = apply(genearray, MARGIN = c(1,2), FUN = mean), nrow = 22810)
dim(means)
```

```
## [1] 22810    11
```

c)

i)

```
#calculate mean of means
means1 <- apply(means, MARGIN = 1, FUN = mean)
totals <- data.frame(genes$Probe, as.numeric(means1)); names(totals) <- c("gene",
"average")
#check to see if we calculated correctly
head(totals)
```

```
##                    gene   average
## 1  AFFX-r2-P1-cre-5_at 3069.8545
## 2  AFFX-r2-P1-cre-3_at 3645.4227
## 3 AFFX-r2-Ec-bioD-5_at  723.3045
## 4 AFFX-r2-Ec-bioD-3_at  829.3182
## 5 AFFX-r2-Ec-bioC-5_at  184.3591
## 6 AFFX-r2-Ec-bioC-3_at  223.9227
```

ii)

```
#replicated matrix of means of means
repped <- matrix(data = means1, nrow = 22810, ncol = 11)
#remove mean effect from averages calculated in part (b)
meaneffect <- means - repped
```

iii)

```
##iii
#standard deviation of each row
stdevs <- apply(X = means, MARGIN = 1, FUN = sd)
#scaled measurements are the standardized genes
ssss <- matrix(data = stdevs, nrow = 22810, ncol = 11)
scaled <- meaneffect/ ssss
```

d)

```
#read in data
measures <- read.table(file = "http://maitra.public.iastate.edu/stat579/datasets/mi
cromeans.dat", sep = "", header = F)
#standardize as above
meansm <- apply(measures, MARGIN = 1, FUN = mean)
#replicated matrix of means of means
reppedm <- matrix(data = meansm, nrow = 20, ncol = 11)
#remove mean effect from averages calculated in part (b)
meaneffectm <- measures - reppedm
#standard deviation of each row
stdevsm <- apply(X = measures, MARGIN = 1, FUN = sd)
#scaled measurements are the standardized genes
scaledm <- as.matrix(meaneffectm/ matrix(data = stdevsm, nrow = 20, ncol = 11), nr
ow = 20, ncol = 11)
```

e)

,

```
#set up arrays of replicated data sets, check dimensions
arrayg <- array(data = scaled, dim = c(22810, 11,20))
arraym <- aperm(array(data = c(scaledm), dim = c(20,11,22810)), perm = c(3,2,1))
dim(arraym); dim(arrayg)
```

```
## [1] 22810    11    20
```

```
## [1] 22810    11    20
```

```
#combine them into a 4-D array
arrayc <- array(data = c(arrayg, arraym), dim = c(22810,11,20,2))
#calculate euclidean distance for each point
#first, a function since dist() is not good
euclid <- function(x){
  eu <- (x[,1]-x[,2])^2
  sum <- sum(eu)
  return(sqrt(sum))
}

#apply the function to each row/3rd dimension to get the appropriate result
edist <- apply(arrayc, MARGIN = c(1,3), FUN = euclid)
dim(edist)
```

```
## [1] 22810    20
```

```
head(edist)
```

```
##          [,1]     [,2]     [,3]     [,4]     [,5]     [,6]     [,7]
## [1,] 5.417885 4.261081 5.207925 3.125414 4.914939 6.096483 4.562500
## [2,] 5.516634 4.434301 5.165336 3.071993 5.058892 6.162220 4.510031
## [3,] 5.792417 4.489249 5.056531 2.773029 5.173668 6.135268 4.342259
## [4,] 5.421806 4.921538 4.593702 2.728476 5.642030 6.192825 3.824113
## [5,] 5.125586 4.153161 5.022716 2.747196 5.116426 6.081829 4.196495
## [6,] 5.490807 4.494354 4.921923 2.645045 5.374061 6.174676 4.142269
##          [,8]     [,9]    [,10]    [,11]    [,12]    [,13]    [,14]
## [1,] 5.011322 5.401339 3.423868 2.711460 2.586746 3.553620 4.287767
## [2,] 5.124380 5.389201 3.452634 2.376768 2.455553 3.376037 4.145981
## [3,] 5.223888 5.332790 3.712574 1.900702 2.409075 3.417172 4.349113
## [4,] 5.063302 5.601996 4.238931 2.104583 3.089493 3.674684 4.364259
## [5,] 4.637203 5.614488 3.804447 2.991776 3.055701 3.972082 4.680032
## [6,] 4.985243 5.572431 3.840632 2.122786 2.716344 3.600823 4.331514
##         [,15]    [,16]    [,17]    [,18]    [,19]    [,20]
## [1,] 3.455173 4.443603 3.807057 4.268661 5.032314 5.147629
## [2,] 3.272239 4.622061 3.531036 4.082220 5.080642 5.343634
## [3,] 3.370305 5.114404 3.007830 3.613390 5.160581 5.622553
## [4,] 2.427275 5.268009 2.870164 3.203122 4.676630 5.686295
## [5,] 3.187997 4.404006 4.082567 4.212892 4.607245 4.952873
## [6,] 2.795264 4.944761 3.358742 3.655613 4.871261 5.486299
```

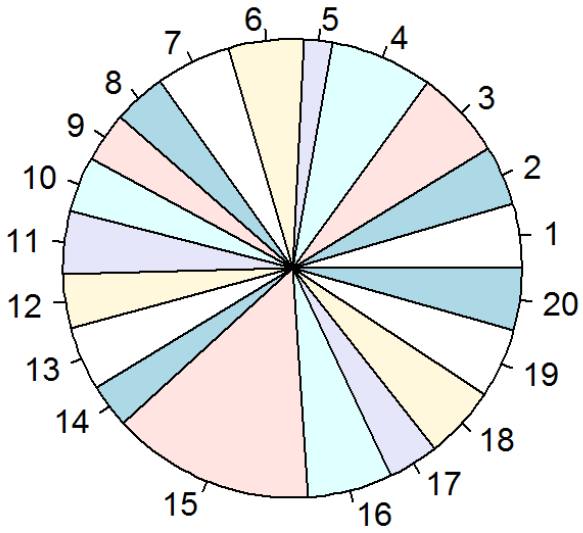
```r
#find the index of the minimum distance in each row
min.idx <- apply(edist, MARGIN = 1, FUN=which.min)
head(min.idx)
```

```
## [1] 12 11 11 11  4 11
```

```r
#frequency table
table(min.idx)
```

```
## min.idx
##    1    2    3    4    5    6    7    8    9   10   11   12   13   14   15
## 1043  959 1424 1641  449 1213 1221  838  807  891 1008  868 1033  709 3246
##   16   17   18   19   20
## 1361  823 1168 1109  999
```

```r
#pie chart of the frequencies
pie(table(min.idx), labels = c(as.character(1:20)))
```



Exercise 2

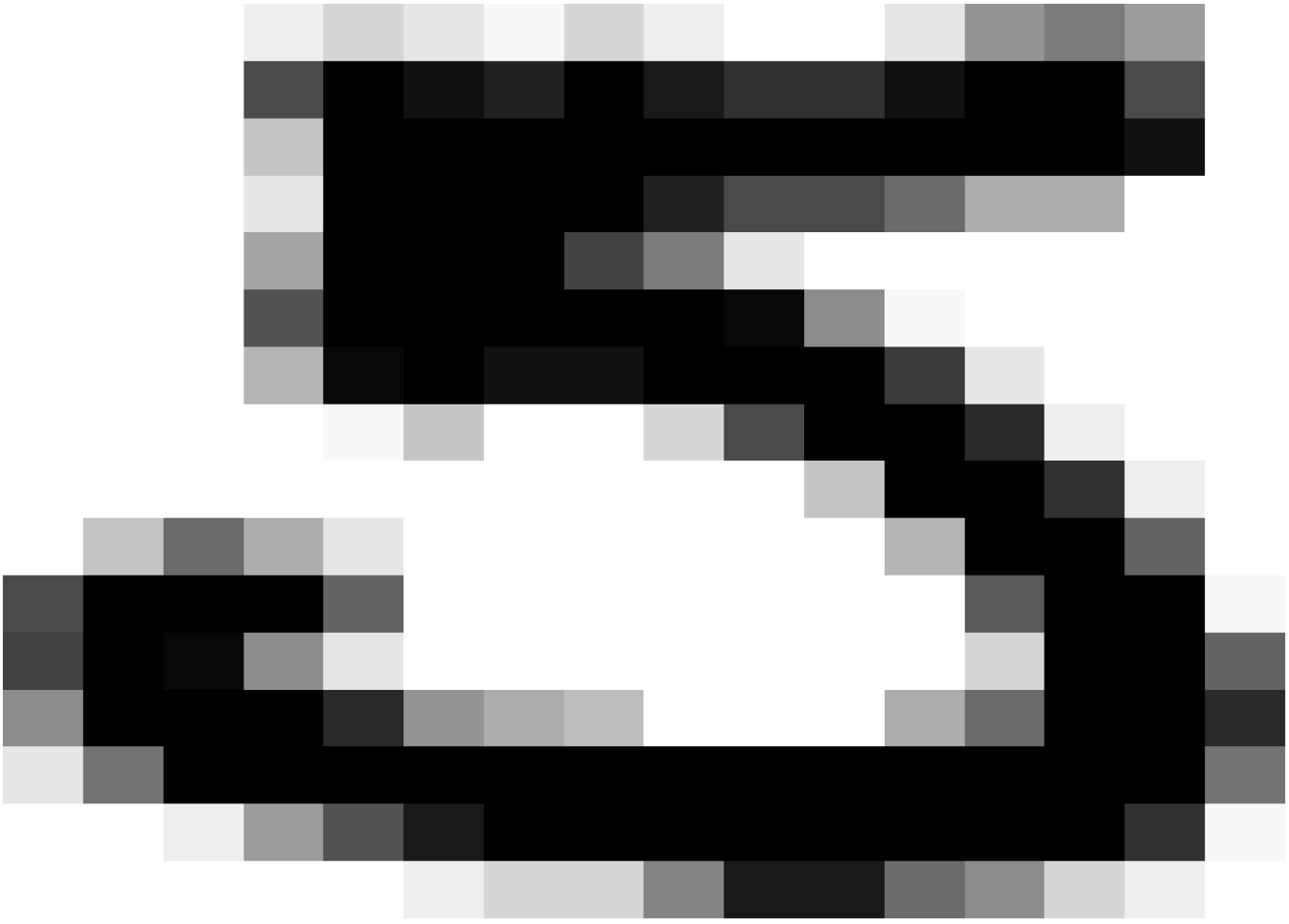
a)

```
#read in the data
ziptrain1 <- as.matrix(read.table(file = "ziptrain.dat", header = F, sep = ""))
#store as an appropriate array
ziptrain2 <- array(data = t(ziptrain1), dim = c(16,16,2000))
```

b)

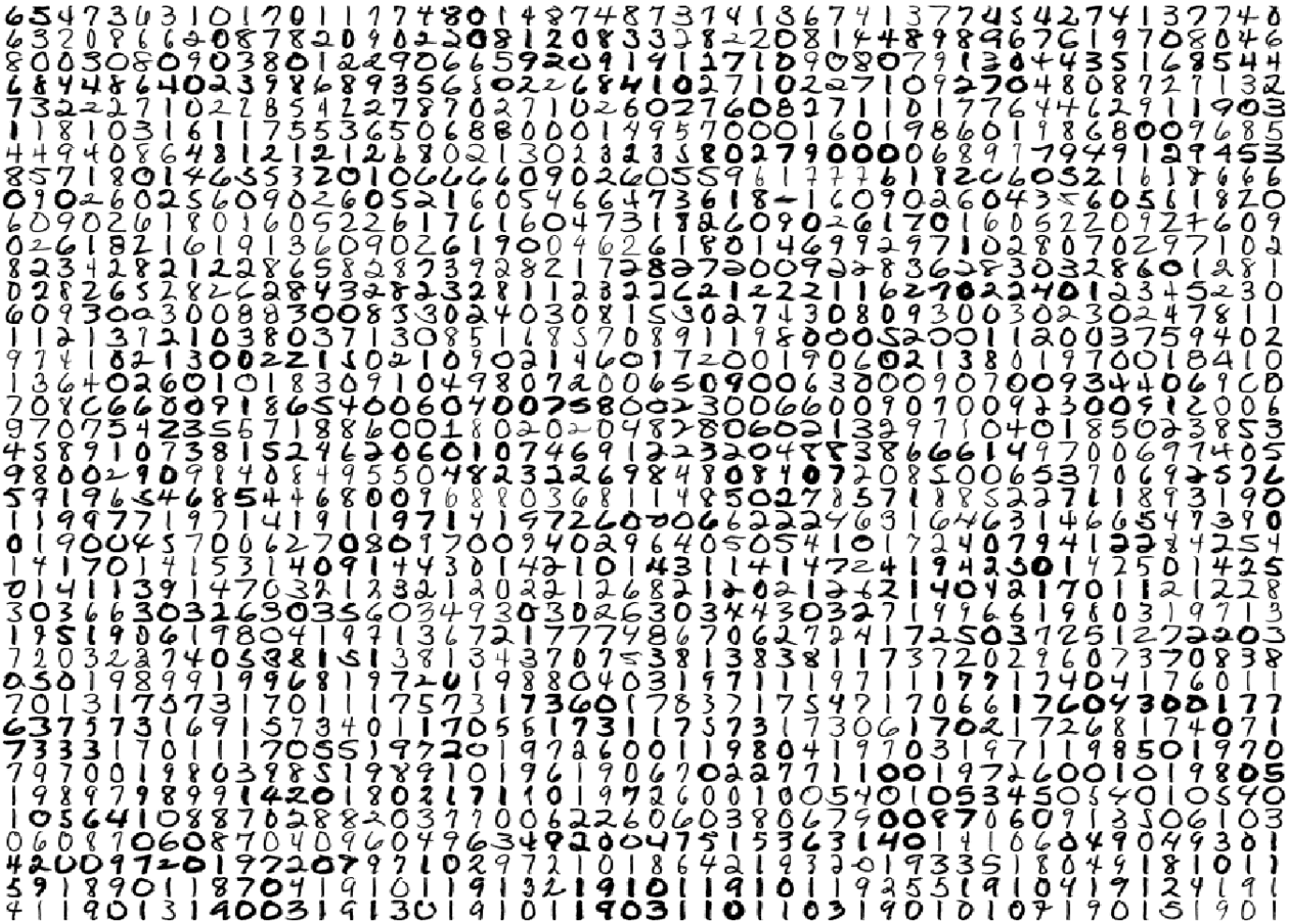
i)

```
#resize plot area
par(mar = rep(0.05, 4))
#plot the image
image(z=ziptrain2[,16:1,2],col = rev(gray(0:31/31)),axes = F )
```



ii)

```
##ii
#first, resize the plot area
par(mfrow = c(40,50), pin=c(6.5,5.2))

#I use a function to plot all of the images, will be useful for later
pics <- function(q){
  par(mar = rep(0.05, 4))
  pic<- image(z = q[1:16,16:1],col = rev(gray(0:31/31)),axes = F )
}

#apply the function to each 16x16 matrix in the array
apply(ziptrain2, MARGIN = 3, FUN = pics)
```



```
## NULL
```

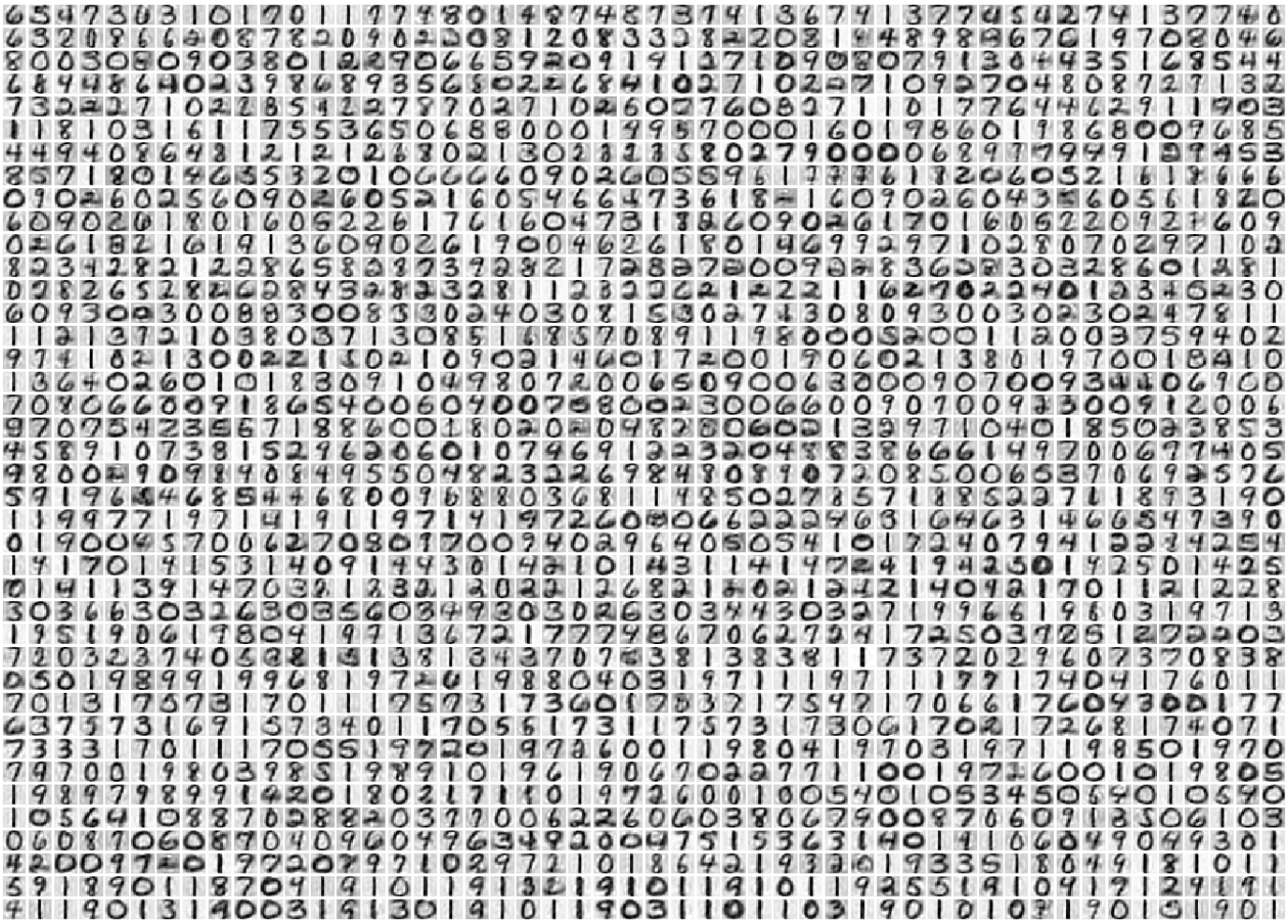
c)

```r
##c#
#Read in the digits index file
digits <- read.table(file = "zipdigit.dat", header = F, sep = "")

#create index matrix of the 10 digits, I made a function to do it with a loop (prob
ably not the easiest)
dig <- 0:9
indexing <- function(v){
  indexmat <- matrix(ncol = 10, nrow= max(table(v)))
  for (y in 0:9){
    indexmat[,y+1] <- c(which(v == y), rep(NA, times = max(table(v) - length(which
(v==y)))))
  }
  return(indexmat)
}
#apply the function to our digits data to get indices
indexes <- indexing(digits)

#Create looping functions for means and standard deviations (again, probably not sm
art to use loops)
means <- function(input, index){
  meanarray <- array(dim = c(16,16,10))
  for (j in 0:9){
    meanarray[,,j+1] <- apply(input[,,c(index[,j+1])], MARGIN = c(1,2), FUN = mean
, na.rm = TRUE)
  }
  return(meanarray)
}

stds <- function(input, index){
  stdarray <- array(dim = c(16,16,10))
  for (j in 0:9){
    stdarray[,,j+1] <- apply(input[,,c(index[,j+1])], MARGIN = c(1,2), FUN = sd, n
a.rm = TRUE)
  }
  return(stdarray)
}

#apply the function to the digits
digmeans <- means(ziptrain2, indexes)
stdarray <- stds(ziptrain2, indexes)

#plot the stds images (should be 1 for each digit). Problem did not ask for mean im
ages so I didn't plot them
par(mfrow = c(3,4))
apply(stdarray, MARGIN = 3, FUN = pics)
```

```
## NULL
```

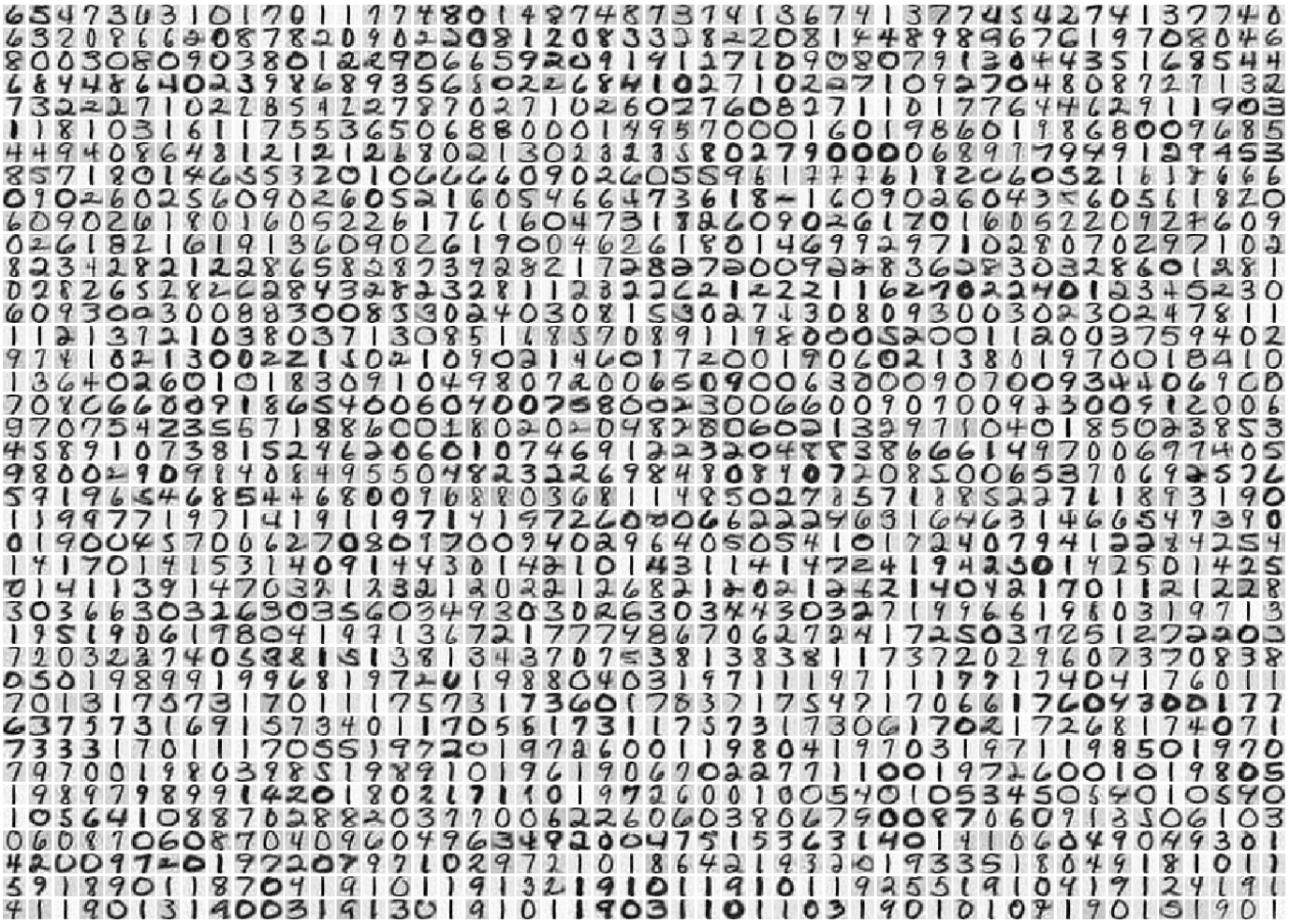
d) **I used a lot of functions for this one.**

```
#First, a function to remove mean effect from each digit based on index
rm.means <- function(input, index, means){
  newarray <- array(dim = c(16,16,2000))
  for (j in 1:2000){
    digindex <- index[j,1]
    newarray[,,j] <- input[,,j] - means[,,digindex+1]
  }
  return(newarray)
}

#apply this function to our image matrices
mean.removed <- rm.means(ziptrain2, digits, digmeans)
records <- matrix(mean.removed, nrow = 2000, ncol = 256, byrow = T)

#Now a function for the svd and diagonalization for k eigenvalues
decompose <- function(input, k){
  decomp <- svd(input)
  Dk <- diag(c(c(decomp$d[1:k]), rep(0, times = 256-k)))
  Y <- decomp$u%*%Dk%*%t(decomp$v)
  return(Y)
}
#Then, a function to add back the mean effect
addback <- function(original, index, means){
  newarray1 <- array(dim = c(16,16,2000))
  z<- array(data = t(original), dim = c(16,16,2000))
  for (j in 1:2000){
    digindex <- index[j,1]
    newarray1[,,j] <- z[,,j] + means[,,digindex+1]
  }
  return(newarray1)
}

#Now we see what the results look like
#First with k=25 eigenvalues

new25 <- decompose(records, k= 25)
image25 <-addback(new25,digits, digmeans)

par(mfrow = c(40,50), pin=c(6.5,5.2))
apply(image25, MARGIN = 3, FUN = pics)
```



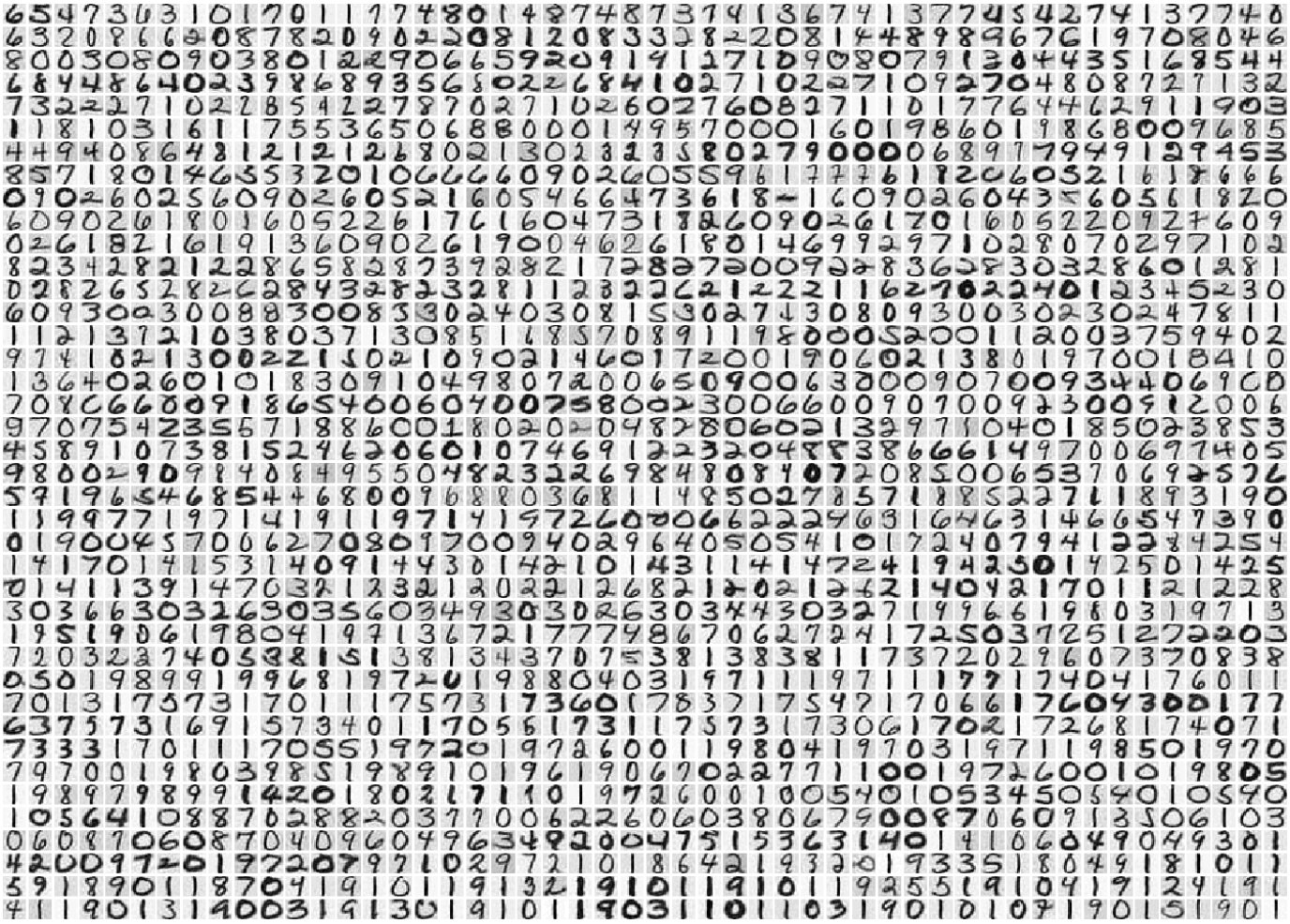
```
## NULL
```

```
#Then with k=50 eigenvalues
new50 <- decompose(records, k=50)
image50 <- addback(new50,digits, digmeans)

par(mfrow = c(40,50), pin=c(6.5,5.2))
apply(image50, MARGIN = 3, FUN = pics)
```



```
## NULL
```

```
#And finally with 75 eigenvalues
new75 <- decompose(records, k=75)
image75 <- addback(new75,digits, digmeans)
par(mfrow = c(40,50), pin=c(6.5,5.2))
apply(image75, MARGIN = 3, FUN = pics)
```



```
## NULL
```

For lower values of k, we remove more of the noise (but also possibly more information), which results in less clear images. This is because only the pixels with the smallest deviations are magnified by the singular value multiplications. As k gets closer to 256, the images get closer to the original. We are basically compressing the images into smaller data storage by choosing small k. Most of the images don't have much deviation so the differences aren't as visible as we would hope. To see the real difference, try k<10 vs k >200.

Exercise 3

a)

```
states <- data.frame(state.x77, state.region)
attach(states)
```

```
## The following object is masked from package:datasets:
##
##     state.region
```

```
#a
#using tapply
percapinc.t <- tapply(Income, INDEX = state.region, FUN = mean)
percapinc.t
```

```
##     Northeast         South North Central          West
##      4570.222      4011.938      4611.083      4702.615
```

```
#using aggregate
percapinc.a <- aggregate(Income, by = list(state.region), FUN = mean)
percapinc.a
```

```
##         Group.1        x
## 1     Northeast 4570.222
## 2         South 4011.938
## 3 North Central 4611.083
## 4          West 4702.615
```

b)

```
#b
#using tapply
maxilliterate.t <- tapply(Illiteracy, INDEX = state.division, FUN=max )
maxilliterate.t
```

```
##        New England    Middle Atlantic     South Atlantic
##                1.3                1.4                2.3
## East South Central West South Central East North Central
##                2.4                2.8                0.9
## West North Central           Mountain            Pacific
##                0.8                2.2                1.9
```

```
#using aggregate
maxilliterate.a <- aggregate(Illiteracy, by = list(state.division), FUN=max)
maxilliterate.a
```

```
##              Group.1   x
## 1        New England 1.3
## 2    Middle Atlantic 1.4
## 3     South Atlantic 2.3
## 4 East South Central 2.4
## 5 West South Central 2.8
## 6 East North Central 0.9
## 7 West North Central 0.8
## 8           Mountain 2.2
## 9            Pacific 1.9
```

c)

```
#c
#The easiest way would be to just use a frequency table
table(state.region)
```

```
## state.region
##     Northeast         South North Central          West
##             9            16            12            13
```

```
#using tapply
regioncount.t <- tapply(state.name, INDEX = state.region, FUN= length )
regioncount.t
```

```
##     Northeast         South North Central          West
##             9            16            12            13
```

```
#using aggregate
regioncount.a <- aggregate(state.name, by = list(state.region), FUN = length)
regioncount.a
```

```
##         Group.1  x
## 1     Northeast  9
## 2         South 16
## 3 North Central 12
## 4          West 13
```

d)

```
#d
#using tapply
names.t <- tapply(state.name, INDEX = state.division, FUN=list)
names.t
```

```
## $`New England`
## [1] "Connecticut"   "Maine"         "Massachusetts" "New Hampshire"
## [5] "Rhode Island"  "Vermont"
##
## $`Middle Atlantic`
## [1] "New Jersey"   "New York"     "Pennsylvania"
##
## $`South Atlantic`
## [1] "Delaware"       "Florida"        "Georgia"        "Maryland"
## [5] "North Carolina" "South Carolina" "Virginia"       "West Virginia"
##
## $`East South Central`
## [1] "Alabama"     "Kentucky"    "Mississippi" "Tennessee"
##
## $`West South Central`
## [1] "Arkansas"  "Louisiana" "Oklahoma"  "Texas"
##
## $`East North Central`
## [1] "Illinois"  "Indiana"   "Michigan"  "Ohio"      "Wisconsin"
##
## $`West North Central`
## [1] "Iowa"         "Kansas"       "Minnesota"    "Missouri"
## [5] "Nebraska"     "North Dakota" "South Dakota"
##
## $Mountain
## [1] "Arizona"    "Colorado"   "Idaho"      "Montana"    "Nevada"
## [6] "New Mexico" "Utah"       "Wyoming"
##
## $Pacific
## [1] "Alaska"     "California" "Hawaii"     "Oregon"     "Washington"
```

```
#using aggregate
names.a <- aggregate(state.name, by=list(state.division), FUN = list)
names.a <- aggregate(formula = state.name~state.division, data=states, FUN = list)
names.a
```

```
##       state.division
## 1        New England
## 2    Middle Atlantic
## 3     South Atlantic
## 4 East South Central
## 5 West South Central
## 6 East North Central
## 7 West North Central
## 8           Mountain
## 9            Pacific
##
state.name
## 1                      Connecticut, Maine, Massachusetts, New Hampshire, Rhode
Island, Vermont
## 2                                                                 New Jersey, New Y
ork, Pennsylvania
## 3 Delaware, Florida, Georgia, Maryland, North Carolina, South Carolina, Virginia
, West Virginia
## 4                                                        Alabama, Kentucky, Missi
ssippi, Tennessee
## 5                                                             Arkansas, Louisiana
, Oklahoma, Texas
## 6                                                   Illinois, Indiana, Michigan,
Ohio, Wisconsin
## 7                      Iowa, Kansas, Minnesota, Missouri, Nebraska, North Dako
ta, South Dakota
## 8                         Arizona, Colorado, Idaho, Montana, Nevada, New Mexic
o, Utah, Wyoming
## 9                                               Alaska, California, Hawaii, Or
egon, Washington
```

e)

```
#e
#first create our variable
state.size <- cut(x = state.x77[, "Population"], breaks = c(0, 2000, 10000, Inf),
                  labels = c("Small", "Medium", "Large"))
#using tapply
pops.t <- tapply(Population, INDEX = list(state.size,state.region), FUN=median)
pops.t
```

```
##        Northeast South North Central    West
## Small      871.5  1189           681   779.5
## Medium    5814.0  3806          4589  2412.5
## Large    14968.0 12237         10966 21198.0
```

```
#using aggregate
pops.a <- aggregate(Population, by=list(state.size, state.region), FUN = median)
pops.a
```

```
##    Group.1       Group.2       x
## 1    Small     Northeast   871.5
## 2   Medium     Northeast  5814.0
## 3    Large     Northeast 14968.0
## 4    Small         South  1189.0
## 5   Medium         South  3806.0
## 6    Large         South 12237.0
## 7    Small North Central   681.0
## 8   Medium North Central  4589.0
## 9    Large North Central 10966.0
## 10   Small          West   779.5
## 11  Medium          West  2412.5
## 12   Large          West 21198.0
```

Exercise 4

a)

```
cars <- data.frame(mtcars)
##a
#using aggregate
mada <- apply(cars, MARGIN = 2, FUN = mad)
mada
```

```
##         mpg         cyl        disp          hp        drat          wt
##   5.4114900   2.9652000 140.4763500  77.0952000   0.7042350   0.7672455
##        qsec          vs          am        gear        carb
##   1.4158830   0.0000000   0.0000000   1.4826000   1.4826000
```

b)

```
##b
#using apply twice and a sweep function to clear it out
#we get the same result as above
meds <- apply(cars, 2, median)
swept <- sweep(cars, 2, meds)
mad2 <- 1.4826 * apply(abs(swept), 2, median)
mad2
```

```
##         mpg         cyl        disp          hp        drat          wt
##   5.4114900   2.9652000 140.4763500  77.0952000   0.7042350   0.7672455
##        qsec          vs          am        gear        carb
##   1.4158830   0.0000000   0.0000000   1.4826000   1.4826000
```