hw7

Hari Rajan

Question 1

```
# load the R.matlab package
library(R.matlab)
```

```
## R.matlab v3.6.2 (2018-09-26) successfully loaded. See ?R.matlab for help.

##
## Attaching package: 'R.matlab'

## The following objects are masked from 'package:base':
##
##     getOption, isOpen
```

```
# read the .mat file and store contents in fmri.p1
fmri.p1 <- readMat("data/data-science-P1.mat")
# unlist each element in the dataset and use rbind to combine into a data fram
fmri <- do.call(rbind, lapply(fmri.p1$data, unlist))
# store the coumn names for the fmri data
colnames <- 1:dim(fmri)[2]
```

```
dim(fmri)
```

```
## [1]   360 21764
```

As indicated above, the diminesions are `360 X 21764` as expected.

```
fmri[172, 2014]
```

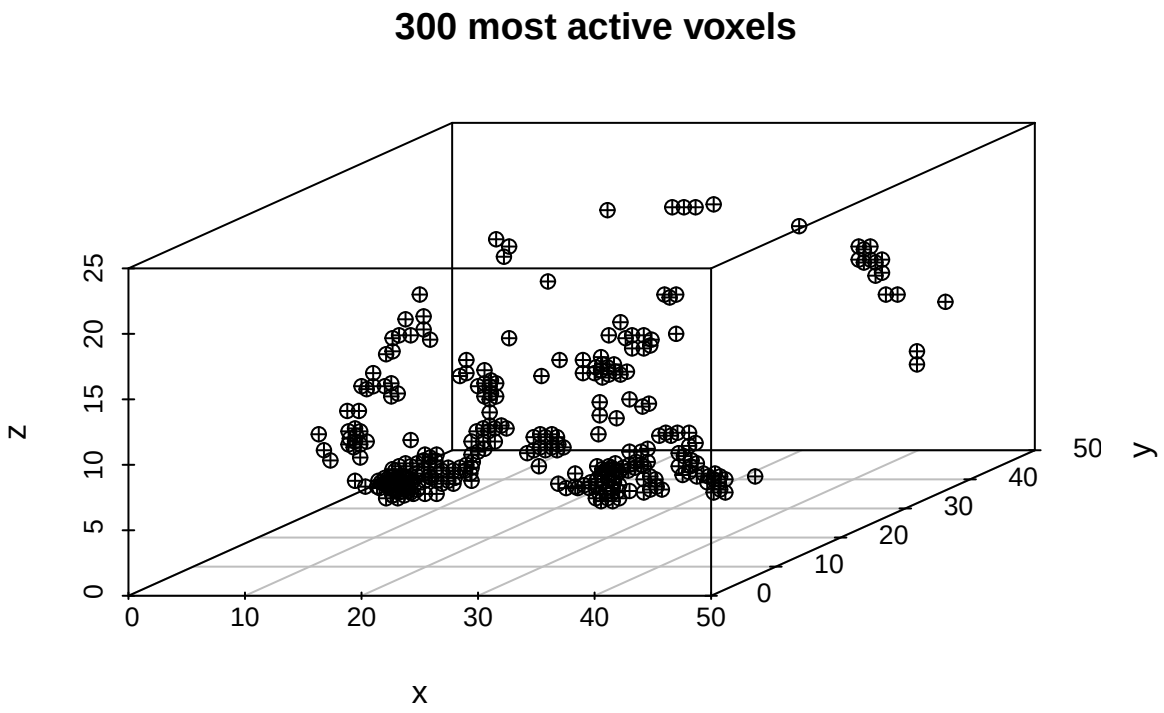
```
##
## -0.06624457
```

As indicated above, the value of `fmri[172,2014]` is ≈ -0.07.

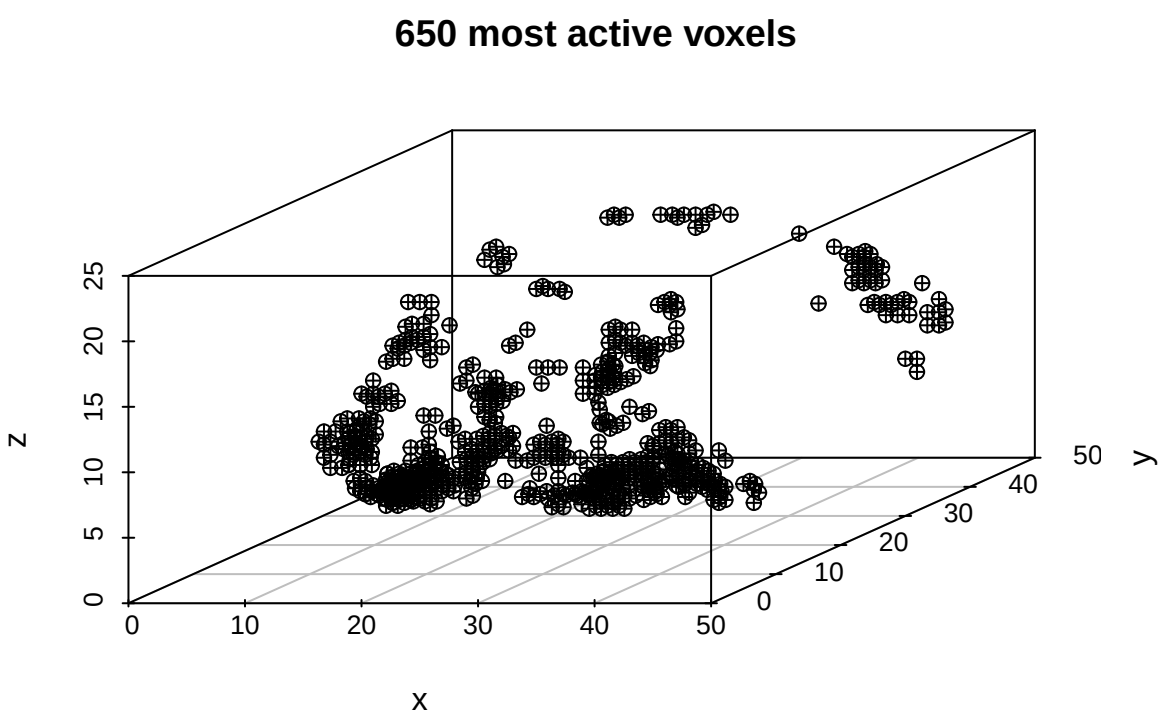
Question 2

```
# load the scatterplot3d package
library(scatterplot3d)
# total number of features
p <- 21764
# store the coordinates needed for the scatterplot in col2coord
col2coord <- fmri.p1$meta[[8]]
```

```r
# compute the means of each column in the fmri data
ave.colMeans <- colMeans(fmri)
# finds the rank of each voxel
rank.fmri <- rank(ave.colMeans)
# we go in reverse order due to the rank() function to get the  300 most active voxels
scatterplot3d(x=col2coord[rank.fmri>(p-300),],pch=10,
  xlab="x", ylab="y", zlab="z", main="300 most active voxels")
```




```r
# repeat as above to plot the 650 most active voxels
scatterplot3d(x=col2coord[rank.fmri>(p-650),],pch=10,
  xlab="x", ylab="y", zlab="z", main="650 most active voxels")
```



Question 3

Question 4

Question 5

Question 6

Question 7

Question 8

Question 9