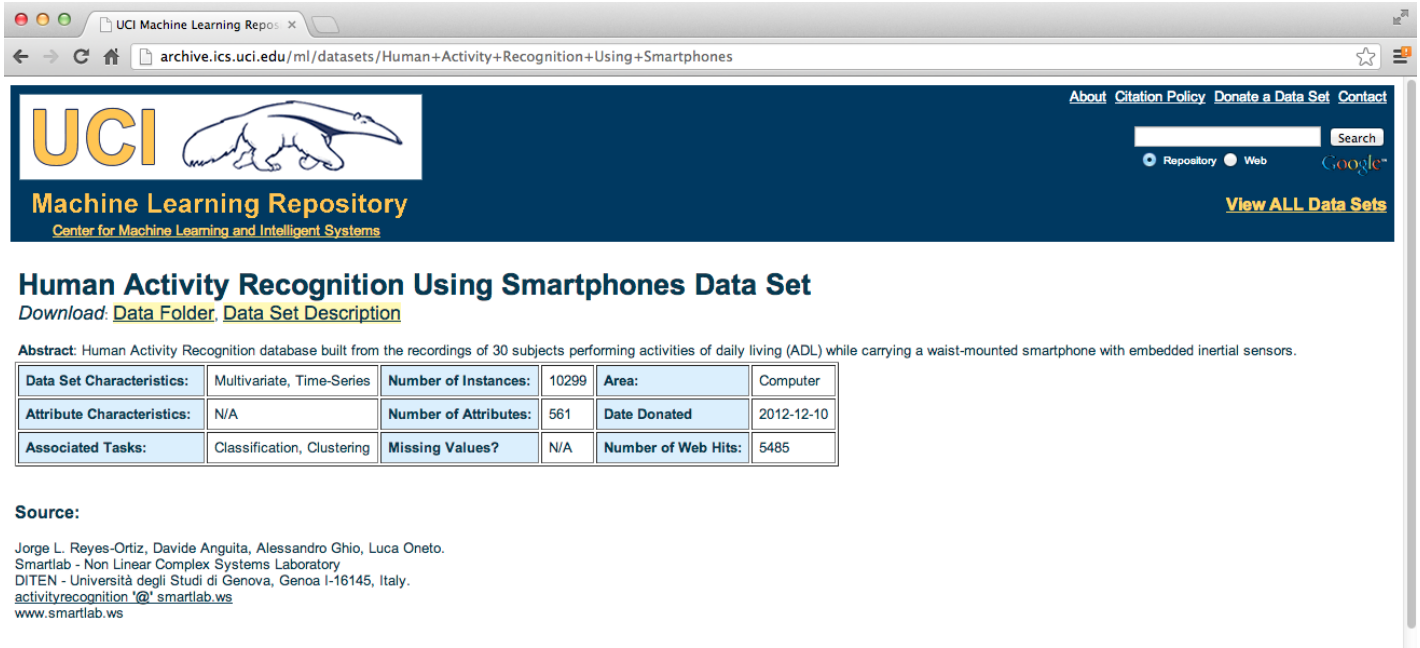
EDA Case Study - Understanding Human Activity with Smart Phones

Roger D. Peng, Associate Professor of Biostatistics
Johns Hopkins Bloomberg School of Public Health

Samsung Galaxy S3

http://www.samsung.com/global/galaxys3/

Samsung Data



http://archive.ics.uci.edu/ml/datasets/Human+Activity+Recognition+Using+Smartphones

Slightly processed data

Samsung data file

```
load("data/samsungData.rda")
names(samsungData)[1:12]
```

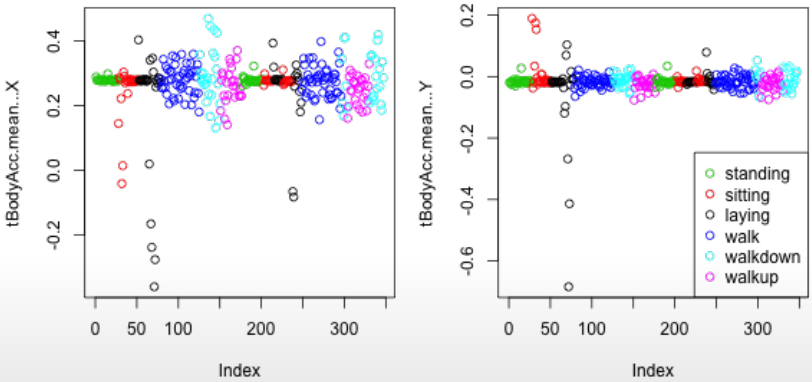
```
##  [1] "tBodyAcc-mean()-X" "tBodyAcc-mean()-Y" "tBodyAcc-mean()-Z"
##  [4] "tBodyAcc-std()-X"  "tBodyAcc-std()-Y"  "tBodyAcc-std()-Z"
##  [7] "tBodyAcc-mad()-X"  "tBodyAcc-mad()-Y"  "tBodyAcc-mad()-Z"
## [10] "tBodyAcc-max()-X"  "tBodyAcc-max()-Y"  "tBodyAcc-max()-Z"
```

```
table(samsungData$activity)
```

```
##
##   laying  sitting standing     walk walkdown   walkup
##     1407     1286     1374     1226      986     1073
```

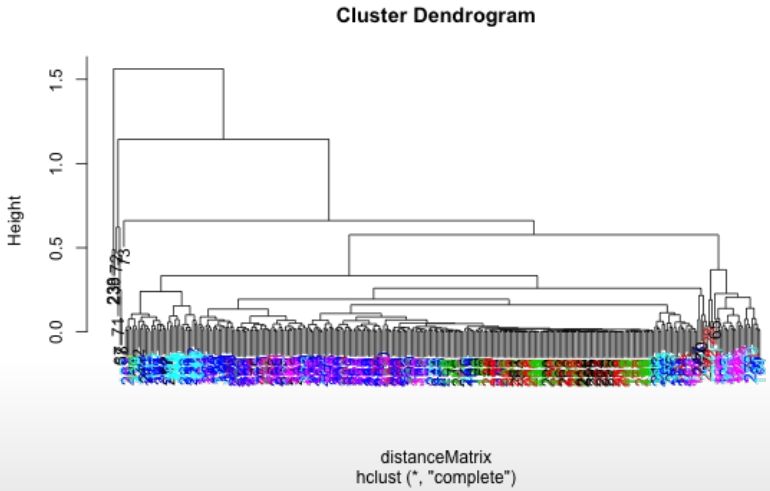
Plotting average acceleration for first subject

```
par(mfrow = c(1, 2), mar = c(5, 4, 1, 1))
samsungData <- transform(samsungData, activity = factor(activity))
sub1 <- subset(samsungData, subject == 1)
plot(sub1[, 1], col = sub1$activity, ylab = names(sub1)[1])
plot(sub1[, 2], col = sub1$activity, ylab = names(sub1)[2])
legend("bottomright", legend = unique(sub1$activity), col = unique(sub1$activity),
    pch = 1)
```



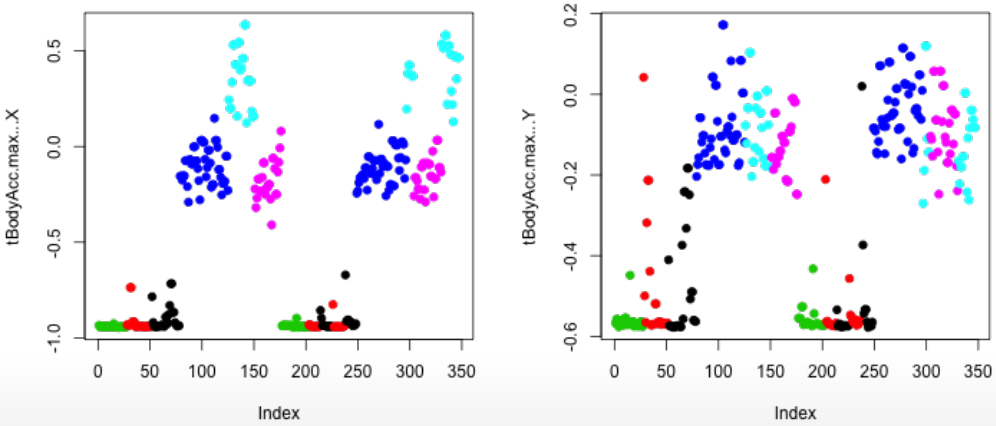
Clustering based just on average acceleration

```
source("myplclust.R")
distanceMatrix <- dist(sub1[, 1:3])
hclustering <- hclust(distanceMatrix)
myplclust(hclustering, lab.col = unclass(sub1$activity))
```



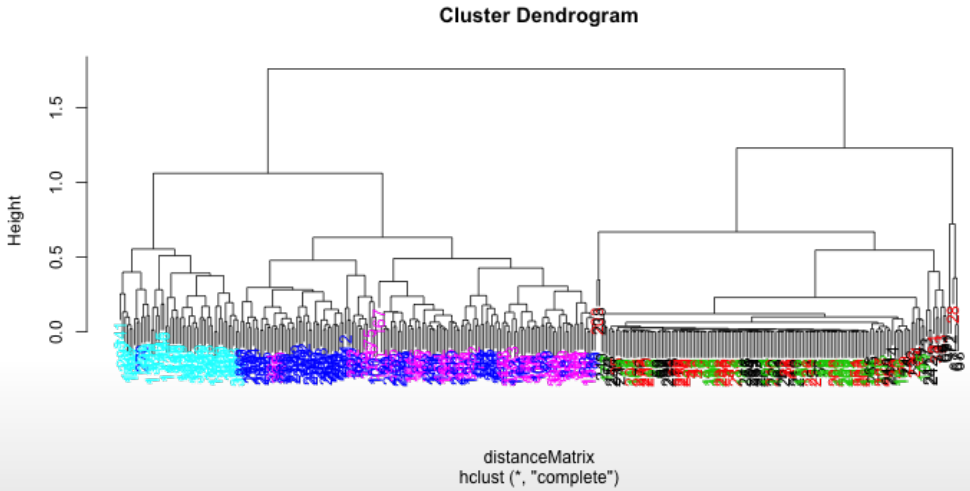
Plotting max acceleration for the first subject

```
par(mfrow = c(1, 2))
plot(sub1[, 10], pch = 19, col = sub1$activity, ylab = names(sub1)[10])
plot(sub1[, 11], pch = 19, col = sub1$activity, ylab = names(sub1)[11])
```



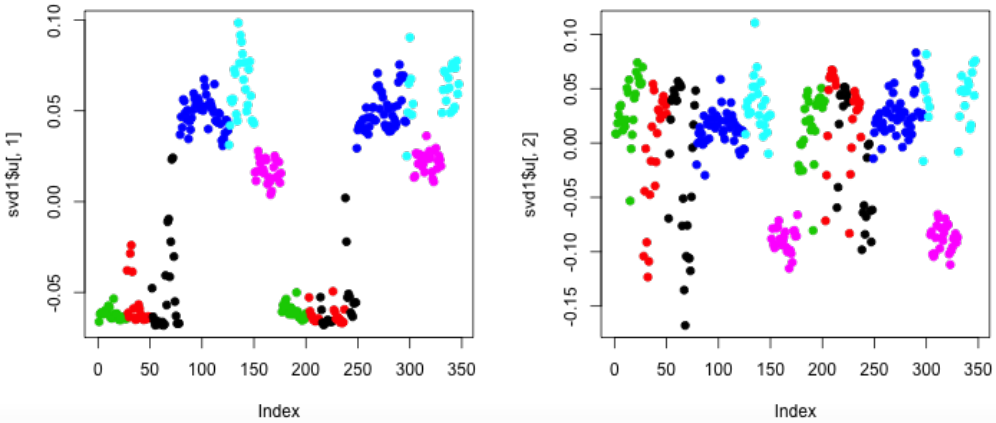
Clustering based on maximum acceleration

```
source("myplclust.R")
distanceMatrix <- dist(sub1[, 10:12])
hclustering <- hclust(distanceMatrix)
myplclust(hclustering, lab.col = unclass(sub1$activity))
```



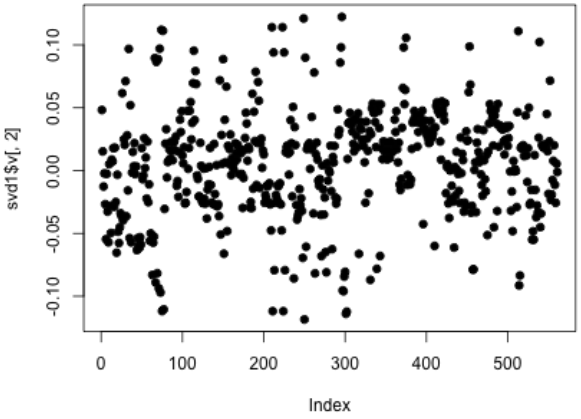
Singular Value Decomposition

```
svd1 = svd(scale(sub1[, -c(562, 563)]))
par(mfrow = c(1, 2))
plot(svd1$u[, 1], col = sub1$activity, pch = 19)
plot(svd1$u[, 2], col = sub1$activity, pch = 19)
```



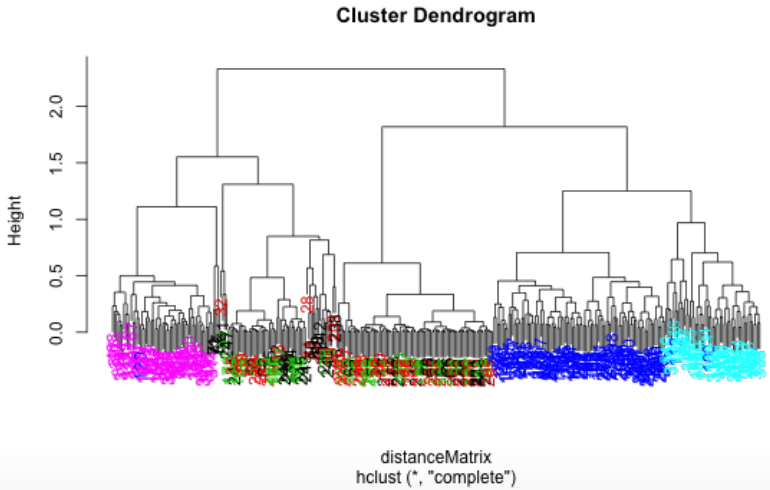
Find maximum contributor

```
plot(svd1$v[, 2], pch = 19)
```



New clustering with maximum contributer

```
maxContrib <- which.max(svd1$v[, 2])
distanceMatrix <- dist(sub1[, c(10:12, maxContrib)])
hclustering <- hclust(distanceMatrix)
myplclust(hclustering, lab.col = unclass(sub1$activity))
```



New clustering with maximum contributer

```
names(samsungData)[maxContrib]
```

```
## [1] "fBodyAcc.meanFreq...Z"
```

K-means clustering (nstart=1, first try)

```
kClust <- kmeans(sub1[, -c(562, 563)], centers = 6)
table(kClust$cluster, sub1$activity)
```

```
##
##      laying sitting standing walk walkdown walkup
##   1       0       0        0   50        1      0
##   2       0       0        0    0       48      0
##   3      27      37       51    0        0      0
##   4       3       0        0    0        0     53
##   5       0       0        0   45        0      0
##   6      20      10        2    0        0      0
```

K-means clustering (nstart=1, second try)

```
kClust <- kmeans(sub1[, -c(562, 563)], centers = 6, nstart = 1)
table(kClust$cluster, sub1$activity)
```

```
##
##     laying sitting standing walk walkdown walkup
##   1      0       0        0    0       49      0
##   2     18      10        2    0        0      0
##   3      0       0        0   95        0      0
##   4     29       0        0    0        0      0
##   5      0      37       51    0        0      0
##   6      3       0        0    0        0     53
```

K-means clustering (nstart=100, first try)

```
kClust <- kmeans(sub1[, -c(562, 563)], centers = 6, nstart = 100)
table(kClust$cluster, sub1$activity)
```

```
##
##      laying sitting standing walk walkdown walkup
##   1      18      10        2    0        0      0
##   2      29       0        0    0        0      0
##   3       0       0        0   95        0      0
##   4       0       0        0    0       49      0
##   5       3       0        0    0        0     53
##   6       0      37       51    0        0      0
```

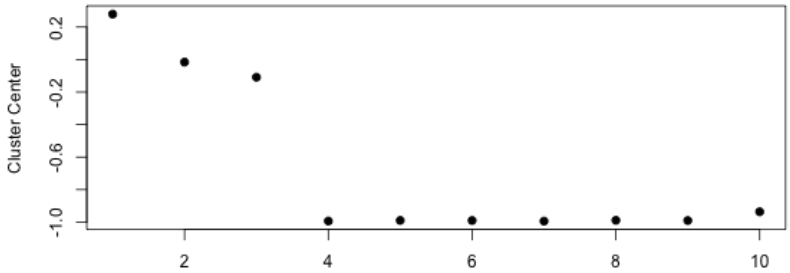
K-means clustering (nstart=100, second try)

```
kClust <- kmeans(sub1[, -c(562, 563)], centers = 6, nstart = 100)
table(kClust$cluster, sub1$activity)
```

```
##
##     laying sitting standing walk walkdown walkup
##   1     29       0        0    0        0      0
##   2      3       0        0    0        0     53
##   3      0       0        0    0       49      0
##   4      0       0        0   95        0      0
##   5      0      37       51    0        0      0
##   6     18      10        2    0        0      0
```

Cluster 1 Variable Centers (Laying)

```
plot(kClust$center[1, 1:10], pch = 19, ylab = "Cluster Center", xlab = "")
```



Cluster 2 Variable Centers (Walking)

```
plot(kClust$center[4, 1:10], pch = 19, ylab = "Cluster Center", xlab = "")
```