Clustering Example

```
> library(swirl)

| Hi! Type swirl() when you are ready to begin.

> swirl()

| Welcome to swirl! Please sign in. If you've been here before, use the same name as you did then
are new,
| call yourself something unique.

What shall I call you? Stephen

| Please choose a course, or type 0 to exit swirl.

1: Data Analysis
2: Exploratory Data Analysis
3: Getting and Cleaning Data
4: Mathematical Biostatistics Boot Camp
5: Open Intro
6: R Programming
7: Regression Models
8: Statistical Inference
9: Take me to the swirl course repository!

Selection: 2

| Please choose a lesson, or type 0 to return to course menu.

 1: Principles of Analytic Graphs   2: Exploratory Graphs             3: Graphics Devices in R
 4: Plotting Systems                5: Base Plotting System           6: Lattice Plotting System
 7: Working with Colors             8: GGPlot2 Part1                  9: GGPlot2 Part2
10: GGPlot2 Extras                 11: Hierarchical Clustering       12: K Means Clustering
13: Dimension Reduction            14: Clustering Example            15: CaseStudy


Selection: 14

| Attempting to load lesson dependencies...

| Package ‘fields’ loaded correctly!

| Package ‘jpeg’ loaded correctly!

| Package ‘datasets’ loaded correctly!

  |
|   0%

| Clustering_Example. (Slides for this and other Data Science courses may be found at github
| https://github.com/DataScienceSpecialization/courses/. If you care to use them, they must be dow
as a zip
| file and viewed locally. This lesson corresponds to 04_ExploratoryAnalysis/clusteringExample.)

...

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| In this lesson we'll apply some of the analytic techniques we learned in this course to data fro
niversity
| of California, Irvine. Specifically, the data we'll use is from UCI's Center for Machine Learni
ntelligent
| Systems. You can find out more about the data at
| http://archive.ics.uci.edu/ml/datasets/Human+Activity+Recognition+Using+Smartphones. As this ado
dicates,
| the data involves smartphones and recognizing human activity. Cool, right?

...
```

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| Our goal is to show you how to use exploratory data analysis to point you in fruitful directions
earch, that
| is, towards answerable questions. Exploratory data analysis is a "rough cut" or filter which he
to find the
| most beneficial areas of questioning so you can set your priorities accordingly.

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| We also hope to show you that "real-world" research isn't always neat and well-defined like tex
estions
| with clearcut answers.

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| We've loaded data from this study for you in a matrix called ssd.  Run the R command dim now to
| dimensions.

> dim(ssd)
[1] 7352  563

| Keep up the great work!

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| Wow - ssd is pretty big, 7352 observations, each of 563 variables. Don't worry we'll only use a
ortion of
| this "Human Activity Recognition database".

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| The study creating this database involved 30 volunteers "performing activities of daily living
ile
| carrying a waist-mounted smartphone with embedded inertial sensors. ... Each person performed s
ities ...
| wearing a smartphone (Samsung Galaxy S II) on the waist. ... The experiments have been video-re
o label the
| data manually.  The obtained dataset has been randomly partitioned into two sets, where 70% of
nteers was
| selected for generating the training data and 30% the test data."

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| Use the R command names with just the last two columns (562 and 563) of ssd to see what data th
in.

> names(ssd[562:563])
[1] "subject"  "activity"

| You got it right!

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```
| These last 2 columns contain subject and activity information. We saw above that the gathered da
"been
| randomly partitioned into two sets, where 70% of the volunteers was selected for generating the
g data and
| 30% the test data." Run the R command table with ssd$subject as its argument to see if the data
contains
| training or test data.

>
> table(ssd$subject)

  1   3   5   6   7   8  11  14  15  16  17  19  21  22  23  25  26  27  28  29  30
347 341 302 325 308 281 316 323 328 366 368 360 408 321 372 409 392 376 382 344 383

| Your dedication is inspiring!

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| From the number of subjects, would you infer that ssd contains training or test data?

1: test
2: training

Selection: 2

| You got it right!

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|  16%

| So ssd contains only training data. If you ran the R command sum with table(ssd$subject) as its
t, what
| would the number you get back represent?

1: the number of rows in ssd
2: Huh?
3: the number of columns in ssd
4: the number of rows and columns of ssd

Selection: 1

| That's correct!

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| Try it now (running sum on table(ssd$subject))to see if you get 7352, the number of rows in ssd
esult.

> sum(table(ssd$subject))
[1] 7352

| You are quite good my friend!

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| So we're looking at training data from a machine learning repository. We can infer that this da
pposed to
| train machines to recognize activity collected from the accelerometers and gyroscopes built int
artphones
| that the subjects had strapped to their waists. Run the R command table on ssd$activity to see w
ivities
| have been characterized by this data.

> table(ssd$activity)

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

```
| You nailed it! Good job!

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| We have 6 activities, 3 passive (laying, standing and sitting) and 3 active which involve walki
ou ran the
| R command sum with table(ssd$activity) as its argument, what would the number you get back repr

1: Huh?
2: the number of rows in ssd
3: the number of columns in ssd
4: the number of rows and columns of ssd

Selection: 2

| You nailed it! Good job!

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| Because it's training data, each row is labeled with the correct activity (from the 6 possible)
ociated
| with the column measurements (from the accelerometer and gyroscope). We're interested in questi
as, "Is
| the correlation between the measurements and activities good enough to train a machine?" so tha
a set of
| 561 measurements, would a trained machine be able to determine which of the 6 activities the pe
doing?"

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| First, let's massage the data a little so it's easier to work with. We've already run the R com
nsform on
| the data so that activities are factors. This will let us color code them when we generate plot
look at
| only the first subject (numbered 1). Create the variable sub1 by assigning to it the output of
mmand
| subset with ssd as the first argument and the boolean, subject equal to 1, as the second.

> sub1 <- subset(ssd, subject == 1)

| You are doing so well!

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| Look at the dimensions of sub1 now.

> dim(sub1)
[1] 347 563

| All that hard work is paying off!

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| So sub1 has fewer than 400 rows now, but still a lot of columns which contain measurements. Use
n the first
| 12 columns of sub1 to see what kind of data we have.

> names(sub1[1:12])
 [1] "tBodyAcc.mean...X" "tBodyAcc.mean...Y" "tBodyAcc.mean...Z" "tBodyAcc.std...X"  "tBodyAcc.st
 [6] "tBodyAcc.std...Z"  "tBodyAcc.mad...X"  "tBodyAcc.mad...Y"  "tBodyAcc.mad...Z"  "tBodyAcc.ma
[11] "tBodyAcc.max...Y"  "tBodyAcc.max...Z"

| You're the best!
```

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| We see X, Y, and Z (3 dimensions) of different aspects of body acceleration measurements, such a
and
| standard deviation. Let's do some comparisons of activities now by looking at plots of mean body
ration in
| the X and Y directions. Call the function myedit with the string "showXY.R" to see the code gene
the plots.
| Make sure your cursor is back in the console window before you hit any more buttons.

> myedit("showXY.R")

| You're the best!

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| You see both the code and its output! The plots are a little squished, but we see that the activ
ities
| related to walking (shown in the two blues and magenta) show more variability than the passive a
es (shown
| in black, red, and green), particularly in the X dimension.

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| The colors are a little hard to distinguish. Just for fun, call the function showMe (we used it
| the Working_with_Colors lesson) which displays color vectors. Use the vector 1:6 as its argument
| and hopefully this will clarify the colors you see in the XY comparison plot.

> showMe(1:6)

| You are doing so well!

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| Nice! We just wanted to show you the beauty and difference in colors. The colors at the bottom,
| black, red and green, mark the passive activities, while the true blues and magenta near the top
| show the walking activities. Let's try clustering to see if we can distinguish the activities mo

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|   34%

| We'll still focus on the 3 dimensions of mean acceleration. (The plot we just saw looked at the
| first 2 dimensions.) Create a distance matrix, mdist, of the first 3 columns of sub1, by using t
| R command dist. Use the x[,1:3] notation to specify the columns.

> mdist <- dist(sub1[,1:3])

| You got it!

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| Now create the variable hclustering by calling the R command hclust and passing it mdist as an
| argument. This will use the Euclidean distance as its default metric.

> hclustering <- hclust(mdist)

| All that hard work is paying off!

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| Now call the pretty plotting function (which we've already sourced) myplclust with 2 arguments.
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| first is hclustering, and the second is the argument lab.col set equal to unclass(sub1$activity)

> myplclust(hclustering, lab.col = unclass(sub1$activity))

| All that practice is paying off!

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| Well that dendrogram doesn't look too helpful, does it? There's no clear grouping of colors, exc
| that active colors (blues and magenta) are near each other as are the passive (black, red, and
| green). So average acceleration doesn't tell us much. How about maximum acceleration? Let's look
| that for the first subject (in our array sub1) for the X and Y dimensions. These are in column 1
| and 11.

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| Here they are plotted side by side, X dimension on the left and Y on the right. The x-axis of ea
| show the 300+ observations and the y-axis indicates the maximum acceleration.

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| From the 2 plots, what separation, if any, do you see?

1: passive activities generate the most acceleration
2: there is no pattern
3: laying generates the most acceleration in the X dimension
4: passive activities mostly fall below the walking activities

Selection: 4

| Perseverance, that's the answer.

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| Finally we're seeing something vaguely interesting! Let's focus then on the 3 dimensions of max
| acceleration, stored in columns 10 through 12 of sub1. Create a new distance matrix, mdist, of
| these 3 columns of sub1, by using the R command dist. Again, use the x[,10:12] notation to catch
| the columns.

> mdist <- dist(sub1[,10:12])

| You nailed it! Good job!

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|  45%

| Now create the variable hclustering by calling hclust with mdist as the argument.

> hclustering <- hclust(mdist)

| You're the best!

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| Again, call the myplclust with 2 arguments. The first is hclustering, and the second is the
| argument lab.col set equal to unclass(sub1$activity).

> myplclust(hclustering, lab.col = unclass(sub1$activity))

| Great job!
```

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| Now we see clearly that the data splits into 2 clusters, active and passive activities. Moreove
| the light blue (walking down) is clearly distinct from the other walking activities. The dark b
| (walking level) also seems to be somewhat clustered. The passive activities, however, seem all
| jumbled together with no clear pattern visible.

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| Let's try some SVD now. Create the variable svd1 by assigning to it the output of a call to the
| command svd. The argument to svd should be scale(sub1[,-c(562,563)]). This will remove the last
| columns from sub1 and scale the data. Recall that the last 2 columns contain activity and subje
| information which we won't need.

> svd1 <- svd(scale(sub1[,-c(562,563)]))

| You are doing so well!

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| To see LEFT singular vectors of sub1, which component of svd1 would we examine?

1: x
2: u
3: d
4: v

Selection: 2

| Excellent job!

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| Call the R command dim with svd1$u as an argument.

> dim(svd1$u)
[1] 347 347

| You are quite good my friend!

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| We see that the u matrix is a 347 by 347 matrix. Each row in u corresponds to a row in the matr
| sub1. Recall that in sub1 each row has an associated activity.

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| Here we're looking at the 2 left singular vectors of svd1 (the first 2 columns of svd1$u). Each
| entry of the columns belongs to a particular row with one of the 6 activities assigned to it. W
| see the activities distinguished by color. Moving from left to right, the first section of rows
| green (standing), the second red (sitting), the third black (laying), etc.  The first column of
| shows separation of the nonmoving (black, red, and green) from the walking activities. The secon
| column is harder to interpret. However, the magenta cluster, which represents walking up, seems
| separate from the others.

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| We'll try to figure out why that is. To do that we'll have to find which of the 500+ measuremen
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| (represented by the columns of sub1) contributes to the variation of that component. Since we're
| interested in sub1 columns, we'll look at the RIGHT singular vectors (the columns of svd1$v), a
| in particular, the second one since the separation of the magenta cluster stood out in the seco
| column of svd1$u.

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| Here's a plot of the second column of svd1$v. We used transparency in our plotting but nothing
| clearly stands out here. Let's use clustering to find the feature (out of the 500+) which
| contributes the most to the variation of this second column of svd1$v.

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| Create the variable maxCon by assigning to it the output of the R command which.max using the
| second column of svd1$v as an argument.

> maxCon <- which.max(svd1$v[,2])

| You got it right!

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| Now create a distance matrix mdist by assigning to it the output of the R command dist using 4
| columns of sub1 as the arguments. These 4 columns are 10 through 12 (10:12) and maxCon. Recall
| you'll have to concatenate these 2 column expressions when specifying them.

> mdist <- dist(c(sub1[,10:12], maxCon)
+
+
+ )
Error in dist(c(sub1[, 10:12], maxCon)) :
  (list) object cannot be coerced to type 'double'
> mdist <- dist(c(10:12, maxCon)
+ )

| Not exactly. Give it another go. Or, type info() for more options.

| Type mdist <- dist(sub1[,c(10:12,maxCon)]) at the command prompt.

> mdist <- dist(sub1[,c(10:12,maxCon)])

| You got it right!

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|   64%

| Now create hclustering, the output of the R command hclust using mdist as the argument.

> hclustering <- hclust(mdist)

| You're the best!

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|   66%

| Call the myplclust with 2 arguments, hclustering, and lab.col set equal to unclass(sub1$activity

> myplclust(hclustering, lab.col = unclass(sub1$activity))

| Great job!

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|   67%
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```
| Now we see some real separation. Magenta (walking up) is on the far left, and the two other wal
| activities, the two blues, are on the far right, but in separate clusters from one another. The
| nonmoving activities still are jumbled together.

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| Run the R command names with the argument sub1[maxCon] to see what measurement is associated wi
| this maximum contributor.

> names(sub1[maxCon])
[1] "fBodyAcc.meanFreq...Z"

| That's correct!

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|  70%

| So the mean body acceleration in the frequency domain in the Z direction is the main contributo
| this clustering phenomenon we're seeing. Let's move on to k-means clustering to see if this
| technique can distinguish between the activities.

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|  72%

| Create the variable kClust by assigning to it the output of the R command kmeans with 2 argumen
| The first is sub1 with the last 2 columns removed. (Recall these don't have pertinent informati
| for clustering analysis.) The second argument to kmeans is centers set equal to 6, the number o
| activities we know we have.

> kclust <- kmeans(sub1[,1:561], centers = 6)

| One more time. You can do it! Or, type info() for more options.

| Type kClust <- kmeans(sub1[, -c(562, 563)], centers = 6) the command prompt.

> kClust <- kmeans(sub1[, -c(562, 563)], centers = 6)

| You got it!

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|  73%

| Recall that without specifying coordinates for the cluster centroids (as we did), kmeans will
| generate starting points randomly. Here we did only 1 random start (the default). To see the
| output, run the R command table with 2 arguments. The first is kClust$cluster (part of the outpu
| from kmeans), and the second is sub1$activity.

> table
function (..., exclude = if (useNA == "no") c(NA, NaN), useNA = c("no",
    "ifany", "always"), dnn = list.names(...), deparse.level = 1)
{
    list.names <- function(...) {
        l <- as.list(substitute(list(...)))[-1L]
        nm <- names(l)
        fixup <- if (is.null(nm))
            seq_along(l)
        else nm == ""
        dep <- vapply(l[fixup], function(x) switch(deparse.level +
            1, "", if (is.symbol(x)) as.character(x) else "",
            deparse(x, nlines = 1)[1L]), "")
        if (is.null(nm))
            dep
        else {
            nm[fixup] <- dep
            nm
        }
```

```
}
miss.use <- missing(useNA)
miss.exc <- missing(exclude)
useNA <- if (miss.use && !miss.exc && !match(NA, exclude,
    nomatch = 0L))
    "ifany"
else match.arg(useNA)
doNA <- useNA != "no"
if (!miss.use && !miss.exc && doNA && match(NA, exclude,
    nomatch = 0L))
    warning("'exclude' containing NA and 'useNA' != \\"no\\"' are a bit contradicting")
args <- list(...)
if (!length(args))
    stop("nothing to tabulate")
if (length(args) == 1L && is.list(args[[1L]])) {
    args <- args[[1L]]
    if (length(dnn) != length(args))
        dnn <- if (!is.null(argn <- names(args)))
            argn
        else paste(dnn[1L], seq_along(args), sep = ".")
}
bin <- 0L
lens <- NULL
dims <- integer()
pd <- 1L
dn <- NULL
for (a in args) {
    if (is.null(lens))
        lens <- length(a)
    else if (length(a) != lens)
        stop("all arguments must have the same length")
    fact.a <- is.factor(a)
    if (doNA)
        aNA <- anyNA(a)
    if (!fact.a) {
        a0 <- a
        a <- factor(a, exclude = exclude)
    }
    add.na <- doNA
    if (add.na) {
        ifany <- (useNA == "ifany")
        anNAc <- anyNA(a)
        add.na <- if (!ifany || anNAc) {
            ll <- levels(a)
            if (add.ll <- !anyNA(ll)) {
              ll <- c(ll, NA)
              TRUE
            }
            else if (!ifany && !anNAc)
              FALSE
            else TRUE
        }
        else FALSE
    }
    if (add.na)
        a <- factor(a, levels = ll, exclude = NULL)
    else ll <- levels(a)
    a <- as.integer(a)
    if (fact.a && !miss.exc) {
        ll <- ll[keep <- which(match(ll, exclude, nomatch = 0L) ==
            0L)]
        a <- match(a, keep)
    }
    else if (!fact.a && add.na) {
        if (ifany && !aNA && add.ll) {
            ll <- ll[!is.na(ll)]
            is.na(a) <- match(a0, c(exclude, NA), nomatch = 0L) >
              0L
        }
        else {
            is.na(a) <- match(a0, exclude, nomatch = 0L) >
```

```
                    0L
                }
            }
            nl <- length(ll)
            dims <- c(dims, nl)
            if (prod(dims) > .Machine$integer.max)
                stop("attempt to make a table with >= 2^31 elements")
            dn <- c(dn, list(ll))
            bin <- bin + pd * (a - 1L)
            pd <- pd * nl
        }
        names(dn) <- dnn
        bin <- bin[!is.na(bin)]
        if (length(bin))
            bin <- bin + 1L
        y <- array(tabulate(bin, pd), dims, dimnames = dn)
        class(y) <- "table"
        y
}
<bytecode: 0x0000000002f6eba0>
<environment: namespace:base>

| You're close...I can feel it! Try it again. Or, type info() for more options.

| Type table(kClust$cluster, sub1$activity) the command prompt.

> table(kClust$cluster, sub1$activity)

    laying sitting standing walk walkdown walkup
  1      0       0        0    0       49      0
  2     16      12        7    0        0      0
  3      0       0        0   95        0      0
  4     24      33       46    0        0      0
  5      0       0        0    0        0     53
  6     10       2        0    0        0      0

| Nice work!

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|   75%

| Your exact output will depend on the state of your random number generator. We notice that when
| just run with 1 random start, the clusters tend to group the nonmoving activities together in o
| cluster. The walking activities seem to cluster individually by themselves. You could run the c
| to kmeans with one random start again and you'll probably get a slightly different result, but.

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|   77%

| ... instead call kmeans with 3 arguments, the last of which will tell it to try more random sta
| and return the best one. The first 2 arguments should be the same as before (sub1 with the last
| columns removed and centers set equal to 6). The third is nstart set equal to 100. Put the resu
| in kClust again.

> kClust <- kmeans(sub1[, -c(562, 563)], centers = 6, nstart=100)

| You got it right!

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|   78%

| Again, run the R command table with 2 arguments. The first is kClust$cluster (part of the outpu
| from kmeans), and the second is sub1$activity.

> table(kClust$cluster, sub1$activity)

    laying sitting standing walk walkdown walkup
  1     18      10        2    0        0      0
  2      0       0        0    0       49      0
```

```
  3      0      37       51    0        0      0
  4      0       0        0   95        0      0
  5     29       0        0    0        0      0
  6      3       0        0    0        0     53

| Great job!

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|   80%

| We see that even with 100 random starts, the passive activities tend to cluster together. One o
| the clusters contains only laying, but in another cluster, standing and sitting group together.

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|   81%

| Use dim to find the dimensions of kClust's centers. Use the x$y notation to access them.

> dim(kclust$centers)
[1]   6 561

| You're close...I can feel it! Try it again. Or, type info() for more options.

| Type dim(kClust$centers) the command prompt.

> dim(kClust$centers)
[1]   6 561

| Excellent work!

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|   83%

| So the centers are a 6 by 561 array. Sometimes it's a good idea to look at the features (columns
| of these centers to see if any dominate.

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|   84%

| Create the variable laying and assign to it the output of the call to the R command which with
| argument kClust$size==29.

> laying <- which(kClust$size==29)

| All that practice is paying off!

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|   86%

| Now call plot with 3 arguments. The first is kClust$centers[laying,1:12], and the second is pch
| to 19. The third is ylab set equal to "Laying Cluster"

> plot(kClust$centers[laying,1:12],pch=19, ylab="Laying Cluster")

| Your dedication is inspiring!

  |======================================================================================
|   88%

| We see the first 3 columns dominate this cluster center. Run names with the first 3 columns of
| as the argument to remind yourself of what these columns contain.

> names(sub1[,1:3])
[1] "tBodyAcc.mean...X" "tBodyAcc.mean...Y" "tBodyAcc.mean...Z"

| Keep up the great work!
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|  89%

| So the 3 directions of mean body acceleration seem to have the biggest effect on laying.

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|  91%

| Create the variable walkdown and assign to it the output of the call to the R command which wit
| the argument kClust$size==49.

> walkdown <- which(kClust$size==49)

| You nailed it! Good job!

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|  92%

| Now call plot with 3 arguments. The first is kClust$centers[walkdown,1:12], and the second is p
| set to 19. The third is ylab set equal to "Walkdown Cluster"

> plot(kClust$centers[walkdown,1:12],pch=19, ylab="Walkdown Cluster")

| You got it!

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|  94%

| We see an interesting pattern here. From left to right, looking at the 12 acceleration measurem
| in groups of 3, the points decrease in value. The X direction dominates, followed by Y then Z. T
| might tell us something more about the walking down activity.

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|  95%

| We'll wrap up here and hope this example convinced you that real world analysis can be frustrat
| sometimes and not always obvious. You might have to try several techniques of exploratory data
| analysis before you hit one that pays off and leads you to the questioms that will be the most
| promising to explore.

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==   |  97%

| We saw here that the sensor measurements were pretty good at discriminating between the 3 walki
| activities, but the passive activities were harder to distinguish from one another. These might
| require more analysis or an entirely different set of sensory measurements.

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===  |  98%

| Congratulations! We hope you enjoyed the 6 activities and 500+ features of this lesson.

...

  |=================================================================================================
=====| 100%

| Would you like to receive credit for completing this course on Coursera.org?

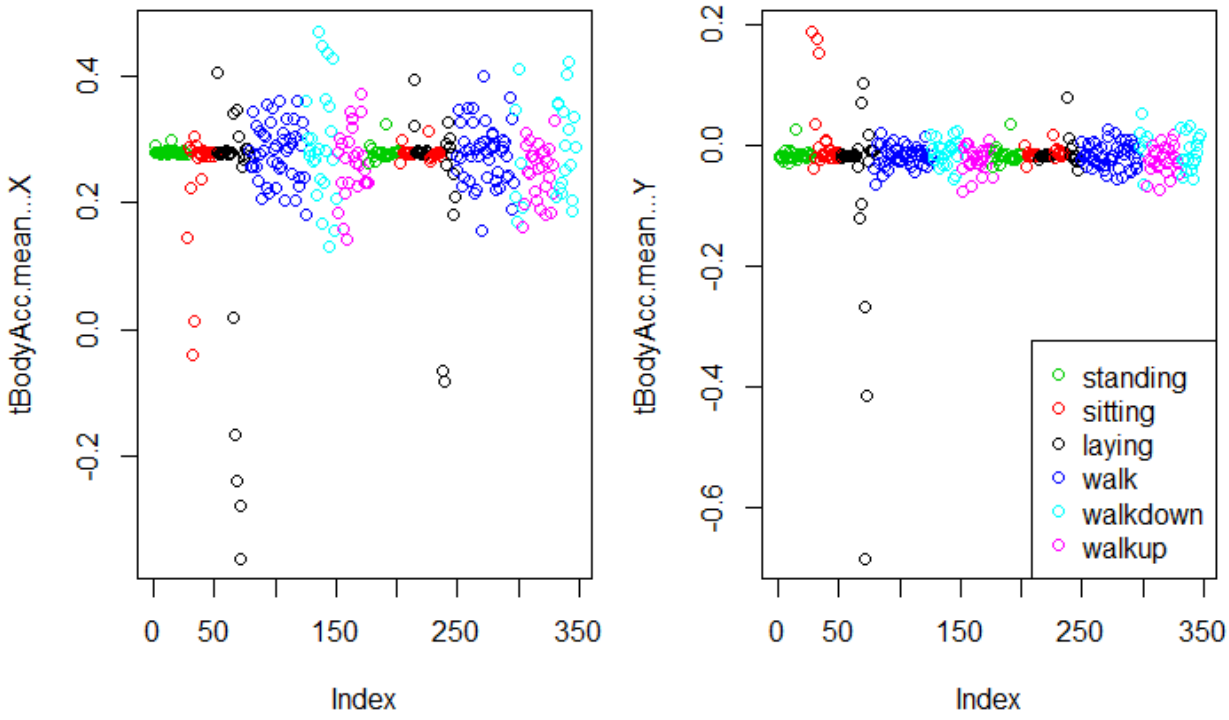
1: No
2: Yes
```

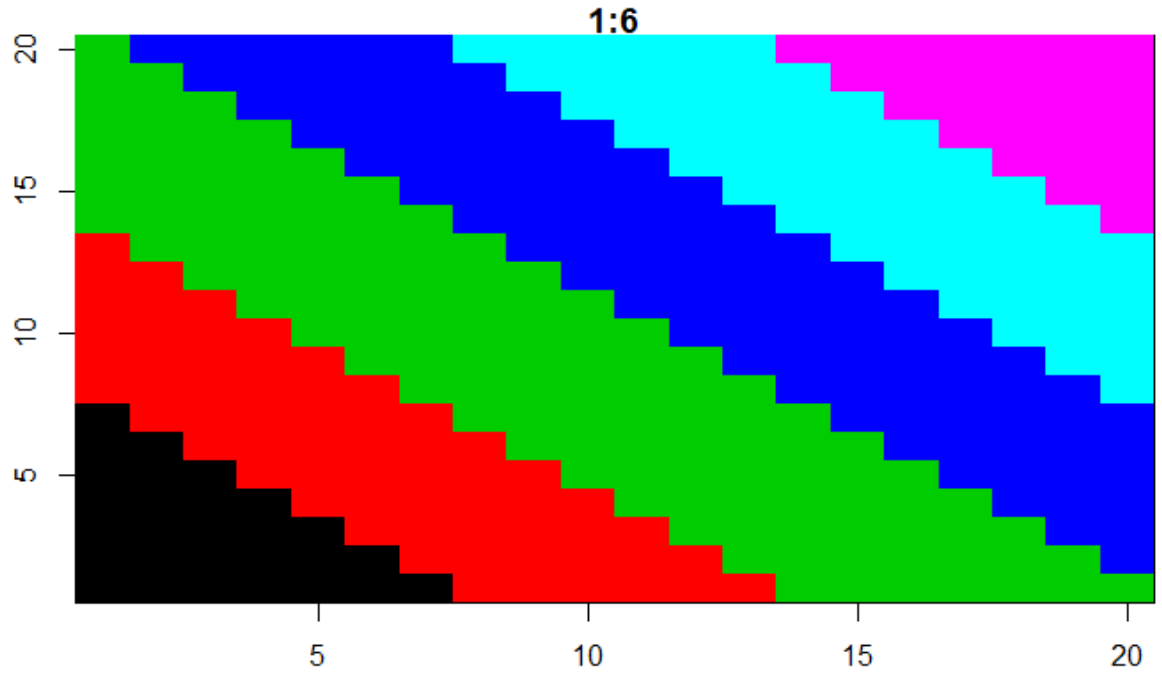
Codes

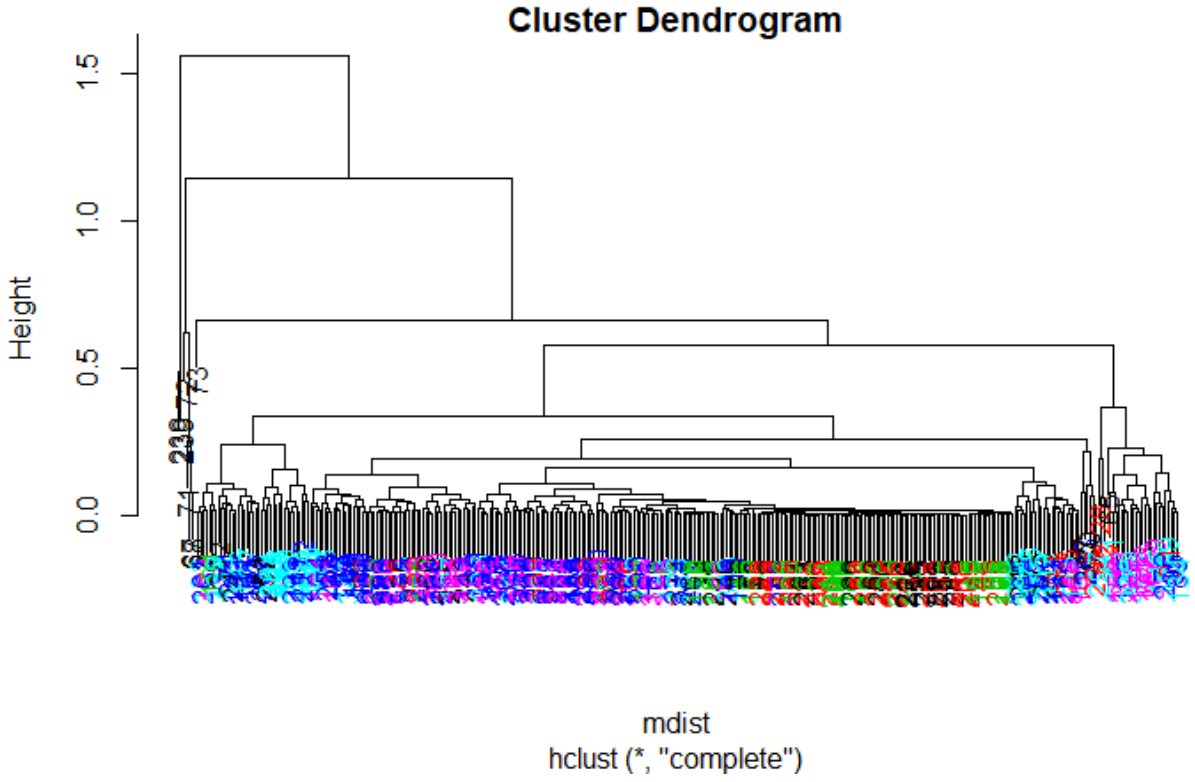
showXY.R

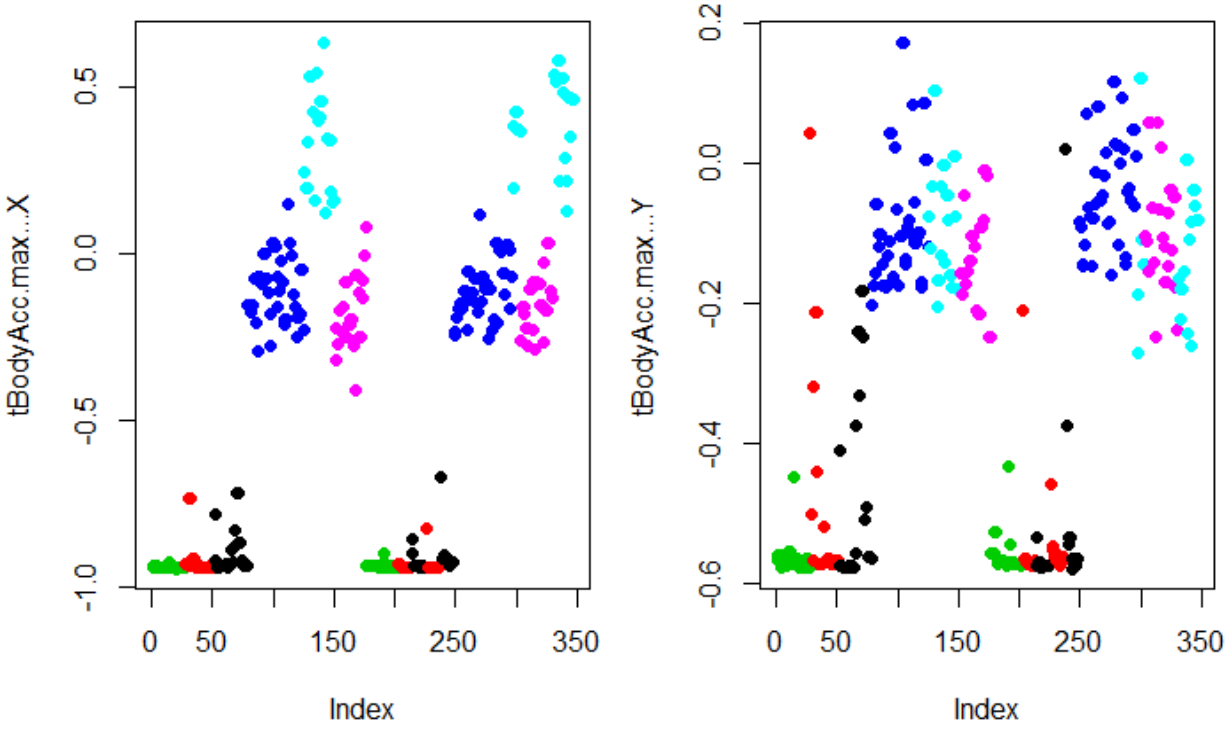
```
par(mfrow=c(1, 2), mar = c(5, 4, 1, 1))
plot(sub1[, 1], col = sub1$activity, ylab = names(sub1)[1])
plot(sub1[, 2], col = sub1$activity, ylab = names(sub1)[2])
legend("bottomright",legend=unique(sub1$activity),col=unique(sub1$activity), pch = 1)
par(mfrow=c(1,1))
```

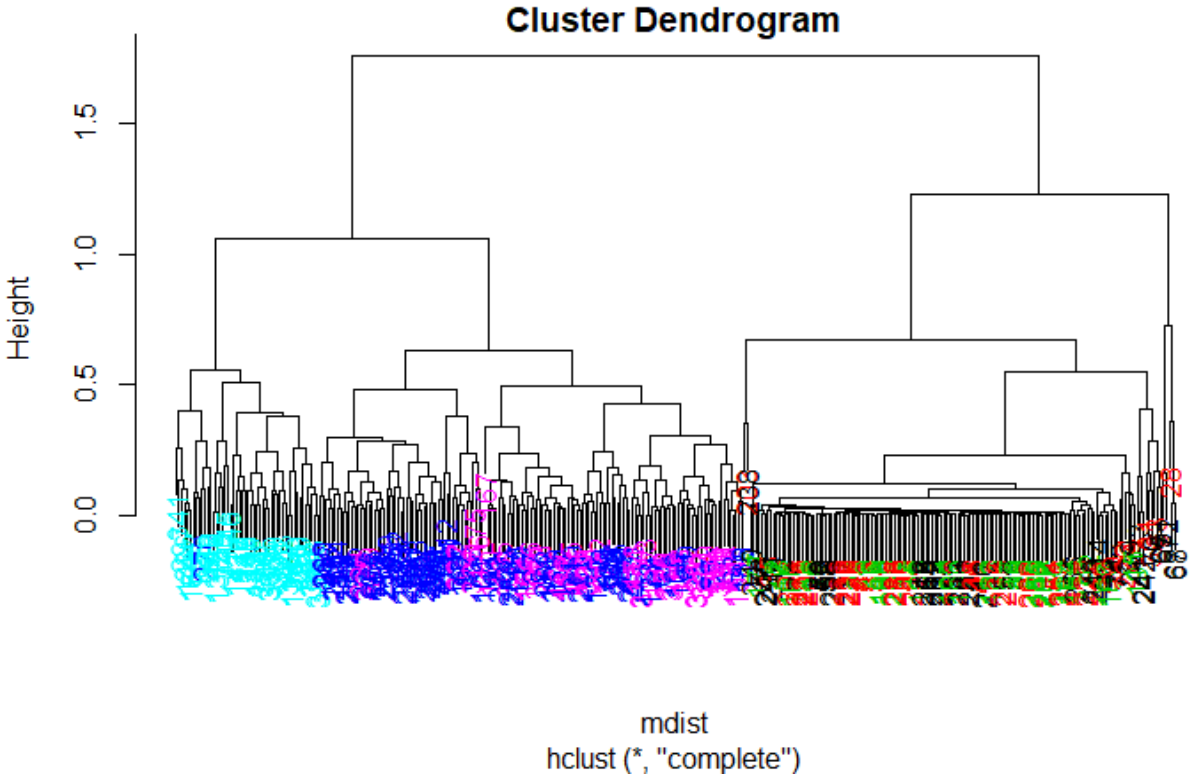
Plots

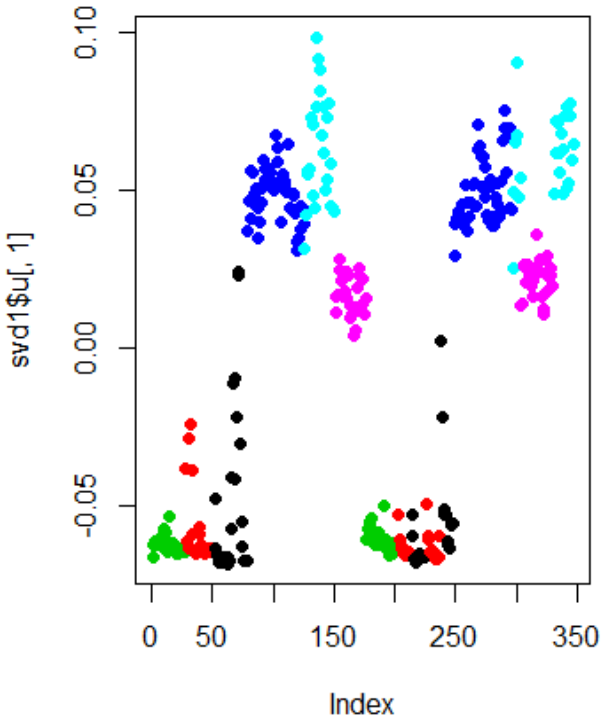


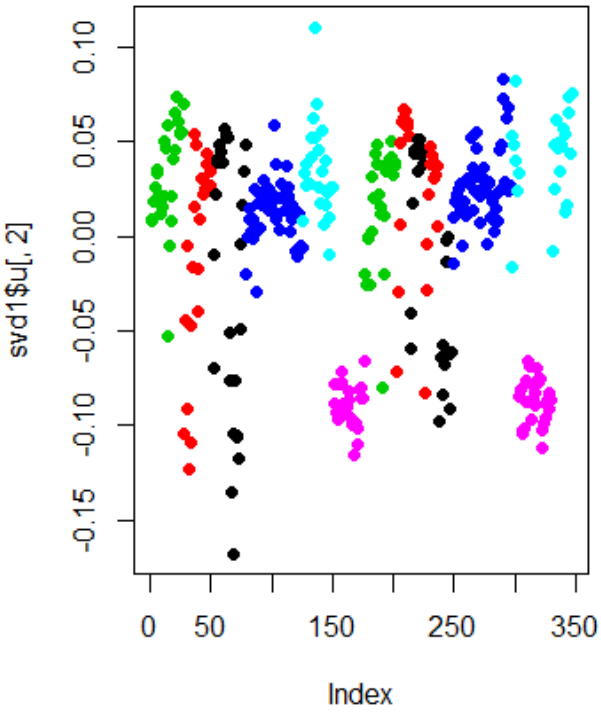

1:6
20
15
10
5
5
10
15
20

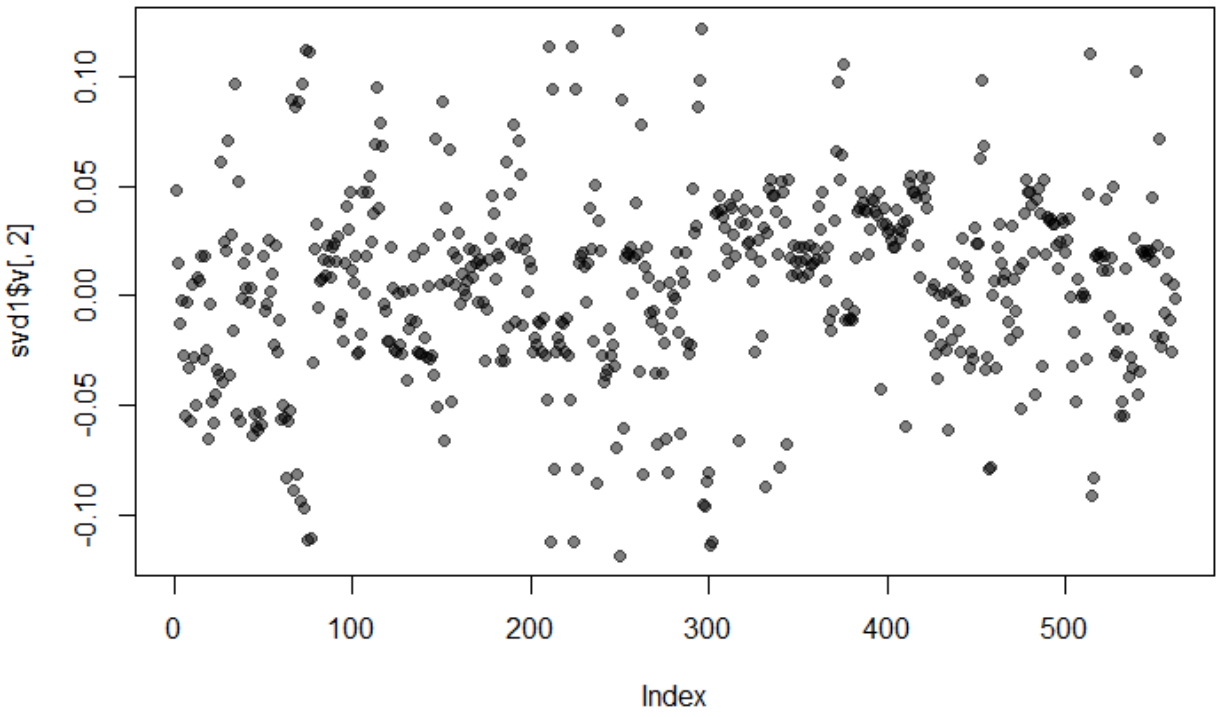

Cluster Dendrogram
Height
1.5
1.0
0.5
0.0
mdist
hclust (*, "complete")

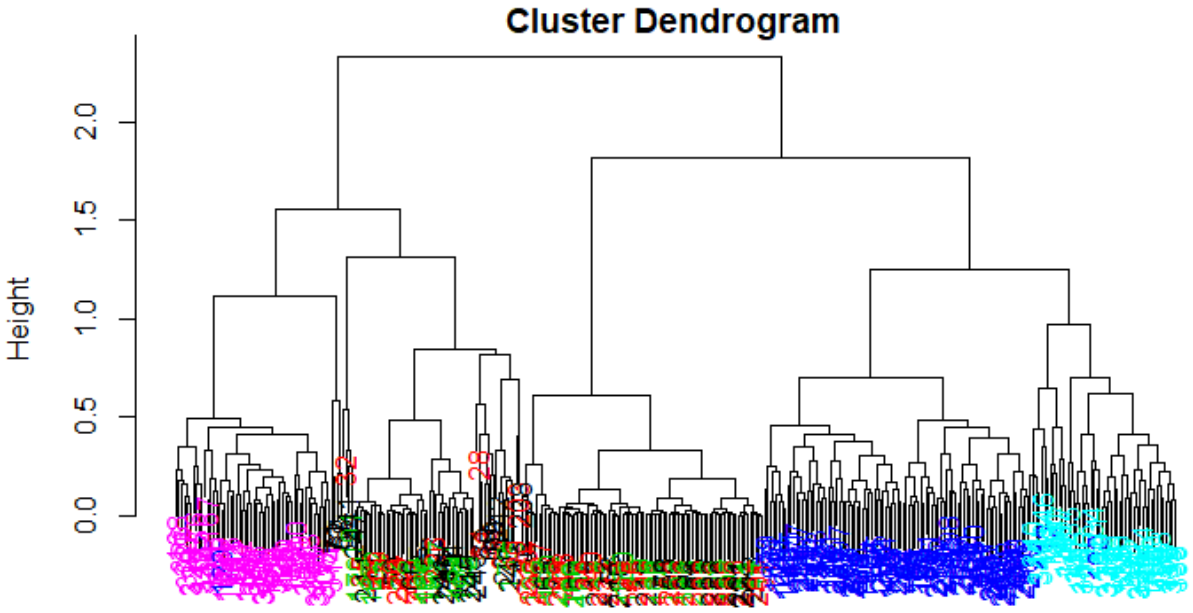

tBodyAcc.max...X
0.5
0.0
-0.5
-1.0
0
50
150
250
350
Index
tBodyAcc.max...Y
0.2
0.0
-0.2
-0.4
-0.6
0
50
150
250
350
Index


Cluster Dendrogram
Height
0.0
0.5
1.0
1.5
mdist
hclust (*, "complete")

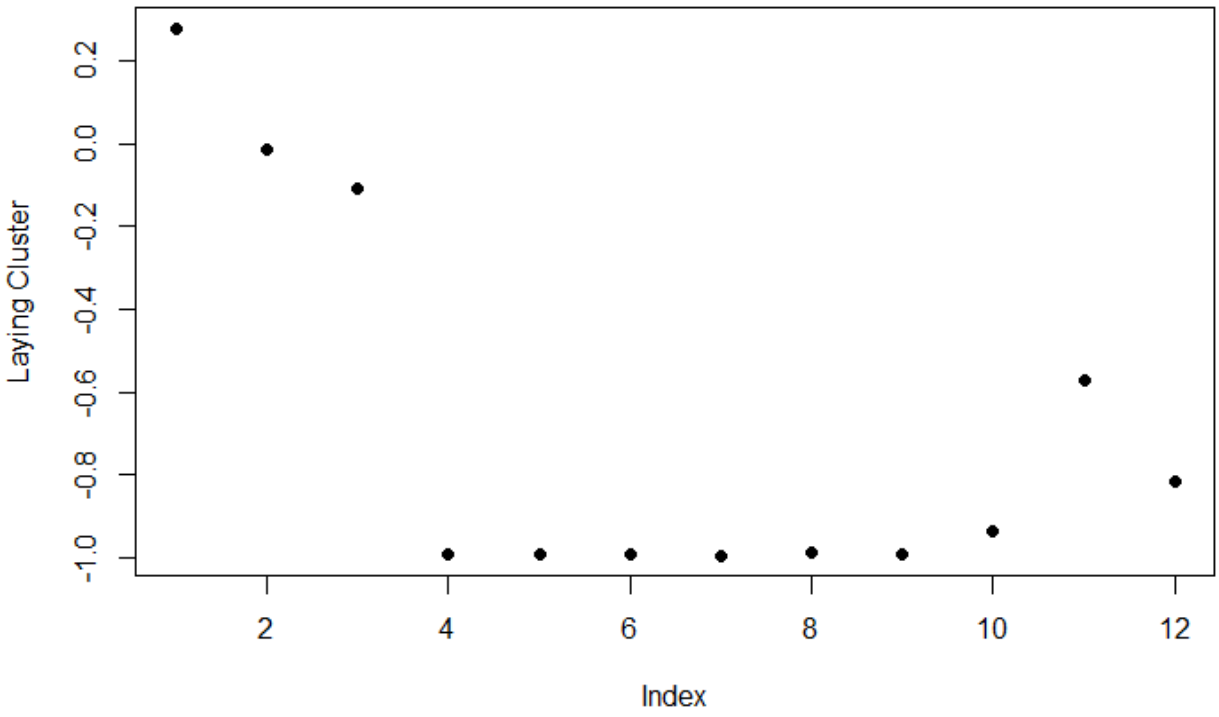

svd1$u[, 1]
0.10
0.05
0.00
-0.05
0
50
150
250
350
Index

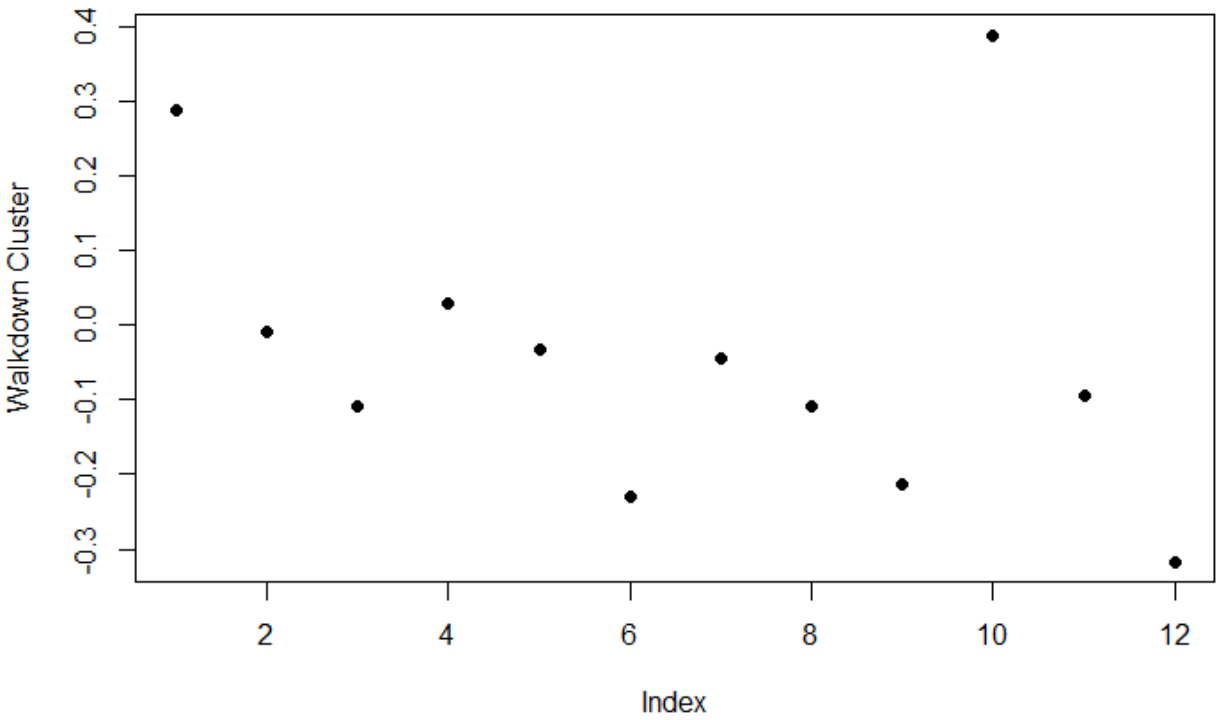

svd1$u[, 2]
0.10
0.05
0.00
-0.05
-0.10
-0.15
0
50
150
250
350
Index


svd1$v[, 2]
0.10
0.05
0.00
-0.05
-0.10
0
100
200
300
400
500
Index



mdist
hclust (*, "complete")




Walkdown Cluster
0.4
0.3
0.2
0.1
0.0
-0.1
-0.2
-0.3
2
4
6
8
10
12
Index