

# BigData II Case 3 Report

Group F

## Introduction

This project works to figure out the correctness of the statement generated by Leo Tolstoy which goes “All happy families are alike; each unhappy family is unhappy in its own way.” And we use the “2017 World Happiness Report” to find whether all happy countries are alike in some ways.

```
library(tidyverse)
library(ggplot2)
library(tidyr)
library(plyr)
library(factoextra)
library(car)
library(GGally)
```

## Data Processing

After having a look at the dataset, we find that there are some missing observations in the variable columns. 8 NAs in the GDPpc and LnGDPpc. 12 NAs in Corruption. 11 NAs in Generosity. 3 NAs in LifeChoice. 1 NA in LifeExp. If we choose to delete all the missing observations, we only have 121 countries in the list, but originally we have 141. We think it is a waste of information. So we decide to solve the missing problem.

```
# Read data
happiness<-read.csv("~/Desktop/whr_2017.csv")

# Input some countries' missing GDP values and get their LnGDPpc
happiness[139,9]<-2325.07
happiness[23,9]<-647.8804
happiness[88,9]<-5305.047
happiness[4,9]<-18489.43
happiness[80,9]<-35705.1
happiness$LnGDPpc<-log(happiness$GDPpc,exp(1))
```

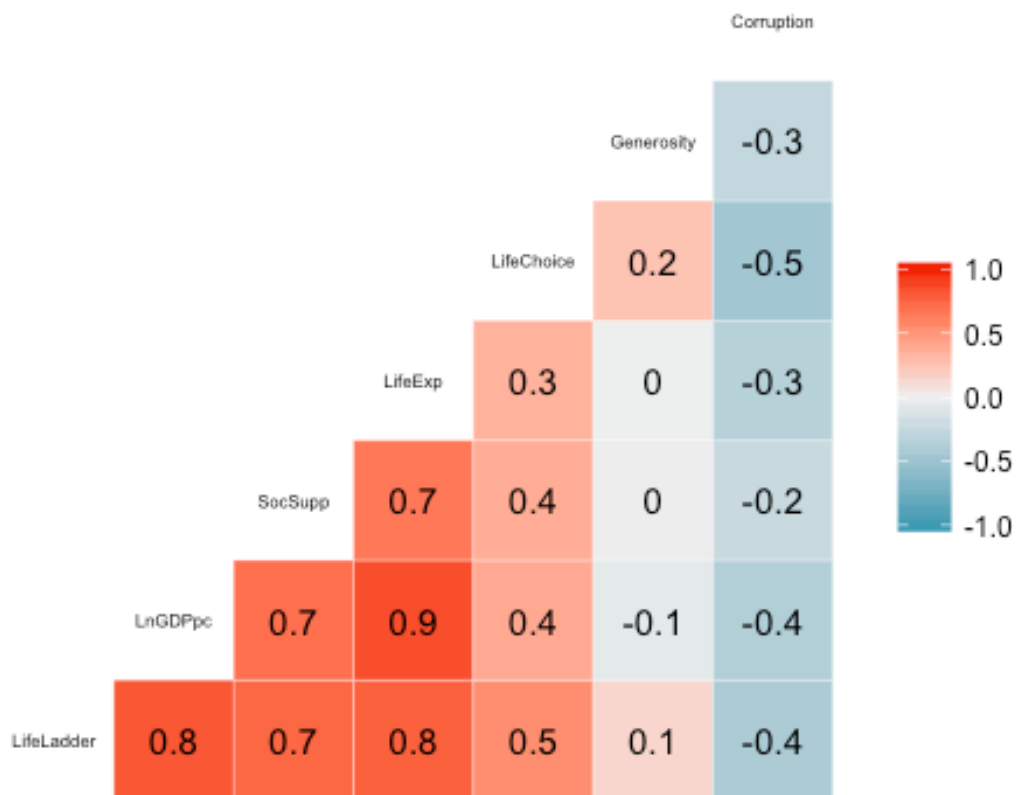
In order to handle the missing value, we first search the dataset of World bank and find the 2016 GDPpc value of 5 missing countries.

```
# Fill out NAs with Average values
for(i in c(2,4,5,6,7,8)){
  happiness[,i][is.na(happiness[,i])] <- mean(happiness[,i], na.rm = TRUE)
}
```

```
# Take out the rows with missing values
happiness<-na.omit(happiness)
```

Then, we have a look at variation of Corruption, Generosity, LifeChoice and LifeExp. The result shows that these 4 variables all have low variations, so they are all close to the mean. Meanwhile, we find that the missing variables of the country is at most 3. If we fill the NAs with mean value of the variables, they still have ability to be clustered. So, we decided to put mean value in the missing observations.

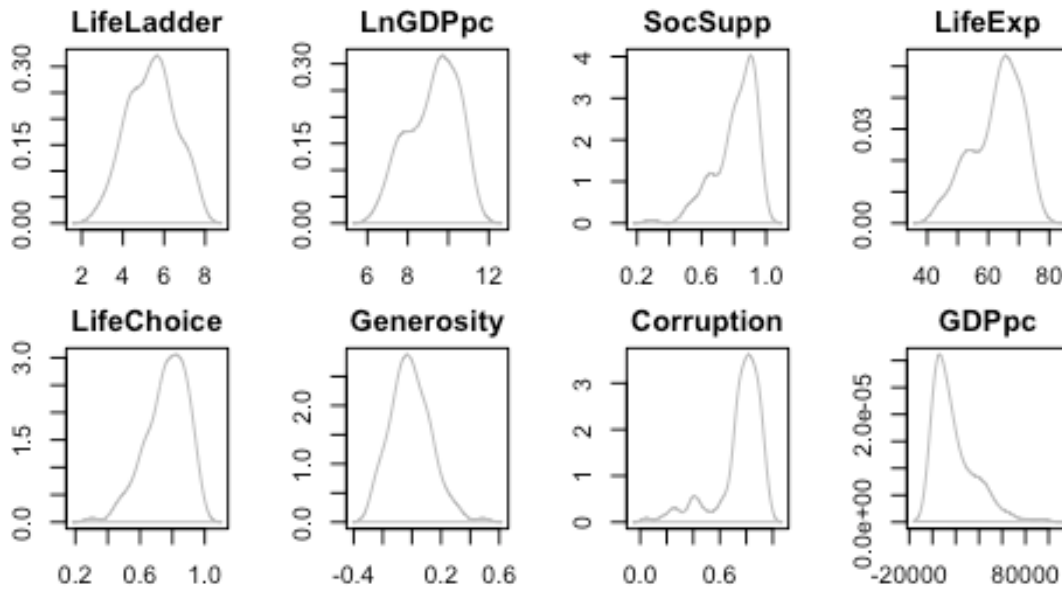
```
# Draw a correlation matrix
ggcorr(happiness[, -c(1,9)], label=TRUE, cex=2)
```



```
# Draw density graphs to see the distribution of all the variables
opar<-par(no.readonly = TRUE)
par(mfrow=c(3, 4))
par(mar = rep(2, 4))

for (i in 2:9) {
  d <- density(happiness[,i])
  plot(d, type="n", main=colnames(happiness)[i])
  polygon(d, border="gray")}
```

```
par(opar)
```



```
# Do power transformation on variables with skewness and redraw density graphs
powerTransform(happiness[,c(4,6,8)]) ## evaluate best power number

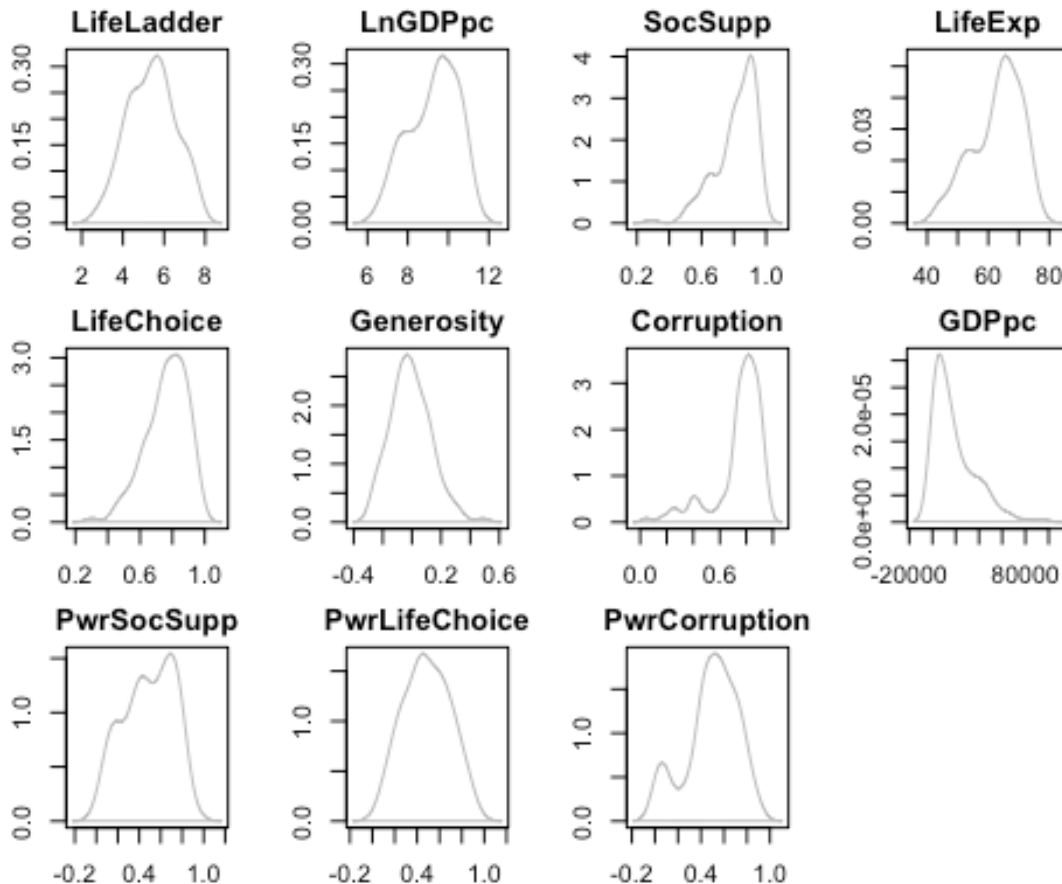
## Estimated transformation parameters
##      SocSupp LifeChoice Corruption
##  4.061827  2.928190  2.836991

happiness$PwrSocSupp<-(happiness$SocSupp)^4.06
happiness$PwrLifeChoice<-(happiness$LifeChoice)^2.93
happiness$PwrCorruption<-(happiness$Corruption)^2.84

opar<-par(no.readonly = TRUE)
par(mfrow=c(3, 4))
par(mar = rep(2, 4))

for (i in 2:12) {
  d <- density(happiness[,i])
  plot(d, type="n", main=colnames(happiness)[i])
  polygon(d, border="gray")}
```

```
par(opar)
```



Before choosing the variables to put into our model, we are curious about the distribution of these variables. Our clustering methods use Euclidean Distance, which computes the square of the distance between data points, and therefore tails of the distribution have the disproportionate effect on the model. We find that SocSupp, LifeChoice and Corruption have negative skewness. And GDPpc has positive skewness. However, LnGDPpc has already solve the problem of GDPpc. So, we decide to only do power transformation of SocSupp, LifeChoice and Corruption. We use powerTransform fuction to find the best power. The second graph shows the result of power transformation.

```
# Select variables after analysis
happiness1<-happiness[,c(1,2,3,5,7,10,11,12)]

# Normalize input variables
happiness.norm <- data.frame(sapply(happiness1[, -1], scale))

# Add row names
row.names(happiness.norm) <- happiness1[,1]

# Draw normalized density graphs of selected variables
```

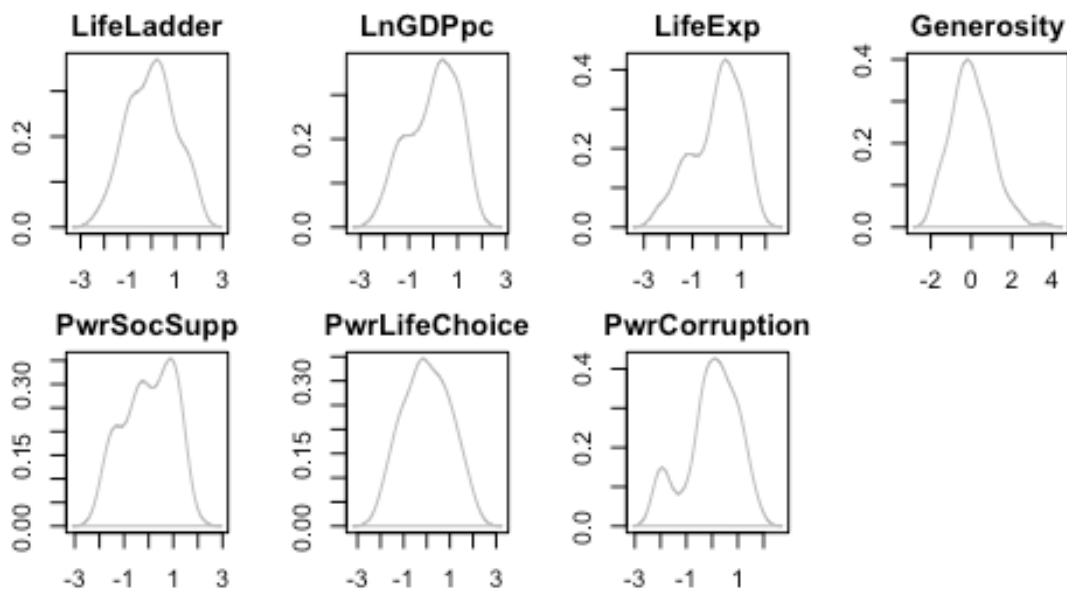
```

opar<-par(no.readonly = TRUE)
par(mfrow=c(3,4))
par(mar = rep(2, 4))

for (i in 1:7) {
  d <- density(na.omit(happiness.norm[,i]))
  plot(d, type="n", main=colnames(happiness.norm)[i])
  polygon(d, border="gray")}

par(opar)

```



Then, we start to choose variables. We use LifeLadder, LnGDPpc, LifeExp, Generosity, powered SocSupp, powered LifeChoice and powered Corruption. Although some variables are highly correlated, for example, LifeExp, SocSupp, LifeLadder and LnGDPpc. It seems like reasonable. Countries with higher GDP may have higher life level because they are able to buy anything they want and get more support from their friends or relatives. Also, people with more money have ability to go to hospital and meet better doctors when they are sick. But we think they measures different dimension of countries, GDP can not explain everything. So we still keep them in the inputs. The last thing building the model we have done is normalizing the variable in order to avoid the impact of scale and calculate the distance between countries more accurate.

## Model Selection

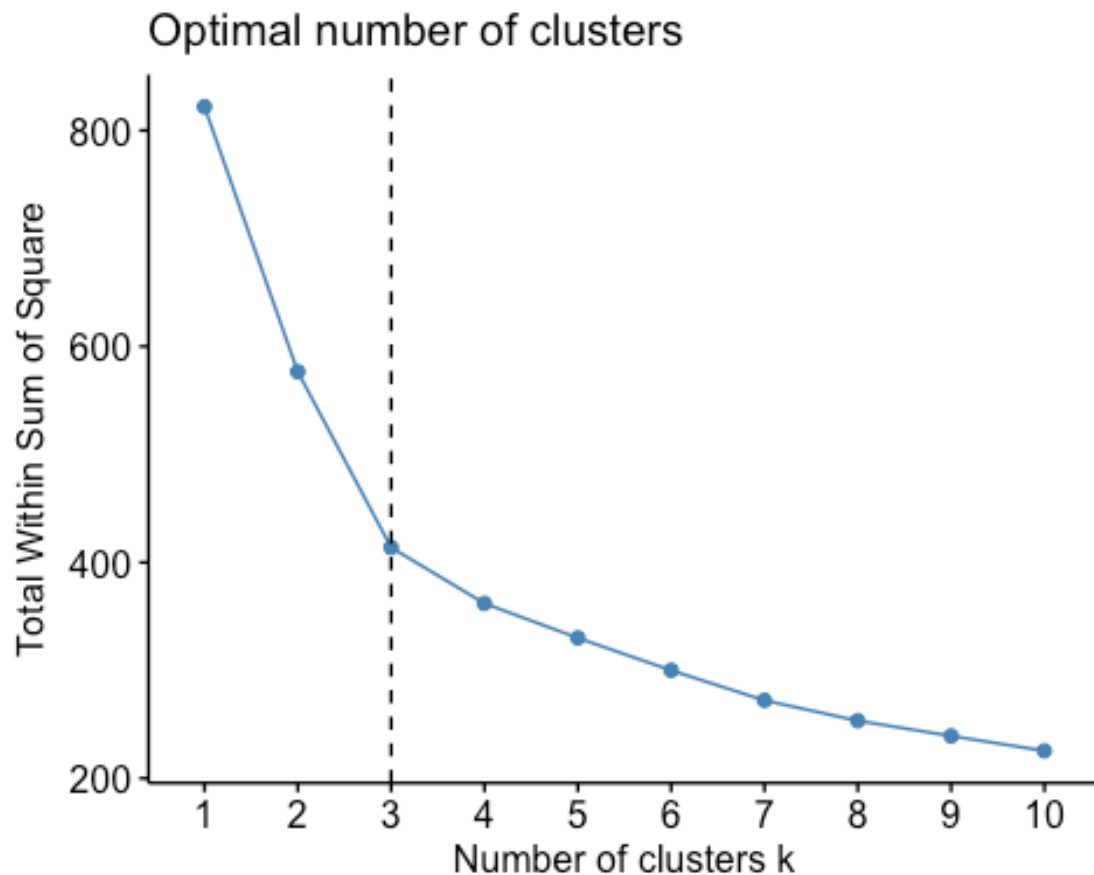
### Clustering

Overall, we choose the number of cluster based on the elbow point in WSS diagram for each cluster model. Then comparing the cluster diagram of each model and combining with educational knowledges, we choose the model which generates the most proportional and non-overlapping clusters and provides meaningful and practical significance.

```
# Exclude LifeLadder  
happiness.norm2<-happiness.norm[, -1]
```

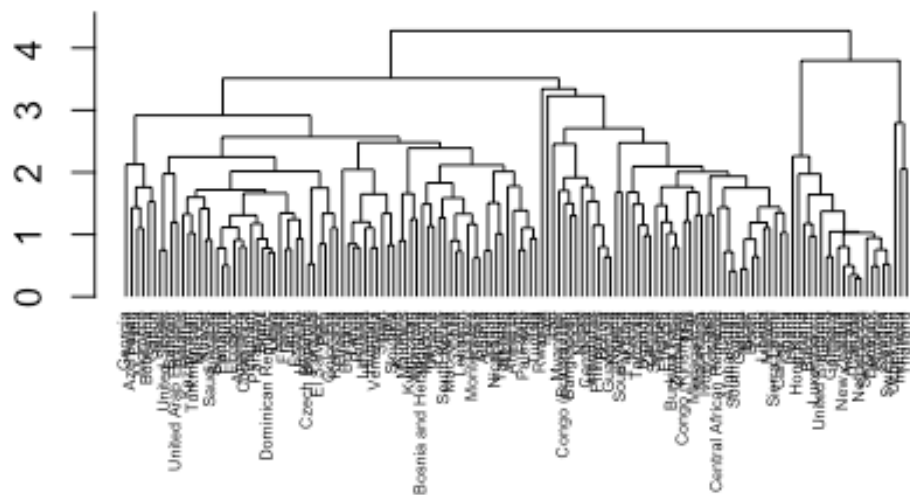
### Model 1 Hierarchical model without LifeLadder

```
## Compute Euclidean distance  
d.norm <- dist(happiness.norm2, method = "euclidean")  
  
## Choose the optimal k based on WSS  
fviz_nbclust(happiness.norm2, hcut, method = "wss") +  
  geom_vline(xintercept = 3, linetype = 2)
```



Based on elbow point in WSS diagram, the k equals to 3 in hierarchical cluster method without LifeLadder.

```
## Compare average and complete method
hc1 <- hclust(d.norm, method = "average")
plot(hc1, hang = -1, ann = FALSE,cex=0.45)
```



```
memb1 <- cutree(hc1, k = 3)
memb1
```

##	Afghanistan	Albania	Algeria
##	1	1	1
##	Argentina	Armenia	Australia
##	1	1	2
##	Austria	Azerbaijan	Bahrain
##	2	1	1
##	Bangladesh	Belarus	Belgium
##	1	1	2

##	Benin	Bolivia	Bosnia and Herzegovina
##	1	1	1
##	Botswana	Brazil	Bulgaria
##	1	1	1
##	Burkina Faso	Cambodia	Cameroon
##	1	1	1
##	Canada	Central African Republic	Chad
##	2	1	1
##	Chile	China	Colombia
##	1	1	1
##	Congo (Brazzaville)	Congo (Kinshasa)	Costa Rica
##	1	1	1
##	Cyprus	Czech Republic	Denmark
##	1	1	2
##	Dominican Republic	Ecuador	Egypt
##	1	1	1
##	El Salvador	Estonia	Ethiopia
##	1	1	1
##	Finland	France	Gabon
##	2	1	1
##	Georgia	Germany	Ghana
##	1	2	1
##	Greece	Guatemala	Guinea
##	1	1	1



##	Haiti	Honduras	Hong Kong
##	1	1	2
##	Hungary	Iceland	India
##	1	2	1
##	Indonesia	Iran	Iraq
##	3	1	1
##	Ireland	Israel	Italy
##	2	1	1
##	Ivory Coast	Japan	Jordan
##	1	1	1
##	Kazakhstan	Kenya	Kosovo
##	1	1	1
##	Kuwait	Kyrgyzstan	Latvia
##	1	1	1
##	Lebanon	Lesotho	Liberia
##	1	1	1
##	Libya	Lithuania	Luxembourg
##	1	1	2
##	Macedonia	Madagascar	Malawi
##	1	1	1
##	Mali	Malta	Mauritania
##	1	1	1
##	Mauritius	Mexico	Moldova
##	1	1	1

##	Mongolia	Montenegro	Morocco
##	1	1	1
##	Myanmar	Nepal	Netherlands
##	1	1	2
##	New Zealand	Nicaragua	Niger
##	2	1	1
##	Nigeria	Norway	Pakistan
##	1	2	1
##	Palestine	Panama	Paraguay
##	1	1	1
##	Peru	Philippines	Poland
##	1	1	1
##	Portugal	Romania	Russia
##	1	1	1
##	Rwanda	Saudi Arabia	Senegal
##	1	1	1
##	Serbia	Sierra Leone	Singapore
##	1	1	2
##	Slovakia	Slovenia	South Africa
##	1	1	1
##	South Korea	South Sudan	Spain
##	1	1	1
##	Sweden	Switzerland	Tajikistan
##	2	2	1

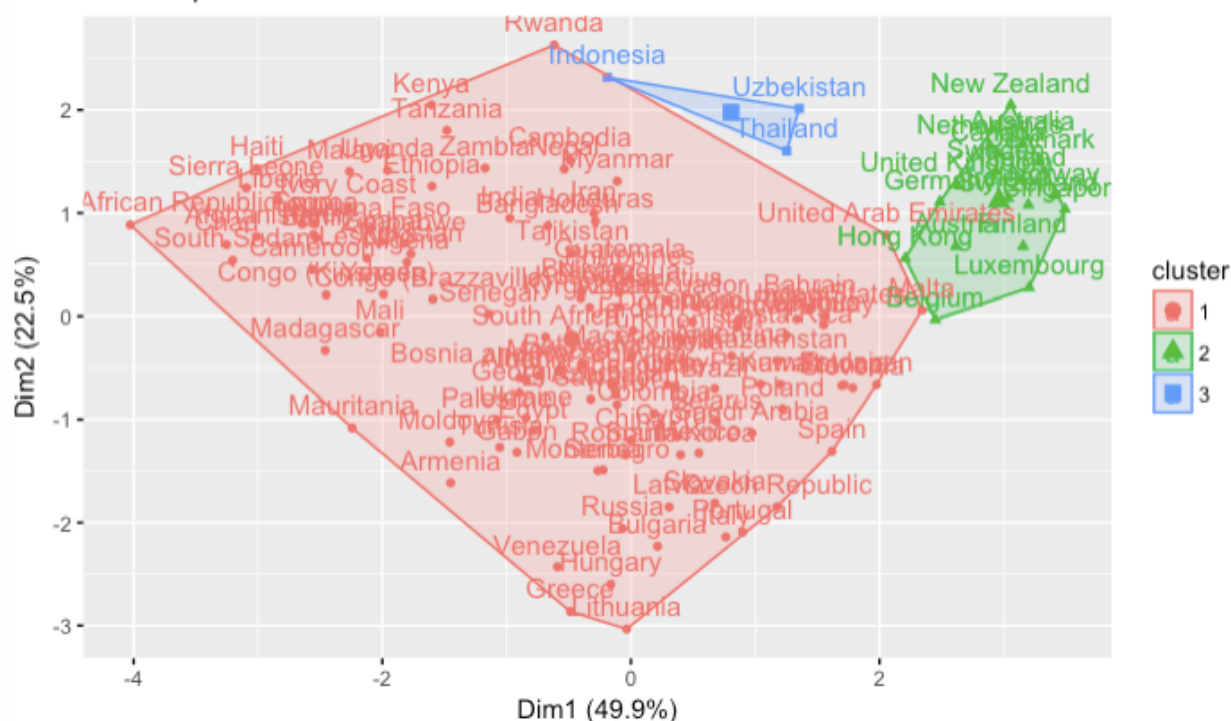
##	Tanzania	Thailand	Togo
##	1	3	1
##	Tunisia	Turkey	Turkmenistan
##	1	1	1
##	Uganda	Ukraine	United Arab Emirates
##	1	1	1
##	United Kingdom	United States	Uruguay
##	2	1	1
##	Uzbekistan	Venezuela	Vietnam
##	3	1	1
##	Yemen	Zambia	Zimbabwe
##	1	1	1

```
table(memb1)
```

```
## memb1
##  1  2  3
## 117 18  3
```

```
fviz_cluster(list(data = happiness.norm2, cluster = memb1))
```

Cluster plot



```
hc2 <- hclust(d.norm, method = "complete")
```

```
memb2 <- cutree(hc2, k = 3)
```

```
memb2
```

##	Afghanistan	Albania	Algeria
##	1	2	2
##	Argentina	Armenia	Australia
##	2	2	3
##	Austria	Azerbaijan	Bahrain
##	3	2	3
##	Bangladesh	Belarus	Belgium
##	1	2	3
##	Benin	Bolivia	Bosnia and Herzegovina
##	1	1	2
##	Botswana	Brazil	Bulgaria

##	2	2	2
##	Burkina Faso	Cambodia	Cameroon
##	1	1	1
##	Canada	Central African Republic	Chad
##	3	1	1
##	Chile	China	Colombia
##	2	2	2
##	Congo (Brazzaville)	Congo (Kinshasa)	Costa Rica
##	1	1	2
##	Cyprus	Czech Republic	Denmark
##	2	2	3
##	Dominican Republic	Ecuador	Egypt
##	2	2	2
##	El Salvador	Estonia	Ethiopia
##	2	2	1
##	Finland	France	Gabon
##	3	2	2
##	Georgia	Germany	Ghana
##	2	3	1
##	Greece	Guatemala	Guinea
##	2	1	1
##	Haiti	Honduras	Hong Kong
##	1	1	3
##	Hungary	Iceland	India

##	2	3	1
##	Indonesia	Iran	Iraq
##	3	1	2
##	Ireland	Israel	Italy
##	3	3	2
##	Ivory Coast	Japan	Jordan
##	1	2	2
##	Kazakhstan	Kenya	Kosovo
##	2	1	2
##	Kuwait	Kyrgyzstan	Latvia
##	2	2	2
##	Lebanon	Lesotho	Liberia
##	2	1	1
##	Libya	Lithuania	Luxembourg
##	2	2	3
##	Macedonia	Madagascar	Malawi
##	2	1	1
##	Mali	Malta	Mauritania
##	1	3	1
##	Mauritius	Mexico	Moldova
##	2	2	2
##	Mongolia	Montenegro	Morocco
##	2	2	2
##	Myanmar	Nepal	Netherlands

##	1	1	3
##	New Zealand	Nicaragua	Niger
##	3	1	1
##	Nigeria	Norway	Pakistan
##	1	3	1
##	Palestine	Panama	Paraguay
##	2	2	2
##	Peru	Philippines	Poland
##	2	1	2
##	Portugal	Romania	Russia
##	2	2	2
##	Rwanda	Saudi Arabia	Senegal
##	1	2	1
##	Serbia	Sierra Leone	Singapore
##	2	1	3
##	Slovakia	Slovenia	South Africa
##	2	2	2
##	South Korea	South Sudan	Spain
##	2	1	2
##	Sweden	Switzerland	Tajikistan
##	3	3	1
##	Tanzania	Thailand	Togo
##	1	3	1
##	Tunisia	Turkey	Turkmenistan

```
##           2           2           2
##           Uganda           Ukraine           United Arab Emirates
##           1           2           3
##           United Kingdom           United States           Uruguay
##           3           3           2
##           Uzbekistan           Venezuela           Vietnam
##           3           2           2
##           Yemen           Zambia           Zimbabwe
##           1           1           1
```

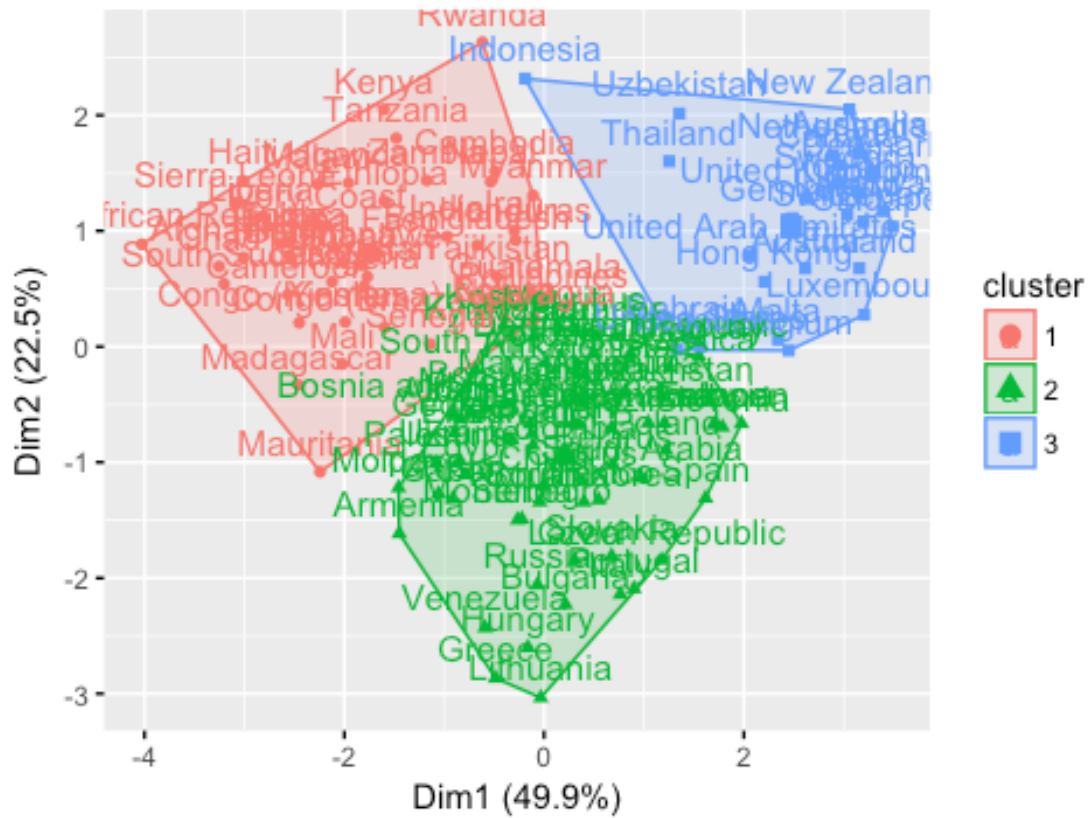
```
table(memb2)
```

```
## memb2
##  1  2  3
## 45 67 26
```

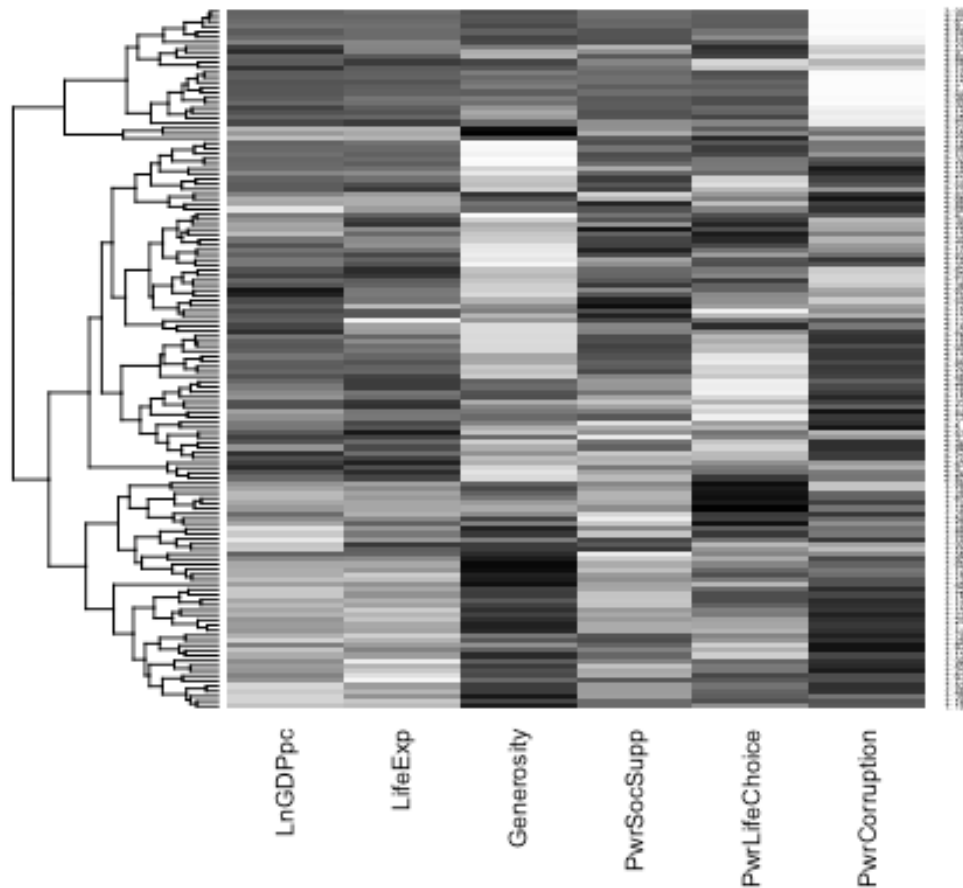
```
fviz_cluster(list(data = happiness.norm2, cluster = memb2))
```



## Cluster plot



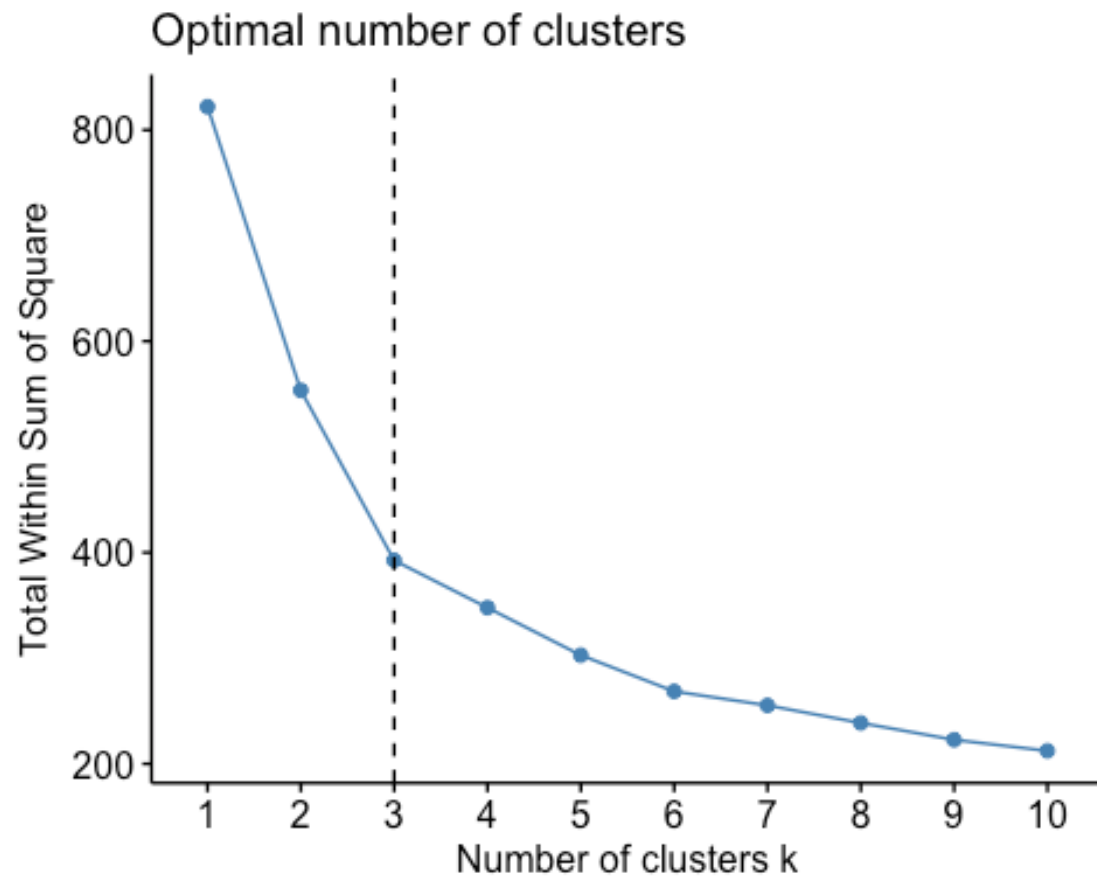
```
## plot heatmap
## rev() reverses the color mapping to large = dark
row.names(happiness.norm2) <- paste(memb2, ":", row.names(happiness), sep =
"")
heatmap(as.matrix(happiness.norm2), dendrogram="row", Colv = NA, hclustfun = h
clust, key.xlab = "Cm",
        col=rev(paste("gray", 1:99, sep="")), cexRow = 0.3, cexCol = 0.8)
```



Comparing average and complete methods, we choose the complete methods which generates more proportional clusters. The number of countries in each cluster respectively is 45, 67 and 26. In Cluster 1, there are countries such as India, Afghanistan, Ethiopia, Liberia and Nepal, where the countries are generally less developed. In Cluster 2, there are countries such as Peru, Portugal, Poland, Vietnam and Japan, where there is a mix of developed and less developed countries. In Cluster 3, there are countries such as Hong Kong, Denmark, United States, United Kingdom and Switzerland, where the countries are generally more developed. The heatmap is showed as below which provides more detailed analysis of each cluster. As the heat diagram shows, the Cluster 3, which is at the top of the heat map, usually has high GDP per capital, life expenditure, generosity, social support and life choice but has low corruption. The Cluster 2 has very similar pattern to Cluster 3 in many attributes except generosity and corruption. It usually has a relative low generosity and a high corruption. In contrast, Cluster 1 generally has a relatively high index in corruption and lowest indexes in other four attributes except generosity. The generosity is in supervise higher than the cluster 2's.

## Model 2 K-means model without LifeLadder

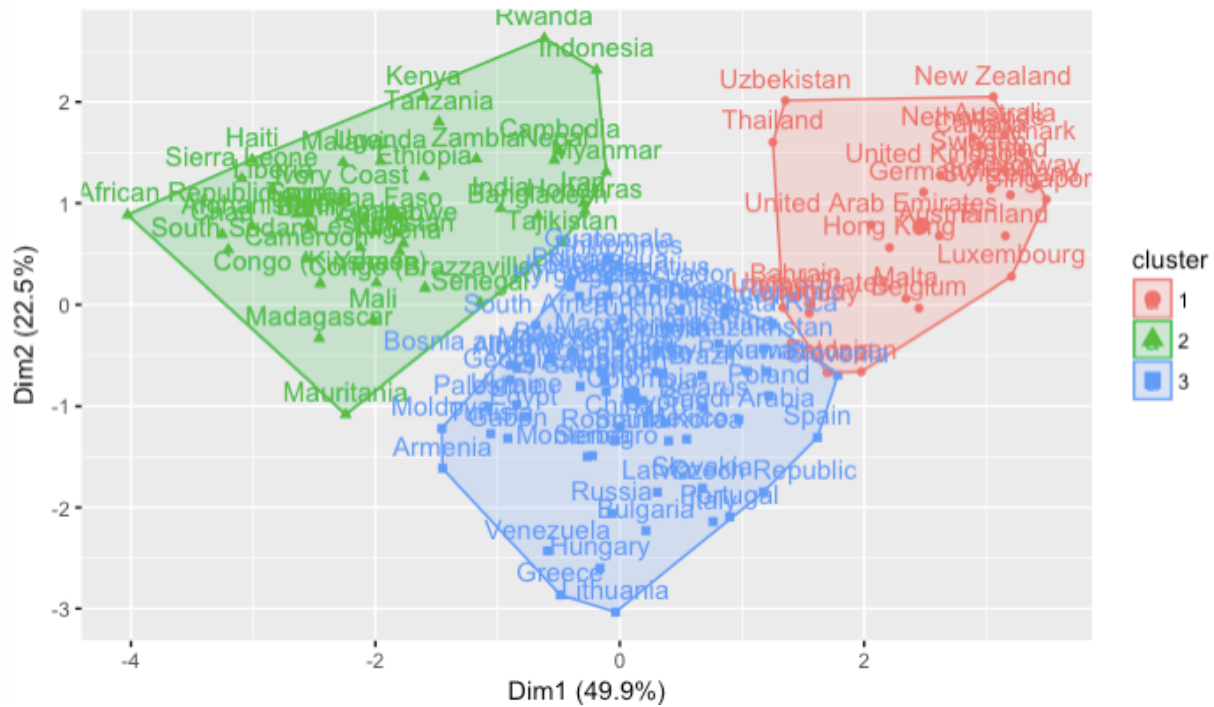
```
## Choose the optimal k based on WSS
set.seed(123)
fviz_nbclust(happiness.norm2, kmeans, method = "wss") +
  geom_vline(xintercept = 3, linetype = 2)
```



Based on elbow point in WSS, the k equals to 3 without LifeLadder. In later discussion it provides BSS/TSS=52.2%.

```
km <- kmeans(happiness.norm2, 3)
fviz_cluster(km, happiness.norm2)
```

Cluster plot



km

```
## K-means clustering with 3 clusters of sizes 29, 42, 67
##
## Cluster means:
##      LnGDPpc  LifeExp  Generosity  PwrSocSupp  PwrLifeChoice  PwrCorruption
## 1  1.114994  1.006658  0.7616236  1.0141274    1.1107057    -1.2865436
## 2 -1.212155 -1.181419  0.3966743 -1.0261713    -0.3767489     0.1317047
## 3  0.277249  0.304873 -0.5783195  0.2043209    -0.2445822     0.4743010
##
## Clustering vector:
##  1: 1   2: 2   2: 3   2: 4   2: 5   3: 6   3: 7   2: 8   3: 9   1: 10
##    2     3     3     3     3     1     1     3     1     2
##  2: 11  3: 12  1: 13  1: 14  2: 15  2: 16  2: 17  2: 18  1: 19  1: 20
##    3     1     2     3     3     3     3     3     2     2
##  1: 21  3: 22  1: 23  1: 24  2: 25  2: 26  2: 27  1: 28  1: 29  2: 30
##    2     1     2     2     3     3     3     2     2     3
##  2: 31  2: 32  3: 33  2: 34  2: 35  2: 36  2: 37  2: 38  1: 39  3: 40
##    3     3     1     3     3     3     3     1     2     1
##  2: 41  2: 42  2: 43  3: 44  1: 45  2: 46  1: 47  1: 48  1: 49  1: 50
##    1     3     3     1     2     3     3     2     2     2
##  3: 51  2: 52  3: 53  1: 54  3: 55  1: 56  2: 57  3: 58  3: 59  2: 60
##    1     3     1     2     2     2     3     1     1     3
##  1: 61  2: 62  2: 63  2: 64  1: 65  2: 66  2: 67  2: 68  2: 69  2: 70
##    2     1     3     3     2     3     3     3     3     3
##  1: 71  1: 72  2: 73  2: 74  3: 75  2: 76  1: 77  1: 78  1: 79  3: 80
##    2     2     3     3     1     3     2     2     2     1
##  1: 81  2: 82  2: 83  2: 84  2: 85  2: 86  2: 87  1: 88  1: 89  3: 90
```

```

##      2      3      3      3      3      3      3      2      2      1
## 3: 91 1: 92 1: 93 1: 94 3: 96 1: 97 2: 98 2: 99 2: 100 2: 101
##      1      3      2      2      1      2      3      3      3      3
## 1: 102 2: 103 2: 104 2: 105 2: 106 1: 107 2: 108 1: 109 2: 110 1: 111
##      3      3      3      3      3      2      3      2      3      2
## 3: 112 2: 113 2: 114 2: 116 2: 117 1: 118 2: 119 3: 120 3: 121 1: 123
##      1      3      3      3      3      2      3      1      1      2
## 1: 124 3: 125 1: 126 2: 127 2: 128 2: 129 1: 130 2: 131 3: 132 3: 133
##      2      1      2      3      3      3      2      3      1      1
## 3: 134 2: 135 3: 136 2: 137 2: 138 1: 139 1: 140 1: 141
##      1      1      1      3      3      2      2      2
##
## Within cluster sum of squares by cluster:
## [1] 70.30303 129.89983 192.41012
## (between_SS / total_SS = 52.2 %)
##
## Available components:
##
## [1] "cluster"      "centers"      "totss"        "withinss"
## [5] "tot.withinss" "betweenss"    "size"         "iter"
## [9] "ifault"

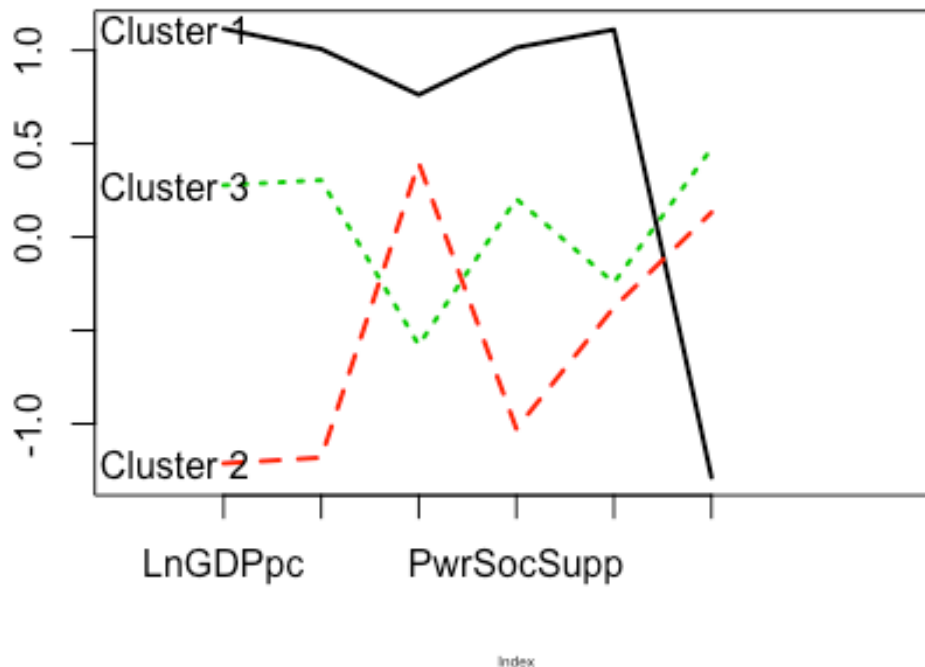
## Plot an empty scatter plot
plot(c(0), xaxt = 'n', ylab = "", type = "l",
      ylim = c(min(km$centers), max(km$centers)), xlim = c(0, 8), cex.lab=0.4)

## Label x-axes
axis(1, at = c(1:6), labels = names(happiness.norm2))

## Plot centroids
for (i in c(1:3))
  lines(km$centers[i,], lty = i, lwd = 2, col = i)

## Name clusters
text(x = 0.5, y = km$centers[, 1], labels = paste("Cluster", c(1:3)))

```

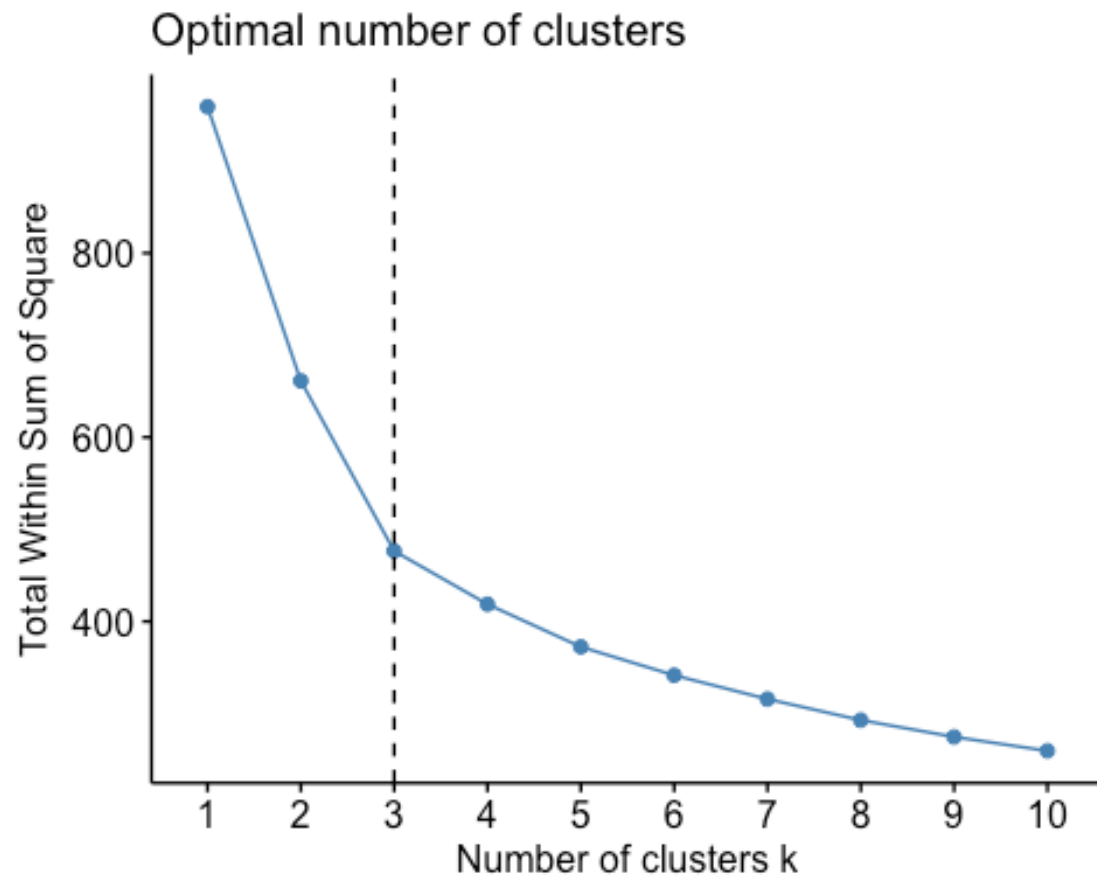


The number of countries in each cluster respectively is 29, 42, 67. In Cluster 1, there are countries such as Austria, Canada, United States, United Kingdom and Singapore, where the countries are generally more developed. In Cluster 2, there are countries such as Afghanistan, India, Nepal, Congo and Liberia, where the countries are less developed. In Cluster 3, there are countries such as Peru, Argentina, Spain, Vietnam and Turkey, where there is a mix of developed and less developed countries. The centroid profile plot is provided as below. The Cluster 1, the same as Cluster 3 in hierarchical clustering, generally has high GDP per capital, life expenditure, generosity, social support and life choice but has a low corruption. The Cluster 2 generally is low in GDP, Life expenditure, social support and life choice, and relatively high in Generosity and Corruption. The Cluster 3 is very similar to Cluster 1 in many attributes except generosity and corruption. It usually has a relatively low generosity and a relatively high corruption.

### Model 3 Hierarchical model with LifeLadder

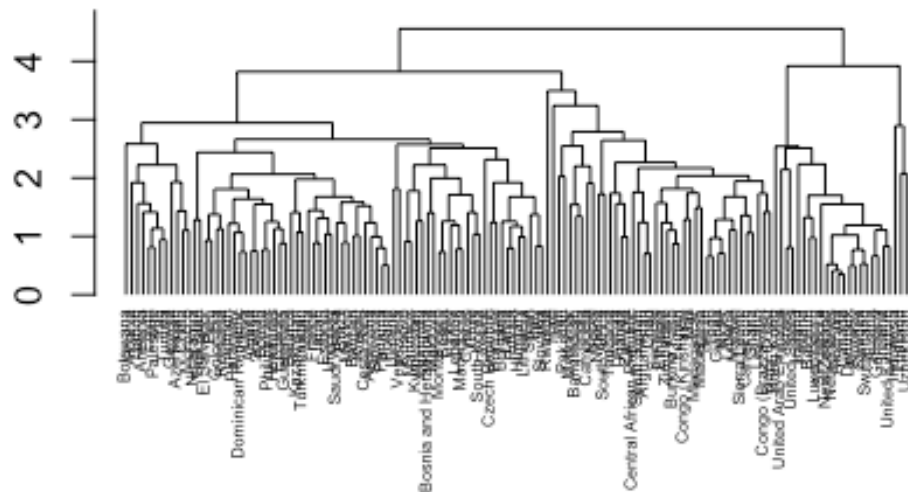
```
# Include LifeLadder and compute Euclidean distance
d.norm1 <- dist(happiness.norm, method = "euclidean")

## Choose the optimal k based on WSS
fviz_nbclust(happiness.norm, hcut, method = "wss") +
  geom_vline(xintercept = 3, linetype = 2)
```



Based on elbow point in WSS diagram, the k equals to 3 in hierarchical cluster method with LifeLadder.

```
## Compare average and complete method  
hc3 <- hclust(d.norm1, method = "average")  
plot(hc3, hang = -1, ann = FALSE, cex=0.45)
```



```
memb3 <- cutree(hc3, k = 3)
```

```
table(memb3)
```

```
## memb3
```

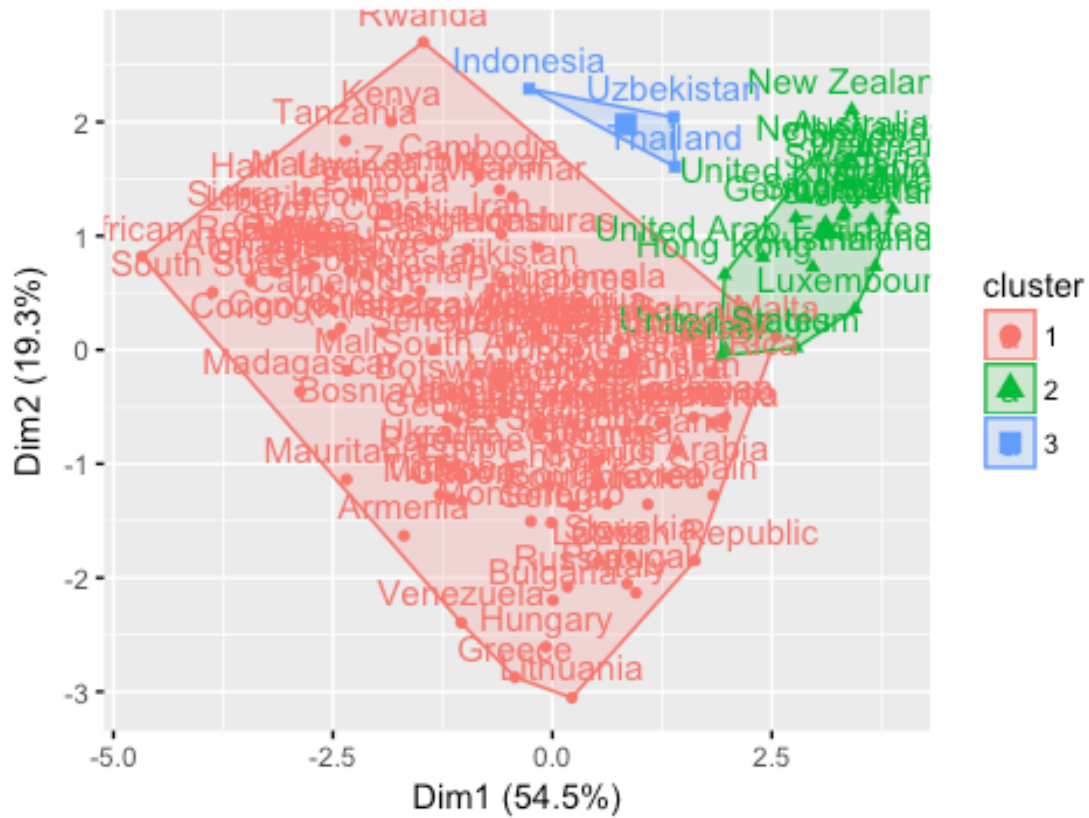
```
##    1    2    3
```

```
## 114   21    3
```

```
fviz_cluster(list(data = happiness.norm, cluster = memb3))
```



## Cluster plot



```
hc4 <- hclust(d.norm1, method = "complete")
memb4 <- cutree(hc4, k = 3)
memb4
```

##	Afghanistan	Albania	Algeria
##	1	2	2
##	Argentina	Armenia	Australia
##	2	2	3
##	Austria	Azerbaijan	Bahrain
##	3	2	3
##	Bangladesh	Belarus	Belgium
##	2	2	3
##	Benin	Bolivia	Bosnia and Herzegovina

##	1	2	2
##	Botswana	Brazil	Bulgaria
##	2	2	2
##	Burkina Faso	Cambodia	Cameroon
##	1	1	1
##	Canada Central African Republic		Chad
##	3	1	1
##	Chile	China	Colombia
##	2	2	2
##	Congo (Brazzaville)	Congo (Kinshasa)	Costa Rica
##	1	1	2
##	Cyprus	Czech Republic	Denmark
##	2	2	3
##	Dominican Republic	Ecuador	Egypt
##	2	2	2
##	El Salvador	Estonia	Ethiopia
##	2	3	1
##	Finland	France	Gabon
##	3	3	2
##	Georgia	Germany	Ghana
##	2	3	1
##	Greece	Guatemala	Guinea
##	2	2	1
##	Haiti	Honduras	Hong Kong

##	1	1	3
##	Hungary	Iceland	India
##	2	3	2
##	Indonesia	Iran	Iraq
##	3	1	2
##	Ireland	Israel	Italy
##	3	3	2
##	Ivory Coast	Japan	Jordan
##	1	3	2
##	Kazakhstan	Kenya	Kosovo
##	2	1	2
##	Kuwait	Kyrgyzstan	Latvia
##	3	2	2
##	Lebanon	Lesotho	Liberia
##	2	1	1
##	Libya	Lithuania	Luxembourg
##	2	2	3
##	Macedonia	Madagascar	Malawi
##	2	1	1
##	Mali	Malta	Mauritania
##	1	3	1
##	Mauritius	Mexico	Moldova
##	2	2	2
##	Mongolia	Montenegro	Morocco

##	2	2	2
##	Myanmar	Nepal	Netherlands
##	2	1	3
##	New Zealand	Nicaragua	Niger
##	3	2	1
##	Nigeria	Norway	Pakistan
##	2	3	1
##	Palestine	Panama	Paraguay
##	2	2	2
##	Peru	Philippines	Poland
##	2	2	2
##	Portugal	Romania	Russia
##	2	2	2
##	Rwanda	Saudi Arabia	Senegal
##	1	2	1
##	Serbia	Sierra Leone	Singapore
##	2	1	3
##	Slovakia	Slovenia	South Africa
##	2	2	2
##	South Korea	South Sudan	Spain
##	2	1	2
##	Sweden	Switzerland	Tajikistan
##	3	3	2
##	Tanzania	Thailand	Togo

##	1	3	1
##	Tunisia	Turkey	Turkmenistan
##	2	2	2
##	Uganda	Ukraine	United Arab Emirates
##	1	2	3
##	United Kingdom	United States	Uruguay
##	3	3	3
##	Uzbekistan	Venezuela	Vietnam
##	3	2	2
##	Yemen	Zambia	Zimbabwe
##	1	1	1

```
table(memb4)
```

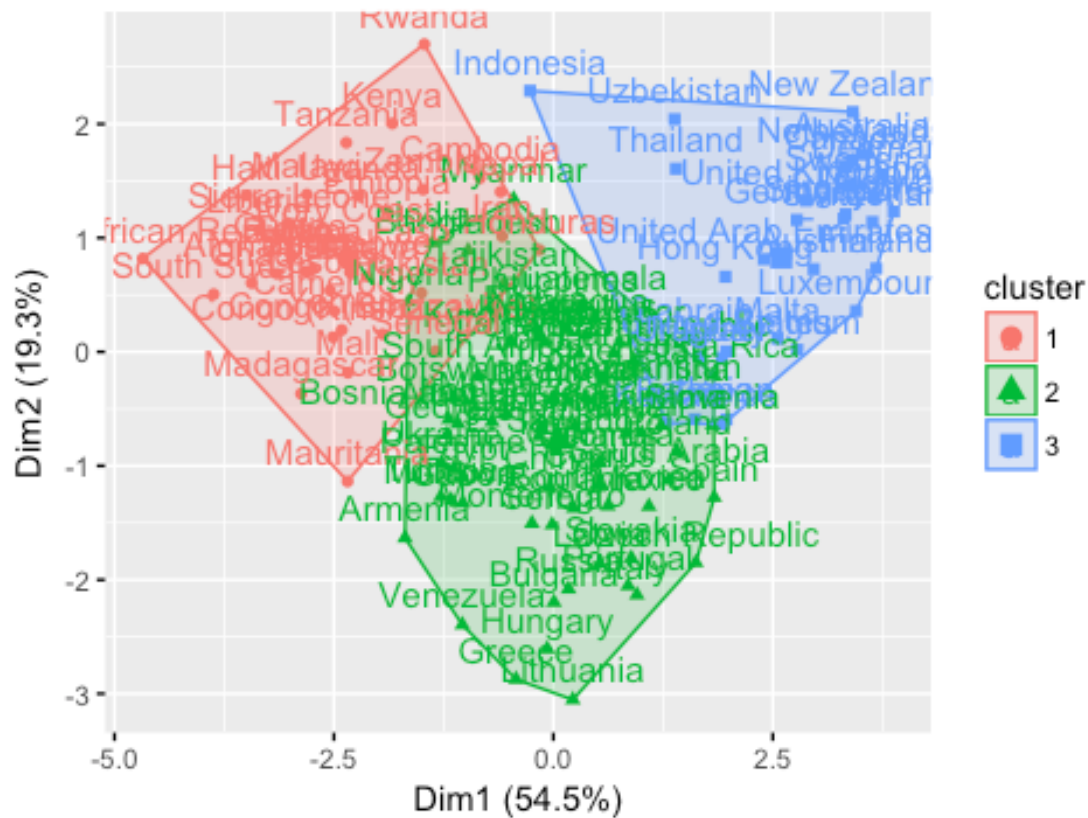
```
## memb4
```

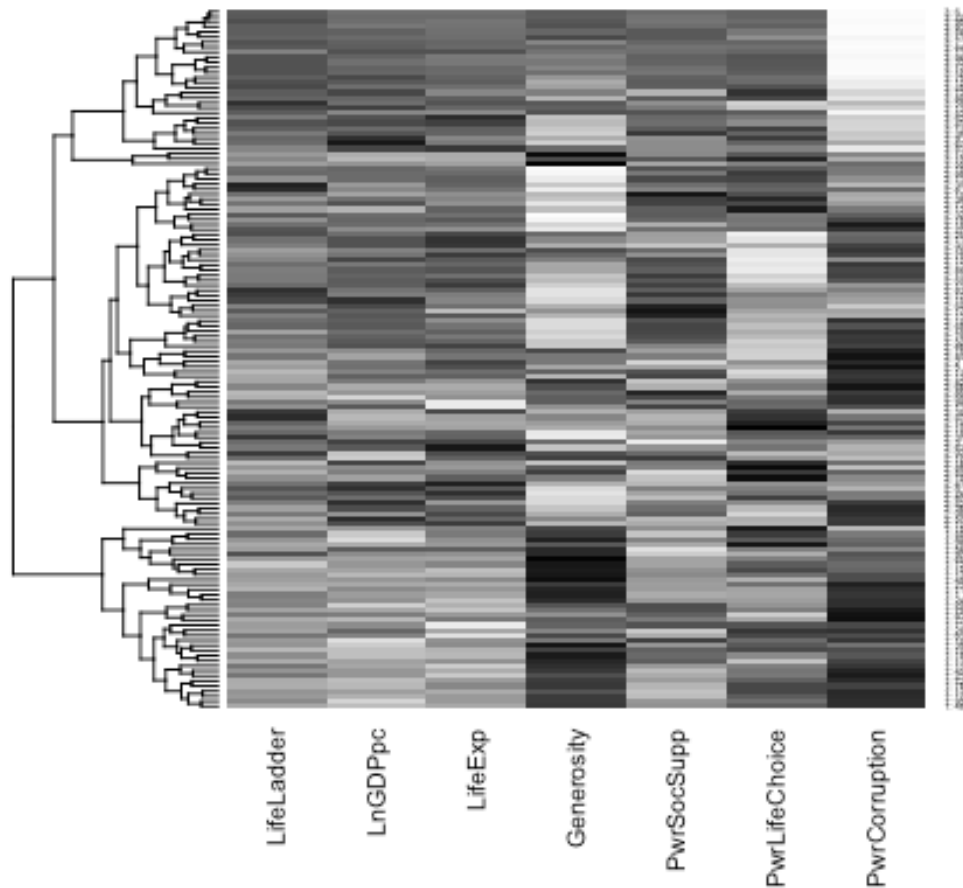
```
## 1 2 3
```

```
## 36 71 31
```

```
fviz_cluster(list(data = happiness.norm, cluster = memb4))
```

Cluster plot

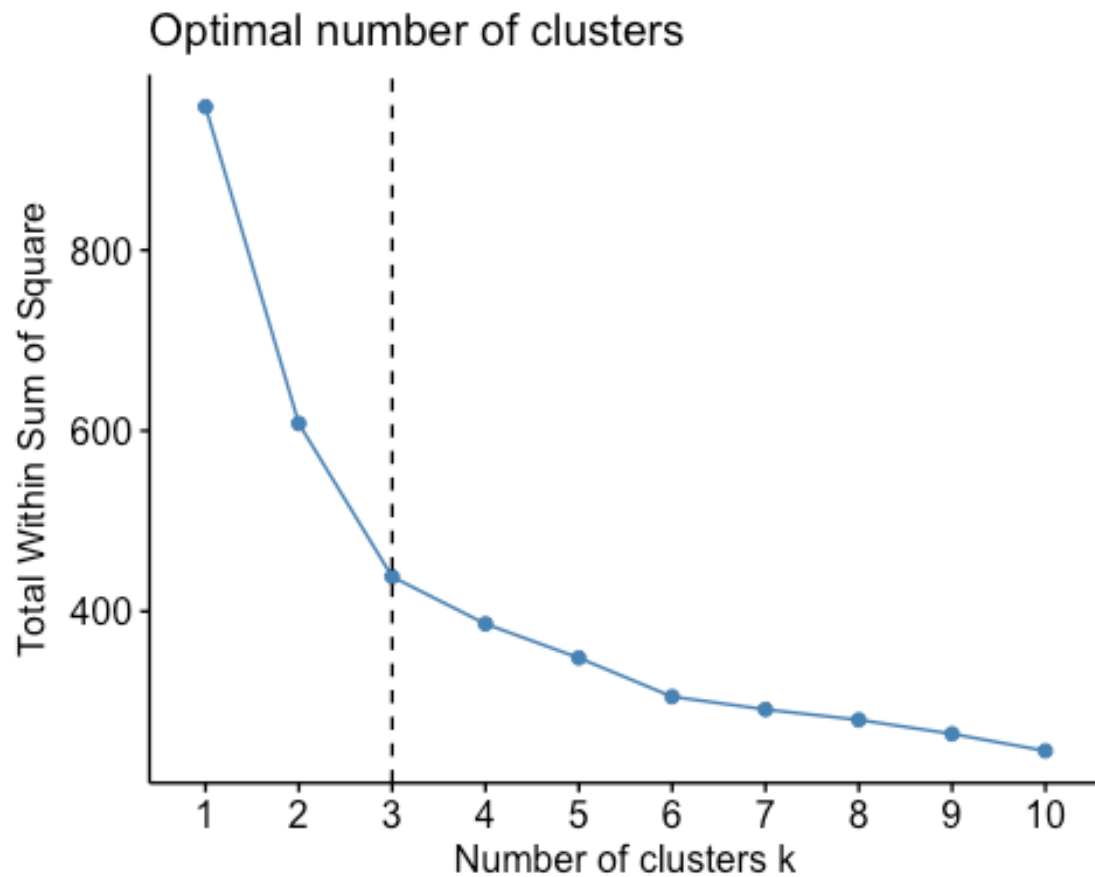




Comparing average and complete methods, we choose the complete methods which generates more proportional clusters. The number of countries in each cluster respectively is 36, 71 and 31. In Cluster 1, there are countries such as India, Afghanistan, Ethiopia, Liberia and Nepal, where the countries are generally less developed. In Cluster 2, there are countries such as Peru, Portugal, Poland, Vietnam and Labia, where there is a mix of developed and less developed countries. In Cluster 3, there are countries such as Hong Kong, Denmark, United States, United Kingdom and Japan, where the countries are generally more developed. The heat map is showed as below which provides more detailed analysis of each cluster. As the heat diagram shows, the Cluster 3, which is at the top of the heat map, usually has high life ladder, GDP per capital, life expenditure, generosity, social support and life choice but has low corruption. The Cluster 2 has very similar pattern to Cluster 3 in many attributes except generosity and corruption. It usually has a relative low generosity and a high corruption. In contrast, Cluster 1 generally has a relatively high index in corruption and lowest indexes in other five attributes except generosity. The generosity is in supervise higher than the cluster 2's.

## Model 4 K-means model with LifeLadder

```
## Choose the optimal k based on WSS
set.seed(123)
fviz_nbclust(happiness.norm, kmeans, method = "wss") +
  geom_vline(xintercept = 3, linetype = 2)
```

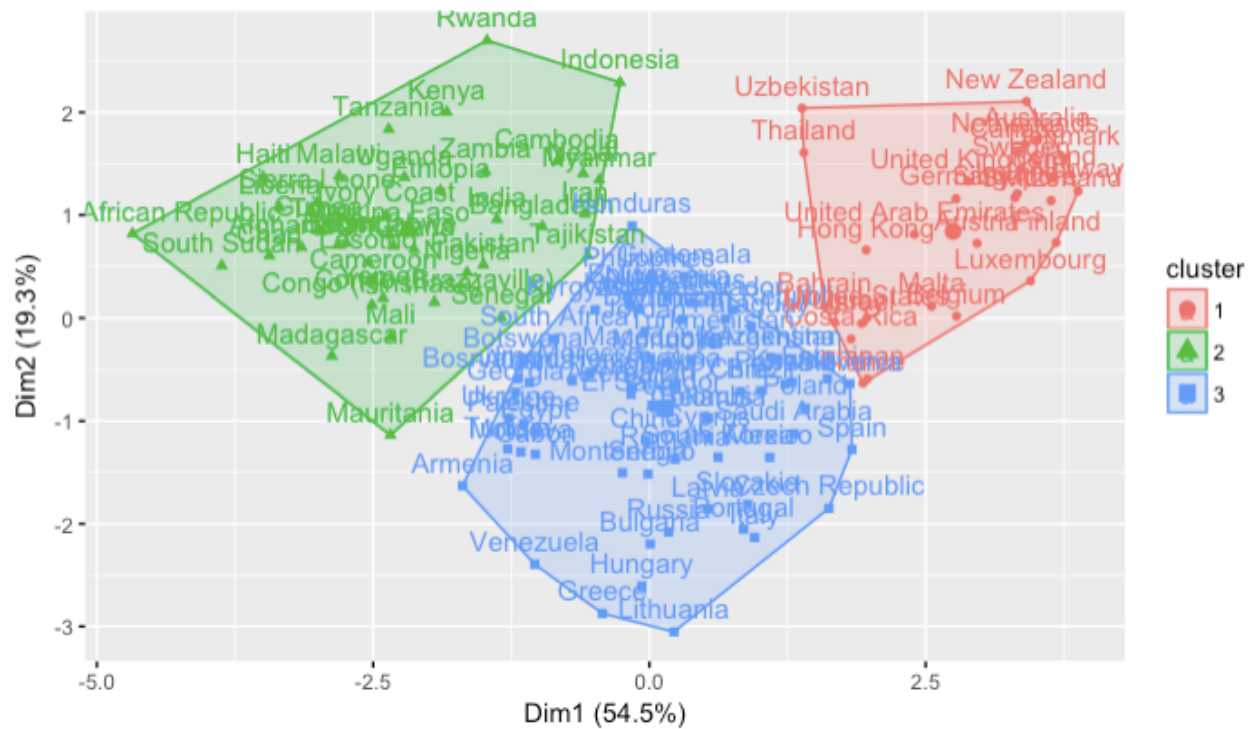


Based on elbow point in WSS, the k equals to 3 with LifeLadder. In later discussion it provides BSS/TSS=54.3%, higher than the k in k-means model without life ladder.

```
km1 <- kmeans(happiness.norm, 3)
fviz_cluster(km, happiness.norm)
```



Cluster plot



```
km1
```

```
## K-means clustering with 3 clusters of sizes 29, 41, 68
##
## Cluster means:
##   LifeLadder   LnGDPpc   LifeExp   Generosity   PwrSocSupp   PwrLifeChoice
## 1  1.27291777  1.0974951  1.0165406  0.7928399  0.9966661  1.1216921
## 2 -1.05425235 -1.2261693 -1.2122245  0.3908106 -1.0368722 -0.4018333
## 3  0.09279016  0.2712586  0.2973754 -0.5737587  0.2001242 -0.2360869
##   PwrCorruption
## 1   -1.2535017
## 2    0.1327160
## 3    0.4545616
##
## Clustering vector:
##   1: 1   2: 2   2: 3   2: 4   2: 5   3: 6   3: 7   2: 8   3: 9   2: 10
##      2      3      3      3      3      1      1      3      1      2
## 2: 11  3: 12  1: 13  2: 14  2: 15  2: 16  2: 17  2: 18  1: 19  1: 20
##      3      1      2      3      3      3      3      3      2      2
## 1: 21  3: 22  1: 23  1: 24  2: 25  2: 26  2: 27  1: 28  1: 29  2: 30
##      2      1      2      2      3      3      3      2      2      1
## 2: 31  2: 32  3: 33  2: 34  2: 35  2: 36  2: 37  3: 38  1: 39  3: 40
##      3      3      1      3      3      3      3      3      2      1
## 3: 41  2: 42  2: 43  3: 44  1: 45  2: 46  2: 47  1: 48  1: 49  1: 50
##      1      3      3      1      2      3      3      2      2      3
## 3: 51  2: 52  3: 53  2: 54  3: 55  1: 56  2: 57  3: 58  3: 59  2: 60
```

```

##      1      3      1      2      2      2      3      1      1      3
## 1: 61 3: 62 2: 63 2: 64 1: 65 2: 66 3: 67 2: 68 2: 69 2: 70
##      2      1      3      3      2      3      3      3      3      3
## 1: 71 1: 72 2: 73 2: 74 3: 75 2: 76 1: 77 1: 78 1: 79 3: 80
##      2      2      3      3      1      3      2      2      2      1
## 1: 81 2: 82 2: 83 2: 84 2: 85 2: 86 2: 87 2: 88 1: 89 3: 90
##      2      3      3      3      3      3      3      2      2      1
## 3: 91 2: 92 1: 93 2: 94 3: 96 1: 97 2: 98 2: 99 2: 100 2: 101
##      1      3      2      2      1      2      3      3      3      3
## 2: 102 2: 103 2: 104 2: 105 2: 106 1: 107 2: 108 1: 109 2: 110 1: 111
##      3      3      3      3      3      2      3      2      3      2
## 3: 112 2: 113 2: 114 2: 116 2: 117 1: 118 2: 119 3: 120 3: 121 2: 123
##      1      3      3      3      3      2      3      1      1      2
## 1: 124 3: 125 1: 126 2: 127 2: 128 2: 129 1: 130 2: 131 3: 132 3: 133
##      2      1      2      3      3      3      2      3      1      1
## 3: 134 3: 135 3: 136 2: 137 2: 138 1: 139 1: 140 1: 141
##      1      1      1      3      3      2      2      2
##
## Within cluster sum of squares by cluster:
## [1] 76.95656 139.38763 221.98106
## (between_SS / total_SS = 54.3 %)
##
## Available components:
##
## [1] "cluster"      "centers"      "totss"        "withinss"
## [5] "tot.withinss" "betweenss"    "size"         "iter"
## [9] "ifault"

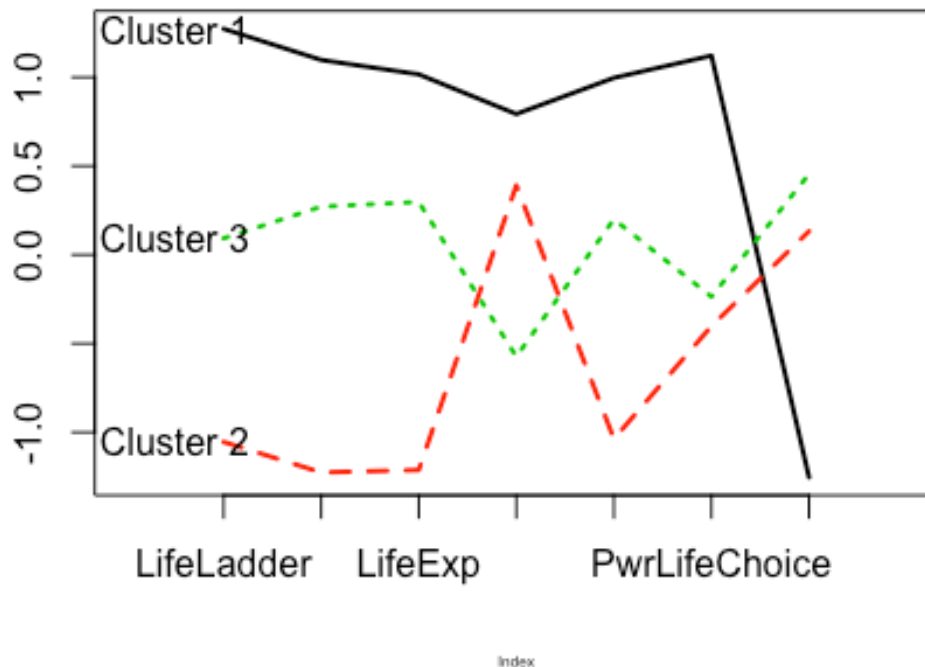
## Plot an empty scatter plot
plot(c(0), xaxt = 'n', ylab = "", type = "l",
      ylim = c(min(km1$centers), max(km1$centers)), xlim = c(0, 8), cex.lab=0.
4)

## Label x-axes
axis(1, at = c(1:7), labels = names(happiness.norm))

## Plot centroids
for (i in c(1:3))
  lines(km1$centers[i,], lty = i, lwd = 2, col = i)

## Name clusters
text(x = 0.5, y = km1$centers[, 1], labels = paste("Cluster", c(1:3)))

```



The number of countries in each cluster respectively is 29, 41, 68, slightly different from kmeans model without life ladder. In Cluster 1, there are countries such as Austria, Canada, United States, United Kingdom and Japan, where the countries are generally more developed. In Cluster 2, there are countries such as Afghanistan, India, Nepal, Congo and Liberia, where the countries are less developed. In Cluster 3, there are countries such as Peru, Argentina, Spain, Vietnam and Turkey, where there is a mix of developed and less developed countries. The centroid profile plot is provided as below. The Cluster 1 generally has high life ladder, GDP per capital, life expenditure, generosity, social support and life choice but has a low corruption. The Cluster 2 generally is low in life ladder, GDP per capital, life expenditure, social support and life choice, and relatively high in generosity and corruption. The Cluster 3 is very similar to Cluster 1 in many attributes except generosity and corruption. It usually has a relatively low generosity and a relatively high corruption.

## Impact of LifeLadder

The impact of LifeLadder on the clustering is first measured by the sum of square index. But here with a new variable added, simply using the sum of squares will cause bias in comparison, so we decide to use the Between Sum of Square/Total Sum of Square to adjust the bias caused by different numbers of variables. We'll only look at the impact of LifeLadder on Kmean clustering because it's the better clustering under both circumstances.

```
## Compare two k-means models
km

## K-means clustering with 3 clusters of sizes 29, 42, 67
##
##
## Within cluster sum of squares by cluster:
## [1] 70.30303 129.89983 192.41012
## (between_SS / total_SS = 52.2 %)
##
##
km1

## K-means clustering with 3 clusters of sizes 29, 41, 68
##
##
## Within cluster sum of squares by cluster:
## [1] 76.95656 139.38763 221.98106
## (between_SS / total_SS = 54.3 %)
##
```

The BSS/TSS of the kmeans clustering without LifeLadder is 52.2% and The BSS/TSS of the kmeans clustering with LifeLadder is 54.3%. A higher BSS/TSS means a better clustering, so, although to a small extent, LifeLadder did improve the performance of our clustering, which means it contains information the other 6 variables don't.

```
opar<-par(no.readonly = TRUE)
par(mfrow=c(1, 2))
par(mar=rep(2,4))

## Plot an empty scatter plot
plot(c(0), xaxt = 'n', ylab = "", type = "l",
      ylim = c(min(km$centers), max(km$centers)), xlim = c(0, 8), cex.lab=
0.2, main = "Clusters without LifeLadder", cex.main=1)

## Label x-axes
axis(1, at = c(1:6), labels = names(happiness.norm2))

## Plot centroids
for (i in c(1:3))
  lines(km$centers[i,], lty = i, lwd = 2, col = i)

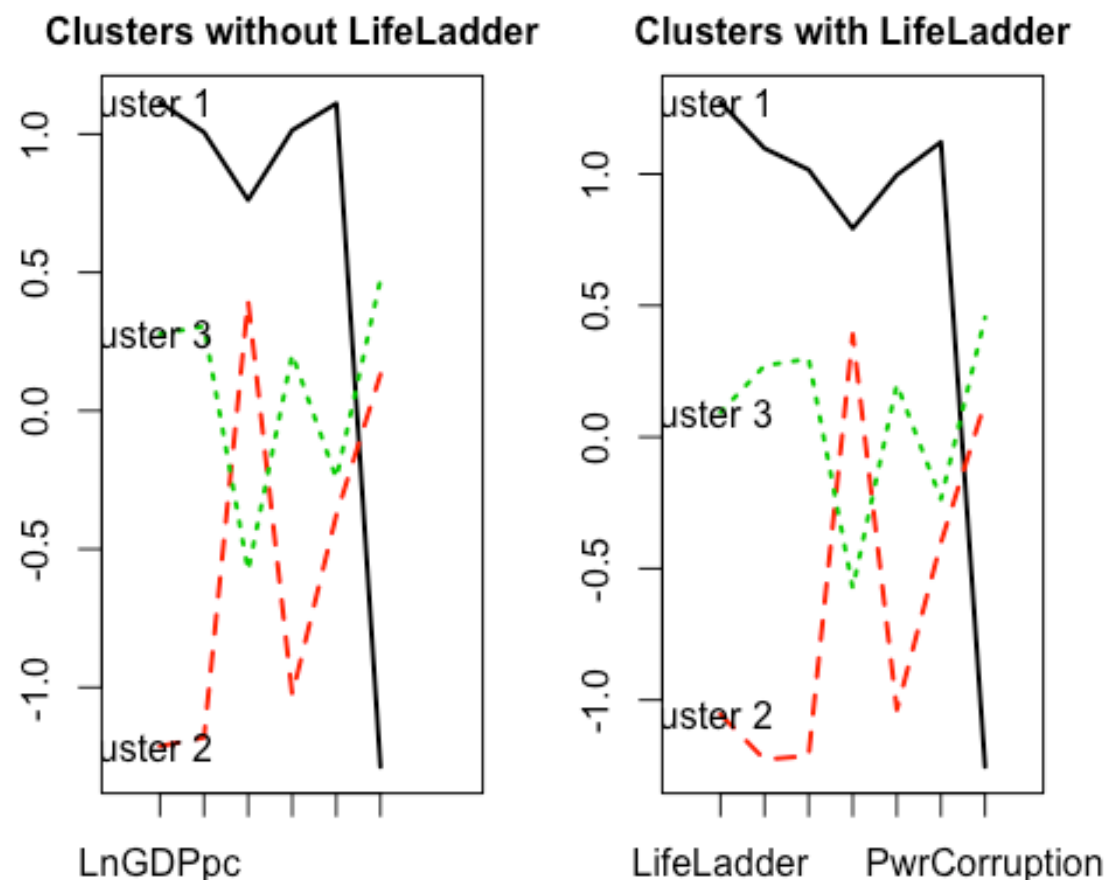
## Name clusters
text(x = 0.5, y = km$centers[, 1], labels = paste("Cluster", c(1:3)))

## Plot an empty scatter plot
plot(c(0), xaxt = 'n', ylab = "", type = "l",
      ylim = c(min(km1$centers), max(km1$centers)), xlim = c(0, 8), cex.lab=
0.2, main = "Clusters with LifeLadder", cex.main=1)
```

```
## Label x-axes
axis(1, at = c(1:7), labels = names(happiness.norm))

## Plot centroids
for (i in c(1:3))
  lines(km1$centers[i,], lty = i, lwd = 2, col = i)

## Name clusters
text(x = 0.5, y = km1$centers[, 1], labels = paste("Cluster", c(1:3)))
```



```
par(opar)
```

From the above graph, we can easily tell that cluster 1 is “the happiest cluster”, cluster 3 is “the second happiest cluster” and cluster 2 is “the least happy” cluster, and that with or without LifeLadder, the clusterings are almost the same, which further proves that the other variables can already describe most of the levels of happiness. However, there are some little fixings LifeLadder did to make the clustering more precise. With LifeLadder, cluster 1, the obviously “happiest” cluster, has a new member, Costa Rica, and Estonia no longer belongs to cluster 1. From the data set we have, although both countries has a GDPpc higher than average, Costa Rica has significantly lower GDPpc and a much high Generosity level than Estonia. The case where a country with lower GDPpc and higher Generosity is happier is rare

because LifeLadder has a very high correlation with GDPpc and very low correlation with Generosity. We can't make a conclusion based on this one case because we can always argue that people in Costa Rica may be easier to be satisfied than people in Estonia, but we can make a guess that although LifeLadder usually agrees with the other 6 variables, it sometimes captures factors related to culture and social environment that can be easily felt but are hard to measure.

## Model comparison

We think that the advantages and disadvantages of these two models are: \*\* Hierarchical Model • Hierarchical model is easy to apply and shows a clear structure on how the choice of k can affect the cluster • Hierarchical model might not show good calculating ability when the dataset is large. • Hierarchical model might be allergic to extreme values. \*\* K-Means Model • K-means model is easy to apply and has a better clustering ability. • K-means model can provide direct numeric comparison on choices of k and don't have methods confusion. • k-means model is likely to be affected by seeds(although not shown in the case).

## Best clustering

As discussed above, we choose k-means model with LifeLadder to be our best clustering model. The reasons are given below. As discussed above, we choose k-means model with LifeLadder to be our best clustering model. First, compared to hierarchical model, k-means models provide more reasonable classifications on the dataset. We can see from the comparison of two different types of graphs that the k-means model manages to separate the countries more completely than the hierarchical model does, which means that the 3 categories in k-means model are more typical to reflect the differences between countries. And when it comes to the question that whether LifeLadder should be included in the model, we think that LifeLadder is an extra supplementary that help us have a better view understanding the situation of certain countries. Although it may not directly separate some of the countries out of previous cluster, it will add another factor to show the differences between countries. For example, the US does not have high LifeLadder compared to other developed countries in Europe (they all have relative high GDP). So that we can generate a conclusion that there are differences between developed countries and GDP is not an absolute factor used to classify different clusters.

## Conclusion

In conclusion, we can see from the "2017 World Happiness Report" that for the most happy countries, they share a few common features and are alike in some ways. However, for countries with not highest happiness index, they are more likely to be different from each other.