FactorAnalysis.R

Mr.Perfectionist

Thu Apr 11 23:02:52 2019

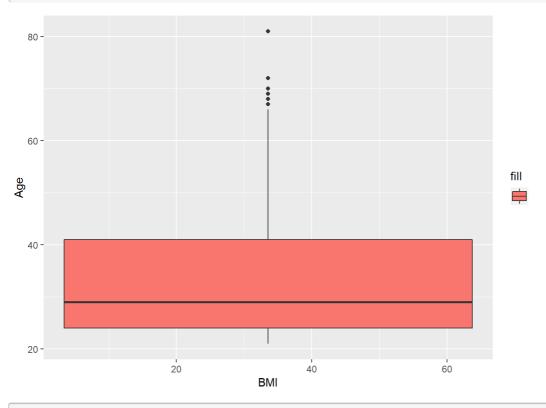
```
diabetes = read.csv("F:/Courses/MVA/diabetes.csv")
str(diabetes)
```

```
## 'data.frame': 768 obs. of 9 variables:
                           : int 6 1 8 1 0 5 3 10 2 8 ...
## $ Pregnancies
## $ Glucose
                           : int 148 85 183 89 137 116 78 115 197 125 ...
## $ BloodPressure
                          : int 72 66 64 66 40 74 50 0 70 96 ...
## $ SkinThickness
                           : int 35 29 0 23 35 0 32 0 45 0 ...
                           : int 0 0 0 94 168 0 88 0 543 0 ...
## $ Insulin
                           : num 33.6 26.6 23.3 28.1 43.1 25.6 31 35.3 30.5 0 ...
## $ BMI
## $ DiabetesPedigreeFunction: num 0.627 0.351 0.672 0.167 2.288 ...
                          : int 50 31 32 21 33 30 26 29 53 54 ...
                           : int 1 0 1 0 1 0 1 0 1 1 ...
   $ Outcome
```

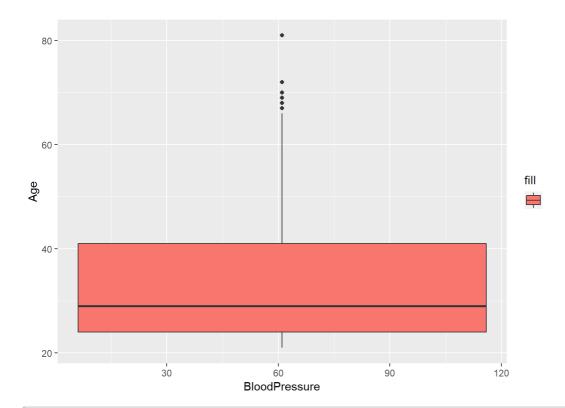
```
attach(diabetes)
library(ggplot2)
```

```
## Warning: package 'ggplot2' was built under R version 3.5.3
```

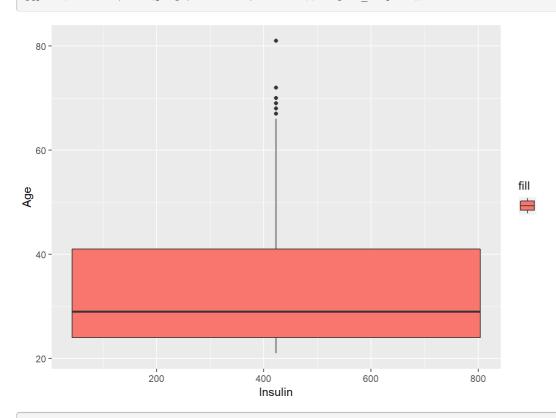
```
ggplot(diabetes, aes(y= Age ,x=BMI, fill='')) + geom_boxplot()
```



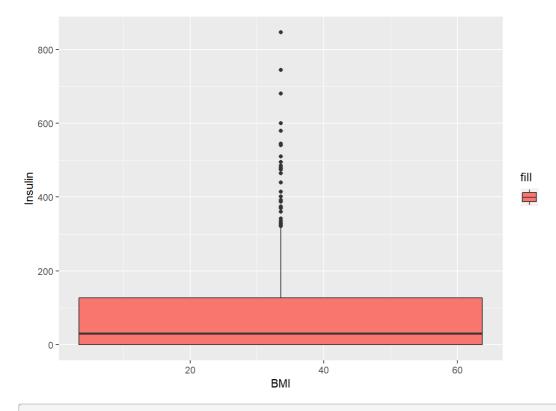
```
ggplot(diabetes, aes(y=Age,x=BloodPressure, fill='')) + geom_boxplot()
```



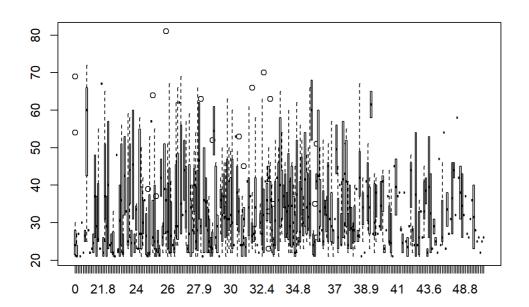
ggplot(diabetes, aes(y=Age,x=Insulin, fill='')) + geom_boxplot()



ggplot(diabetes, aes(y=Insulin,x=BMI, fill='')) + geom_boxplot()



boxplot(Age ~ BMI)



```
unique(diabetes$default)

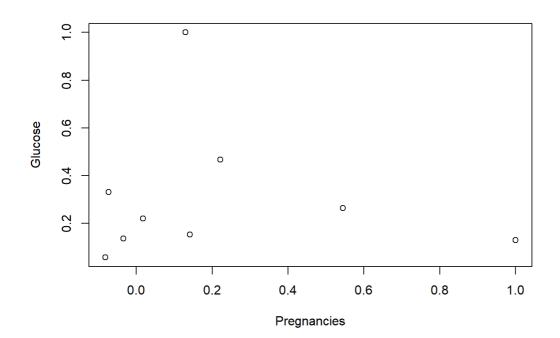
## NULL

default_dummy=ifelse(diabetes$default=='yes',1,0)
unique(diabetes$BMI)
```

```
[1] 33.6 26.6 23.3 28.1 43.1 25.6 31.0 35.3 30.5 0.0 37.6 38.0 27.1 30.1
    [15] 25.8 30.0 45.8 29.6 43.3 34.6 39.3 35.4 39.8 29.0 36.6 31.1 39.4 23.2
##
##
   [29] 22.2 34.1 36.0 31.6 24.8 19.9 27.6 24.0 33.2 32.9 38.2 37.1 34.0 40.2
   [43] 22.7 45.4 27.4 42.0 29.7 28.0 39.1 19.4 24.2 24.4 33.7 34.7 23.0 37.7
##
   [57] 46.8 40.5 41.5 25.0 25.4 32.8 32.5 42.7 19.6 28.9 28.6 43.4 35.1 32.0
##
## [71] 24.7 32.6 43.2 22.4 29.3 24.6 48.8 32.4 38.5 26.5 19.1 46.7 23.8 33.9
## [85] 20.4 28.7 49.7 39.0 26.1 22.5 39.6 29.5 34.3 37.4 33.3 31.2 28.2 53.2
## [99] 34.2 26.8 55.0 42.9 34.5 27.9 38.3 21.1 33.8 30.8 36.9 39.5 27.3 21.9
## [113] 40.6 47.9 50.0 25.2 40.9 37.2 44.2 29.9 31.9 28.4 43.5 32.7 67.1 45.0
## [127] 34.9 27.7 35.9 22.6 33.1 30.4 52.3 24.3 22.9 34.8 30.9 40.1 23.9 37.5
## [141] 35.5 42.8 42.6 41.8 35.8 37.8 28.8 23.6 35.7 36.7 45.2 44.0 46.2 35.0
## [155] 43.6 44.1 18.4 29.2 25.9 32.1 36.3 40.0 25.1 27.5 45.6 27.8 24.9 25.3
## [169] 37.9 27.0 26.0 38.7 20.8 36.1 30.7 32.3 52.9 21.0 39.7 25.5 26.2 19.3
## [183] 38.1 23.5 45.5 23.1 39.9 36.8 21.8 41.0 42.2 34.4 27.2 36.5 29.8 39.2
## [197] 38.4 36.2 48.3 20.0 22.3 45.7 23.7 22.1 42.1 42.4 18.2 26.4 45.3 37.0
## [211] 24.5 32.2 59.4 21.2 26.7 30.2 46.1 41.3 38.8 35.2 42.3 40.7 46.5 33.5
## [225] 37.3 30.3 26.3 21.7 36.4 28.5 26.9 38.6 31.3 19.5 20.1 40.8 23.4 28.3
## [239] 38.9 57.3 35.6 49.6 44.6 24.1 44.5 41.2 49.3 46.3
BMI dummy=ifelse(diabetes$BMI=='yes',1,0)
unique (diabetes $Outcome)
## [1] 1 0
Outcome_dummy=ifelse(diabetes$Outcome=='yes',1,0)
unique(diabetes$Insulin)
    [1]
         0 94 168 88 543 846 175 230 83 96 235 146 115 140 110 245
    [18] 192 207 70 240 82 36 23 300 342 304 142 128 38 100
                                                               90 270
   [35] 125 176 48 64 228 76 220 40 152 18 135 495 37 51
                                                               99 145 225
##
   [52] 49 50 92 325 63 284 119 204 155 485 53 114 105 285 156 78 130
## [69] 55 58 160 210 318 44 190 280 87 271 129 120 478 56 32 744 370
## [86] 45 194 680 402 258 375 150 67 57 116 278 122 545 75 74 182 360
## [103] 215 184   42 132 148 180 205   85 231   29   68   52 255 171   73 108   43
## [120] 167 249 293 66 465 89 158 84 72 59 81 196 415 275 165 579 310
## [137] 61 474 170 277 60 14 95 237 191 328 250 480 265 193 79 86 326
## [154] 188 106 65 166 274 77 126 330 600 185 25 41 272 321 144 15 183
## [171] 91 46 440 159 540 200 335 387 22 291 392 178 127 510 16 112
Insulin_dummy=ifelse(diabetes$Insulin=='yes',1,0)
unique (diabetes$BloodPressure)
## [1] 72 66 64 40 74 50 0 70 96 92 80 60 84 30 88 90 94
## [18] 76 82 75 58 78 68 110 56 62 85 86 48 44 65 108 55 122
## [35] 54 52 98 104 95 46 102 100 61 24 38 106 114
BloodPressure dummy=ifelse(diabetes$BloodPressure=='yes',1,0)
diabetes1 =data.frame(Age,BMI,Outcome,Insulin,BloodPressure)
# Computing Correlation Matrix
corrm.z = cor(diabetes)
corrm.z
```

```
##
                           Pregnancies Glucose BloodPressure
## Pregnancies
                           1.00000000 0.12945867 0.14128198
                                                  0.15258959
                           0.12945867 1.00000000
## Glucose
                                                  1.00000000
## BloodPressure
                           0.14128198 0.15258959
## SkinThickness
                           -0.08167177 0.05732789
                                                  0.20737054
## Insulin
                           -0.07353461 0.33135711
                                                  0.08893338
## BMI
                           0.01768309 0.22107107
                                                  0.28180529
## DiabetesPedigreeFunction -0.03352267 0.13733730
                                                  0.04126495
## Age
                           0.54434123 0.26351432
                                                  0.23952795
                           0.22189815 0.46658140
                                                  0.06506836
## Outcome
##
                           SkinThickness Insulin
                                                       BMT
## Pregnancies
                            -0.08167177 -0.07353461 0.01768309
## Glucose
                             0.05732789 0.33135711 0.22107107
## BloodPressure
                             0.20737054 0.08893338 0.28180529
## SkinThickness
                              1.00000000 0.43678257 0.39257320
## Insulin
                              0.43678257
                                         1.00000000 0.19785906
## BMI
                             0.39257320 0.19785906 1.00000000
## DiabetesPedigreeFunction 0.18392757 0.18507093 0.14064695
## Age
                            -0.11397026 -0.04216295 0.03624187
## Outcome
                             0.07475223 0.13054795 0.29269466
##
                           DiabetesPedigreeFunction
                                                          Age
                                                                 Outcome
## Pregnancies
                                        -0.03352267 0.54434123 0.22189815
## Glucose
                                        0.13733730 0.26351432 0.46658140
                                        0.04126495 0.23952795 0.06506836
## BloodPressure
                                        0.18392757 -0.11397026 0.07475223
## SkinThickness
## Insulin
                                        0.18507093 -0.04216295 0.13054795
## BMI
                                        0.14064695 0.03624187 0.29269466
## DiabetesPedigreeFunction
                                        1.00000000 0.03356131 0.17384407
                                        0.03356131 1.00000000 0.23835598
## Age
                                        0.17384407 0.23835598 1.00000000
## Outcome
```

plot(corrm.z)



diabetes_pca <- prcomp(diabetes, scale=TRUE)
diabetes_pca</pre>

```
## Standard deviations (1, ..., p=9):
## [1] 1.5337867 1.3320330 1.0584069 0.9391245 0.9190340 0.8572446 0.6988730
## [8] 0.6466693 0.6204113
##
## Rotation (n x k) = (9 \times 9):
##
                               PC1
                                        PC2
                                                 PC3
                        -0.2159984 0.52744611 -0.1645123 0.16088274
## Pregnancies
                        -0.4367568 0.09563451 0.3914174 -0.32712336
## Glucose
## BloodPressure
                        -0.3004554 0.04625339 -0.6297053 0.01105718
## SkinThickness
                        -0.3072920 -0.44839783 -0.2943260 0.07401586
                        -0.3363324 -0.35534569 0.1416535 -0.09763514
## Insulin
                        -0.3973420 -0.21031643 -0.2519303 -0.16321892
## BMI
## DiabetesPedigreeFunction -0.2376345 -0.17519467 0.2853247 0.87352658
             -0.2786556 0.53320237 -0.1261179 0.17111166
## Age
## Outcome
                        -0.4156528 0.15476805 0.3946151 -0.18167421
##
                               PC5
                                       PC6
                                                   PC7
                       -0.21176571 0.456773101 -0.07851795 -0.54064221
## Pregnancies
                        -0.10877916 -0.382749448 0.20799965 0.02524536
## Glucose
## BloodPressure
                        0.05937792 -0.607867100 -0.32670833 -0.16280013
## SkinThickness
                       -0.17180950 0.397956778 -0.28199843 0.43491377
                       -0.65037442 0.008730189 0.08221649 -0.26883758
## BMI
                        ## DiabetesPedigreeFunction 0.15655457 -0.171628373 0.05719014 -0.09316407
          -0.20428857 -0.001054913 0.29942807 0.61489048
## Age
                        0.37793701 0.171378976 -0.58037812 0.06827401
## Outcome
##
                                PC9
                  -0.26505155
## Pregnancies
                        -0.58107579
## Glucose
                         0.06830645
## BloodPressure
                        -0.39477039
## SkinThickness
## Insulin
                         0.47845101
## BMI
                         0.12644026
## DiabetesPedigreeFunction -0.04961786
## Age
## Outcome
                         0.31756221
summary(diabetes pca)
## Importance of components:
                      PC1 PC2 PC3 PC4 PC5
##
## Standard deviation 1.5338 1.3320 1.0584 0.93912 0.91903 0.85724
## Proportion of Variance 0.2614 0.1971 0.1245 0.09799 0.09385 0.08165
## Cumulative Proportion 0.2614 0.4585 0.5830 0.68100 0.77485 0.85650
##
                        PC7 PC8 PC9
## Standard deviation 0.69887 0.64667 0.62041
## Proportion of Variance 0.05427 0.04646 0.04277
## Cumulative Proportion 0.91077 0.95723 1.00000
plot(diabetes pca)
(eigen_diabetes <- diabetes_pca$sdev^2)</pre>
## [1] 2.3525016 1.7743120 1.1202251 0.8819549 0.8446234 0.7348682 0.4884234
## [8] 0.4181811 0.3849102
names(eigen_diabetes) <- paste("PC",1:9,sep="")</pre>
```

```
head(diabetes_pca$x)
```

PC1 PC2 PC3 PC4 PC5 PC6 PC7 ## 2.3525016 1.7743120 1.1202251 0.8819549 0.8446234 0.7348682 0.4884234

eigen_diabetes

PC8

0.4181811 0.3849102

PC9

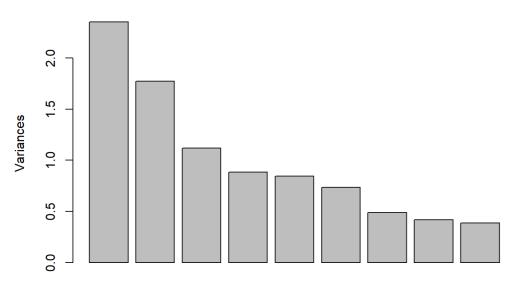
```
PC2
                                  PC3
## [1,] -1.7558028 1.1110186 0.2086554 0.33348787 0.481394261
## [2,] 1.5064398 -0.5590413 -0.6502039 0.22978395 -0.004884372 0.11923298
## [3,] -0.6503982 1.9283197 2.0064327 -0.02611202 0.233903264 -0.67360542
## [4,] 1.5863640 -1.0643810 -0.4741330 -0.58027536 -0.297234935 0.07085043
## [5,] -2.4817566 -2.3580258 2.9236096 3.93404759 1.565329993 0.20026682
## [6,] 1.4426872 1.0547347 -0.2776812 -0.41570434 -0.145266364 -0.63711649
               PC7
                          PC8
## [1,] -0.457360625 1.12367812 -0.49362490
## [2,] -0.366229199 0.85188754 -0.03130377
## [3,] -0.721004746 -0.79284183 -1.06301081
## [4,] -0.344525279 -0.03060397 0.24081177
## [5,] 0.814600055 0.39844558 0.24900243
## [6,] -0.004113885 -0.61235146 -0.18157474
```

```
dim(diabetes_pca$x)
```

```
## [1] 768 9
```

```
plot(diabetes_pca)
```

diabetes_pca

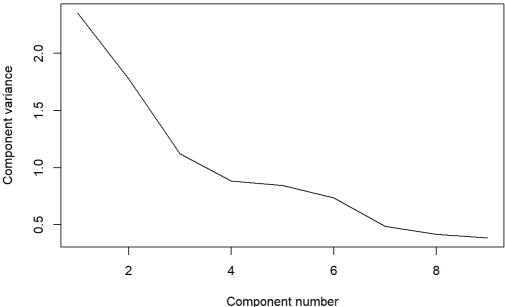


summary(diabetes pca)

```
## Importance of components:
                                    PC2
                                           PC3
                             PC1
                                                   PC4
                                                           PC5
## Standard deviation
                         1.5338 1.3320 1.0584 0.93912 0.91903 0.85724
## Proportion of Variance 0.2614 0.1971 0.1245 0.09799 0.09385 0.08165
## Cumulative Proportion 0.2614 0.4585 0.5830 0.68100 0.77485 0.85650
##
                             PC7
                                     PC8
                                              PC9
                         0.69887 0.64667 0.62041
## Standard deviation
## Proportion of Variance 0.05427 0.04646 0.04277
## Cumulative Proportion 0.91077 0.95723 1.00000
```

```
plot(eigen_diabetes, xlab = "Component number", ylab = "Component variance", type = "l", main = "Scree diagr
am")
```

Scree diagram

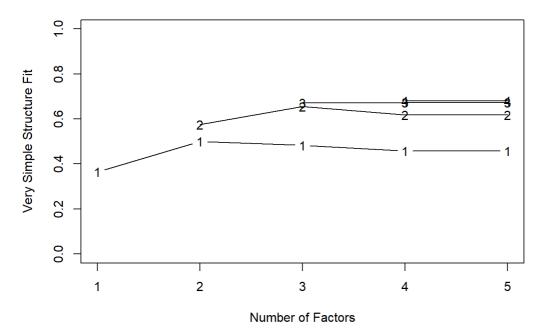


```
Component number
library (psych)
## Warning: package 'psych' was built under R version 3.5.3
##
## Attaching package: 'psych'
\#\# The following objects are masked from 'package:ggplot2':
##
##
      %+%, alpha
vss(diabetes1)
## Warning in fac(r = r, nfactors = nfactors, n.obs = n.obs, rotate =
## rotate, : A loading greater than abs(1) was detected. Examine the loadings
## carefully.
\#\# Warning in fa.stats(r = r, f = f, phi = phi, n.obs = n.obs, np.obs
\#\# = np.obs, : The estimated weights for the factor scores are probably
```

```
## incorrect. Try a different factor extraction method.
```

```
\#\# Warning in fac(r = r, nfactors = nfactors, n.obs = n.obs, rotate =
## rotate, : An ultra-Heywood case was detected. Examine the results carefully
```

Very Simple Structure



```
## Very Simple Structure
## Call: vss(x = diabetes1)
\#\# VSS complexity 1 achieves a maximimum of 0.5 with 2 factors
## VSS complexity 2 achieves a maximimum of 0.66 with 3 factors
##
\#\# The Velicer MAP achieves a minimum of NA with 1 factors
\#\# BIC achieves a minimum of NA with 2 factors
## Sample Size adjusted BIC achieves a minimum of NA with 2 factors
##
## Statistics by number of factors
## vssl vss2 map dof chisq prob sqresid fit RMSEA BIC SABIC
## 1 0.36 0.00 0.081 5 9.5e+01 7.3e-19
                                       3.6 0.36 0.15 61.4
## 2 0.50 0.57 0.191 1 1.5e+01 8.4e-05
                                         2.4 0.57 0.14 8.8
## 3 0.48 0.66 0.393 -2 2.0e-09 NA
                                        1.9 0.67
                                                   NA
                                                        NA
                                                               NA
## 4 0.46 0.62 1.000 -4 0.0e+00
                                 NA
                                                   NA
                                         1.8 0.68
                                                         NA
## 5 0.46 0.62
              NA -5 0.0e+00
                                  NA
                                         1.8 0.68
                                                   NA
                                                        NA
                                                               NA
##
  complex eChisq
                    SRMR eCRMS eBIC
       1.0 1.2e+02 8.8e-02 0.12
## 2
        1.4 1.7e+01 3.3e-02 0.11
## 3
        1.4 1.8e-09 3.4e-07
## 4
       1.7 5.4e-14 1.9e-09
                             NA
                                  NA
       1.7 5.4e-14 1.9e-09
## 5
                             NA
```

```
#therefore choosing 5 Factors

#Oblique rotation
fit.pc <- fa(diabetes1, nfactors=5, rotate="oblimin")</pre>
```

```
## Loading required namespace: GPArotation
```

```
fit.pc
```

```
## Factor Analysis using method = minres
## Call: fa(r = diabetes1, nfactors = 5, rotate = "oblimin")
## Standardized loadings (pattern matrix) based upon correlation matrix
                MR2 MR1 MR3 MR4 MR5 h2 u2 com
##
                0.67 -0.07 0.12 -0.01 0 0.47 0.53 1.1
## Age
               -0.07 0.65 0.11 0.01 0 0.47 0.53 1.1
## BMI
               0.33 0.30 -0.21 0.30 0 0.51 0.49 3.7
## Outcome
              -0.19 0.00 0.19 0.37 0 0.13 0.87 2.1
## BloodPressure 0.13 0.13 0.61 0.01 0 0.49 0.51 1.2
##
##
                        MR2 MR1 MR3 MR4 MR5
                       0.64 0.63 0.51 0.30 0.00
## SS loadings
## Proportion Var
                       0.13 0.13 0.10 0.06 0.00
## Cumulative Var
                       0.13 0.25 0.35 0.41 0.41
## Proportion Explained 0.31 0.30 0.25 0.14 0.00
## Cumulative Proportion 0.31 0.61 0.86 1.00 1.00
## With factor correlations of
##
    MR2 MR1 MR3 MR4 MR5
## MR2 1.00 0.19 0.19 0.30 0
## MR1 0.19 1.00 0.31 0.70 0
## MR3 0.19 0.31 1.00 -0.17 0
## MR4 0.30 0.70 -0.17 1.00 0
## MR5 0.00 0.00 0.00 0.00
##
## Mean item complexity = 1.8
## Test of the hypothesis that 5 factors are sufficient.
##
## The degrees of freedom for the null model are 10 and the objective function was 0.35 with Chi Square o
f 268.92
\#\# The degrees of freedom for the model are -5 and the objective function was 0
##
## The root mean square of the residuals (RMSR) is 0
## The df corrected root mean square of the residuals is NA
## The harmonic number of observations is 768 with the empirical chi square 0 with prob < NA
\#\# The total number of observations was 768 with Likelihood Chi Square = 0 with prob < NA
## Tucker Lewis Index of factoring reliability = 1.039
## Fit based upon off diagonal values = 1
## Measures of factor score adequacy
##
                                                   MR2 MR1 MR3 MR4 MR5
## Correlation of (regression) scores with factors 0.75 0.78 0.72 0.71 0
## Multiple R square of scores with factors
                                                 0.56 0.61 0.52 0.51 0
## Minimum correlation of possible factor scores
                                                 0.12 0.22 0.03 0.01 -1
```

```
#what are factors for each variable , what is affectin and
#Fit based upon off diagonal values = 0.96 higher the better
#residual should be less
round(fit.pc$values, 3)
```

```
## [1] 1.107 0.497 0.433 0.032 0.000
```

fit.pc\$loadings

```
## Loadings:
              MR2 MR1 MR3
\# \#
                                  MR4
                                         MR5
## Age
                            0.117
               0.669
                       0.647 0.109
## BMI
               0.330 0.296 -0.209 0.298
## Outcome
## Insulin
               -0.192
                            0.193 0.368
## BloodPressure 0.133 0.130 0.610
##
##
                 MR2 MR1 MR3 MR4 MR5
## SS loadings 0.616 0.528 0.478 0.225 0.000
## Proportion Var 0.123 0.106 0.096 0.045 0.000
## Cumulative Var 0.123 0.229 0.324 0.369 0.369
```

```
# Loadings with more digits
for (i in c(1,2,3,4,5)) { print(fit.pc$loadings[[1,i]])}
## [1] 0.6691348
## [1] -0.06577584
## [1] 0.1173003
## [1] -0.01371583
## [1] 7.517829e-15
# Communalities
fit.pc$communality
##
           Age
                         BMI
                                  Outcome
                                               Insulin BloodPressure
                                             0.1274868
##
      0.4696878
                   0.4706203
                                0.5081298
                                                        0.4929153
# Rotated factor scores, Notice the columns ordering: RC1, RC3, RC2 and RC4
fit.pc$scores
                 MR2
                              MR1
                                           MR3
##
    [1,] 1.293781717 0.4488283514 -0.0347154073 0.687675487 1.792075e-13
    [2,] -0.276899150 -0.6956025483 -0.1005076314 -0.678256768 -1.565038e-13
##
    [3,] 0.457321352 -0.2101551616 -0.7208675256 0.371503907 3.022903e-14
##
    [4,] -0.820158918 -0.4638932263 -0.1454118736 -0.503918008 -1.415069e-13
##
    [5,] 0.071752833 0.9799937756 -0.9444880017 1.375256974 2.164896e-13
##
##
    [6,] -0.257292578 -0.6767428839 0.1143696332 -0.749417238 -1.547352e-13
    \#\,\#
    [8,] -0.932771058 -0.7798376663 -1.9770023140 -0.083140408 -1.920539e-13
##
    [9,] 1.144362838 0.7656255590 0.0496265536 1.354851802 3.055703e-13
   [10,] 1.937378359 -1.4715963015 -0.0156046510 -0.535483604 -7.168909e-14
##
   ##
   [12,] 0.507109084 0.8151690639 -0.0494276261 0.813466573 1.827942e-13
##
   [13,]
         1.066828031 -0.6350113011 0.6361617769 -0.709589207 -6.569371e-14
         1.191275871 0.9220210351 -0.1010938067 1.815594603 3.839124e-13
##
         1.307517124 0.1241906322 -0.1434445438 0.674262501 1.603385e-13
##
   [15,]
   [16,] -0.071702341 -0.4104470199 -2.5588257689 0.892327736 -1.502363e-14
##
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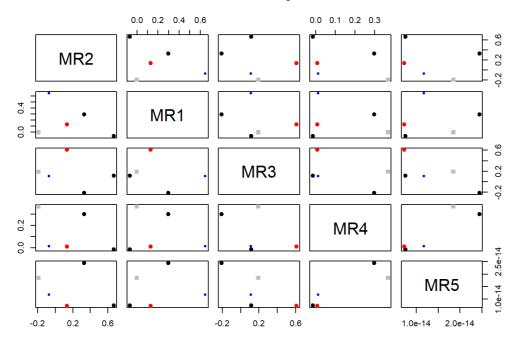
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```

eigenvalues of principal components and factor analysis **Parallel Analysis Scree Plots** PC Actual Data PC Simulated Data PC Resampled Data FA Actual Data FA Simulated Data 0. FA Resampled Data 0.5 0.0 2 3 5 1 Factor/Component Number

Parallel analysis suggests that the number of factors = 0 and the number of components = 2

fa.plot(fit.pc) # See Correlations within Factors

Factor Analysis



fa.diagram(fit.pc) # Visualize the relationship

Factor Analysis

