

# Multivariate Analysis of diabetes data

Jas Sur, Hassasn Sarr, Pushpalatha Solligi, Priyadarshini Thota

5/6/2022

## Reducing the dimesionality of diabetes factors by using PCA, factor analysis and non-metric MDS techniques

### Data Source

source : <http://odds.cs.stonybrook.edu/pima-indians-diabetes-dataset>

Following data is observed and used for predicting if a person has diabetes.

```
diabetes <- readMat('C:/Users/JasSu/Downloads/pima.mat')
diabetesX <- data.frame(diabetes$X)
diabetesY <- data.frame(diabetes$y)
colnames(diabetesY) <- "Y"
colnames(diabetesX) <- c("Pregnancies", "Glucose", "BloodPressure", "SkinThickness", "Insulin", "BMI", "DiabetesPedigreeFunction", "Age")
str(diabetesX)
```

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

```
str(diabetesY$Y)
```

```
## num [1:768] 1 0 1 0 1 0 1 0 1 1 ...
```

```
summary(diabetesX)
```

|             | Pregnancies | Glucose       | BloodPressure  | SkinThickness |
|-------------|-------------|---------------|----------------|---------------|
| ## Min.     | : 0.000     | Min. : 0.0    | Min. : 0.00    | Min. : 0.00   |
| ## 1st Qu.: | : 1.000     | 1st Qu.: 99.0 | 1st Qu.: 62.00 | 1st Qu.: 0.00 |
| ## Median : | : 3.000     | Median :117.0 | Median : 72.00 | Median :23.00 |
| ## Mean :   | : 3.845     | Mean :120.9   | Mean : 69.11   | Mean :20.54   |

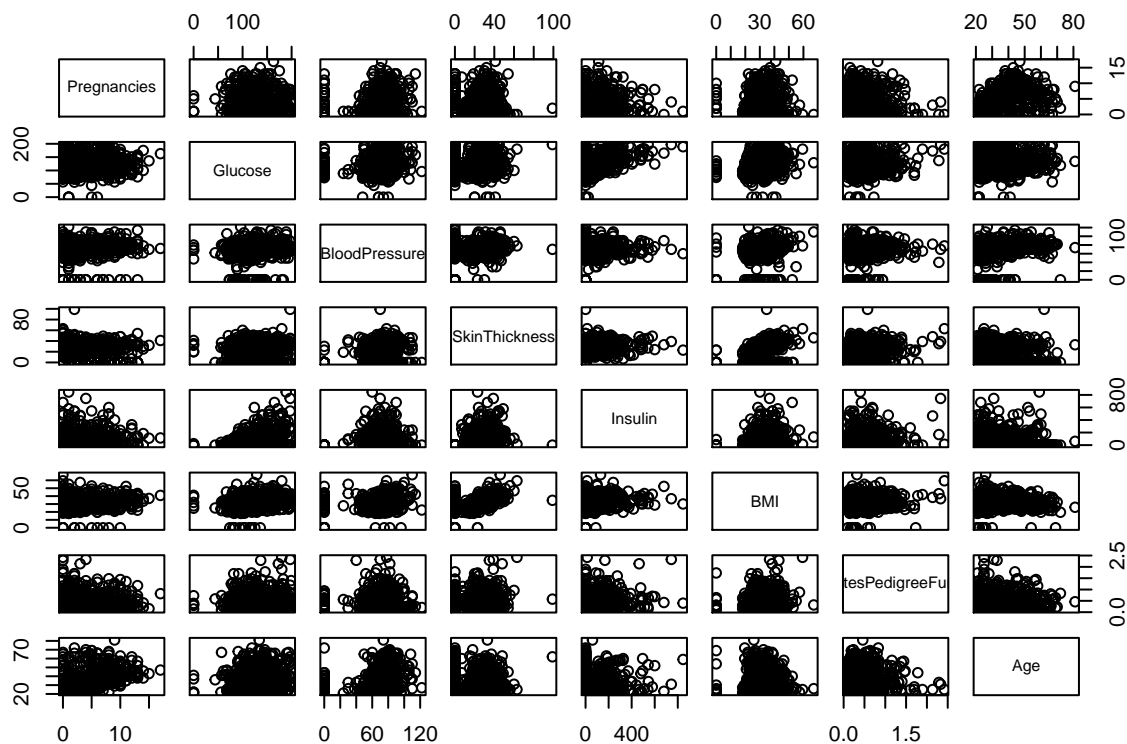
```
## 3rd Qu.: 6.000 3rd Qu.:140.2 3rd Qu.: 80.00 3rd Qu.:32.00
## Max. :17.000 Max. :199.0 Max. :122.00 Max. :99.00
## Insulin BMI DiabetesPedigreeFunction Age
## Min. : 0.0 Min. : 0.00 Min. :0.0780 Min. :21.00
## 1st Qu.: 0.0 1st Qu.:27.30 1st Qu.:0.2437 1st Qu.:24.00
## Median : 30.5 Median :32.00 Median :0.3725 Median :29.00
## Mean : 79.8 Mean :31.99 Mean :0.4719 Mean :33.24
## 3rd Qu.:127.2 3rd Qu.:36.60 3rd Qu.:0.6262 3rd Qu.:41.00
## Max. :846.0 Max. :67.10 Max. :2.4200 Max. :81.00
```

```
#m <- dist(diabetesX[,1:8])
#m1 <- as.matrix(m)[1:5,1:8]

#palette(rainbow(8)) # set colors
#stars( diabetesX, len=1, cex=0.5, key.loc=c(12.5, 2),
#labels=row.names(diabetesX), draw.segments=TRUE)
```

Check for the correlation between

```
pairs(diabetesX)
```



Reduce dependent variables which are correlated with each other.

```
diabetes.pc <- princomp(scale(diabetesX), cor = T)
summary(diabetes.pc)
```

```
## Importance of components:
##               Comp.1   Comp.2   Comp.3   Comp.4   Comp.5
## Standard deviation    1.4471973 1.3157546 1.0147068 0.9356971 0.87312335
## Proportion of Variance 0.2617975 0.2164013 0.1287037 0.1094411 0.09529305
## Cumulative Proportion 0.2617975 0.4781988 0.6069025 0.7163436 0.81163667
##               Comp.6   Comp.7   Comp.8
## Standard deviation    0.82621328 0.64793223 0.63597331
## Proportion of Variance 0.08532855 0.05247702 0.05055776
## Cumulative Proportion 0.89696522 0.94944224 1.00000000
```

```
sapply(diabetesX, sd)
```

```
##           Pregnancies           Glucose           BloodPressure
##           3.3695781           31.9726182           19.3558072
##           SkinThickness           Insulin           BMI
##           15.9522176           115.2440024           7.8841603
## DiabetesPedigreeFunction           Age
##           0.3313286           11.7602315
```

```
loadings<- diabetes.pc$loadings
print(loadings)
```

```
##
## Loadings:
##               Comp.1 Comp.2 Comp.3 Comp.4 Comp.5 Comp.6 Comp.7
## Pregnancies      0.128  0.594           0.476  0.194  0.589
## Glucose          0.393  0.174 -0.468 -0.404 -0.466
## BloodPressure    0.360  0.184  0.535           -0.328 -0.634  0.192
## SkinThickness    0.440 -0.332  0.238           0.488           -0.282
## Insulin          0.435 -0.251 -0.337 -0.350  0.347 -0.271  0.132
## BMI              0.452 -0.101  0.362           -0.253  0.685
## DiabetesPedigreeFunction 0.271 -0.122 -0.433  0.834 -0.120
## Age              0.198  0.621           0.109           -0.712
##               Comp.8
## Pregnancies      0.118
## Glucose          0.450
## BloodPressure
## SkinThickness    0.566
## Insulin          -0.549
## BMI              -0.342
## DiabetesPedigreeFunction
## Age              -0.212
##
##               Comp.1 Comp.2 Comp.3 Comp.4 Comp.5 Comp.6 Comp.7 Comp.8
## SS loadings      1.000  1.000  1.000  1.000  1.000  1.000  1.000  1.000
## Proportion Var    0.125  0.125  0.125  0.125  0.125  0.125  0.125  0.125
## Cumulative Var    0.125  0.250  0.375  0.500  0.625  0.750  0.875  1.000
```

```
print(loadings, digits=2, cutoff=0.2, sort=T)
```

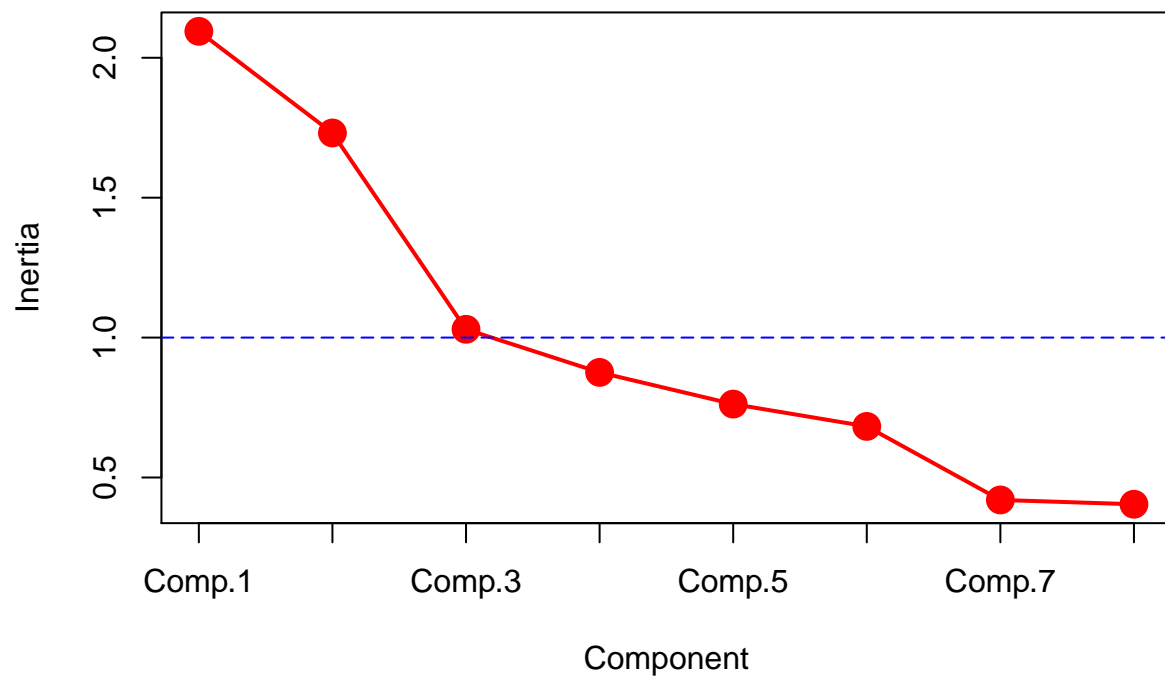
```
##
## Loadings:
##
```

|                             | Comp.1 | Comp.2 | Comp.3 | Comp.4 | Comp.5 | Comp.6 | Comp.7 |
|-----------------------------|--------|--------|--------|--------|--------|--------|--------|
| ## Pregnancies              |        | 0.59   |        |        | 0.48   |        | 0.59   |
| ## DiabetesPedigreeFunction | 0.27   |        | -0.43  | 0.83   |        |        |        |
| ## BloodPressure            | 0.36   |        | 0.54   |        | -0.33  | -0.63  |        |
| ## BMI                      | 0.45   |        | 0.36   |        | -0.25  | 0.69   |        |
| ## Age                      |        | 0.62   |        |        |        |        | -0.71  |
| ## SkinThickness            | 0.44   | -0.33  | 0.24   |        | 0.49   |        | -0.28  |
| ## Insulin                  | 0.44   | -0.25  | -0.34  | -0.35  | 0.35   | -0.27  |        |
| ## Glucose                  | 0.39   |        | -0.47  | -0.40  | -0.47  |        |        |

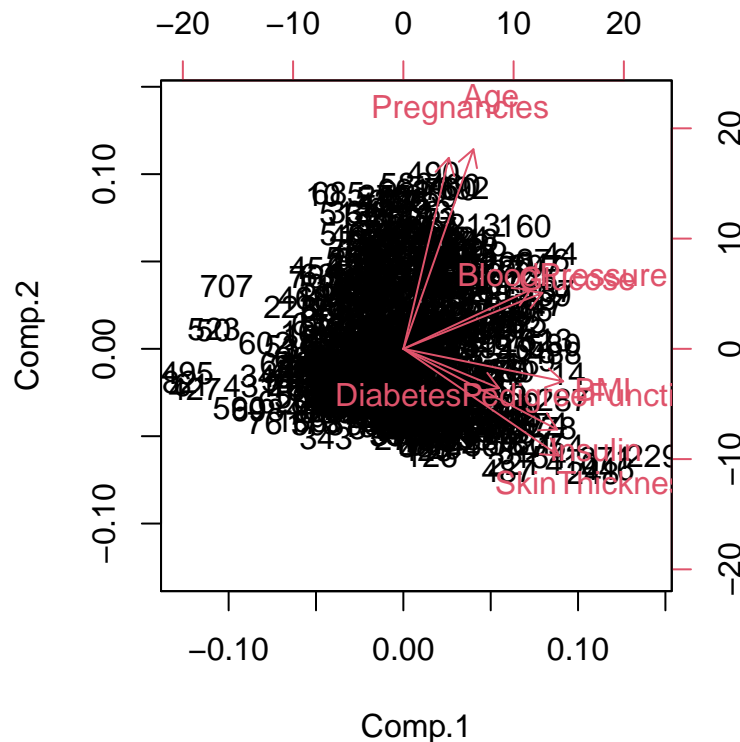
```
##
## Comp.8
## Pregnancies
## DiabetesPedigreeFunction
## BloodPressure
## BMI
## Age
## SkinThickness
## Insulin
## Glucose
##
```

|                   | Comp.1 | Comp.2 | Comp.3 | Comp.4 | Comp.5 | Comp.6 | Comp.7 | Comp.8 |
|-------------------|--------|--------|--------|--------|--------|--------|--------|--------|
| ## SS loadings    | 1.00   | 1.00   | 1.00   | 1.00   | 1.00   | 1.00   | 1.00   | 1.00   |
| ## Proportion Var | 0.12   | 0.13   | 0.12   | 0.12   | 0.13   | 0.12   | 0.13   | 0.12   |
| ## Cumulative Var | 0.12   | 0.25   | 0.37   | 0.50   | 0.62   | 0.75   | 0.88   | 1.00   |

```
screeplot(diabetes.pc, col = "red", pch = 16,
           type = "lines", cex = 2, lwd = 2, main = "")
abline(h=1, col='blue', lwd=1, lty=5)
```



```
biplot(diabetes.pc)
```



ScreePlot suggest that 3 should be sufficient to represent the model with  $\text{var} \geq 1$ , Looking at the biplot, it can be ascertained that Pregnancies and Age contribute to comp2, and factors other than Blood Pressure Glucose are orthogonal to it.

We can check these factors further by doing Factor analysis.

### Exploitory check using Factor analysis

```
diabetes.std = as.data.frame(diabetesX)
str(diabetes.std)
```

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

```
fact = factanal(diabetes.std, factors=3, rotation = 'none', na.omit=TRUE)
fact
```

```
##
## Call:
## factanal(x = diabetes.std, factors = 3, rotation = "none", na.omit = TRUE)
##
## Uniquenesses:
##           Pregnancies           Glucose           BloodPressure
##           0.614             0.005             0.845
##           SkinThickness       Insulin             BMI
##           0.188             0.674             0.767
## DiabetesPedigreeFunction      Age
##           0.939             0.230
##
## Loadings:
##           Factor1 Factor2 Factor3
## Pregnancies    -0.298   0.133   0.529
## Glucose         0.000   0.997   0.000
## BloodPressure   0.125   0.155   0.339
## SkinThickness   0.849   0.000   0.297
## Insulin         0.459   0.333   0.000
## BMI             0.379   0.223   0.199
## DiabetesPedigreeFunction 0.187   0.138   0.000
## Age            -0.408   0.268   0.729
##
##           Factor1 Factor2 Factor3
## SS loadings    1.381   1.292   1.065
## Proportion Var 0.173   0.161   0.133
## Cumulative Var 0.173   0.334   0.467
##
## Test of the hypothesis that 3 factors are sufficient.
## The chi square statistic is 39 on 7 degrees of freedom.
## The p-value is 1.95e-06
```

```
#three factors are not sufficient
fact = factanal(diabetes.std, factors=4, rotation = 'none', na.omit=TRUE)
fact
```

```
##
## Call:
## factanal(x = diabetes.std, factors = 4, rotation = "none", na.omit = TRUE)
##
## Uniquenesses:
##           Pregnancies           Glucose           BloodPressure
##           0.658             0.592             0.813
##           SkinThickness       Insulin             BMI
##           0.005             0.472             0.356
## DiabetesPedigreeFunction      Age
##           0.924             0.119
##
## Loadings:
##           Factor1 Factor2 Factor3 Factor4
## Pregnancies         0.570
## Glucose             0.321   0.439   0.330
## BloodPressure       0.208   0.297   0.191 -0.139
## SkinThickness       0.997
```

```
## Insulin          0.440          0.301  0.494
## BMI              0.396   0.131   0.602 -0.327
## DiabetesPedigreeFunction 0.185          0.154  0.119
## Age              -0.118   0.929
##
##               Factor1 Factor2 Factor3 Factor4
## SS loadings    1.447   1.402   0.716   0.497
## Proportion Var  0.181   0.175   0.090   0.062
## Cumulative Var  0.181   0.356   0.446   0.508
##
## Test of the hypothesis that 4 factors are sufficient.
## The chi square statistic is 2.9 on 2 degrees of freedom.
## The p-value is 0.235
```

```
print(fact, digits=2, cutoff=0.3, sort=T)
```

```
##
## Call:
## factanal(x = diabetes.std, factors = 4, rotation = "none", na.omit = TRUE)
##
## Uniquenesses:
##               Pregnancies          Glucose          BloodPressure
##               0.66              0.59              0.81
##               SkinThickness          Insulin              BMI
##               0.00              0.47              0.36
## DiabetesPedigreeFunction          Age
##               0.92              0.12
##
## Loadings:
##               Factor1 Factor2 Factor3 Factor4
## SkinThickness    1.00
## Pregnancies          0.57
## Age              0.93
## BMI              0.40          0.60 -0.33
## Glucose          0.32   0.44   0.33
## BloodPressure
## Insulin          0.44          0.30   0.49
## DiabetesPedigreeFunction
##
##               Factor1 Factor2 Factor3 Factor4
## SS loadings    1.45   1.40   0.72   0.50
## Proportion Var  0.18   0.18   0.09   0.06
## Cumulative Var  0.18   0.36   0.45   0.51
##
## Test of the hypothesis that 4 factors are sufficient.
## The chi square statistic is 2.9 on 2 degrees of freedom.
## The p-value is 0.235
```

It looks like factors 3 are insufficient and factor 4 are sufficient to explain the model. We fail to reject the null hypothesis that the factor 4 would be sufficient to represent a reduced dimensions model

Check residuals to be small so that the reduced dimensions are sufficient to represent a reduced model.



## Rotate the model

```
fact = factanal(diabetes.std, factors=4, rotation = 'varimax', na.omit=TRUE)
fact

##
## Call:
## factanal(x = diabetes.std, factors = 4, rotation = "varimax",      na.omit = TRUE)
##
## Uniquenesses:
##           Pregnancies           Glucose           BloodPressure
##           0.658           0.592           0.813
##           SkinThickness           Insulin           BMI
##           0.005           0.472           0.356
## DiabetesPedigreeFunction           Age
##           0.924           0.119
##
## Loadings:
##           Factor1 Factor2 Factor3 Factor4
## Pregnancies      0.582
## Glucose           0.205 -0.115  0.569  0.171
## BloodPressure     0.236  0.125          0.325
## SkinThickness          0.922  0.238  0.280
## Insulin            0.282  0.662
## BMI                0.141  0.195  0.766
## DiabetesPedigreeFunction 0.110  0.233
## Age               0.929
##
##           Factor1 Factor2 Factor3 Factor4
## SS loadings    1.319  0.997  0.931  0.816
## Proportion Var 0.165  0.125  0.116  0.102
## Cumulative Var 0.165  0.289  0.406  0.508
##
## Test of the hypothesis that 4 factors are sufficient.
## The chi square statistic is 2.9 on 2 degrees of freedom.
## The p-value is 0.235
```

```
print(fact, digits=2, cutoff=0.3, sort=T)
```

```
##
## Call:
## factanal(x = diabetes.std, factors = 4, rotation = "varimax",      na.omit = TRUE)
##
## Uniquenesses:
##           Pregnancies           Glucose           BloodPressure
##           0.66           0.59           0.81
##           SkinThickness           Insulin           BMI
##           0.00           0.47           0.36
## DiabetesPedigreeFunction           Age
##           0.92           0.12
##
## Loadings:
```

```
##                               Factor1 Factor2 Factor3 Factor4
## Pregnancies                   0.58
## Age                           0.93
## SkinThickness                 0.92
## Glucose                       0.57
## Insulin                       0.66
## BMI                           0.77
## BloodPressure                 0.33
## DiabetesPedigreeFunction
##
##                               Factor1 Factor2 Factor3 Factor4
## SS loadings                   1.32    1.00    0.93    0.82
## Proportion Var                0.16    0.12    0.12    0.10
## Cumulative Var                0.16    0.29    0.41    0.51
##
## Test of the hypothesis that 4 factors are sufficient.
## The chi square statistic is 2.9 on 2 degrees of freedom.
## The p-value is 0.235
```

It's much clear that the Factor1 can be explained by Pregnancies and Age, Factor2 by Skintickness, Factor 3 by Flucose and Insulin, and Factor4 can be explained by BloodPressure and DiabetesPedigreeFunction.

The test provides a p-value of 0.235, which suggests that a 4 dimensions reduction of the data is sufficient at 5% significance level.

## Check residuals

```
L = fact$loadings; L; Psi = diag(fact$uniquenesses);Psi
```

```
##
## Loadings:
##                               Factor1 Factor2 Factor3 Factor4
## Pregnancies                   0.582
## Glucose                       0.205 -0.115  0.569  0.171
## BloodPressure                 0.236  0.125      0.325
## SkinThickness                 0.922  0.238  0.280
## Insulin                       0.282  0.662
## BMI                           0.141  0.195  0.766
## DiabetesPedigreeFunction      0.110  0.233
## Age                           0.929
##
##                               Factor1 Factor2 Factor3 Factor4
## SS loadings                   1.319  0.997  0.931  0.816
## Proportion Var                0.165  0.125  0.116  0.102
## Cumulative Var                0.165  0.289  0.406  0.508
##
##          [,1]    [,2]    [,3]    [,4]    [,5]    [,6]    [,7]    [,8]
## [1,] 0.6578437 0.000000 0.0000000 0.000 0.0000000 0.0000000 0.0000000 0.000000
## [2,] 0.0000000 0.591578 0.0000000 0.000 0.0000000 0.0000000 0.0000000 0.000000
## [3,] 0.0000000 0.000000 0.8127369 0.000 0.0000000 0.0000000 0.0000000 0.000000
## [4,] 0.0000000 0.000000 0.0000000 0.005 0.0000000 0.0000000 0.0000000 0.000000
## [5,] 0.0000000 0.000000 0.0000000 0.000 0.4716588 0.0000000 0.0000000 0.000000
```

```
## [6,] 0.0000000 0.000000 0.0000000 0.000 0.0000000 0.3558406 0.0000000 0.000000
## [7,] 0.0000000 0.000000 0.0000000 0.000 0.0000000 0.0000000 0.9237768 0.000000
## [8,] 0.0000000 0.000000 0.0000000 0.000 0.0000000 0.0000000 0.0000000 0.119118
```

```
resids = cor(diabetesX) - (L%*%t(L) + Psi) ; resids
```

```
##              Pregnancies      Glucose BloodPressure
## Pregnancies      1.318673e-06  5.994472e-03 -4.994879e-03
## Glucose          5.994472e-03 -9.223485e-07  6.603275e-03
## BloodPressure   -4.994879e-03  6.603275e-03  7.026252e-08
## SkinThickness   2.702657e-05 -6.497846e-06  2.705642e-05
## Insulin         1.271592e-03  8.830411e-04 -4.408838e-04
## BMI             1.088344e-03 -1.027914e-03 -5.630390e-05
## DiabetesPedigreeFunction -3.516193e-02 -1.079072e-03 -2.928254e-02
## Age             6.612853e-05 -9.240893e-04  3.603548e-04
##              SkinThickness      Insulin      BMI
## Pregnancies      2.702657e-05  1.271592e-03  1.088344e-03
## Glucose          -6.497846e-06  8.830411e-04 -1.027914e-03
## BloodPressure    2.705642e-05 -4.408838e-04 -5.630390e-05
## SkinThickness   -5.265443e-08  3.221339e-06 -4.305107e-06
## Insulin         3.221339e-06 -5.297747e-09  2.999977e-05
## BMI            -4.305107e-06  2.999977e-05  7.209581e-08
## DiabetesPedigreeFunction 2.816875e-05 -3.204163e-03 4.977742e-03
## Age            -3.888883e-06 -1.552557e-04 -9.100591e-05
##              DiabetesPedigreeFunction      Age
## Pregnancies      -3.516193e-02  6.612853e-05
## Glucose          -1.079072e-03 -9.240893e-04
## BloodPressure    -2.928254e-02  3.603548e-04
## SkinThickness    2.816875e-05 -3.888883e-06
## Insulin         -3.204163e-03 -1.552557e-04
## BMI             4.977742e-03 -9.100591e-05
## DiabetesPedigreeFunction -1.469487e-06 5.143935e-03
## Age             5.143935e-03  1.220708e-07
```

```
summary(resids[row(resids)!=col(resids)])
```

```
##      Min.    1st Qu.    Median      Mean    3rd Qu.      Max.
## -3.516e-02 -5.617e-04 -3.300e-07 -1.783e-03  4.910e-04  6.603e-03
```

The residuals are small so we can ascertain that the reduced dimension represent original model fairly well with around 51 of variance.

## Verify factors with non-metric MDS

Since this is non-distance (metric) data, we checked goodness of fit using Shepard and Stress plots.

```
D <- dist(diabetesX)
head(D)
```

```
## [1] 66.90348 54.29634 115.73012 172.58913 52.13618 117.17040
```

```

#
#
# mds <- isoMDS(D)
#
# stress2 = vector(length = 7)
# for(k in 1:length(stress2)) {
#   fit2 = isoMDS(D, y = cmdscale(D, k), k, trace = FALSE)
#   stress2[k] = fit2$stress
# }
# plot(stress2, main = "Stress vs. k") # k = 2 is good enough?
#
# x <- mds$points[,1]
# y <- mds$points[,2]
#
# plot(x, y, xlab = "Coordinate 1", ylab = "Coordinate 2", xlim = range(mds$points[,1])*1.2, type = "n")
# text(x, y, labels = colnames(diabetesX), cex = 0.6)
#
# diabetes_sh <- Shepard(diabetesX[lower.tri(diabetesX)], mds$points)
#
# #x-axis= orig proximity (similarity or dissimilarity) x(i,j)
# #y-axis = d(i,j) =asterisk
# plot(diabetes_sh, pch = "*", cex=1, col="red",
#       xlab = "Dissimilarity",
#       ylab = "Distance",
#       xlim = range(diabetes_sh$x),
#       ylim = range(diabetes_sh$y))
#
# #x-axis= orig proximity(similarity or dissimilarity)
# #y-axis= the fit( \hat{d(i,j)}) =dash
# lines(diabetes_sh$x, diabetes_sh$yf, type = "S", lwd=2,col="blue")

```

```

library(vegan)
diabetes_mds2 <- metaMDS(diabetesX, k=4)

```

```

## Square root transformation
## Wisconsin double standardization
## Run 0 stress 0.06121611
## Run 1 stress 0.06177514
## Run 2 stress 0.06122449
## ... Procrustes: rmse 0.0009288842  max resid 0.01537085
## Run 3 stress 0.0612629
## ... Procrustes: rmse 0.004047671  max resid 0.06568366
## Run 4 stress 0.06122993
## ... Procrustes: rmse 0.0006380424  max resid 0.01288919
## Run 5 stress 0.06123394
## ... Procrustes: rmse 0.0008310833  max resid 0.01344095
## Run 6 stress 0.06127028
## ... Procrustes: rmse 0.004125378  max resid 0.06583423
## Run 7 stress 0.06173031
## Run 8 stress 0.06125167
## ... Procrustes: rmse 0.003827134  max resid 0.06549385
## Run 9 stress 0.06122064
## ... Procrustes: rmse 0.0002877605  max resid 0.005498155

```

```

## ... Similar to previous best
## Run 10 stress 0.0621178
## Run 11 stress 0.06129146
## ... Procrustes: rmse 0.003438192  max resid 0.0651043
## Run 12 stress 0.06121638
## ... Procrustes: rmse 0.0007245537  max resid 0.008143436
## ... Similar to previous best
## Run 13 stress 0.06136674
## ... Procrustes: rmse 0.004540835  max resid 0.06631846
## Run 14 stress 0.06122968
## ... Procrustes: rmse 0.0008300005  max resid 0.01930606
## Run 15 stress 0.06129681
## ... Procrustes: rmse 0.004245805  max resid 0.06578371
## Run 16 stress 0.06124696
## ... Procrustes: rmse 0.001511969  max resid 0.01839689
## Run 17 stress 0.06137857
## ... Procrustes: rmse 0.00512532  max resid 0.06656211
## Run 18 stress 0.06126185
## ... Procrustes: rmse 0.003701733  max resid 0.06546292
## Run 19 stress 0.06125783
## ... Procrustes: rmse 0.003828786  max resid 0.06505558
## Run 20 stress 0.06122108
## ... Procrustes: rmse 0.0008207116  max resid 0.009888921
## ... Similar to previous best
## *** Solution reached

```

```

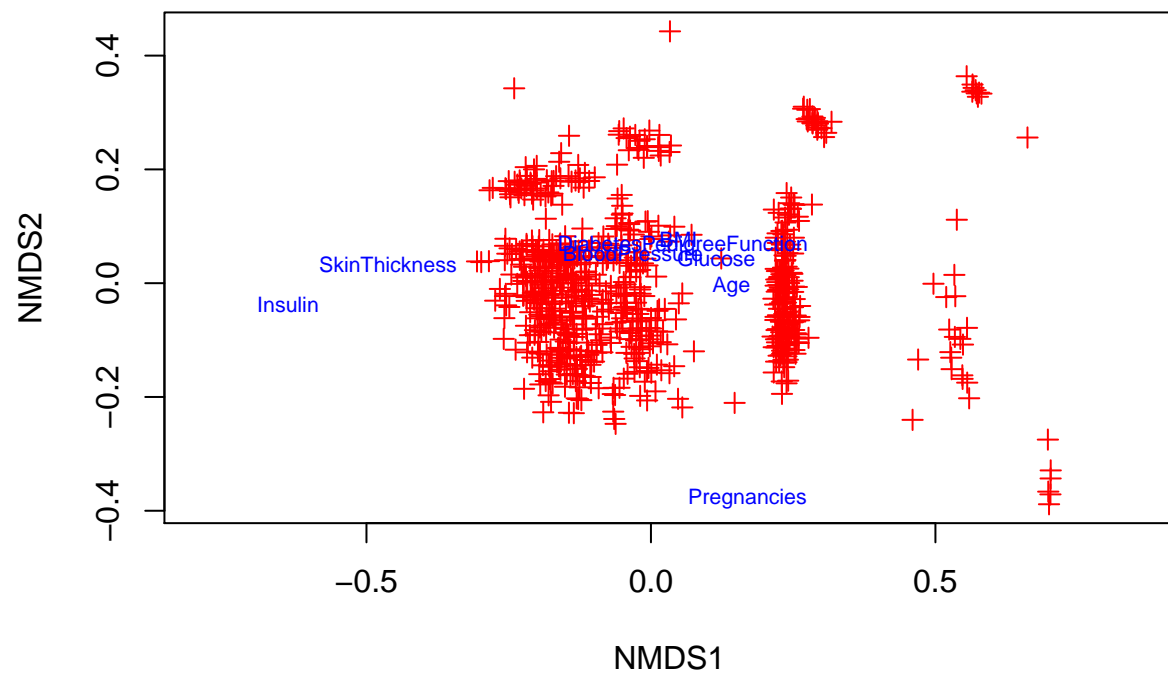
plot(diabetes_mds2, type="n")
points(diabetes_mds2, display=c("sites"), choices=c(1,2), pch=3, col="red")
text(diabetes_mds2, display=c("species"), choicec=c(1,2), col="blue", cex=0.7)

```

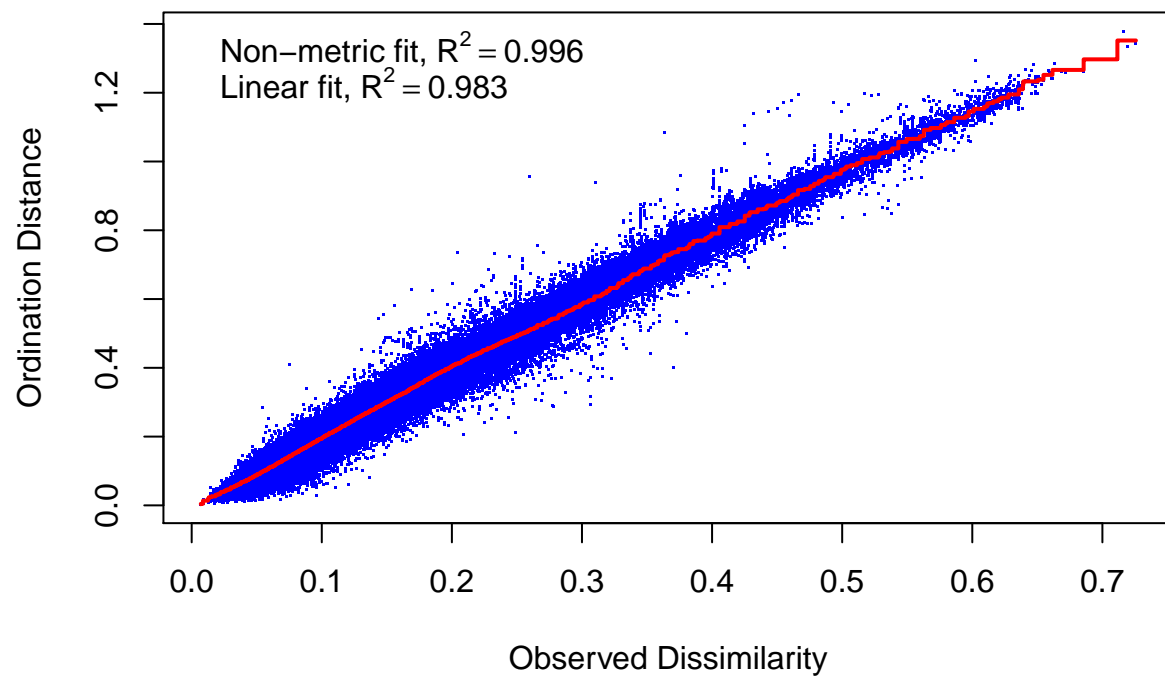
```

## Warning in text.default(x, labels = rownames(x), ...): "choicec" is not a
## graphical parameter

```



```
stressplot(diabetes_mds2)
```



The plot shows a  $R^2$  value of 0.966, which is close to zero, so we can claim that there is a good fit.