

## Factor\_Analysis.R

saiprasad

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```
# Factor Analysis
HCV<- read.csv("HCV-Egy-Data.csv")

View(HCV)
attach(HCV)
library(dplyr)

##
## Attaching package: 'dplyr'

## The following objects are masked from 'package:stats':
##
##   filter, lag

## The following objects are masked from 'package:base':
##
##   intersect, setdiff, setequal, union

Survivorship = HCV$Survivorship <- if_else( RNA.EOT>= 400000 , 'NC','C')
cbind(data.frame(Survivorship),HCV)

##      Survivorship Age Gender BMI Fever Nausea.Vomting Headache Diarrhea
## 1                C  56      1  35     2              1          1          1
## 2                C  46      1  29     1              2          2          1
## 3               NC  57      1  33     2              2          2          2
## 4               NC  49      2  33     1              2          1          2
## 5                C  59      1  32     1              1          2          1
## 6                C  58      2  22     2              2          2          1
## 7                C  42      2  26     1              1          2          2
## 8                C  48      2  30     1              1          2          2
## 9                C  44      1  23     1              1          2          2
## 10               C  45      1  30     2              1          2          2
## 11               NC  37      2  24     2              1          2          1
## 12               C  36      1  22     2              2          1          1
## 13               C  45      2  25     2              1          1          1
## 14               C  34      1  22     1              2          1          1
## 15               NC  40      2  32     2              2          2          1
## 16               NC  58      1  34     2              1          1          1
## 17               C  61      1  35     1              2          2          2
## 18               C  55      2  24     2              1          2          2
## 19               NC  56      1  27     1              2          2          2
## 20               NC  35      2  23     2              2          1          1
## 21               NC  57      2  23     1              1          2          2
```

```

hcv_pca <- prcomp(HCV_pca, scale=TRUE)
summary(hcv_pca)

## Importance of components:
##
##          PC1      PC2      PC3      PC4      PC5      PC6
## Standard deviation  1.08404 1.05059 1.0387 1.02934 1.01426 1.01148
## Proportion of Variance 0.09793 0.09198 0.0899 0.08829 0.08573 0.08526
## Cumulative Proportion 0.09793 0.18991 0.2798 0.36810 0.45383 0.53909
##
##          PC7      PC8      PC9      PC10     PC11     PC12
## Standard deviation  0.9962 0.98907 0.97517 0.95981 0.9327 0.90452
## Proportion of Variance 0.0827 0.08152 0.07925 0.07677 0.0725 0.06818
## Cumulative Proportion 0.6218 0.70331 0.78255 0.85932 0.9318 1.00000

plot(hcv_pca)
# A table containing eigenvalues and %'s accounted, follows. Eigenvalues are
the sdev^2
(eigen_hcv <- round(hcv_pca$sdev^2,2))

## [1] 1.18 1.10 1.08 1.06 1.03 1.02 0.99 0.98 0.95 0.92 0.87 0.82

names(eigen_hcv) <- paste("PC",1:12,sep="")
eigen_hcv

## PC1 PC2 PC3 PC4 PC5 PC6 PC7 PC8 PC9 PC10 PC11 PC12
## 1.18 1.10 1.08 1.06 1.03 1.02 0.99 0.98 0.95 0.92 0.87 0.82

sumlambdas <- sum(eigen_hcv)
sumlambdas

## [1] 12

propvar <- round(eigen_hcv/sumlambdas,2)
propvar

## PC1 PC2 PC3 PC4 PC5 PC6 PC7 PC8 PC9 PC10 PC11 PC12
## 0.10 0.09 0.09 0.09 0.09 0.08 0.08 0.08 0.08 0.08 0.07 0.07

cumvar_hcv <- cumsum(propvar)
cumvar_hcv

## PC1 PC2 PC3 PC4 PC5 PC6 PC7 PC8 PC9 PC10 PC11 PC12
## 0.10 0.19 0.28 0.37 0.46 0.54 0.62 0.70 0.78 0.86 0.93 1.00

matlambdas <- rbind(eigen_hcv,propvar,cumvar_hcv)
matlambdas

##
##          PC1 PC2 PC3 PC4 PC5 PC6 PC7 PC8 PC9 PC10 PC11 PC12
## eigen_hcv  1.18 1.10 1.08 1.06 1.03 1.02 0.99 0.98 0.95 0.92 0.87 0.82
## propvar    0.10 0.09 0.09 0.09 0.09 0.08 0.08 0.08 0.08 0.08 0.07 0.07
## cumvar_hcv 0.10 0.19 0.28 0.37 0.46 0.54 0.62 0.70 0.78 0.86 0.93 1.00

```

```

rownames(matlambdas) <- c("Eigenvalues", "Prop. variance", "Cum. prop.
variance")
rownames(matlambdas)

## [1] "Eigenvalues"          "Prop. variance"          "Cum. prop. variance"

eigvec.hcv <- hcv_pca$rotation
print(hcv_pca)

## Standard deviations (1, ..., p=12):
## [1] 1.0840427 1.0505938 1.0386641 1.0293370 1.0142649 1.0114786 0.9961803
## [8] 0.9890660 0.9751702 0.9598120 0.9327088 0.9045197
##
## Rotation (n x k) = (12 x 12):
##
##          PC1          PC2          PC3          PC4
## Age      -0.09529935  0.284882543  0.31747295  0.338906000
## Gender   -0.01044315 -0.316250295 -0.07203548  0.198455085
## Nausea.Vomting  0.52480080  0.088540649 -0.24781518  0.107734234
## Jaundice  -0.10889929  0.057223969 -0.15761428  0.550381317
## Epigastric.pain -0.36243330  0.087014225 -0.40100204 -0.424062232
## WBC       -0.31925445 -0.018338105  0.01645813  0.205418062
## Plat      0.55719490 -0.204281272 -0.04274376  0.006393138
## AST.1     0.02697707  0.443073086 -0.19135091 -0.310995830
## ALT.1     0.32045717  0.407795297 -0.33720628  0.061155423
## ALT.after.24.w -0.18820970  0.008476448 -0.38978528 -0.004039055
## RNA.Base  -0.13955452  0.282607286 -0.34255100  0.449136202
## RNA.EOT   -0.03831018 -0.561716624 -0.47462581  0.083473231
##
##          PC5          PC6          PC7          PC8
## Age      -0.002212279 -0.37355037 -0.04875916 -0.44436803
## Gender   -0.677696273 -0.22936402 -0.29458461  0.28262743
## Nausea.Vomting  0.236489116 -0.03939247  0.38658341  0.10081836
## Jaundice  -0.091079291  0.59055330  0.08817802  0.01018116
## Epigastric.pain -0.107455186 -0.04176427  0.06035269 -0.49894025
## WBC       -0.350199687 -0.12886045  0.73719558 -0.05030833
## Plat      -0.184948482 -0.16921682  0.24574326 -0.29402786
## AST.1     -0.299205035  0.29242475  0.12604131  0.24969134
## ALT.1     -0.327303100 -0.10706918 -0.28177087 -0.18531477
## ALT.after.24.w  0.206078032 -0.52920937  0.11414766  0.44898794
## RNA.Base  0.234651816 -0.12214543 -0.17512225 -0.01675482
## RNA.EOT   0.118014180  0.13640232 -0.08457018 -0.27551387
##
##          PC9          PC10          PC11          PC12
## Age      0.520792542  0.13577096 -0.23596778  0.09689700
## Gender   -0.006169086  0.07272571 -0.35241526 -0.21735019
## Nausea.Vomting -0.014602955 -0.13365869 -0.63442826 -0.07783699
## Jaundice  0.320862480 -0.27375624  0.14539380 -0.30519221
## Epigastric.pain -0.014426575 -0.14347333 -0.19835482 -0.44093897
## WBC       -0.281821277 -0.02758649  0.05666123  0.29435529
## Plat      0.091339000  0.28486892  0.47530120 -0.34763250
## AST.1     0.326466725  0.53259952 -0.04585550  0.15495592
## ALT.1     -0.134042709 -0.42464147  0.19333300  0.38153525

```

```
## ALT.after.24.w    0.401358681 -0.17496164  0.28277459 -0.06118809
## RNA.Base         -0.456743248  0.49191702  0.04710736 -0.16687657
## RNA.EOT          0.208196459  0.21070746 -0.07972966  0.49099507
```

*# Taking the first four PCs to generate linear combinations for all the variables with four factors*

```
pcafactors.hcv <- eigvec.hcv[,1:4]
pcafactors.hcv
```

##	PC1	PC2	PC3	PC4
## Age	-0.09529935	0.284882543	0.31747295	0.338906000
## Gender	-0.01044315	-0.316250295	-0.07203548	0.198455085
## Nausea.Vomting	0.52480080	0.088540649	-0.24781518	0.107734234
## Jaundice	-0.10889929	0.057223969	-0.15761428	0.550381317
## Epigastric.pain	-0.36243330	0.087014225	-0.40100204	-0.424062232
## WBC	-0.31925445	-0.018338105	0.01645813	0.205418062
## Plat	0.55719490	-0.204281272	-0.04274376	0.006393138
## AST.1	0.02697707	0.443073086	-0.19135091	-0.310995830
## ALT.1	0.32045717	0.407795297	-0.33720628	0.061155423
## ALT.after.24.w	-0.18820970	0.008476448	-0.38978528	-0.004039055
## RNA.Base	-0.13955452	0.282607286	-0.34255100	0.449136202
## RNA.EOT	-0.03831018	-0.561716624	-0.47462581	0.083473231

*# Multiplying each column of the eigenvector's matrix by the square-root of the corresponding eigenvalue in order to get the factor loadings*

```
unrot.fact.hcv <- sweep(pcafactors.hcv,MARGIN=2,hcv_pca$sdev[1:4],`*`)
unrot.fact.hcv
```

##	PC1	PC2	PC3	PC4
## Age	-0.10330856	0.299295831	0.32974776	0.348848478
## Gender	-0.01132082	-0.332250596	-0.07482067	0.204277158
## Nausea.Vomting	0.56890646	0.093020256	-0.25739673	0.110894831
## Jaundice	-0.11805147	0.060119147	-0.16370829	0.566527842
## Epigastric.pain	-0.39289316	0.091416605	-0.41650642	-0.436502936
## WBC	-0.34608544	-0.019265900	0.01709447	0.211444407
## Plat	0.60402305	-0.214616636	-0.04439641	0.006580694
## AST.1	0.02924429	0.465489833	-0.19874933	-0.320119508
## ALT.1	0.34738924	0.428427207	-0.35024406	0.062949538
## ALT.after.24.w	-0.20402735	0.008905303	-0.40485597	-0.004157549
## RNA.Base	-0.15128305	0.296905460	-0.35579542	0.462312501
## RNA.EOT	-0.04152987	-0.590135998	-0.49297679	0.085922083

*# Computing communalities*

```
communalities.hcv <- rowSums(unrot.fact.hcv^2)
communalities.hcv
```

##	Age	Gender	Nausea.Vomting	Jaundice
##	0.3306795	0.1578459	0.4108581	0.3653047
##	Epigastric.pain	WBC	Plat	AST.1
##	0.5267344	0.1651473	0.4129185	0.3595138

```
##          ALT.1  ALT.after.24.w          RNA.Base          RNA.EOT
##          0.4308627      0.2056321      0.4513626      0.6003939
```

*# Performing the varimax rotation. The default in the varimax function is norm=TRUE thus, Kaiser normalization is carried out*

```
rot.fact.hcv <- varimax(unrot.fact.hcv)
```

```
View(unrot.fact.hcv)
```

```
rot.fact.hcv
```

```
## $loadings
```

```
##
```

```
## Loadings:
```

```
##          PC1      PC2      PC3      PC4
## Age          -0.190   0.142   0.439   0.287
## Gender                -0.390
## Nausea.Vomting  0.630                0.112
## Jaundice          -0.190                0.568
## Epigastric.pain -0.228   0.247  -0.639
## WBC             -0.322  -0.103                0.226
## Plat            0.570  -0.203   0.115  -0.184
## AST.1           0.107   0.546  -0.223
## ALT.1           0.470   0.343                0.287
## ALT.after.24.w                -0.403   0.204
## RNA.Base                -0.105   0.661
## RNA.EOT         0.117  -0.595  -0.480
```

```
##
```

```
##          PC1      PC2      PC3      PC4
## SS loadings  1.162  1.096  1.085  1.074
## Proportion Var 0.097  0.091  0.090  0.090
## Cumulative Var 0.097  0.188  0.279  0.368
```

```
##
```

```
## $rotmat
```

```
##          [,1]      [,2]      [,3]      [,4]
## [1,]  0.93119621 -0.005476209  0.3020940 -0.2039187
## [2,]  0.04203690  0.906775699  0.1510461  0.3913768
## [3,] -0.36023297  0.049131561  0.8413855 -0.3998608
## [4,]  0.03658853 -0.418705066  0.4218941  0.8033385
```

*# The print method of varimax omits Loadings less than abs(0.1). In order to display all the loadings, it is necessary to ask explicitly the contents of the object \$loadings*

```
fact.load.hcv <- rot.fact.hcv$loadings[1:9,1:4]
```

```
fact.load.hcv
```

```
##          PC1      PC2      PC3      PC4
## Age          -0.189641232  0.14209632  0.438620690  0.286594181
## Gender          0.009918388 -0.39042271 -0.030374813  0.066294905
## Nausea.Vomting  0.630454087  0.02215453  0.016129583  0.112404278
## Jaundice        -0.027700318 -0.19009027  0.074691098  0.568176281
## Epigastric.pain -0.227949410  0.24734830 -0.639483053 -0.068218412
## WBC             -0.321504881 -0.10326758 -0.003870194  0.226059074
```

```
## Plat          0.569675983 -0.20285354  0.115476608 -0.184128639
## AST.1         0.106683282  0.54620552 -0.223136385 -0.001473782
## ALT.1         0.469969986  0.34301968 -0.098475760  0.287455983
```

*# Computing the rotated factor scores for the 30 European Countries. Notice that signs are reversed for factors F2 (PC2), F3 (PC3) and F4 (PC4)*

```
scale.hcv <- scale(HCV[1:29])
scale.hcv
```

```
##           Age      Gender      BMI      Fever Nausea.Vomting
## [1,]  1.10241532 -0.9789225  1.56795830  0.9690704  -1.0047041
## [2,] -0.03634155 -0.9789225  0.09600468 -1.0311717   0.9945993
## [3,]  1.21629100 -0.9789225  1.07730709  0.9690704   0.9945993
## [4,]  0.30528551  1.0207938  1.07730709 -1.0311717   0.9945993
## [5,]  1.44404238 -0.9789225  0.83198149 -1.0311717  -1.0047041
## [6,]  1.33016669  1.0207938 -1.62127455  0.9690704   0.9945993
## [7,] -0.49184430  1.0207938 -0.63997214 -1.0311717  -1.0047041
## [8,]  0.19140982  1.0207938  0.34133028 -1.0311717  -1.0047041
## [9,] -0.26409293 -0.9789225 -1.37594895 -1.0311717  -1.0047041
## [10,] -0.15021724 -0.9789225  0.34133028  0.9690704  -1.0047041
## [11,] -1.06122274  1.0207938 -1.13062334  0.9690704  -1.0047041
## [12,] -1.17509843 -0.9789225 -1.62127455  0.9690704   0.9945993
## [13,] -0.15021724  1.0207938 -0.88529774  0.9690704  -1.0047041
## [14,] -1.40284980 -0.9789225 -1.62127455 -1.0311717   0.9945993
## [15,] -0.71959568  1.0207938  0.83198149  0.9690704   0.9945993
## [16,]  1.33016669 -0.9789225  1.32263270  0.9690704  -1.0047041
## [17,]  1.67179375 -0.9789225  1.56795830 -1.0311717   0.9945993
## [18,]  0.98853963  1.0207938 -1.13062334  0.9690704  -1.0047041
## [19,]  1.10241532 -0.9789225 -0.39464653 -1.0311717   0.9945993
## [20,] -1.28897411  1.0207938 -1.37594895  0.9690704   0.9945993
## [21,]  1.21629100  1.0207938 -1.37594895 -1.0311717  -1.0047041
## [22,] -1.51672549 -0.9789225 -0.88529774  0.9690704  -1.0047041
## [23,] -0.60571999 -0.9789225 -1.37594895 -1.0311717   0.9945993
## [24,] -0.83347136  1.0207938  0.09600468 -1.0311717   0.9945993
## [25,] -1.51672549  1.0207938 -1.13062334 -1.0311717   0.9945993
## [26,] -0.37796862  1.0207938  1.32263270  0.9690704   0.9945993
## [27,]  0.53303688 -0.9789225  1.32263270  0.9690704  -1.0047041
```

```
## attr(,"scaled:center")
```

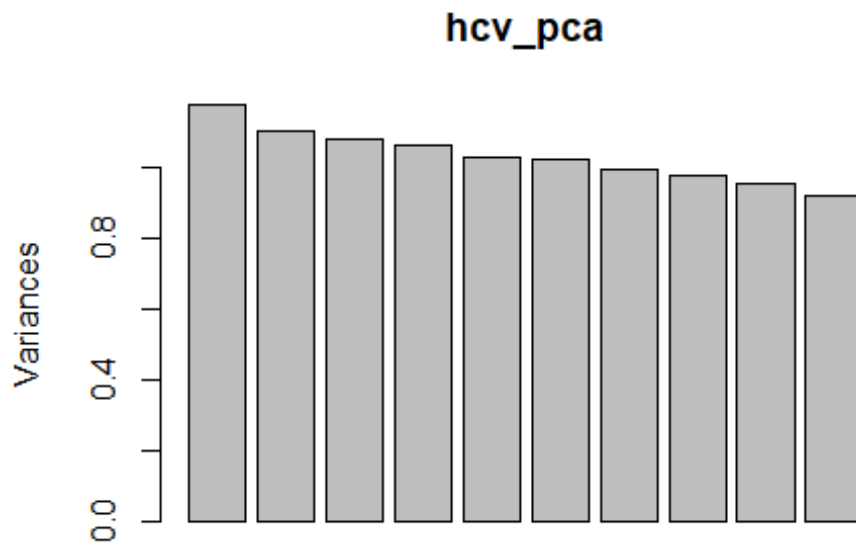
```
##           Age      Gender
## 4.631913e+01  1.489531e+00
##           BMI      Fever
## 2.860866e+01  1.515523e+00
## Nausea.Vomting Headache
## 1.502527e+00  1.496029e+00
## Diarrhea Fatigue...generalized.bone.ache
## 1.502527e+00  1.498917e+00
## Jaundice Epigastric.pain
## 1.501083e+00  1.503971e+00
##           WBC      RBC
```

```

##          7.533386e+03          4.422130e+06
##          HGB          Plat
##          1.258773e+01          1.583481e+05
##          AST.1          ALT.1
##          8.277473e+01          8.391625e+01
##          ALT4          ALT.12
##          8.340578e+01          8.351047e+01
##          ALT.24          ALT.36
##          8.370903e+01          8.311769e+01
##          ALT.48          ALT.after.24.w
##          8.362960e+01          3.343827e+01
##          RNA.Base          RNA.4
##          5.909512e+05          6.008956e+05
##          RNA.12          RNA.EOT
##          2.887536e+05          2.876603e+05
##          RNA.EF          Baseline.histological.Grading
##          2.913783e+05          9.761733e+00
##          Baselinehistological.staging
##          2.536462e+00
## attr(,"scaled:scale")
##          Age          Gender
##          8.781506e+00          5.000709e-01
##          BMI          Fever
##          4.076215e+00          4.999395e-01
##          Nausea.Vomting          Headache
##          5.001742e-01          5.001648e-01
##          Diarrhea          Fatigue...generalized.bone.ache
##          5.001742e-01          5.001794e-01
##          Jaundice          Epigastric.pain
##          5.001794e-01          5.001648e-01
##          WBC          RBC
##          2.668220e+03          3.463577e+05
##          HGB          Plat
##          1.713511e+00          3.879479e+04
##          AST.1          ALT.1
##          2.599324e+01          2.592280e+01
##          ALT4          ALT.12
##          2.652973e+01          2.606448e+01
##          ALT.24          ALT.36
##          2.620599e+01          2.639903e+01
##          ALT.48          ALT.after.24.w
##          2.622395e+01          7.073569e+00
##          RNA.Base          RNA.4
##          3.539354e+05          3.623151e+05
##          RNA.12          RNA.EOT
##          2.853507e+05          2.645595e+05
##          RNA.EF          Baseline.histological.Grading
##          2.677007e+05          4.023896e+00
##          Baselinehistological.staging
##          1.121392e+00

```

```
library(psych)
```



```
fit.pc <- principal(HCV[1:29], nfactors=4, rotate="varimax")
fit.pc
```

```
## Principal Components Analysis
## Call: principal(r = HCV[1:29], nfactors = 4, rotate = "varimax")
## Standardized loadings (pattern matrix) based upon correlation matrix
##
```

	RC1	RC2	RC3	RC4	h2	u2	com
## Age	-0.10	0.06	-0.05	0.27	0.091	0.91	1.4
## Gender	-0.01	0.05	0.08	-0.09	0.017	0.98	2.6
## BMI	-0.02	-0.04	0.15	-0.51	0.287	0.71	1.2
## Fever	0.02	0.09	0.18	0.01	0.043	0.96	1.5
## Nausea.Vomting	0.05	-0.52	0.26	0.08	0.346	0.65	1.5
## Headache	-0.02	-0.08	0.05	0.35	0.129	0.87	1.1
## Diarrhea	0.03	0.03	0.35	0.16	0.148	0.85	1.5
## Fatigue...generalized.bone.ache	0.05	0.13	0.00	-0.02	0.021	0.98	1.3
## Jaundice	0.04	0.07	-0.09	0.34	0.133	0.87	1.3
## Epigastric.pain	0.11	0.39	0.03	-0.09	0.169	0.83	1.3
## WBC	-0.10	0.18	-0.09	-0.18	0.084	0.92	3.1
## RBC	-0.06	-0.32	-0.04	-0.03	0.109	0.89	1.1
## HGB	0.04	-0.17	-0.17	-0.41	0.227	0.77	1.7
## Plat	0.11	-0.34	0.36	-0.15	0.281	0.72	2.6
## AST.1	-0.04	0.01	0.07	0.00	0.007	0.99	1.6
## ALT.1	-0.04	-0.08	0.58	0.11	0.356	0.64	1.1
## ALT4	0.05	-0.10	-0.24	0.17	0.101	0.90	2.3
## ALT.12	-0.08	0.04	-0.46	0.16	0.242	0.76	1.3



```

## ALT.24          0.06 -0.38 -0.33  0.02 0.260 0.74 2.0
## ALT.36          0.06 -0.07  0.01  0.19 0.044 0.96 1.5
## ALT.48         -0.01  0.40  0.19  0.13 0.212 0.79 1.6
## ALT.after.24.w  0.00  0.22  0.09  0.09 0.066 0.93 1.6
## RNA.Base       -0.02  0.11  0.15  0.31 0.131 0.87 1.8
## RNA.4          -0.07  0.19  0.01 -0.21 0.083 0.92 2.2
## RNA.12         0.76  0.05  0.01  0.04 0.581 0.42 1.0
## RNA.EOT        0.78  0.08 -0.04  0.00 0.613 0.39 1.0
## RNA.EF         0.78  0.06 -0.03  0.05 0.620 0.38 1.0
## Baseline.histological.Grading -0.07  0.16  0.04 -0.14 0.050 0.95 2.5
## Baselinehistological.staging  0.03 -0.20  0.03  0.28 0.118 0.88 1.9
##
##              RC1  RC2  RC3  RC4
## SS loadings    1.88 1.25 1.22 1.22
## Proportion Var  0.06 0.04 0.04 0.04
## Cumulative Var  0.06 0.11 0.15 0.19
## Proportion Explained 0.34 0.22 0.22 0.22
## Cumulative Proportion 0.34 0.56 0.78 1.00
##
## Mean item complexity = 1.7
## Test of the hypothesis that 4 components are sufficient.
##
## The root mean square of the residuals (RMSR) is 0.06
## with the empirical chi square 3895.88 with prob < 0
##
## Fit based upon off diagonal values = -0.68

round(fit.pc$values, 3)

## [1] 1.896 1.249 1.235 1.192 1.163 1.147 1.129 1.107 1.062 1.059 1.035
## [12] 1.028 1.024 1.010 0.985 0.974 0.962 0.959 0.928 0.908 0.885 0.866
## [23] 0.862 0.847 0.833 0.796 0.766 0.565 0.529

fit.pc$loadings

##
## Loadings:
##              RC1  RC2  RC3  RC4
## Age                                0.275
## Gender
## BMI                                0.147 -0.514
## Fever                                0.183
## Nausea.Vomting                    -0.520  0.255
## Headache                                0.347
## Diarrhea                            0.346  0.165
## Fatigue...generalized.bone.ache      0.135
## Jaundice                                0.343
## Epigastric.pain                    0.106  0.385
## WBC                               -0.105  0.180 -0.180
## RBC                                -0.320
## HGB                               -0.169 -0.172 -0.408

```

```

## Plat                                0.112 -0.340  0.359 -0.154
## AST.1
## ALT.1                                0.580  0.111
## ALT4                               -0.104 -0.243  0.171
## ALT.12                             -0.455  0.162
## ALT.24                             -0.381 -0.334
## ALT.36                                0.190
## ALT.48                               0.402  0.186  0.128
## ALT.after.24.w                      0.225
## RNA.Base                           0.112  0.151  0.308
## RNA.4                              0.189      -0.206
## RNA.12                             0.759
## RNA.EOT                            0.778
## RNA.EF                             0.783
## Baseline.histological.Grading        0.158      -0.138
## Baselinehistological.staging       -0.199      0.277
##
##              RC1   RC2   RC3   RC4
## SS loadings   1.884 1.250 1.219 1.219
## Proportion Var 0.065 0.043 0.042 0.042
## Cumulative Var 0.065 0.108 0.150 0.192

```

#### # Loadings with more digits

```
for (i in c(1,3,2,4)) { print(fit.pc$loadings[[1,i]])}
```

```

## [1] -0.0958724
## [1] -0.04948666
## [1] 0.06362426
## [1] 0.2745433

```

#### # Communalities

```
fit.pc$communality
```

```

##              Age                                Gender
##              0.091062507                        0.017148673
##              BMI                                Fever
##              0.287460763                        0.042658501
## Nausea.Vomting                                Headache
##              0.345852672                        0.129429831
## Diarrhea Fatigue...generalized.bone.ache
##              0.148330647                        0.020932605
## Jaundice Epigastric.pain
##              0.133236702                        0.168757196
## WBC RBC
##              0.084375524                        0.108709457
## HGB Plat
##              0.226575779                        0.280929541
## AST.1 ALT.1
##              0.006993762                        0.356042693
## ALT4 ALT.12
##              0.101470264                        0.241949189

```

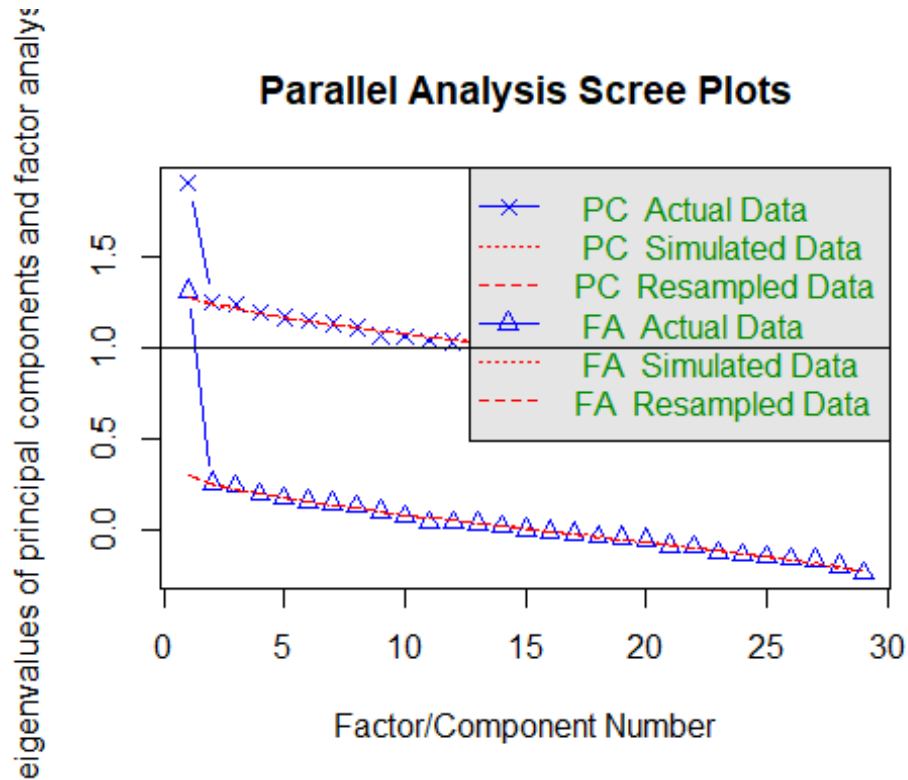
```
##          ALT.24          ALT.36
##          0.260153753          0.044408419
##          ALT.48          ALT.after.24.w
##          0.212487180          0.066164981
##          RNA.Base          RNA.4
##          0.131088563          0.083108957
##          RNA.12          RNA.EOT
##          0.581119980          0.612871462
##          RNA.EF          Baseline.histological.Grading
##          0.619617868          0.050100301
##          Baselinehistological.staging
##          0.118334956
```

*# Rotated factor scores, Notice the columns ordering: RC1, RC3, RC2 and RC4*  
fit.pc\$scores

```
##          RC1          RC2          RC3          RC4
## [1,] -1.0622643100  0.080761668 -1.5094106350 -1.962632045
## [2,] -0.0026786175 -0.044020173  0.0736538382  0.886102392
## [3,]  0.6996290407 -3.216649251 -1.4067382361 -0.057261850
## [4,]  1.5163346531 -0.776414526 -0.1281427476  0.681424373
## [5,]  4.9057352496  0.476636781  0.5326617845  0.313016961
## [6,] -1.5191976947  0.402707723 -0.2361002782  1.890172046
## [7,]  0.3715288048  0.243918957 -1.6544416873  0.508715596
## [8,]  1.0528134353  0.282429290  1.0349324442  0.572492606
## [9,] -0.4624751429  0.369648174 -0.6615023183  0.590944129
## [10,]  0.2959360322  0.303746811 -1.0721971649  1.098803257
## [11,]  0.5072113382  0.695569255  1.0678222322  1.621447274
## [12,]  0.8254115604  0.458076783 -0.2398940534 -1.405320375
## [13,] -1.2033769829  1.014090963  0.9403751880 -1.245043164
## [14,]  1.1785640985 -0.271905934 -0.4626974933 -0.298366405
## [15,]  0.1100394954 -0.289805069  1.3012403268 -0.563134500
## [16,] -0.1863439454  0.279091024 -0.8554825546 -1.323897864
## [17,] -1.3677347159 -0.953862198  1.3649506001  0.674939536
## [18,]  0.3117828097  0.018360917 -0.0056293649  1.556618732
## [19,]  0.7823548200 -0.657807268  1.3852125249  0.765636497
## [20,]  0.9836496936  0.349039338  0.5334288872  1.673576535
## [21,]  0.6756799086  0.411599173 -0.7863017569  0.876200476
## [22,] -1.3528130191  0.296732421 -0.6216050314  1.033441596
## [23,] -0.8954196002  0.212892557 -0.2961383286  0.921981624
## [24,]  0.7115976706 -1.271476758  1.4876628894 -0.352473825
## [25,]  0.6025828120  0.394462546  0.8027628881  0.636466590
## [26,] -1.3885480928 -1.030634107  0.5949796104 -0.150762610
## [27,]  1.4395069145  1.561371569 -0.8770405460 -0.728553346
## [28,]  0.0552936021 -0.007343432  0.9477563169 -0.451740170
## [29,] -1.2756600924 -0.847188753  0.5566900065  0.433490670
## [30,]  0.7423287554  0.672957693 -1.8607013524 -0.525549256
## [31,] -0.6595104332  0.686749854  0.1452406500 -1.149481326
## [32,] -0.2485054317 -1.229862373  1.4107446897  0.815026590
## [33,]  1.1758079231  1.387365844 -0.1315387113  0.188171397
```

```
## [34,] 0.0311235683 -0.219399571 -0.6624545051 0.098782267
## [35,] 0.8008224945 1.339360078 1.0819966981 1.121787320
# Play with FA utilities
```

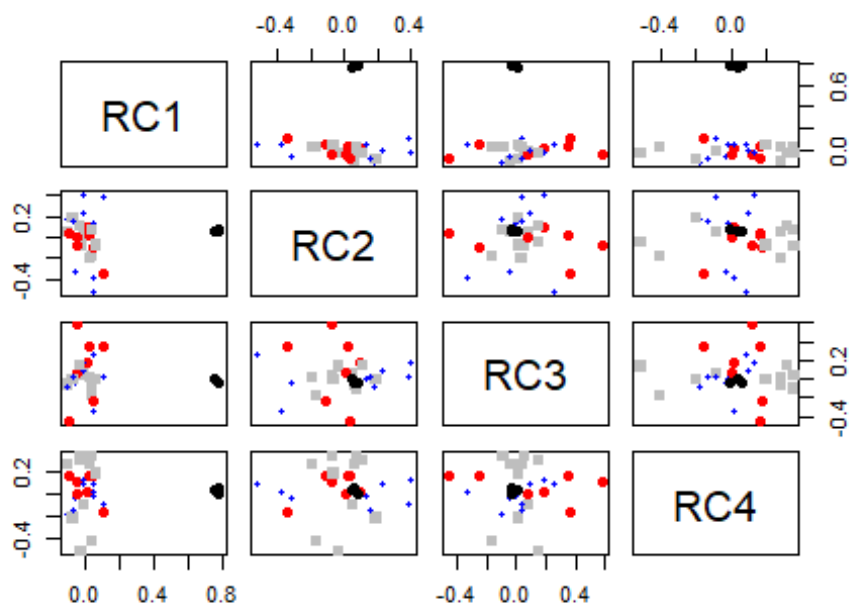
```
fa.parallel(HCV[1:29]) # See factor recommendation
```



```
## Parallel analysis suggests that the number of factors = 1 and the number
of components = 1
```

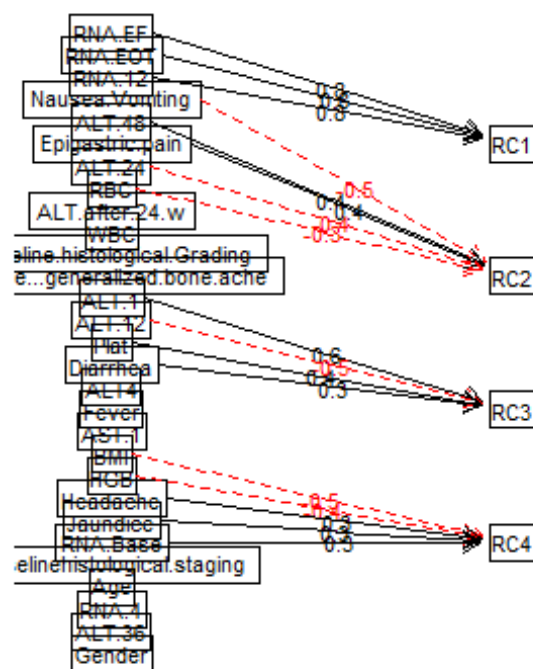
```
fa.plot(fit.pc) # See Correlations within Factors
```

## Principal Component Analysis



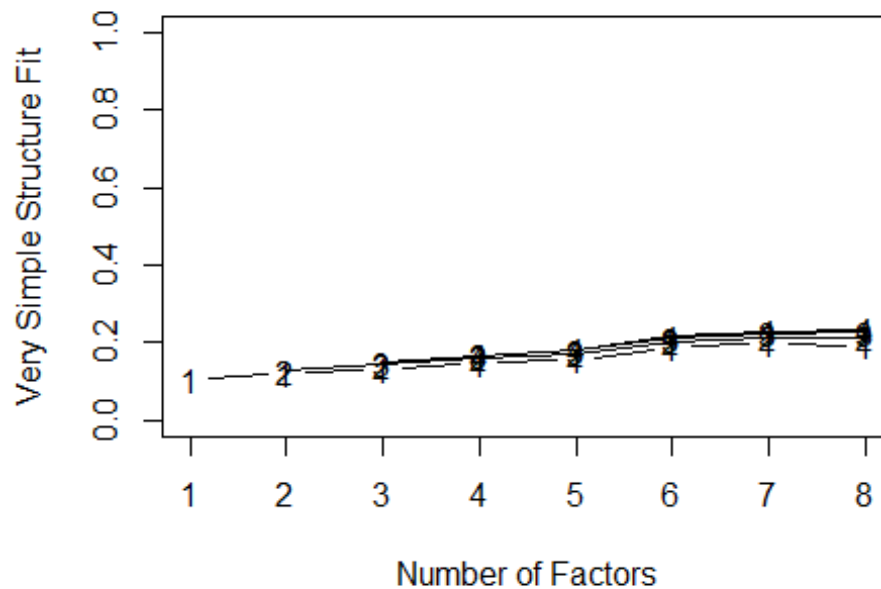
```
fa.diagram(fit.pc) # Visualize the relationship
```

## Components Analysis



```
vss(HCV[1:29]) # See Factor recommendations for a simple structure
```

## Very Simple Structure



```
##
## Very Simple Structure
## Call: vss(x = HCV[1:29])
## VSS complexity 1 achieves a maximum of 0.2 with 7 factors
## VSS complexity 2 achieves a maximum of 0.22 with 7 factors
##
## The Velicer MAP achieves a minimum of 0 with 1 factors
## BIC achieves a minimum of -2353.19 with 1 factors
## Sample Size adjusted BIC achieves a minimum of -1155.61 with 1 factors
##
## Statistics by number of factors
##   vss1 vss2   map dof chisq prob sqresid fit RMSEA   BIC SABIC complex
## 1 0.11 0.00 0.0024 377 374 0.54 27 0.11 0 -2353 -1156 1.0
## 2 0.12 0.13 0.0038 349 327 0.80 27 0.13 0 -2198 -1089 1.3
## 3 0.13 0.14 0.0052 322 283 0.94 26 0.15 0 -2046 -1023 1.6
## 4 0.15 0.16 0.0068 296 248 0.98 26 0.17 0 -1893 -953 1.7
## 5 0.16 0.17 0.0085 271 221 0.99 25 0.18 0 -1740 -879 1.8
## 6 0.19 0.20 0.0104 247 189 1.00 24 0.22 0 -1598 -814 1.8
## 7 0.20 0.22 0.0123 224 157 1.00 23 0.24 0 -1464 -752 2.1
## 8 0.19 0.21 0.0145 202 133 1.00 23 0.24 0 -1328 -686 2.0
##   eChisq SRMR eCRMS eBIC
## 1 699 0.025 0.026 -2028
## 2 594 0.023 0.025 -1931
## 3 499 0.021 0.024 -1830
## 4 425 0.019 0.023 -1716
## 5 369 0.018 0.022 -1591
## 6 311 0.017 0.021 -1475
```

## 7	255	0.015	0.020	-1365
## 8	209	0.014	0.019	-1252