

HW5

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5.1

The covariance matrix of the observed variables can be written as: $\Sigma = \text{Cov}(\Lambda F + \epsilon)$, where F is the matrix of common factors and ϵ is the matrix of specific factor, due to the assumption of unique variance. And then we can apply some transformation on the equation: $\Sigma = \text{Cov}(\Lambda F) + \text{Cov}(\epsilon) = \Lambda \text{Cov}(F) \Lambda^T + \Psi$, where $\text{Cov}(F)$ is the covariance matrix of the common factors, and since the factors are uncorrelated, it is a diagonal matrix with variances on the diagonal. Ψ is the covariance matrix of the specific factors, which is also a diagonal matrix with specific variances on the diagonal. Thus, we got $\Sigma = \Lambda \Lambda^T + \Psi$. If the factor allowed correlated, we will have the previous form, that is: $\Sigma = \Lambda \text{Cov}(F) \Lambda^T + \Psi$, since the covariance matrix of the common factors will no longer be a diagonal matrix.

5.2

Let's compute the communalities using the transformed factor loadings, denoted as h_i : $h_i = \sum (\lambda_{ij})^2$. Since $\Lambda^* = \Lambda M$, we can write λ_{ij} as: $\lambda_{ij} = \sum (\lambda_{ik} m_{kj})$, Substituting this expression in the equation for h_i : $h_i = \sum (\sum (\lambda_{ik} m_{kj}))^2 = \sum (\lambda_{ik} m_{kj} \lambda_{il} m_{lj}) = \sum (\lambda_{ik} \lambda_{il} \sum (m_{kj} m_{lj}))$ Applying the property of the orthogonal matrix ($M^T M = I$): $h_i^* = \sum (\lambda_{ik} \lambda_{il} \delta_{kl})$ Now, applying the Kronecker delta property: $h_i^* = \sum (\lambda_{ik} \lambda_{ik})$, that is $h_i^* = h_i$. DONE.

5.3

Proportion of Variance Explained for the j th factor = (Eigenvalue of j th factor) / (Total variance), that is $PVE_j = \lambda_j / \sum \lambda_i$

5.4

```
d <- c(0.447,
  0.422, 0.619,
  0.435, 0.604, 0.583,
  0.114, 0.068, 0.053, 0.115,
  0.203, 0.146, 0.139, 0.258, 0.349,
  0.091, 0.103, 0.110, 0.122, 0.209, 0.221,
  0.082, 0.063, 0.066, 0.097, 0.321, 0.355, 0.201,
  0.513, 0.445, 0.365, 0.482, 0.186, 0.315, 0.150, 0.154,
  0.304, 0.318, 0.240, 0.368, 0.303, 0.377, 0.163, 0.219, 0.534,
  0.245, 0.203, 0.183, 0.255, 0.272, 0.323, 0.310, 0.288, 0.301, 0.302,
  0.101, 0.088, 0.074, 0.139, 0.279, 0.367, 0.232, 0.320, 0.204, 0.368, 0.340,
  0.245, 0.199, 0.184, 0.293, 0.278, 0.545, 0.232, 0.314, 0.394, 0.467, 0.392, 0.511)
```

```

druguse <- diag(13) / 2

druguse[upper.tri(druguse)] <- d

druguse <- druguse + t(druguse)

rownames(druguse) <- colnames(druguse) <- c("cigarettes", "beer", "wine", "liquor", "cocaine",
      "tranquillizers", "drug store medication", "heroin",
      "marijuana", "hashish", "inhalants", "hallucinogenics", "amphetamine")

"life" <- structure(.Data = list(c(63., 34., 38., 59., 56., 62., 50., 65., 56., 69., 65., 64., 56., 60.
, c(51., 29., 30., 42., 38., 44., 39., 44., 46., 47., 48., 50., 44., 44., 45., 40., 42., 44., 44., 48.
43., 45., 40., 46., 45., 46., 43., 44., 46.)
, c(30., 13., 17., 20., 18., 24., 20., 22., 24., 24., 26., 28., 25., 22., 22., 22., 22., 23., 24., 28.
21., 23., 21., 23., 23., 24., 23., 24., 28.)
, c(13., 5., 7., 6., 7., 7., 7., 7., 11., 8., 9., 11., 10., 6., 8., 9., 6., 8., 8., 14., 9., 7., 6., 8.
8., 9., 10., 9., 9.)
, c(67., 38., 38., 64., 62., 69., 55., 72., 63., 75., 68., 66., 61., 65., 65., 51., 61., 67., 63., 68.
68., 74., 67., 75., 74., 71., 66., 62., 60.)
, c(54., 32., 34., 46., 46., 50., 43., 50., 54., 53., 50., 51., 48., 45., 49., 41., 43., 48., 46., 51.
47., 51., 46., 52., 51., 51., 49., 47., 49.)
, c(34., 17., 20., 25., 25., 28., 23., 27., 33., 29., 27., 29., 27., 25., 27., 23., 22., 26., 25., 29.
24., 28., 25., 29., 28., 28., 27., 25., 28.)
, c(15., 6., 7., 8., 10., 14., 8., 9., 19., 10., 10., 11., 12., 9., 10., 8., 7., 9., 8., 13., 10., 9.,
10., 10., 10., 12., 10., 11.)
),
class = "data.frame"
, names = c("m0", "m25", "m50", "m75", "w0", "w25", "w50", "w75")
, row.names = c("Algeria", "Cameroon", "Madagascar", "Mauritius", "Reunion", "Seychelles", "South Africa",
"Tunisia", "Canada", "Costa Rica", "Dominican Rep.", "El Salvador", "Greenland", "Grenada", "Guatemala",
"Honduras", "Jamaica", "Mexico", "Nicaragua", "Panama", "Trinidad (62)", "Trinidad (67)",
"United States (66)", "United States (NW66)", "United States (W66)", "United States (67)", "Argentina",
"Chile", "Colombia", "Ecuador")
)

toLatex(HSAURtable(life), pcol = 1, rownames = TRUE,
caption = "Life expectancies for different countries by age and gender.",
label = "ch:EFA:life:tab")

## \index{life data@\Robject{life} data}
## \begin{center}
## \begin{longtable}[l rrrrrrr ]
## \caption{\Robject{life} data. Life expectancies for different countries by age and gender. \label{ch:
## \\
## \hline
## & \Robject{m0} & \Robject{m25} & \Robject{m50} & \Robject{m75} & \Robject{w0} & \Robject{w25} & \Robject{w50} & \Robject{w75} \\
## \endfirsthead
## \caption[]{\Robject{life} data (continued).} \\
## \hline
## & \Robject{m0} & \Robject{m25} & \Robject{m50} & \Robject{m75} & \Robject{w0} & \Robject{w25} & \Robject{w50} & \Robject{w75} \\
## \endhead
## Algeria & 63 & 51 & 30 & 13 & 67 & 54 & 34 & 15 \\

```

```

## Cameroon    & 34 & 29 & 13 & 5 & 38 & 32 & 17 & 6 \\
## Madagascar  & 38 & 30 & 17 & 7 & 38 & 34 & 20 & 7 \\
## Mauritius   & 59 & 42 & 20 & 6 & 64 & 46 & 25 & 8 \\
## Reunion     & 56 & 38 & 18 & 7 & 62 & 46 & 25 & 10 \\
## Seychelles  & 62 & 44 & 24 & 7 & 69 & 50 & 28 & 14 \\
## South Africa (C) & 50 & 39 & 20 & 7 & 55 & 43 & 23 & 8 \\
## South Africa (W) & 65 & 44 & 22 & 7 & 72 & 50 & 27 & 9 \\
## Tunisia     & 56 & 46 & 24 & 11 & 63 & 54 & 33 & 19 \\
## Canada      & 69 & 47 & 24 & 8 & 75 & 53 & 29 & 10 \\
## Costa Rica  & 65 & 48 & 26 & 9 & 68 & 50 & 27 & 10 \\
## Dominican Rep. & 64 & 50 & 28 & 11 & 66 & 51 & 29 & 11 \\
## El Salvador & 56 & 44 & 25 & 10 & 61 & 48 & 27 & 12 \\
## Greenland   & 60 & 44 & 22 & 6 & 65 & 45 & 25 & 9 \\
## Grenada     & 61 & 45 & 22 & 8 & 65 & 49 & 27 & 10 \\
## Guatemala   & 49 & 40 & 22 & 9 & 51 & 41 & 23 & 8 \\
## Honduras    & 59 & 42 & 22 & 6 & 61 & 43 & 22 & 7 \\
## Jamaica     & 63 & 44 & 23 & 8 & 67 & 48 & 26 & 9 \\
## Mexico      & 59 & 44 & 24 & 8 & 63 & 46 & 25 & 8 \\
## Nicaragua   & 65 & 48 & 28 & 14 & 68 & 51 & 29 & 13 \\
## Panama      & 65 & 48 & 26 & 9 & 67 & 49 & 27 & 10 \\
## Trinidad (62) & 64 & 63 & 21 & 7 & 68 & 47 & 25 & 9 \\
## Trinidad (67) & 64 & 43 & 21 & 6 & 68 & 47 & 24 & 8 \\
## United States (66) & 67 & 45 & 23 & 8 & 74 & 51 & 28 & 10 \\
## United States (NW66) & 61 & 40 & 21 & 10 & 67 & 46 & 25 & 11 \\
## United States (W66) & 68 & 46 & 23 & 8 & 75 & 52 & 29 & 10 \\
## United States (67) & 67 & 45 & 23 & 8 & 74 & 51 & 28 & 10 \\
## Argentina   & 65 & 46 & 24 & 9 & 71 & 51 & 28 & 10 \\
## Chile       & 59 & 43 & 23 & 10 & 66 & 49 & 27 & 12 \\
## Colombia    & 58 & 44 & 24 & 9 & 62 & 47 & 25 & 10 \\
## Ecuador     & 57 & 46 & 28 & 9 & 60 & 49 & 28 & 11 \\
## \hline
## \end{longtable}
## \end{center}

```

```

m <- life[,1:4]
f <- life[,5:8]
factanal(m, factors = 1, method = "mle", scores = "regression")

```

```

##
## Call:
## factanal(x = m, factors = 1, scores = "regression", method = "mle")
##
## Uniquenesses:
##      m0      m25      m50      m75
## 0.594 0.552 0.005 0.434
##
## Loadings:
##      Factor1
## m0 0.638
## m25 0.669
## m50 0.998
## m75 0.752
##
##
##      Factor1

```

```
## SS loadings      2.415
## Proportion Var   0.604
##
## Test of the hypothesis that 1 factor is sufficient.
## The chi square statistic is 14.45 on 2 degrees of freedom.
## The p-value is 0.000728
```

```
factanal(f, factors = 1, method = "mle", scores = "regression")
```

```
##
## Call:
## factanal(x = f, factors = 1, scores = "regression", method = "mle")
##
## Uniquenesses:
##      w0   w25   w50   w75
## 0.220 0.005 0.115 0.526
##
## Loadings:
##      Factor1
## w0  0.883
## w25 0.998
## w50 0.941
## w75 0.689
##
##              Factor1
## SS loadings      3.134
## Proportion Var   0.784
##
## Test of the hypothesis that 1 factor is sufficient.
## The chi square statistic is 52.15 on 2 degrees of freedom.
## The p-value is 4.74e-12
```

The factor analysis results indicate that the life expectancy variables for women have a stronger association with the factor and a larger proportion of the variance explained than those for men. However, one factor may not be sufficient to explain the relationships among the variables for both groups, since the p-value of both groups are less than 0.05.

5.5

Factor analysis:

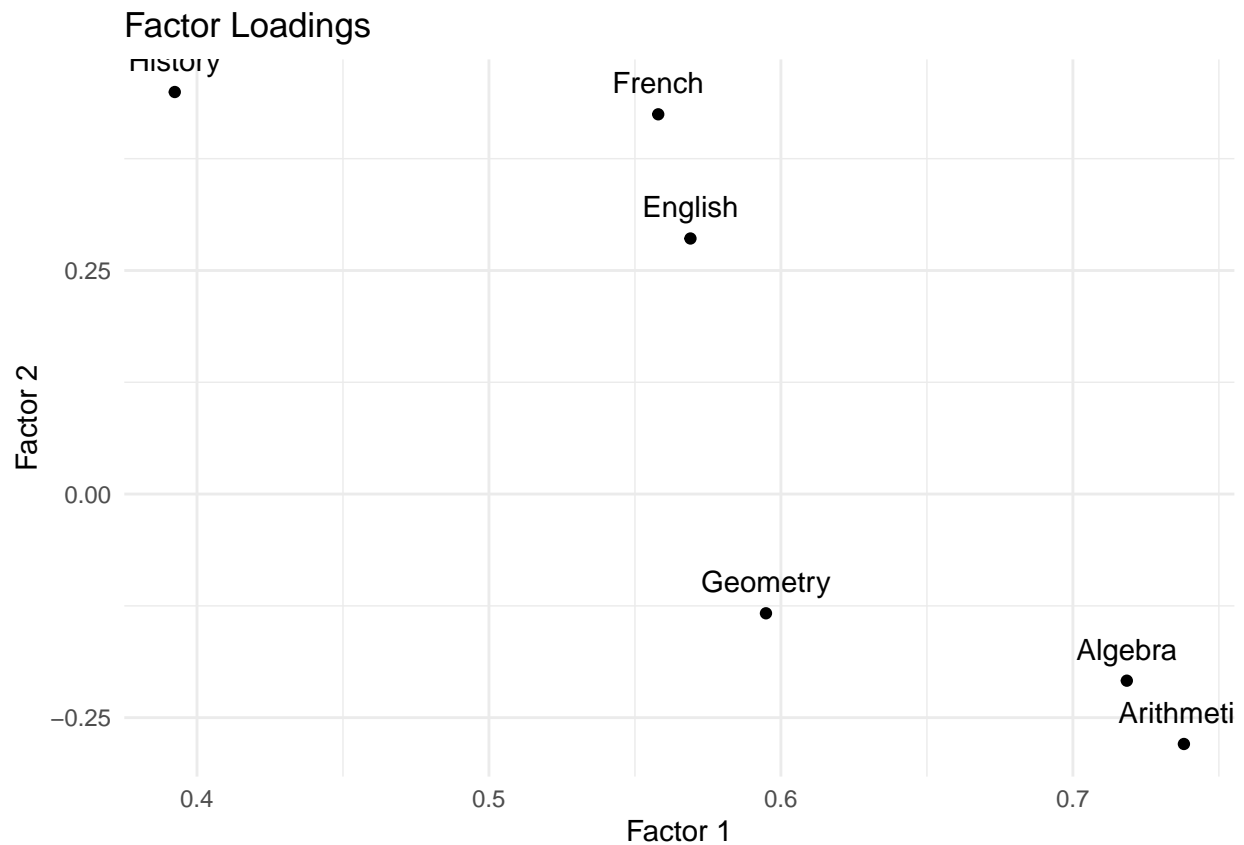
```
R <- matrix(c(1.00, 0.44, 0.41, 0.29, 0.33, 0.25,
              0.44, 1.00, 0.35, 0.35, 0.32, 0.33,
              0.41, 0.35, 1.00, 0.16, 0.19, 0.18,
              0.29, 0.35, 0.16, 1.00, 0.59, 0.47,
              0.33, 0.32, 0.19, 0.59, 1.00, 0.46,
              0.25, 0.33, 0.18, 0.47, 0.46, 1.00), nrow = 6, ncol = 6, byrow = TRUE)
rownames(R) <- colnames(R) <- c("French", "English", "History", "Arithmetic", "Algebra", "Geometry")

fa <- factanal(R, factors = 2, covmat = R, method = "mle", rotation = "none")
```

Plot the derived loadings:

```
loadings <- data.frame(Subject = rownames(fa$loadings),
                      Factor1 = fa$loadings[, 1],
                      Factor2 = fa$loadings[, 2])

# Plot the derived loadings
ggplot(loadings, aes(x = Factor1, y = Factor2, label = Subject)) +
  geom_point() +
  geom_text(vjust = -1) +
  ggtitle("Factor Loadings") +
  xlab("Factor 1") +
  ylab("Factor 2") +
  theme_minimal()
```



Find the orthogonal rotation:

```
rotated <- factanal(R, factors = 2, covmat = R, method = "mle", rotation = "varimax")
print(rotated)
```

##

Call:

factanal(x = R, factors = 2, covmat = R, rotation = "varimax", method = "mle")

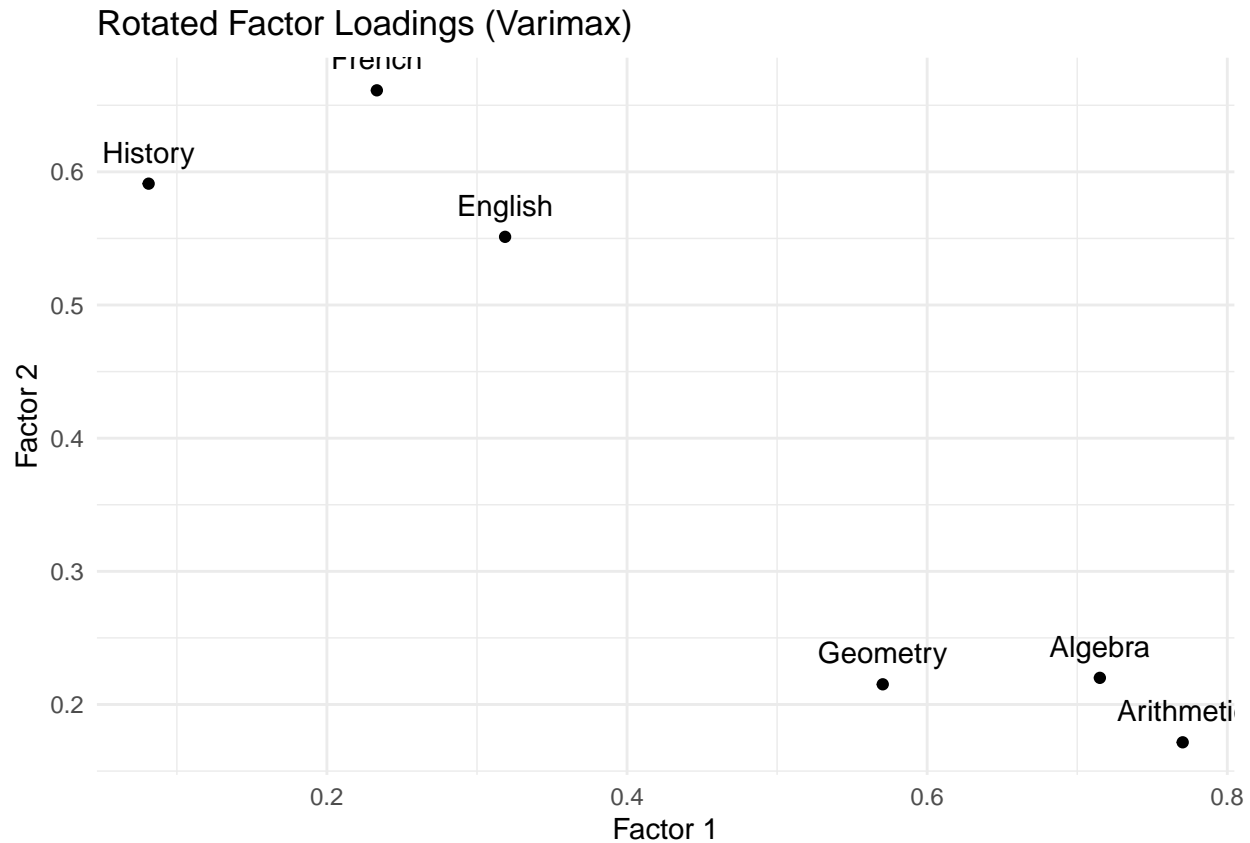
##

Uniquenesses:

```
##      French      English      History Arithmetic      Algebra      Geometry
##      0.508        0.595        0.644        0.377        0.440        0.628
##
## Loadings:
##           Factor1 Factor2
## French      0.233  0.661
## English     0.319  0.551
## History           0.591
## Arithmetic  0.770  0.172
## Algebra     0.715  0.220
## Geometry    0.570  0.215
##
##           Factor1 Factor2
## SS loadings      1.593  1.215
## Proportion Var   0.265  0.202
## Cumulative Var   0.265  0.468
##
## The degrees of freedom for the model is 4 and the fit was 0.0101
```

```
rotation <- data.frame(Subject = rownames(rotated$loadings),
                      Factor1 = rotated$loadings[, 1],
                      Factor2 = rotated$loadings[, 2])

# Plot the rotated loadings
ggplot(rotation, aes(x = Factor1, y = Factor2, label = Subject)) +
  geom_point() +
  geom_text(vjust = -1) +
  ggtitle("Rotated Factor Loadings (Varimax)") +
  xlab("Factor 1") +
  ylab("Factor 2") +
  theme_minimal()
```



5.6

(a)

From the screen plot we can see that the appropriate number of components is 2.

```
cor_matrix <- matrix(c(1.00, -0.04, 0.61, 0.45, 0.03, -0.29, -0.30, 0.45, 0.30,
  -0.04, 1.00, -0.07, -0.12, 0.49, 0.43, 0.30, -0.31, -0.17,
  0.61, -0.07, 1.00, 0.59, 0.03, -0.13, -0.24, 0.59, 0.32,
  0.45, -0.12, 0.59, 1.00, -0.08, -0.21, -0.19, 0.63, 0.37,
  0.03, 0.49, 0.03, -0.08, 1.00, 0.47, 0.41, -0.14, -0.24,
  -0.29, 0.43, -0.13, -0.21, 0.47, 1.00, 0.63, -0.13, -0.15,
  -0.30, 0.30, -0.24, -0.19, 0.41, 0.63, 1.00, -0.26, -0.29,
  0.45, -0.31, 0.59, 0.63, -0.14, -0.13, -0.26, 1.00, 0.40,
  0.30, -0.17, 0.32, 0.37, -0.24, -0.15, -0.29, 0.40, 1.00),
  nrow = 9, ncol = 9, byrow = TRUE)
```

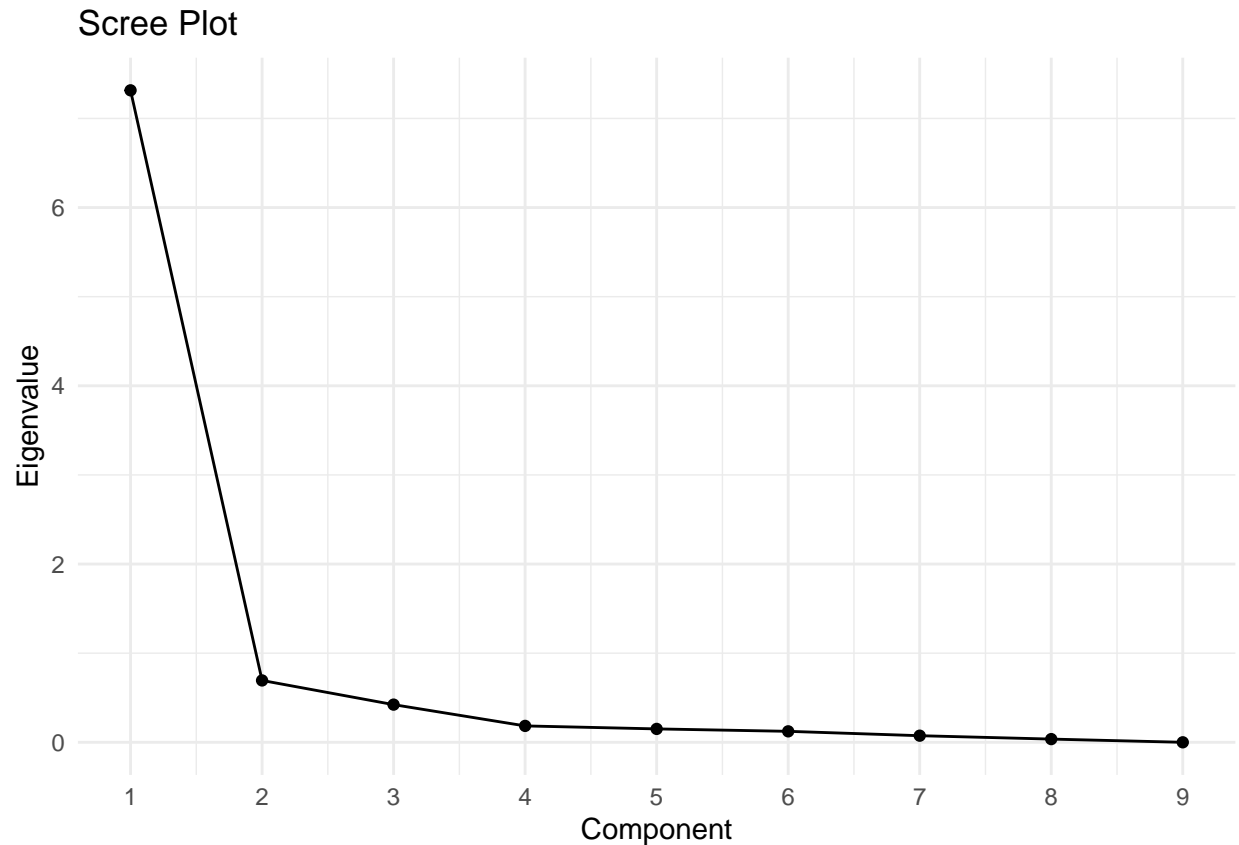
```
pca <- prcomp(cor_matrix, scale. = TRUE)
print(pca)
```

```
## Standard deviations (1, ..., p=9):
## [1] 2.704736e+00 8.331771e-01 6.502194e-01 4.289716e-01 3.876030e-01
## [6] 3.508762e-01 2.721774e-01 1.897039e-01 4.758338e-17
##
```

```
## Rotation (n x k) = (9 x 9):
##          PC1          PC2          PC3          PC4          PC5          PC6
## [1,] -0.3239653 -0.47987694  0.1241538 -0.40348183  0.41325092 -0.0931845
## [2,]  0.3178757 -0.37284396  0.4857942  0.56201002 -0.03307198 -0.1938381
## [3,] -0.3377157 -0.33866672 -0.2124359  0.03519881 -0.17586275 -0.5074909
## [4,] -0.3437808 -0.07315301 -0.2697679  0.60211229 -0.04019514  0.4474441
## [5,]  0.3178574 -0.48032358 -0.1340633 -0.33971984 -0.56418824  0.4381370
## [6,]  0.3487105  0.20107781 -0.2212017 -0.00391355 -0.30421581 -0.5130034
## [7,]  0.3460985  0.20036455 -0.3718775 -0.05831799  0.42733208  0.1115798
## [8,] -0.3482022  0.07254992 -0.3861045  0.05725338 -0.29142654 -0.1342968
## [9,] -0.3132142  0.44057522  0.5257503 -0.18832195 -0.34232850  0.1018233
##          PC7          PC8          PC9
## [1,]  0.19037918 -0.423666881  0.30225047
## [2,]  0.12178767  0.118849408  0.37478899
## [3,] -0.62072863  0.224729996  0.02454897
## [4,] -0.16148166 -0.453019642  0.08957952
## [5,] -0.07654837  0.001816995  0.13688696
## [6,]  0.05023732 -0.649522288  0.09434210
## [7,] -0.30591479  0.153172375  0.62150432
## [8,]  0.60633561  0.312875676  0.39068910
## [9,] -0.26063958 -0.086112460  0.43932523
```

```
eigenvalues_df <- data.frame(Component = 1:length(pca$sdev), Eigenvalue = pca$sdev^2)
```

```
# Plot the scree plot
ggplot(eigenvalues_df, aes(x = Component, y = Eigenvalue)) +
  geom_point() +
  geom_line() +
  ggtitle("Scree Plot") +
  xlab("Component") +
  ylab("Eigenvalue") +
  theme_minimal() +
  scale_x_continuous(limits = c(1, 9),
                     breaks = seq(1, 9, 1),
                     labels = seq(1, 9, 1))
```

(b)

Compare the results we can see that factors 5 has lowest value of fit score (0.0087), which indicate a better fit, and df is not equal to 0 (1), therefore, we choose factor 5.

```
factanal(factors = 1, covmat = cor_matrix, method = "mle")
```

```
##
## Call:
## factanal(factors = 1, covmat = cor_matrix, method = "mle")
##
## Uniquenesses:
## [1] 0.574 0.929 0.425 0.441 0.969 0.895 0.839 0.399 0.758
##
## Loadings:
##      Factor1
## [1,] 0.653
## [2,] -0.267
## [3,] 0.758
## [4,] 0.748
## [5,] -0.176
## [6,] -0.324
## [7,] -0.402
## [8,] 0.775
## [9,] 0.492
```

```
##
##               Factor1
## SS loadings      2.771
## Proportion Var   0.308
##
## The degrees of freedom for the model is 27 and the fit was 1.4689
```

```
factanal(factors = 2, covmat = cor_matrix, method = "mle")
```

```
##
## Call:
## factanal(factors = 2, covmat = cor_matrix, method = "mle")
##
## Uniquenesses:
## [1] 0.539 0.695 0.318 0.448 0.579 0.356 0.464 0.436 0.766
##
## Loadings:
##      Factor1 Factor2
## [1,]  0.664 -0.139
## [2,] -0.107  0.542
## [3,]  0.826
## [4,]  0.736
## [5,]      0.648
## [6,] -0.144  0.789
## [7,] -0.253  0.687
## [8,]  0.739 -0.134
## [9,]  0.432 -0.218
##
##      Factor1 Factor2
## SS loadings    2.494  1.904
## Proportion Var  0.277  0.212
## Cumulative Var  0.277  0.489
##
## The degrees of freedom for the model is 19 and the fit was 0.5171
```

```
factanal(factors = 3, covmat = cor_matrix, method = "mle")
```

```
##
## Call:
## factanal(factors = 3, covmat = cor_matrix, method = "mle")
##
## Uniquenesses:
## [1] 0.404 0.518 0.336 0.455 0.499 0.171 0.496 0.239 0.754
##
## Loadings:
##      Factor1 Factor2 Factor3
## [1,]  0.649 -0.372  0.190
## [2,] -0.126  0.194  0.655
## [3,]  0.794 -0.144  0.116
## [4,]  0.725 -0.106
## [5,]      0.292  0.645
## [6,]      0.825  0.377
## [7,] -0.225  0.590  0.325
```

```
## [8,] 0.815          -0.304
## [9,] 0.437          -0.221
##
##               Factor1 Factor2 Factor3
## SS loadings    2.507    1.331    1.291
## Proportion Var 0.279    0.148    0.143
## Cumulative Var 0.279    0.426    0.570
##
## The degrees of freedom for the model is 12 and the fit was 0.1653
```

```
factanal(factors = 4, covmat = cor_matrix, method = "mle")
```

```
##
## Call:
## factanal(factors = 4, covmat = cor_matrix, method = "mle")
##
## Uniquenesses:
## [1] 0.433 0.600 0.297 0.482 0.169 0.005 0.536 0.005 0.731
##
## Loadings:
##      Factor1 Factor2 Factor3 Factor4
## [1,] 0.707  -0.243
## [2,]      0.335   0.447  -0.296
## [3,] 0.833
## [4,] 0.654  -0.126      0.265
## [5,]      0.289   0.864
## [6,] -0.108   0.966   0.224
## [7,] -0.259   0.553   0.297
## [8,] 0.643      -0.164   0.745
## [9,] 0.421      -0.278   0.111
##
##      Factor1 Factor2 Factor3 Factor4
## SS loadings    2.293    1.514    1.202    0.734
## Proportion Var 0.255    0.168    0.134    0.082
## Cumulative Var 0.255    0.423    0.557    0.638
##
## The degrees of freedom for the model is 6 and the fit was 0.0841
```

```
factanal(factors = 5, covmat = cor_matrix, method = "mle")
```

```
##
## Call:
## factanal(factors = 5, covmat = cor_matrix, method = "mle")
##
## Uniquenesses:
## [1] 0.393 0.043 0.317 0.005 0.467 0.005 0.445 0.372 0.646
##
## Loadings:
##      Factor1 Factor2 Factor3 Factor4 Factor5
## [1,] 0.737  -0.221      0.103
## [2,]      0.248   0.937      -0.118
## [3,] 0.780      0.237   0.131
## [4,] 0.464      0.865   0.160
```

```
## [5,] 0.153 0.440 0.358 -0.432
## [6,] -0.108 0.966 0.198
## [7,] -0.235 0.617 0.105 -0.327
## [8,] 0.589 -0.250 0.347 0.313
## [9,] 0.305 -0.105 0.166 0.465
##
## Factor1 Factor2 Factor3 Factor4 Factor5
## SS loadings 1.899 1.636 1.128 0.975 0.667
## Proportion Var 0.211 0.182 0.125 0.108 0.074
## Cumulative Var 0.211 0.393 0.518 0.627 0.701
##
## The degrees of freedom for the model is 1 and the fit was 0.0087
```

(c)

For the orthogonal rotation, we can see that the loadings are mostly high for each variable on only one factor, which suggests that the factors are relatively independent of each other. For the oblique rotation, we can see that the loadings are also high for each variable on one factor, but there is more overlap between factors. The correlations between factors, represented by the phi matrix, suggest that there is some correlation between factors 1 and 3, factors 2 and 5, and factors 3 and 5. Overall, based on the context provided in the question, we can say that the results from orthogonal rotation and oblique rotation suggest that people's beliefs about pain are multifaceted and can be related to beliefs about doctors' skills and control over pain, personal responsibility for pain, seeking medical advice, pain resulting from carelessness, and a less clear factor related to beliefs about pain and behavior.

```
library(GPArotation)
fa_solution <- factanal(factors = 5, covmat = cor_matrix, rotation = "varimax")
(varimax_solution <- varimax(fa_solution$loadings))
```

```
## $loadings
##
## Loadings:
## Factor1 Factor2 Factor3 Factor4 Factor5
## [1,] 0.737 -0.220 0.104
## [2,] 0.249 0.937 -0.118
## [3,] 0.780 0.238 0.132
## [4,] 0.463 0.865 0.161
## [5,] 0.153 0.440 0.358 -0.431
## [6,] -0.108 0.966 0.197
## [7,] -0.235 0.618 0.105 -0.326
## [8,] 0.589 -0.250 0.347 0.314
## [9,] 0.304 -0.105 0.166 0.466
##
## Factor1 Factor2 Factor3 Factor4 Factor5
## SS loadings 1.897 1.637 1.128 0.977 0.666
## Proportion Var 0.211 0.182 0.125 0.109 0.074
## Cumulative Var 0.211 0.393 0.518 0.627 0.701
##
## $rotmat
## [,1] [,2] [,3] [,4] [,5]
## [1,] 0.9999991487 3.521370e-04 -1.448696e-04 7.885263e-04 9.673639e-04
## [2,] -0.0003533005 9.999992e-01 -1.716262e-04 -7.718607e-06 1.183285e-03
## [3,] 0.0001447679 1.715461e-04 1.000000e+00 -8.292712e-05 1.104832e-04
```

```
## [4,] -0.0007884647 7.518677e-06 8.304596e-05 9.999997e-01 -5.440686e-05
## [5,] -0.0009670050 -1.183645e-03 -1.101356e-04 5.366241e-05 9.999988e-01
```

```
(oblimin_solution <- oblimin(fa_solution$loadings))
```

```
## Oblique rotation method Oblimin Quartimin converged.
```

```
## Loadings:
```

```
##      Factor1 Factor2 Factor3 Factor4 Factor5
## [1,] 0.763595 -0.1811 -0.0247 0.0426 0.03640
## [2,] -0.000842 0.0300 0.0302 0.9779 -0.01460
## [3,] 0.731846 0.0635 0.1363 -0.0340 -0.03012
## [4,] 0.009097 -0.0470 0.9931 0.0286 0.00635
## [5,] 0.273101 0.2176 -0.0486 0.2137 0.49283
## [6,] -0.021343 0.9609 -0.0645 0.0608 0.00103
## [7,] -0.210372 0.4549 0.1058 -0.0329 0.40308
## [8,] 0.431933 0.1967 0.2979 -0.2503 -0.19668
## [9,] 0.189381 0.1076 0.1362 0.0139 -0.47718
```

```
##
```

```
##      Factor1 Factor2 Factor3 Factor4 Factor5
## SS loadings      1.626   1.368   1.293   1.157   0.862
## Proportion Var   0.181   0.152   0.144   0.129   0.096
## Cumulative Var   0.181   0.333   0.476   0.605   0.701
```

```
##
```

```
## Phi:
```

```
##      Factor1 Factor2 Factor3 Factor4 Factor5
## Factor1 1.0000 -0.1348 0.6051 -0.0598 -0.252
## Factor2 -0.1348 1.0000 -0.0933 0.3617 0.387
## Factor3 0.6051 -0.0933 1.0000 -0.1682 -0.281
## Factor4 -0.0598 0.3617 -0.1682 1.0000 0.435
## Factor5 -0.2521 0.3871 -0.2812 0.4353 1.000
```