Solution for the assignment of the eight class

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9/29/2021

Importing data

```
##
## -- Column specification ------
## cols(
## .default = col_double(),
## neme = col_character(),
## isk = col_character()
## i Use `spec()` for the full column specifications.
```

Data exploration

nume**niy**cugtala0

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```
skimr::skim(processed) %>%
kable()
```

```
skim skippe variabilseingleberrauthennanthennanthenenopelyaracheingundeiniuspuneniunudeniump@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@niuup@ni
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1. PCA on Diener flourishing scale

First, we select the variables of interest.

```
diener_data <- dplyr::select(processed, contains("diener"))</pre>
```

In R, we can run the PCA with just one function. We can set the scale argument to true to scale our variables to unit variance and center the variables.

```
pca <-
  diener_data %>%
  prcomp(scale = TRUE, center = TRUE)

summary(pca)
```

```
## Importance of components:
##
                             PC1
                                     PC2
                                             PC3
                                                    PC4
                                                             PC5
                                                                     PC6
                                                                             PC7
## Standard deviation
                          2.3837 0.70037 0.67176 0.6203 0.55088 0.54801 0.46048
## Proportion of Variance 0.7102 0.06131 0.05641 0.0481 0.03793 0.03754 0.02651
## Cumulative Proportion 0.7102 0.77154 0.82795 0.8760 0.91399 0.95153 0.97803
##
                              PC8
## Standard deviation
                          0.41922
## Proportion of Variance 0.02197
## Cumulative Proportion 1.00000
```

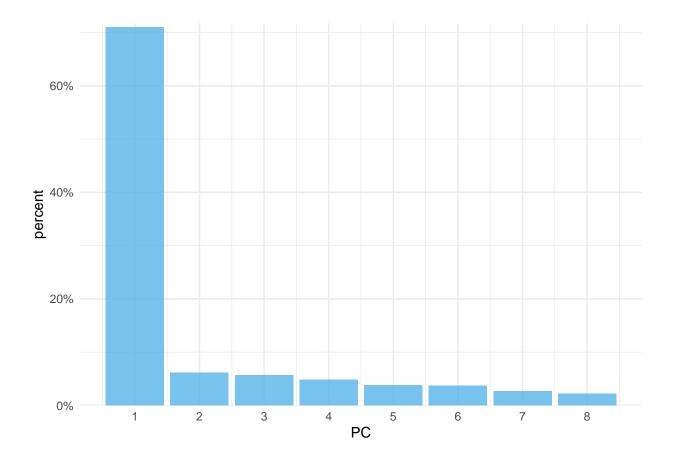
As the data are standardized the standard deviation values for each principal component are the Eigenvalues.

As we can see only the first PC has an Eigenvalue greater than 1.

The first PC accounts for 71.02% of the variance, while the second PC accounts for the 6.13% of the variance. Together they explain 77.15% of the variance.

Lets plot the results.

```
pca %>%
  tidy(matrix = "eigenvalues") %>%
  ggplot(aes(PC, percent)) +
  geom_col(fill = "#56B4E9", alpha = 0.8) +
  scale_x_continuous(breaks = 1:8) +
  scale_y_continuous(
    labels = scales::percent_format(),
    expand = expansion(mult = c(0, 0.01))
  ) +
  theme_minimal()
```



2. PCA of MET

First, we select the variables of interest.

```
met_subscales <- c("jollet", "savor", "a_vhat", "onreg", "rezil")
met_data <- dplyr::select(processed, all_of(met_subscales))</pre>
```

We run the PCA while standardizing the variables.

```
pca_met <-
  met_data %>%
  prcomp(scale = TRUE, center = TRUE)

summary(pca_met)

## Importance of components:
```

```
## Importance of components:

## PC1 PC2 PC3 PC4 PC5

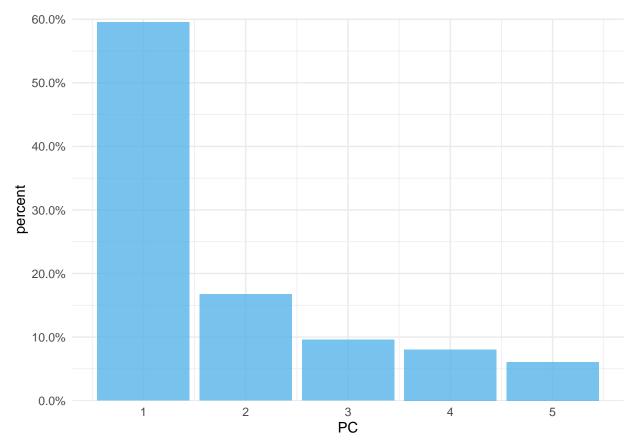
## Standard deviation 1.7254 0.9153 0.69228 0.63458 0.55085

## Proportion of Variance 0.5954 0.1676 0.09585 0.08054 0.06069

## Cumulative Proportion 0.5954 0.7629 0.85878 0.93931 1.00000
```

As we can see only the first PC has an Eigenvalue greater than 1, and it accounts for 59.54% of the variance.

```
pca_met %>%
  tidy(matrix = "eigenvalues") %>%
  ggplot(aes(PC, percent)) +
  geom_col(fill = "#56B4E9", alpha = 0.8) +
  scale_x_continuous(breaks = 1:5) +
  scale_y_continuous(
    labels = scales::percent_format(),
    expand = expansion(mult = c(0, 0.01))
  ) +
  theme_minimal()
```



3. Use varimax and promax rotation on the first three principal components of the second task.

I could use the prcomp function ad before, but we would have to use a cutting point for the Eigenvalues to only include 3 PC. Thus, I will use the psych::principal function, where I can set the number of PC in the function call.

Thus, I run a new PCA with three components and varimax rotation. This function returns the standardized scores by default. The function calculates the correlation matrix by pairwise deletion of the missing values.

```
pca_met_varimax <- psych::principal(met_data, rotate = "varimax", nfactors = 3, scores = TRUE)</pre>
```

Lets take a look at the Eigenvalues.

```
pca_met_varimax$value
```

[1] 2.9768986 0.8377353 0.4792455 0.4026888 0.3034318

The rest of the results.

```
pca_met_varimax
```

```
## Principal Components Analysis
## Call: psych::principal(r = met_data, nfactors = 3, rotate = "varimax",
       scores = TRUE)
## Standardized loadings (pattern matrix) based upon correlation matrix
          RC1 RC3 RC2
                          h2
                                 u2 com
## jollet 0.67 0.55 0.14 0.77 0.230 2.0
## savor 0.91 0.10 0.12 0.86 0.144 1.1
## a_vhat 0.74 0.45 0.12 0.76 0.240 1.7
## onreg 0.14 0.22 0.97 1.00 0.002 1.1
## rezil 0.24 0.89 0.25 0.91 0.090 1.3
##
##
                         RC1 RC3 RC2
                        1.90 1.36 1.04
## SS loadings
## Proportion Var
                        0.38 0.27 0.21
## Cumulative Var
                        0.38 0.65 0.86
## Proportion Explained 0.44 0.32 0.24
## Cumulative Proportion 0.44 0.76 1.00
##
## Mean item complexity = 1.5
## Test of the hypothesis that 3 components are sufficient.
##
## The root mean square of the residuals (RMSR) is 0.08
  with the empirical chi square 57.46 with prob < NA
##
## Fit based upon off diagonal values = 0.98
```

The factor loadings are quite small for *onreg* and *rezil* on RC1. Based on the communalities (h2) it seems that most of the variance explained by these two items can be explained by other items.

The complexity scores suggest that jollet and maybe a_vhat the items measure more than one latent construct.

The proportion var suggest that the RC1 explains 38% of the variance in the responses, while RC3 27% and RC2 21%.

The fit based upon off diagonal values support a good fit.

Now we should run the same analysis but allow factors to correlate, therefore we use an oblique rotation called promax.

```
pca_met_promax <- psych::principal(met_data, rotate = "promax", nfactors = 3, scores = TRUE)</pre>
```

Lets see the results of this solution.

```
pca_met_promax
```

```
## Principal Components Analysis
## Call: psych::principal(r = met_data, nfactors = 3, rotate = "promax",
       scores = TRUE)
## Standardized loadings (pattern matrix) based upon correlation matrix
                 RC3
           RC1
                       RC2
                             h2
                                   u2 com
## jollet 0.54 0.43 -0.03 0.77 0.230 1.9
## savor
          1.07 -0.27 0.04 0.86 0.144 1.1
## a_vhat 0.68 0.27 -0.03 0.76 0.240 1.3
          0.02
                0.04 0.97 1.00 0.002 1.0
## onreg
## rezil -0.16 1.04 0.04 0.91 0.090 1.0
##
                         RC1 RC3 RC2
## SS loadings
                        1.92 1.40 0.98
## Proportion Var
                        0.38 0.28 0.20
## Cumulative Var
                        0.38 0.66 0.86
## Proportion Explained 0.45 0.33 0.23
## Cumulative Proportion 0.45 0.77 1.00
##
##
   With component correlations of
##
        RC1 RC3 RC2
## RC1 1.00 0.66 0.29
## RC3 0.66 1.00 0.42
## RC2 0.29 0.42 1.00
## Mean item complexity = 1.3
## Test of the hypothesis that 3 components are sufficient.
## The root mean square of the residuals (RMSR) is 0.08
## with the empirical chi square 57.46 with prob < NA
##
## Fit based upon off diagonal values = 0.98
```

Allowing for correlation reduced the complexity and we have a much cleaner latent structure than before with varimax. RC1 highly correlates (0.66) with RC3 and only medium with RC2 (0.29), there is a medium to high correlation (0.42) between RC3 and RC2.

4. Save the factors from the promax rotation and correlate the with the PERMA test's items. Which items has the highest correlattion with the first factor.

Calculating the factor scores.

```
scores <- factor.scores(met_data, pca_met_promax)
scores <- as.data.frame(scores$scores)</pre>
```

Binding calculated scores to the original data.

```
perma_vars <- c("p_poz_erz", "p_elmely", "p_poz_kapc", "p_ert_cel", "p_telj", "p_boldog", "p_egeszs", "processed_scores <-
processed %>%
bind_cols(., scores) %>%
select(RC1, RC2, RC3, all_of(perma_vars))
```

Running the correlations.

```
corr_matrix <- rcorr(as.matrix(processed_scores))
corr_matrix$r</pre>
```

```
##
                  R.C1
                           RC2
                                     RC3 p_poz_erz
                                                   p_elmely p_poz_kapc
## RC1
             1.0000000 0.2864299
                               0.6621899
                                        0.6913069 0.4993597 0.5658908
## RC2
            0.2864299 \quad 1.0000000 \quad 0.4246157 \quad 0.4356578 \quad 0.2492797 \quad 0.2877081
## RC3
            0.6621899 0.4246157
                               1.0000000 0.7040195
                                                  0.4838113
                                                            0.5060462
            ## p_poz_erz
## p_elmely
            ## p_poz_kapc 0.5658908 0.2877081 0.5060462 0.6774156
                                                  0.4796039
                                                           1.0000000
## p_ert_cel
            0.6604940 0.2450133 0.6050290 0.7531407
                                                  0.6305894 0.6495659
            0.6053890 0.2457362 0.5759880 0.7229889 0.5485736 0.5369546
## p_telj
## p_boldog
            ## p_egeszs
            ## p_neg_erz -0.5526917 -0.4805750 -0.6201278 -0.6866772 -0.4282924 -0.4972611
## p_magany
            -0.3836024 -0.2836810 -0.4253238 -0.4525517 -0.2901264 -0.4671761
            p_ert_cel
                        p_telj
                                p_boldog
                                         p_egeszs p_neg_erz
                                                             p_magany
            0.6604940 \quad 0.6053890 \quad 0.6577439 \quad 0.4361927 \quad -0.5526917 \quad -0.3836024
## RC1
## RC2
            ## RC3
            0.6050290 \quad 0.5759880 \quad 0.6490360 \quad 0.4511676 \ -0.6201278 \ -0.4253238
            ## p_poz_erz
## p_elmely
            0.6305894 0.5485736 0.5095568 0.3379240 -0.4282924 -0.2901264
## p_poz_kapc 0.6495659 0.5369546 0.7279601 0.4356007 -0.4972611 -0.4671761
## p_ert_cel
            1.0000000 \quad 0.7500587 \quad 0.7304123 \quad 0.4943210 \quad -0.5041553 \quad -0.3912630
## p_telj
            0.7500587 \quad 1.0000000 \quad 0.6500552 \quad 0.5273559 \quad -0.5219503 \quad -0.3331066
## p_boldog
            0.7304123 0.6500552
                               1.0000000 0.4527424 -0.6081244 -0.5236918
            0.4943210 \quad 0.5273559 \quad 0.4527424 \quad 1.0000000 \quad -0.4147676 \quad -0.2980372
## p_egeszs
## p_neg_erz -0.5041553 -0.5219503 -0.6081244 -0.4147676 1.0000000 0.5487226
            -0.3912630 -0.3331066 -0.5236918 -0.2980372 0.5487226 1.0000000
## p_magany
```

Interestingly there is a strong correlation between almost all of the variables. The strongest correlation is between RC1 and and the PERMA items is with p_poz_erz (r = 0.69)