

EFA

```
set.seed(42)

library(igraph)

##
## Attaching package: 'igraph'
## The following objects are masked from 'package:stats':
##
##      decompose, spectrum
## The following object is masked from 'package:base':
##
##      union
library(QuantPsyc) # for the multivariate normality test

## Loading required package: boot
## Loading required package: dplyr
##
## Attaching package: 'dplyr'
## The following objects are masked from 'package:igraph':
##
##      as_data_frame, groups, union
## The following objects are masked from 'package:stats':
##
##      filter, lag
## The following objects are masked from 'package:base':
##
##      intersect, setdiff, setequal, union
## Loading required package: purrr
##
## Attaching package: 'purrr'
## The following objects are masked from 'package:igraph':
##
##      compose, simplify
## Loading required package: MASS
##
## Attaching package: 'MASS'
## The following object is masked from 'package:dplyr':
##
##      select
```

```

##
## Attaching package: 'QuantPsyc'
## The following object is masked from 'package:base':
##
##      norm
library(dunn.test)
library(nFactors) # for the scree plot

## Loading required package: lattice
##
## Attaching package: 'lattice'
## The following object is masked from 'package:boot':
##
##      melanoma
##
## Attaching package: 'nFactors'
## The following object is masked from 'package:lattice':
##
##      parallel
library(psych) # for PA FA

##
## Attaching package: 'psych'
## The following object is masked from 'package:boot':
##
##      logit
library(caret) # highly correlated features removal

## Loading required package: ggplot2
##
## Attaching package: 'ggplot2'
## The following objects are masked from 'package:psych':
##
##      %+%, alpha
##
## Attaching package: 'caret'
## The following object is masked from 'package:purrr':
##
##      lift
library(tidyverse)

## -- Attaching core tidyverse packages ----- tidyverse 2.0.0 --
## v forcats   1.0.0      v stringr   1.5.1
## v lubridate 1.9.3      v tibble   3.2.1
## v readr     2.1.5      v tidyr    1.3.1

## -- Conflicts ----- tidyverse_conflicts() --
## x lubridate::%--%()      masks igraph::%--%()

```

```
## x ggplot2::%+%( ) masks psych::%+%( )
## x ggplot2::alpha( ) masks psych::alpha( )
## x tibble::as_data_frame( ) masks dplyr::as_data_frame( ), igraph::as_data_frame( )
## x purrr::compose( ) masks igraph::compose( )
## x tidyr::crossing( ) masks igraph::crossing( )
## x dplyr::filter( ) masks stats::filter( )
## x dplyr::lag( ) masks stats::lag( )
## x caret::lift( ) masks purrr::lift( )
## x MASS::select( ) masks dplyr::select( )
## x purrr::simplify( ) masks igraph::simplify( )
## i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become errors.
```

```
library(paletteer) # color palettes
```

```
library(conflicted) # to resolve QuantPsyc x dplyr conflicts
conflict_prefer("select", "dplyr")
```

```
## [conflicted] Will prefer dplyr::select over any other package.
```

```
conflict_prefer("filter", "dplyr")
```

```
## [conflicted] Will prefer dplyr::filter over any other package.
```

Load and tidy data

```
pretty_names <- read_csv("../feat_name_mapping.csv")
```

```
## Rows: 85 Columns: 2
## -- Column specification -----
## Delimiter: ","
## chr (2): name_orig, name_pretty
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```
data <- read_csv("../measurements/measurements.csv")
```

```
## Rows: 754 Columns: 108
## -- Column specification -----
## Delimiter: ","
## chr (20): fpath, KUK_ID, FileName, FileFormat, FolderPath, subcorpus, Source...
## dbl (85): RuleAbstractNouns, RuleAmbiguousRegards, RuleAnaphoricReferences, ...
## lgl (3): ClarityPursuit, SyllogismBased, Bindingness
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```
.firstnonmetacolumn <- 17
```

```
data_no_nas <- data %>%
  select(!c(
    fpath,
    # KUK_ID,
    # FileName,
    FolderPath,
    # subcorpus,
```

```

DocumentTitle,
ClarityPursuit,
Readability,
SyllogismBased,
SourceDB
)) %>%
# replace -1s in variation coefficients with NAs
mutate(across(c(
  `RuleDoubleAdpos.max_allowable_distance.v`,
  `RuleTooManyNegations.max_negation_frac.v`,
  `RuleTooManyNegations.max_allowable_negations.v`,
  `RuleTooManyNominalConstructions.max_noun_frac.v`,
  `RuleTooManyNominalConstructions.max_allowable_nouns.v`,
  `RuleCaseRepetition.max_repetition_count.v`,
  `RuleCaseRepetition.max_repetition_frac.v`,
  `RulePredSubjDistance.max_distance.v`,
  `RulePredObjDistance.max_distance.v`,
  `RuleInfVerbDistance.max_distance.v`,
  `RuleMultiPartVerbs.max_distance.v`,
  `RuleLongSentences.max_length.v`,
  `RulePredAtClauseBeginning.max_order.v`,
  `mattr.v`,
  `maentropy.v`
), ~ na_if(.x, -1))) %>%
# replace NAs with 0s
replace_na(list(
  RuleGPcoordovs = 0,
  RuleGPdeverbaddr = 0,
  RuleGPpatinstr = 0,
  RuleGPdeverbsubj = 0,
  RuleGPadjective = 0,
  RuleGPpatbenperson = 0,
  RuleGPwordorder = 0,
  RuleDoubleAdpos = 0,
  RuleDoubleAdpos.max_allowable_distance = 0,
  RuleDoubleAdpos.max_allowable_distance.v = 0,
  RuleAmbiguousRegards = 0,
  RuleReflexivePassWithAnimSubj = 0,
  RuleTooManyNegations = 0,
  RuleTooManyNegations.max_negation_frac = 0,
  RuleTooManyNegations.max_negation_frac.v = 0,
  RuleTooManyNegations.max_allowable_negations = 0,
  RuleTooManyNegations.max_allowable_negations.v = 0,
  RuleTooManyNominalConstructions.max_noun_frac.v = 0,
  RuleTooManyNominalConstructions.max_allowable_nouns.v = 0,
  RuleFunctionWordRepetition = 0,
  RuleCaseRepetition.max_repetition_count.v = 0,
  RuleCaseRepetition.max_repetition_frac.v = 0,
  RuleWeakMeaningWords = 0,
  RuleAbstractNouns = 0,
  RuleRelativisticExpressions = 0,
  RuleConfirmationExpressions = 0,
  RuleRedundantExpressions = 0,

```

```

RuleTooLongExpressions = 0,
RuleAnaphoricReferences = 0,
RuleLiteraryStyle = 0,
RulePassive = 0,
RulePredSubjDistance = 0,
RulePredSubjDistance.max_distance = 0,
RulePredSubjDistance.max_distance.v = 0,
RulePredObjDistance = 0,
RulePredObjDistance.max_distance = 0,
RulePredObjDistance.max_distance.v = 0,
RuleInfVerbDistance = 0,
RuleInfVerbDistance.max_distance = 0,
RuleInfVerbDistance.max_distance.v = 0,
RuleMultiPartVerbs = 0,
RuleMultiPartVerbs.max_distance = 0,
RuleMultiPartVerbs.max_distance.v = 0,
RuleLongSentences.max_length.v = 0,
RulePredAtClauseBeginning.max_order.v = 0,
RuleVerbalNouns = 0,
RuleDoubleComparison = 0,
RuleWrongValencyCase = 0,
RuleWrongVerbominalCase = 0,
RuleIncompleteConjunction = 0
))

data_clean <- data_no_nas %>%
  # norm data expected to correlate with text length
  mutate(across(c(
    RuleGPcoordovs,
    RuleGPdeverbaddr,
    RuleGPpatinstr,
    RuleGPdeverbsubj,
    RuleGPadjective,
    RuleGPpatbenperson,
    RuleGPwordorder,
    RuleDoubleAdpos,
    RuleAmbiguousRegards,
    RuleFunctionWordRepetition,
    RuleWeakMeaningWords,
    RuleAbstractNouns,
    RuleRelativisticExpressions,
    RuleConfirmationExpressions,
    RuleRedundantExpressions,
    RuleTooLongExpressions,
    RuleAnaphoricReferences,
    RuleLiteraryStyle,
    RulePassive,
    RuleVerbalNouns,
    RuleDoubleComparison,
    RuleWrongValencyCase,
    RuleWrongVerbominalCase,
    RuleIncompleteConjunction,
    num_hapax,

```

```

RuleReflexivePassWithAnimSubj,
RuleTooManyNominalConstructions,
RulePredSubjDistance,
RuleMultiPartVerbs,
RulePredAtClauseBeginning
), ~ .x / word_count)) %>%
mutate(across(c(
  RuleTooFewVerbs,
  RuleTooManyNegations,
  RuleCaseRepetition,
  RuleLongSentences,
  RulePredObjDistance,
  RuleInfVerbDistance
), ~ .x / sent_count)) %>%
# remove variables identified as "u counts"
select(!c(
  RuleTooFewVerbs,
  RuleTooManyNegations,
  RuleTooManyNominalConstructions,
  RuleCaseRepetition,
  RuleLongSentences,
  RulePredAtClauseBeginning,
  sent_count,
  word_count,
  syllab_count,
  char_count
)) %>%
# remove variables identified as unreliable
select(!c(
  RuleAmbiguousRegards,
  RuleFunctionWordRepetition,
  RuleDoubleComparison,
  RuleWrongValencyCase,
  RuleWrongVerbonominalCase
)) %>%
# remove artificially limited variables
select(!c(
  RuleCaseRepetition.max_repetition_frac,
  RuleCaseRepetition.max_repetition_frac.v
)) %>%
# remove further variables belonging to the 'acceptability' category
select(!c(RuleIncompleteConjunction)) %>%
mutate(across(c(
  class,
  FileFormat,
  subcorpus,
  DocumentVersion,
  LegalActType,
  Objectivity,
  AuthorType,
  RecipientType,
  RecipientIndividuation,
  Anonymized

```

```

), ~ as.factor(.x)))

# no NAs should be present now
data_clean[!complete.cases(data_clean), ]

## # A tibble: 754 x 83
##   KUK_ID      FileName FileFormat subcorpus SourceID DocumentVersion
##   <chr>      <chr>      <fct>      <fct>      <chr>      <fct>
## 1 673b7a37c6537d54ff062~ 002_Kom~  TXT      KUKY      <NA>      Original
## 2 673b7a37c6537d54ff062~ 006_Chc~  TXT      KUKY      <NA>      Redesign
## 3 673b7a37c6537d54ff062~ 004_Nev~  TXT      KUKY      <NA>      Original
## 4 673b7a37c6537d54ff062~ 008_Pol~  TXT      KUKY      <NA>      Original
## 5 673b7a37c6537d54ff062~ 005_Och~  TXT      KUKY      <NA>      Original
## 6 673b7a37c6537d54ff062~ 016_Obc~  TXT      KUKY      <NA>      Original
## 7 673b7a37c6537d54ff062~ 019_Dét~  TXT      KUKY      <NA>      Redesign
## 8 673b7a37c6537d54ff062~ 007_DÜC~  TXT      KUKY      <NA>      Redesign
## 9 673b7a37c6537d54ff062~ 024_Opa~  TXT      KUKY      <NA>      Original
## 10 673b7a37c6537d54ff062~ 047_Dav~  TXT      KUKY      <NA>      Original
## # i 744 more rows
## # i 77 more variables: ParentDocumentID <chr>, LegalActType <fct>,
## #   Objectivity <fct>, Bindingness <lgl>, AuthorType <fct>,
## #   RecipientType <fct>, RecipientIndividuation <fct>, Anonymized <fct>,
## #   `Recipient Type` <chr>, class <fct>, RuleAbstractNouns <dbl>,
## #   RuleAnaphoricReferences <dbl>,
## #   RuleCaseRepetition.max_repetition_count <dbl>, ...
data_clean_scaled <- data_clean %>%
  mutate(across(class, ~ .x == "good")) %>%
  mutate(across(.firstnonmetacolumn:length(names(data_clean)), ~ scale(.x)))

## Warning: There was 1 warning in `mutate()`.
## i In argument: `across(.firstnonmetacolumn:length(names(data_clean)),
##   ~scale(.x))`.
## Caused by warning:
## ! Using an external vector in selections was deprecated in tidysselect 1.1.0.
## i Please use `all_of()` or `any_of()` instead.
## # Was:
##   data %>% select(.firstnonmetacolumn)
##
## # Now:
##   data %>% select(all_of(.firstnonmetacolumn))
##
## See <https://tidysselect.r-lib.org/reference/faq-external-vector.html>.

```

Important features identification

```

data_clean_good <- data_clean_scaled %>% filter(class == "good")
data_clean_bad <- data_clean_scaled %>% filter(class == "bad")

feature_importances <- tibble(
  feat_name = character(), p_value = numeric()
)

```

```

for (i in .firstnonmetacolumn:ncol(data_clean)) {
  fname <- names(data_clean)[i]

  formula_single <- reformulate(fname, "class")

  glm_model <- glm(formula_single, data_clean, family = "binomial")
  glm_coefficients <- summary(glm_model)$coefficients
  row_index <- which(rownames(glm_coefficients) == fname)
  p_value <- glm_coefficients[row_index, 4]

  feature_importances <- feature_importances %>%
    add_row(feet_name = fname, p_value = p_value)
}
feature_importances

```

```

## # A tibble: 67 x 2
##   feat_name                p_value
##   <chr>                  <dbl>
## 1 RuleAbstractNouns      0.00187
## 2 RuleAnaphoricReferences 0.660
## 3 RuleCaseRepetition.max_repetition_count 0.0722
## 4 RuleCaseRepetition.max_repetition_count.v 0.00479
## 5 RuleConfirmationExpressions 0.0985
## 6 RuleDoubleAdpos        0.312
## 7 RuleDoubleAdpos.max_allowable_distance 0.000154
## 8 RuleDoubleAdpos.max_allowable_distance.v 0.00000356
## 9 RuleGPadjective        0.380
## 10 RuleGPcoordovs        0.828
## # i 57 more rows

```

```

selected_features <- feature_importances %>%
  mutate(selected = p_value <= 0.05)
selected_features %>% write_csv("selected_features.csv")
selected_features_names <- selected_features %>%
  filter(selected) %>%
  pull(feet_name)

```

Correlations

See Levshina (2015: 353–54).

```

analyze_correlation <- function(data) {
  cor_matrix <- cor(data)

  cor_tibble_long <- cor_matrix %>%
    as_tibble() %>%
    mutate(feet1 = rownames(cor_matrix)) %>%
    pivot_longer(!feet1, names_to = "feet2", values_to = "cor") %>%
    mutate(abs_cor = abs(cor))

  cor_matrix_upper <- cor_matrix
  cor_matrix_upper[lower.tri(cor_matrix_upper)] <- 0

  cor_tibble_long_upper <- cor_matrix_upper %>%

```



```

as_tibble() %>%
mutate(feats1 = rownames(cor_matrix)) %>%
pivot_longer(!feats1, names_to = "feat2", values_to = "cor") %>%
mutate(abs_cor = abs(cor)) %>%
filter(feats1 != feat2 & abs_cor > 0)

list(
  cor_matrix = cor_matrix,
  cor_matrix_upper = cor_matrix_upper,
  cor_tibble_long = cor_tibble_long,
  cor_tibble_long_upper = cor_tibble_long_upper
)
}

data_purish <- data_clean %>% select(any_of(selected_features_names)) %>%
# remove features expected to have low communalities
select(!c(
  RuleDoubleAdpos.max_allowable_distance,
  RuleDoubleAdpos.max_allowable_distance.v,
  RuleGPwordorder,
  RuleLiteraryStyle,
  maentropy.v,
  RuleTooManyNegations.max_negation_frac,
  RulePredSubjDistance.max_distance,
  RuleTooManyNegations.max_allowable_negations,
  RuleTooManyNegations.max_allowable_negations.v,
  RuleTooManyNominalConstructions.max_allowable_nouns.v,
  RuleTooFewVerbs.min_verb_frac.v,
  RulePredObjDistance.max_distance.v,
  RulePredObjDistance.max_distance,
  RulePredAtClauseBeginning.max_order.v,
  RuleInfVerbDistance
)) %>%
# remove features expected to have low loadings
select(!c(
  RuleMultiPartVerbs.max_distance.v,
  RulePredSubjDistance.max_distance.v,
  RuleLongSentences.max_length
))

```

Extremely non-normal data

```

# # remove where median == 0?
# keep <- character()
# for (i in seq_along(colnames(data_purish))) {
#   cname <- colnames(data_purish)[i]
#   q <- quantile(data_purish[, i][[1]], probs = 0.10)[[1]]
#   if (q > 0) {
#     keep <- c(keep, cname)
#     cat("keep", cname, "\n")
#   } else {
#     cat("throw out", cname, "\n")
#   }
# }

```

```
# }
# data_purish <- data_purish %>% select(any_of(keep))
```

High correlations

```
.hcorrcutoff <- 0.9

analyze_correlation(data_purish)$cor_tibble_long %>%
  filter(featl1 != featl2 & abs_cor > .hcorrcutoff) %>%
  arrange(featl1, -abs_cor) %>%
  print(n = 100)
```

```
## # A tibble: 16 x 4
##   featl1    featl2      cor abs_cor
##   <chr>    <chr>    <dbl> <dbl>
## 1 ari      fkgl      0.984  0.984
## 2 ari      gf        0.978  0.978
## 3 ari      smog      0.951  0.951
## 4 atl      cli        0.960  0.960
## 5 cli      atl        0.960  0.960
## 6 fkgl     ari        0.984  0.984
## 7 fkgl     gf        0.967  0.967
## 8 fkgl     smog      0.949  0.949
## 9 gf       smog      0.987  0.987
## 10 gf      ari        0.978  0.978
## 11 gf      fkgl      0.967  0.967
## 12 maentropy mattr    0.964  0.964
## 13 mattr    maentropy 0.964  0.964
## 14 smog     gf        0.987  0.987
## 15 smog     ari        0.951  0.951
## 16 smog     fkgl      0.949  0.949
```

exclude:

- **ari:** corr. w/ RuleLongSentences.max_length > 0.94; sentence length seems more universal, let's make it a substitute
- **gf:** corr. w/ RuleLongSentences.max_length > 0.92; sentence length seems more universal, let's make it a substitute
- **maentropy:** corr. w/ mattr > 0.96, but mattr is implemented in QuitaUp. besides, the interesting thing about maentropy is its variation
- **smog:** corr. w/ fkgl almost 0.95, but fkgl coefficients adjusted for Czech are available
- **atl:** corr. w/ cli around 0.96; unlike cli, atl is not a readability metric

```
high_correlations <- findCorrelation(cor(data_purish), verbose = TRUE)
```

```
## Compare row 20 and column 26 with corr 0.978
## Means: 0.399 vs 0.207 so flagging column 20
## Compare row 26 and column 32 with corr 0.987
## Means: 0.378 vs 0.195 so flagging column 26
## Compare row 32 and column 24 with corr 0.949
## Means: 0.35 vs 0.184 so flagging column 32
## Compare row 21 and column 22 with corr 0.96
## Means: 0.27 vs 0.176 so flagging column 21
## Compare row 28 and column 30 with corr 0.964
## Means: 0.194 vs 0.171 so flagging column 28
```

```
## All correlations <= 0.9
names(data_purish)[high_correlations]

## [1] "ari"          "gf"          "smog"        "atl"         "maentropy"

data_pureish_striphigh <- data_purish %>% select(!all_of(high_correlations))

analyze_correlation(data_pureish_striphigh)$cor_tibble_long %>%
  filter(featl != feat2 & abs_cor > .hcorrcutoff) %>%
  arrange(featl, -abs_cor) %>%
  print(n = 100)

## # A tibble: 0 x 4
## # i 4 variables: feat1 <chr>, feat2 <chr>, cor <dbl>, abs_cor <dbl>
```

Low correlations

```
# 0.35 instead of 0.3 otherwise the FA bootstrapping would freeze
.lcorrcutoff <- 0.35

low_correlating_features <- analyze_correlation(data_pureish_striphigh)$
  cor_tibble_long %>%
  filter(featl != feat2) %>%
  group_by(featl) %>%
  summarize(max_cor = max(abs_cor)) %>%
  filter(max_cor < .lcorrcutoff) %>%
  pull(featl)

feature_importances %>% filter(featl_name %in% low_correlating_features)

## # A tibble: 11 x 2
##   feat_name                                p_value
##   <chr>                                <dbl>
## 1 RuleAbstractNouns                      0.00187
## 2 RuleCaseRepetition.max_repetition_count.v 0.00479
## 3 RuleGPdeverbaddr                      0.0112
## 4 RuleGPdeverbsubj                     0.0133
## 5 RuleMultiPartVerbs.max_distance        0.00320
## 6 RuleRedundantExpressions              0.0104
## 7 RuleRelativisticExpressions          0.00205
## 8 RuleTooManyNegations.max_negation_frac.v 0.0365
## 9 RuleTooManyNominalConstructions.max_noun_frac.v 0.00000311
## 10 RuleVerbalNouns                     0.0000748
## 11 RuleWeakMeaningWords                 0.0386

data_pure <- data_pureish_striphigh %>%
  select(!any_of(low_correlating_features))

cnames <- map(
  colnames(data_pure),
  function(x) {
    pull(pretty_names %>%
      filter(name_orig == x), name_pretty)
  }
) %>% unlist()
```

```
colnames(data_pure) <- cnames
```

Visualisation

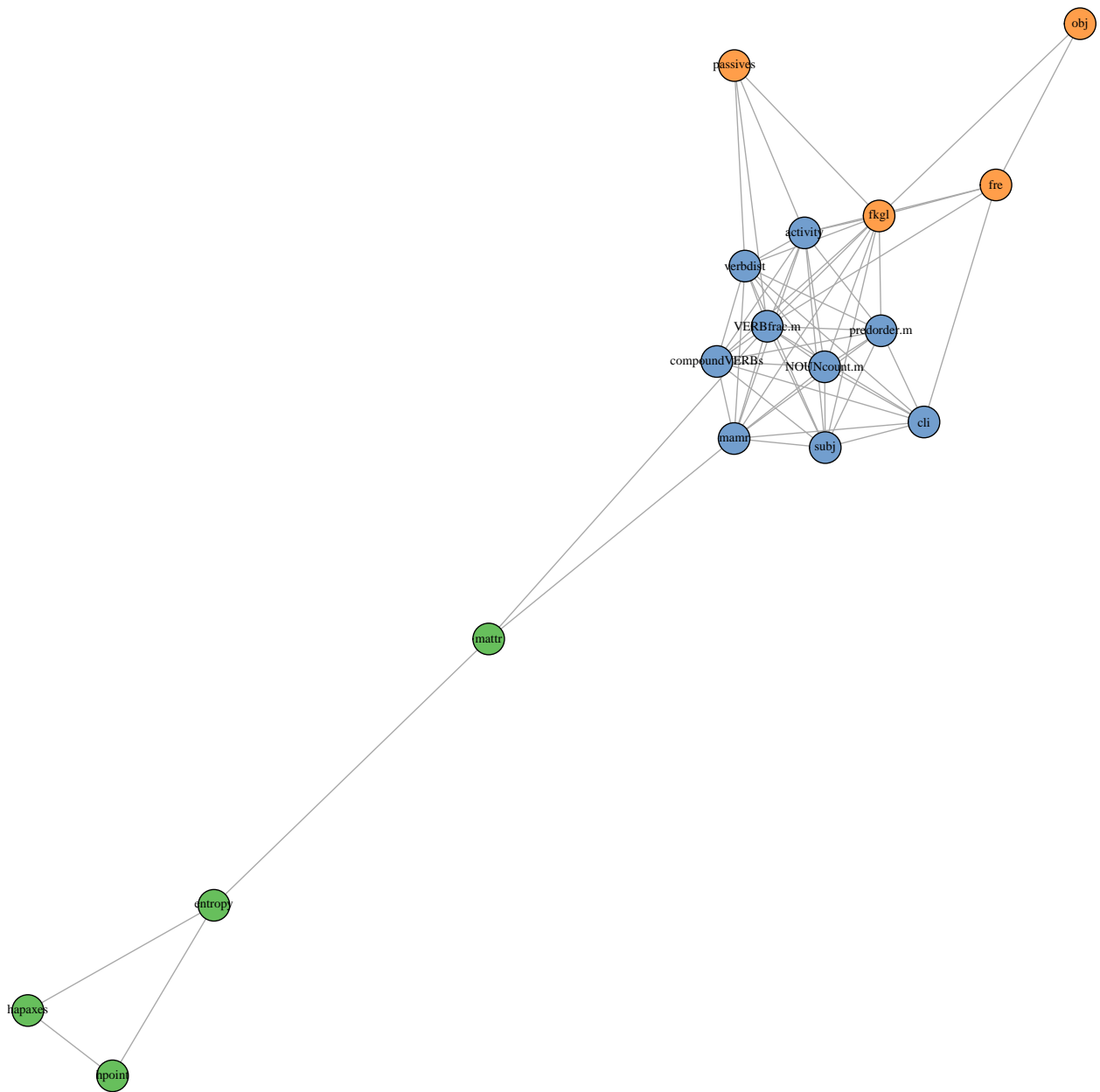
```
my_colors <- paletteer::paletteer_d("ggthemes::Classic_10_Medium")

network_edges <- analyze_correlation(data_pure)$cor_tibble_long_upper %>%
  filter(abs_cor > 0.3)

network <- graph_from_data_frame(
  network_edges,
  directed = FALSE
)
E(network)$weight <- network_edges$abs_cor
network_communities <- cluster_optimal(network)

network_membership <- membership(network_communities)

plot(
  network,
  layout = layout_fruchterman_reingold,
  vertex.color = map(
    network_communities$membership,
    function(x) my_colors[x]
  ) %>% unlist(use.names = FALSE),
  vertex.size = 6,
  vertex.label.color = "black",
  vertex.label.cex = 0.7
)
```



Scaling

```
data_scaled <- data_pure %>%
  mutate(across(seq_along(data_pure), ~ scale(.x)[, 1])))

final_collist <- data_scaled %>% colnames()
```

Check for normality

```
mult.norm(data_scaled %>% as.data.frame())$mult.test
```

```
##          Beta-hat      kappa p-val
```

```
## Skewness 351.5182 44174.1153    0
## Kurtosis 858.5678  289.3036    0
```

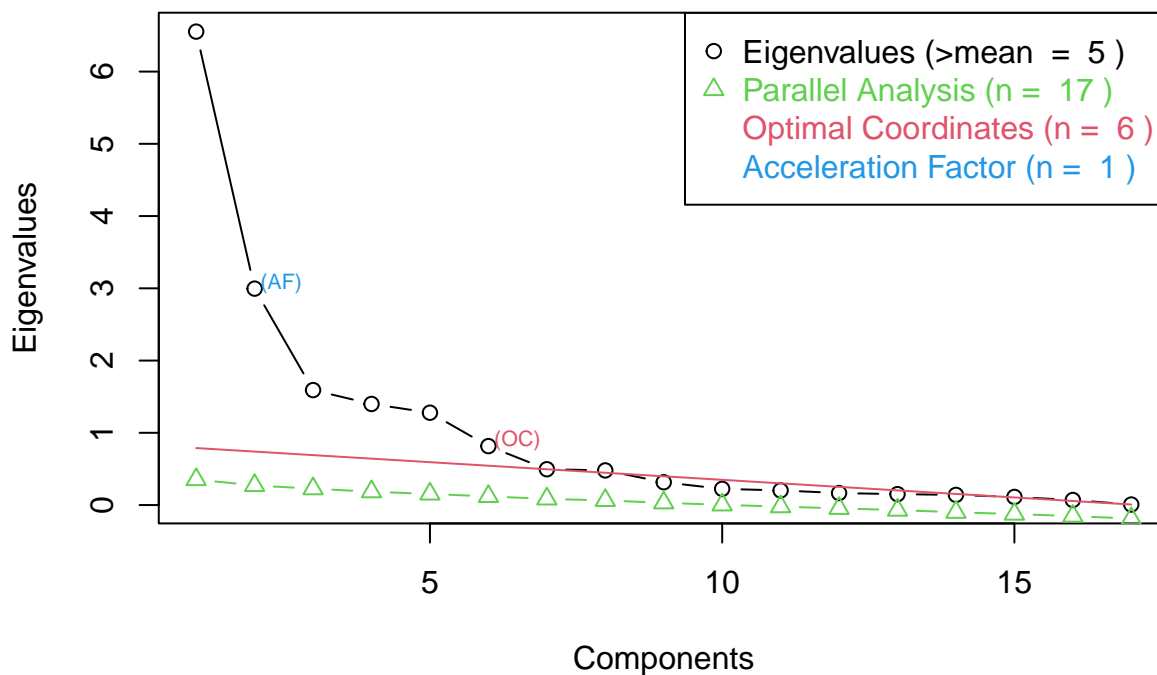
Low (null) p-values show that we can reject the hypothesis that the data would be in a multivariate normal distribution. I.e. the distribution isn't multivariate normal.

FA

No. of factors

```
eigen <- eigen(cor(data_scaled))
par <- nFactors::parallel(
  subject = nrow(data_scaled),
  var = ncol(data_scaled),
  rep = 100,
  quantile = .95,
  model = "factors"
)
scree <- nScree(x = eigen$values, aparallel = par$eigen$gevpea)
plotnScree(scree)
```

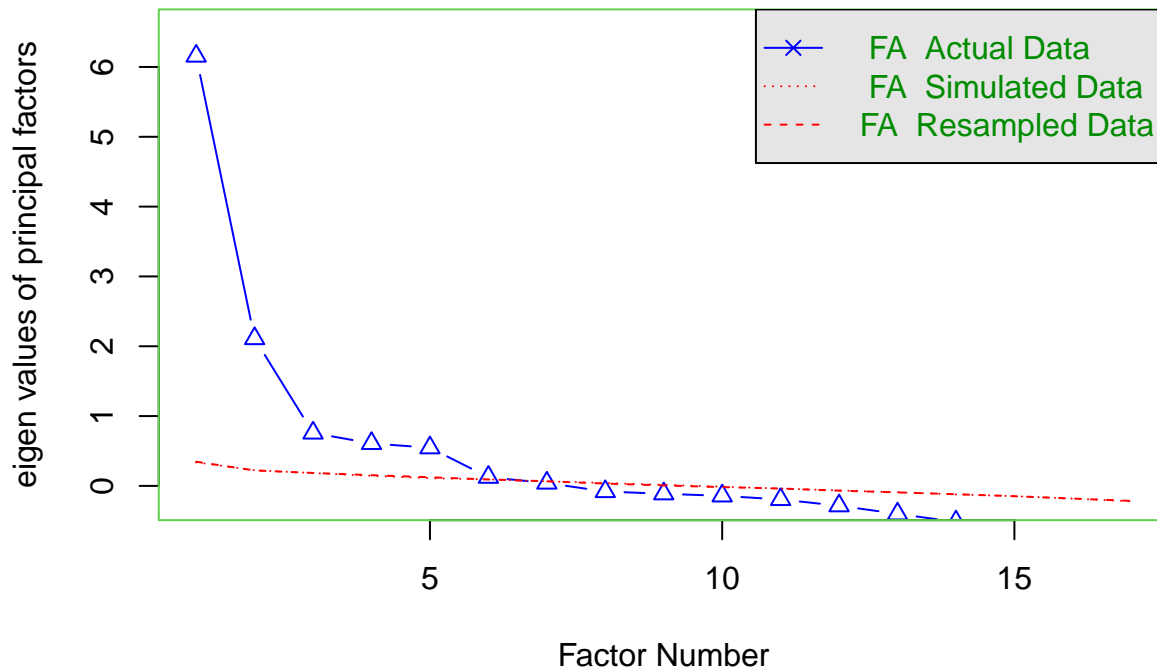
Non Graphical Solutions to Scree Test



```
fa.parallel(data_scaled, fm = "pa", fa = "fa", n.iter = 20)
```

```
## 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 score estimation method.
```

Parallel Analysis Scree Plots



Parallel analysis suggests that the number of factors = 6 and the number of components = NA

Model

<https://www.rdocumentation.org/packages/psych/versions/2.5.3/topics/fa>

```
# appears to be the happiest when nfactors = 6 or 7
# throws the The estimated weights for the factor scores are probably incorrect.
# Try a different factor score estimation method. warning otherwise
```

```
fa_res <- fa(
  data_scaled,
  nfactors = 7,
  fm = "pa",
  rotate = "promax",
  oblique.scores = TRUE,
  scores = "tenBerge",
  n.iter = 100
)
```

Loading required namespace: GPArotation

```
fa_res
```

```
## Factor Analysis with confidence intervals using method = fa(r = data_scaled, nfactors = 7, n.iter = 100)
##   scores = "tenBerge", fm = "pa", oblique.scores = TRUE)
## Factor Analysis using method = pa
## Call: fa(r = data_scaled, nfactors = 7, n.iter = 100, rotate = "promax",
##   scores = "tenBerge", fm = "pa", oblique.scores = TRUE)
## Standardized loadings (pattern matrix) based upon correlation matrix
##               PA1  PA2  PA6  PA3  PA4  PA5  PA7  h2    u2 com
## compoundVERBs 0.79 0.00 -0.17 -0.01 0.04 0.24 0.51 0.78 0.2219 2.0
## passives      0.10 -0.03 0.00 -0.17 0.03 0.82 0.12 0.59 0.4143 1.2
```

```

## predorder.m    -0.72 -0.02  0.13 -0.07 -0.11 -0.05  0.02 0.55 0.4487 1.1
## obj            0.24 -0.01  0.96 -0.15 -0.02 -0.05 -0.12 0.71 0.2887 1.2
## subj           0.72  0.09  0.02  0.09 -0.15  0.18 -0.01 0.53 0.4684 1.3
## VERBfrac.m     0.75 -0.01 -0.03 -0.01 -0.03 -0.31  0.24 0.91 0.0932 1.6
## NOUNcount.m    -1.06  0.06 -0.16  0.11 -0.07 -0.13 -0.07 0.86 0.1443 1.1
## activity        0.72  0.01  0.15 -0.15 -0.02 -0.43  0.18 0.93 0.0695 2.0
## cli            0.20 -0.04 -0.14  0.95  0.08 -0.23 -0.03 0.91 0.0852 1.3
## entropy         0.12  0.74 -0.05  0.04  0.54  0.00  0.03 0.95 0.0461 1.9
## fkg1           -0.40  0.04  0.60  0.07  0.04  0.19  0.08 1.00 0.0013 2.1
## fre            0.17 -0.03 -0.53 -0.53 -0.04 -0.07 -0.11 0.99 0.0127 2.4
## hpoint          0.01  0.94  0.01 -0.02 -0.01 -0.02 -0.02 0.87 0.1348 1.0
## mamr           0.68 -0.06 -0.04  0.22 -0.32  0.04  0.06 0.75 0.2506 1.7
## mattr          -0.06 -0.12 -0.01  0.08  0.83  0.04  0.02 0.72 0.2818 1.1
## hapaxes         0.09 -0.94 -0.02  0.03  0.29  0.04 -0.01 0.86 0.1397 1.2
## verbdist       -0.94  0.02 -0.27 -0.09 -0.10  0.08  0.07 0.82 0.1803 1.2
##
##
##              PA1  PA2  PA6  PA3  PA4  PA5  PA7
## SS loadings      5.52 2.34 1.71 1.31 1.26 1.22 0.35
## Proportion Var    0.32 0.14 0.10 0.08 0.07 0.07 0.02
## Cumulative Var    0.32 0.46 0.56 0.64 0.71 0.79 0.81
## Proportion Explained 0.40 0.17 0.13 0.10 0.09 0.09 0.03
## Cumulative Proportion 0.40 0.57 0.70 0.79 0.89 0.97 1.00
##
## With factor correlations of
##      PA1  PA2  PA6  PA3  PA4  PA5  PA7
## PA1  1.00  0.02 -0.38 0.04 -0.27 -0.49 -0.09
## PA2  0.02  1.00  0.30 0.17  0.17  0.19 -0.01
## PA6 -0.38  0.30  1.00 0.27  0.13  0.22  0.28
## PA3  0.04  0.17  0.27 1.00  0.10  0.29  0.33
## PA4 -0.27  0.17  0.13 0.10  1.00  0.11 -0.05
## PA5 -0.49  0.19  0.22 0.29  0.11  1.00  0.22
## PA7 -0.09 -0.01  0.28 0.33 -0.05  0.22  1.00
##
## Mean item complexity = 1.5
## Test of the hypothesis that 7 factors are sufficient.
##
## df null model = 136 with the objective function = 17.23 with Chi Square = 12859.06
## df of the model are 38 and the objective function was 0.41
##
## The root mean square of the residuals (RMSR) is 0.01
## The df corrected root mean square of the residuals is 0.02
##
## The harmonic n.obs is 754 with the empirical chi square 19.64 with prob < 0.99
## The total n.obs was 754 with Likelihood Chi Square = 305.8 with prob < 1.5e-43
##
## Tucker Lewis Index of factoring reliability = 0.924
## RMSEA index = 0.097 and the 90 % confidence intervals are 0.087 0.107
## BIC = 54.04
## Fit based upon off diagonal values = 1
## Measures of factor score adequacy
##
##              PA1  PA2  PA6  PA3  PA4  PA5
## Correlation of (regression) scores with factors 0.99 0.98 0.99 0.99 0.95 0.93
## Multiple R square of scores with factors        0.97 0.96 0.98 0.98 0.90 0.86
## Minimum correlation of possible factor scores    0.95 0.91 0.96 0.96 0.80 0.73

```



```

##
## Correlation of (regression) scores with factors    PA7    0.85
## Multiple R square of scores with factors          0.72
## Minimum correlation of possible factor scores      0.44
##
## Coefficients and bootstrapped confidence intervals
##
##          low  PA1 upper  low  PA2 upper  low  PA6 upper  low  PA3
## compoundVERBs  0.74  0.79  0.86 -0.05  0.00  0.03 -0.21 -0.17 -0.09 -0.06 -0.01
## passives      0.04  0.10  0.15 -0.06 -0.03  0.00 -0.05  0.00  0.03 -0.21 -0.17
## predorder.m   -0.81 -0.72 -0.62 -0.07 -0.02  0.03  0.06  0.13  0.21 -0.21 -0.07
## obj           0.15  0.24  0.30 -0.04 -0.01  0.03  0.88  0.96  1.03 -0.20 -0.15
## subj          0.59  0.72  0.83  0.04  0.09  0.17 -0.07  0.02  0.11  0.03  0.09
## VERBfrac.m    0.68  0.75  0.84 -0.05 -0.01  0.01 -0.07 -0.03  0.02 -0.05 -0.01
## NOUNcount.m   -1.13 -1.06 -0.93  0.01  0.06  0.08 -0.20 -0.16 -0.10  0.07  0.11
## activity      0.65  0.72  0.79 -0.02  0.01  0.03  0.12  0.15  0.20 -0.18 -0.15
## cli           0.16  0.20  0.24 -0.05 -0.04 -0.01 -0.17 -0.14 -0.11  0.90  0.95
## entropy       0.08  0.12  0.15  0.71  0.74  0.78 -0.07 -0.05 -0.01  0.01  0.04
## fkg1          -0.46 -0.40 -0.34  0.01  0.04  0.06  0.54  0.60  0.67  0.05  0.07
## fre           0.12  0.17  0.20 -0.05 -0.03 -0.01 -0.60 -0.53 -0.48 -0.59 -0.53
## hpoint        -0.02  0.01  0.05  0.91  0.94  0.96 -0.02  0.01  0.05 -0.05 -0.02
## mamr          0.57  0.68  0.79 -0.12 -0.06  0.00 -0.11 -0.04  0.02  0.16  0.22
## mattr         -0.11 -0.06 -0.01 -0.16 -0.12 -0.09 -0.06 -0.01  0.04  0.04  0.08
## hapaxes       0.05  0.09  0.13 -0.97 -0.94 -0.90 -0.05 -0.02  0.02  0.00  0.03
## verbdist      -1.00 -0.94 -0.84 -0.02  0.02  0.07 -0.35 -0.27 -0.16 -0.13 -0.09
##
##          upper  low  PA4 upper  low  PA5 upper  low  PA7 upper
## compoundVERBs  0.04  0.01  0.04  0.07  0.18  0.24  0.35  0.41  0.51  0.70
## passives      -0.13  0.00  0.03  0.06  0.73  0.82  0.92  0.01  0.12  0.34
## predorder.m   0.02 -0.15 -0.11 -0.04 -0.17 -0.05  0.11 -0.16  0.02  0.18
## obj           -0.11 -0.05 -0.02  0.00 -0.13 -0.05  0.00 -0.21 -0.12 -0.03
## subj          0.15 -0.21 -0.15 -0.09  0.07  0.18  0.29 -0.19 -0.01  0.21
## VERBfrac.m    0.01 -0.05 -0.03  0.00 -0.36 -0.31 -0.23  0.17  0.24  0.35
## NOUNcount.m   0.16 -0.10 -0.07 -0.03 -0.18 -0.13 -0.06 -0.26 -0.07  0.03
## activity      -0.11 -0.05 -0.02  0.00 -0.47 -0.43 -0.37  0.13  0.18  0.23
## cli           1.01  0.06  0.08  0.11 -0.28 -0.23 -0.18 -0.09 -0.03  0.04
## entropy       0.06  0.49  0.54  0.57 -0.03  0.00  0.04 -0.02  0.03  0.09
## fkg1          0.11  0.02  0.04  0.06  0.14  0.19  0.26  0.00  0.08  0.15
## fre          -0.47 -0.06 -0.04 -0.02 -0.13 -0.07 -0.04 -0.17 -0.11 -0.07
## hpoint        0.01 -0.04 -0.01  0.02 -0.05 -0.02  0.02 -0.07 -0.02  0.02
## mamr          0.27 -0.36 -0.32 -0.26 -0.06  0.04  0.14 -0.11  0.06  0.29
## mattr         0.11  0.78  0.83  0.87 -0.01  0.04  0.10 -0.07  0.02  0.13
## hapaxes       0.07  0.26  0.29  0.32 -0.01  0.04  0.08 -0.07 -0.01  0.06
## verbdist      -0.05 -0.14 -0.10 -0.07  0.00  0.08  0.23 -0.09  0.07  0.21
##
## Interfactor correlations and bootstrapped confidence intervals
##
##          lower estimate upper
## PA1-PA2 -0.0877    0.017  0.112
## PA1-PA6 -0.5341   -0.381 -0.162
## PA1-PA3 -0.6045    0.044  0.354
## PA1-PA4 -0.5989   -0.270  0.234
## PA1-PA5 -0.6290   -0.486 -0.041
## PA1-PA7 -0.4863   -0.093  0.202
## PA2-PA6  0.1897    0.297  0.384
## PA2-PA3  0.0313    0.170  0.309
## PA2-PA4  0.0366    0.168  0.270

```

```
## PA2-PA5 0.0535 0.193 0.285
## PA2-PA7 -0.2668 -0.013 0.217
## PA6-PA3 0.0765 0.269 0.387
## PA6-PA4 0.0059 0.134 0.367
## PA6-PA5 0.0187 0.219 0.326
## PA6-PA7 -0.0514 0.285 0.535
## PA3-PA4 -0.0959 0.100 0.432
## PA3-PA5 -0.0525 0.288 0.410
## PA3-PA7 -0.1248 0.328 0.548
## PA4-PA5 -0.1071 0.113 0.306
## PA4-PA7 -0.2233 -0.053 0.483
## PA5-PA7 -0.3407 0.225 0.547
```

Loadings

```
fa_res$loadings
```

```
##
## Loadings:
##          PA1    PA2    PA6    PA3    PA4    PA5    PA7
## compoundVERBs 0.794      -0.165      0.239 0.505
## passives      0.101      -0.169      0.817 0.123
## predorder.m -0.719      0.129    -0.107
## obj           0.236      0.965 -0.155      -0.124
## subj          0.721      -0.154 0.183
## VERBfrac.m    0.745      -0.312 0.240
## NOUNcount.m -1.060      -0.158 0.109    -0.131
## activity      0.716      0.151 -0.147    -0.432 0.176
## cli           0.203      -0.138 0.955    -0.229
## entropy       0.121 0.742      0.541
## fkg1          -0.404      0.605      0.194
## fre           0.171      -0.535 -0.527      -0.113
## hpoint        0.936
## mamr           0.685      0.222 -0.318
## mattr         -0.122      0.826
## hapaxes       -0.942      0.294
## verbdist      -0.937      -0.272    -0.105
##
##          PA1    PA2    PA6    PA3    PA4    PA5    PA7
## SS loadings 5.533 2.351 1.774 1.360 1.227 1.171 0.411
## Proportion Var 0.325 0.138 0.104 0.080 0.072 0.069 0.024
## Cumulative Var 0.325 0.464 0.568 0.648 0.720 0.789 0.813
```

```
for (i in 1:fa_res$nfactors) {
  cat("\n-----", colnames(fa_res$loadings)[i], "-----\n")

  loadings <- fa_res$loadings[, i]
  load_df <- data.frame(loading = loadings)

  load_df_filtered <- load_df %>%
    mutate(abs_l = abs(loading)) %>%
    mutate(str = case_when(
      abs_l > 0.7 ~ "***",
      abs_l <= 0.7 & abs_l > 0.5 ~ "** ",
    ))
}
```

```

    abs_1 <= 0.5 & abs_1 > 0.3 ~ "*" ",
    abs_1 <= 0.3 & abs_1 > 0.1 ~ "." ",
    .default = ""
  )) %>%
  arrange(-abs_1) %>%
  filter(abs_1 > 0.1)

load_df_filtered %>%
  mutate(across(c(loading, abs_1), ~ round(.x, 3))) %>%
  print()

cat("\n")
}

```

```

##
## ----- PA1 -----
##           loading abs_1 str
## NOUNcount.m   -1.060 1.060 ***
## verbdist      -0.937 0.937 ***
## compoundVERBs  0.794 0.794 ***
## VERBfrac.m    0.745 0.745 ***
## subj          0.721 0.721 ***
## predorder.m   -0.719 0.719 ***
## activity       0.716 0.716 ***
## mamr           0.685 0.685 **
## fkg1           -0.404 0.404 *
## obj            0.236 0.236 .
## cli            0.203 0.203 .
## fre            0.171 0.171 .
## entropy        0.121 0.121 .
## passives       0.101 0.101 .
##
##
## ----- PA2 -----
##           loading abs_1 str
## hapaxes       -0.942 0.942 ***
## hpoint         0.936 0.936 ***
## entropy        0.742 0.742 ***
## mattr         -0.122 0.122 .
##
##
## ----- PA6 -----
##           loading abs_1 str
## obj            0.965 0.965 ***
## fkg1           0.605 0.605 **
## fre            -0.535 0.535 **
## verbdist      -0.272 0.272 .
## compoundVERBs -0.165 0.165 .
## NOUNcount.m   -0.158 0.158 .
## activity       0.151 0.151 .
## cli            -0.138 0.138 .
## predorder.m    0.129 0.129 .
##
##
##

```

```

## ----- PA3 -----
##          loading abs_l str
## cli      0.955 0.955 ***
## fre      -0.527 0.527 **
## mamr      0.222 0.222 .
## passives -0.169 0.169 .
## obj       -0.155 0.155 .
## activity -0.147 0.147 .
## NOUNcount.m 0.109 0.109 .
##
##
## ----- PA4 -----
##          loading abs_l str
## mattr     0.826 0.826 ***
## entropy   0.541 0.541 **
## mamr      -0.318 0.318 *
## hapaxes   0.294 0.294 .
## subj      -0.154 0.154 .
## predorder.m -0.107 0.107 .
## verbdist  -0.105 0.105 .
##
##
## ----- PA5 -----
##          loading abs_l str
## passives   0.817 0.817 ***
## activity   -0.432 0.432 *
## VERBfrac.m -0.312 0.312 *
## compoundVERBs 0.239 0.239 .
## cli        -0.229 0.229 .
## fkg1        0.194 0.194 .
## subj        0.183 0.183 .
## NOUNcount.m -0.131 0.131 .
##
##
## ----- PA7 -----
##          loading abs_l str
## compoundVERBs 0.505 0.505 **
## VERBfrac.m   0.240 0.240 .
## activity      0.176 0.176 .
## obj           -0.124 0.124 .
## passives      0.123 0.123 .
## fre           -0.113 0.113 .

```

hypotheses:

- **PA1:** register – narrativity, richness of expression; shorter clauses (-technical / +narrative)
 - narrativity? (1st and 2nd persons etc.)
- **PA2:** text length (-short / +long)
 - hapaxes load negatively, because I normed them over word count
- **PA6:** sentence complexity (more clauses) (-simple / +complex)
 - slightly longer nominal constructions / more objects, more years of education necessary, predicates slightly further in the clause, slightly more verbs
 - fkg1 in strong correlation with `sentlen.m`
- **PA3:** word length (-short / +long)
 - cli highly correlates with `at1`, meaning the factor likely expresses mostly token lengths

- slightly more passives, slightly more objects, slightly less verbal overall / slightly longer nom. constructions, slightly morphologically richer, many years of education necessary
- more enumerations? but one would expect higher **activity** differences to occur if that was the case
- **PA4:** lexical richness (-poor / +rich)
- **PA5:** passivity (-active / +passive)
 - compound verbs, because that's what passives are in Czech
 - smaller activity, because passive participles count as ADJ in UD.
- **PA7:** compound verbs (-less / +more)

strong correlations:

- **PA1–PA6:** (-0.38) narrativity leads to simple clauses
- **PA2–PA6:** (+0.30) longer texts include more complex sentences
- **PA1–PA5:** (-0.49, topconf = +0.09) narrative texts more active

NOTE: variables with low communalities are excluded from the analysis, yet still likely play a role in legal writing readability. this includes both those selected for the analysis and the excluded ones.

NOTE: some high-correlating variables were excluded from the FA.

Healthiness diagnostics

```
fa_res$loadings[] %>%
  as_tibble() %>%
  mutate(feats = cnames) %>%
  select(feats, everything()) %>%
  pivot_longer(!feats) %>%
  mutate(value = abs(value)) %>%
  group_by(feats) %>%
  summarize(maxload = max(value)) %>%
  arrange(maxload)
```

```
## # A tibble: 17 x 2
##   feats      maxload
##   <chr>      <dbl>
## 1 fre        0.535
## 2 fkg1       0.605
## 3 mamr       0.685
## 4 activity   0.716
## 5 predorder.m 0.719
## 6 subj       0.721
## 7 entropy    0.742
## 8 VERBfrac.m 0.745
## 9 compoundVERBs 0.794
## 10 passives   0.817
## 11 mattr      0.826
## 12 hpoint     0.936
## 13 verbdist   0.937
## 14 hapaxes    0.942
## 15 cli        0.955
## 16 obj        0.965
## 17 NOUNcount.m 1.06
```

```
fa_res$communality %>% sort()
```

```
##      subj  predorder.m  passives      obj      mattr
## 0.5315955 0.5512988 0.5856923 0.7113441 0.7181813
##  mamr compoundVERBs  verbdist  NOUNcount.m  hapaxes
## 0.7493974 0.7781089 0.8196810 0.8557424 0.8602815
##  hpoint  VERBfrac.m      cli  activity  entropy
## 0.8652002 0.9067914 0.9147991 0.9305464 0.9539003
##      fre      fkg1
## 0.9872669 0.9987222
```

Uniquenesses

```
fa_res$uniquenesses %>% round(3)
```

```
## compoundVERBs  passives  predorder.m      obj      subj
##      0.222      0.414      0.449      0.289      0.468
##  VERBfrac.m  NOUNcount.m  activity      cli  entropy
##      0.093      0.144      0.069      0.085      0.046
##      fkg1      fre      hpoint      mamr      mattr
##      0.001      0.013      0.135      0.251      0.282
##      hapaxes  verbdist
##      0.140      0.180
```

Distributions over factors

```
analyze_distributions <- function(data_factors_long, variable) {
  plot <- data_factors_long %>%
    ggplot(aes(x = factor_score, y = !!sym(variable))) +
    geom_boxplot() +
    facet_grid(factor ~ .)
  print(plot)

  formula <- reformulate(variable, "factor_score")
  factors <- levels(data_factors_long$factor)

  min_p_values <- numeric()
  for (f in factors) {
    data <- data_factors_long %>% filter(factor == f)

    cat(
      "\nTest for the significance of differences in",
      variable, "over", f, ":\n\n"
    )

    dunn <- dunn.test(
      data$factor_score, data[[variable]],
      altP = TRUE, method = "bonferroni"
    )
    min_p_values <- c(min_p_values, min(dunn$altP.adjusted))
  }

  cat(
```

```

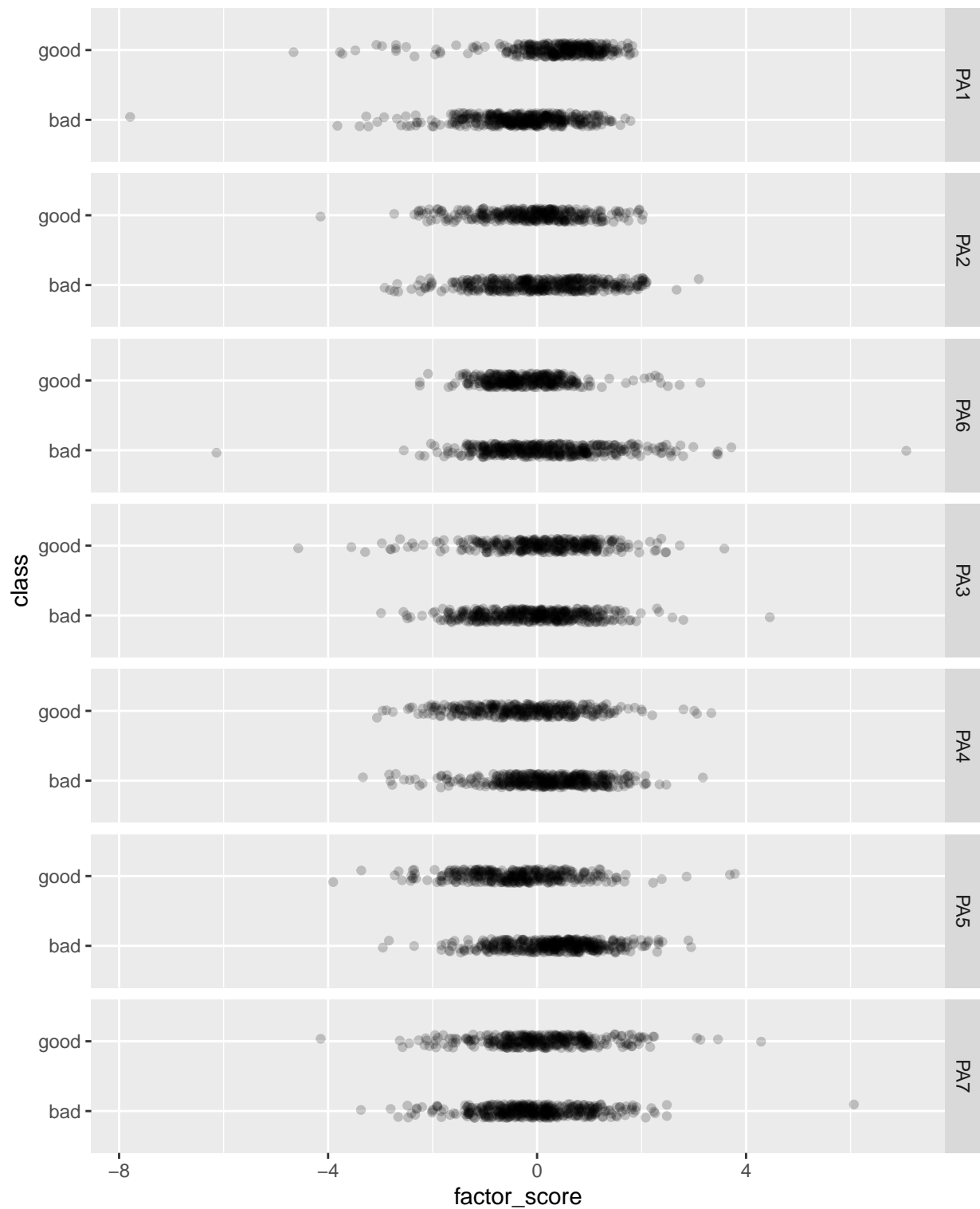
    "\np < 5e-2\tfound in:",
    factors[min_p_values < 0.05],
    "\np < 1e-2\tfound in:",
    factors[min_p_values < 0.01],
    "\np < 1e-3\tfound in:",
    factors[min_p_values < 0.001],
    "\np < 1e-4\tfound in:",
    factors[min_p_values < 0.0001], "\n"
  )
}

data_factors <- bind_cols(data_clean, fa_res$scores %>% as.data.frame())
cnames <- map(
  colnames(data_factors),
  function(x) {
    name <- pull(pretty_names %>%
      filter(name_orig == x), name_pretty)
    if (length(name) == 1) {
      return(name)
    } else {
      return(x)
    }
  }
) %>% unlist()
colnames(data_factors) <- cnames

data_factors_long <- data_factors %>%
  pivot_longer(PA1:PA7, names_to = "factor", values_to = "factor_score") %>%
  mutate(across(
    factor,
    ~ factor(.x, levels = c("PA1", "PA2", "PA6", "PA3", "PA4", "PA5", "PA7"))
  ))

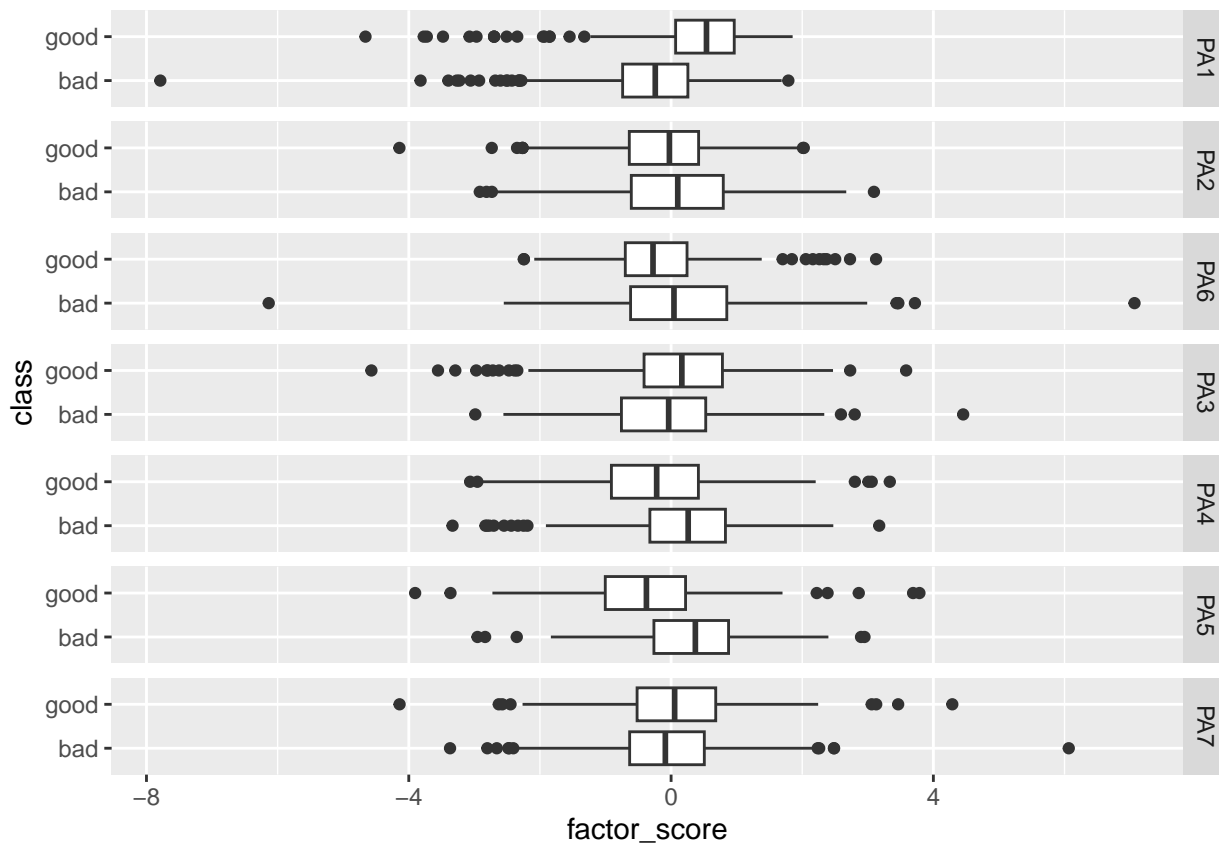
data_factors_long %>%
  ggplot(aes(x = factor_score, y = class)) +
  facet_grid(factor ~ .) +
  theme(legend.position = "bottom") +
  geom_jitter(width = 0, height = 0.1, alpha = 0.2)

```



class

```
analyze_distributions(data_factors_long, "class")
```

```
##
## Test for the significance of differences in class over PA1 :
##
##   Kruskal-Wallis rank sum test
##
## data: x and group
## Kruskal-Wallis chi-squared = 147.6724, df = 1, p-value = 0
##
##
##               Comparison of x by group
##               (Bonferroni)
## Col Mean-|
## Row Mean |      bad
## -----+-----
##   good | -12.15205
##       |  0.0000*
##
## alpha = 0.05
## Reject Ho if p <= alpha
##
## Test for the significance of differences in class over PA2 :
##
##   Kruskal-Wallis rank sum test
##
## data: x and group
## Kruskal-Wallis chi-squared = 8.0515, df = 1, p-value = 0
##
```

```

##
##                                     Comparison of x by group
##                                     (Bonferroni)
## Col Mean-|
## Row Mean |          bad
## -----+-----
##      good |    2.837517
##          |    0.0045*
##
## alpha = 0.05
## Reject Ho if p <= alpha
##
## Test for the significance of differences in class over PA6 :
##
##      Kruskal-Wallis rank sum test
##
## data: x and group
## Kruskal-Wallis chi-squared = 23.4951, df = 1, p-value = 0
##
##
##                                     Comparison of x by group
##                                     (Bonferroni)
## Col Mean-|
## Row Mean |          bad
## -----+-----
##      good |    4.847174
##          |    0.0000*
##
## alpha = 0.05
## Reject Ho if p <= alpha
##
## Test for the significance of differences in class over PA3 :
##
##      Kruskal-Wallis rank sum test
##
## data: x and group
## Kruskal-Wallis chi-squared = 11.9438, df = 1, p-value = 0
##
##
##                                     Comparison of x by group
##                                     (Bonferroni)
## Col Mean-|
## Row Mean |          bad
## -----+-----
##      good |   -3.455977
##          |    0.0005*
##
## alpha = 0.05
## Reject Ho if p <= alpha
##
## Test for the significance of differences in class over PA4 :
##
##      Kruskal-Wallis rank sum test
##

```

```

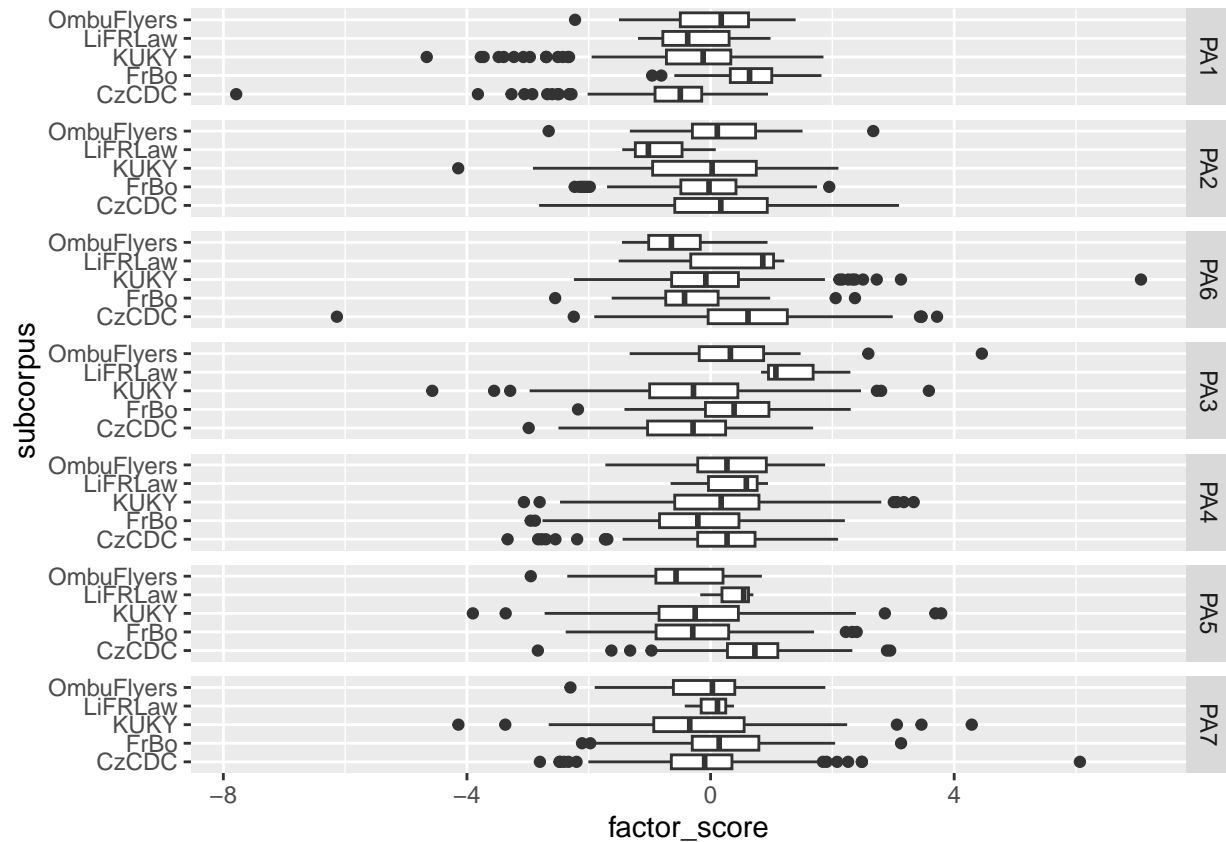
## data: x and group
## Kruskal-Wallis chi-squared = 46.5471, df = 1, p-value = 0
##
##
##                                     Comparison of x by group
##                                     (Bonferroni)
## Col Mean-|
## Row Mean |          bad
## -----+-----
##      good |    6.822546
##          |    0.0000*
##
## alpha = 0.05
## Reject Ho if p <= alpha
##
## Test for the significance of differences in class over PA5 :
##
##   Kruskal-Wallis rank sum test
##
## data: x and group
## Kruskal-Wallis chi-squared = 101.1707, df = 1, p-value = 0
##
##
##                                     Comparison of x by group
##                                     (Bonferroni)
## Col Mean-|
## Row Mean |          bad
## -----+-----
##      good |   10.05836
##          |    0.0000*
##
## alpha = 0.05
## Reject Ho if p <= alpha
##
## Test for the significance of differences in class over PA7 :
##
##   Kruskal-Wallis rank sum test
##
## data: x and group
## Kruskal-Wallis chi-squared = 4.3737, df = 1, p-value = 0.04
##
##
##                                     Comparison of x by group
##                                     (Bonferroni)
## Col Mean-|
## Row Mean |          bad
## -----+-----
##      good |  -2.091333
##          |    0.0365*
##
## alpha = 0.05
## Reject Ho if p <= alpha
##
## p < 5e-2 found in: PA1 PA2 PA6 PA3 PA4 PA5 PA7

```

```
## p < 1e-2 found in: PA1 PA2 PA6 PA3 PA4 PA5
## p < 1e-3 found in: PA1 PA6 PA3 PA4 PA5
## p < 1e-4 found in: PA1 PA6 PA4 PA5
```

subcorpus

```
analyze_distributions(data_factors_long, "subcorpus")
```



```
##
## Test for the significance of differences in subcorpus over PA1 :
##
```

```
## Kruskal-Wallis rank sum test
```

```
##
```

```
## data: x and group
```

```
## Kruskal-Wallis chi-squared = 324.6698, df = 4, p-value = 0
```

```
##
```

```
##
```

```
## Comparison of x by group
## (Bonferroni)
```

```
## Col Mean-|
## Row Mean |      CzCDC      FrBo      KUKY      LiFRLaw
## -----|-----
## FrBo | -17.35858
##      |  0.0000*
##      |
## KUKY | -5.082162  11.31002
##      |  0.0000*  0.0000*
```

```

##
## LiFRLaw | -0.872398 1.790209 -0.003452
##          | 1.0000 0.7342 1.0000
##
## OmbuFlye | -4.533034 4.348685 -1.649043 -0.484868
##          | 0.0001* 0.0001* 0.9914 1.0000
##
## alpha = 0.05
## Reject Ho if p <= alpha
##
## Test for the significance of differences in subcorpus over PA2 :
##
## Kruskal-Wallis rank sum test
##
## data: x and group
## Kruskal-Wallis chi-squared = 9.8975, df = 4, p-value = 0.04
##
##
## Comparison of x by group
## (Bonferroni)
## Col Mean-|
## Row Mean | CzCDC FrBo KUKY LiFRLaw
## -----+-----
## FrBo | 2.438507
##       | 0.1475
##
## KUKY | 2.006418 -0.192445
##       | 0.4481 1.0000
##
## LiFRLaw | 1.738831 1.368187 1.394671
##         | 0.8206 1.0000 1.0000
##
## OmbuFlye | -0.091483 -1.356400 -1.214028 -1.712554
##          | 1.0000 1.0000 1.0000 0.8679
##
## alpha = 0.05
## Reject Ho if p <= alpha
##
## Test for the significance of differences in subcorpus over PA6 :
##
## Kruskal-Wallis rank sum test
##
## data: x and group
## Kruskal-Wallis chi-squared = 137.7653, df = 4, p-value = 0
##
##
## Comparison of x by group
## (Bonferroni)
## Col Mean-|
## Row Mean | CzCDC FrBo KUKY LiFRLaw
## -----+-----
## FrBo | 10.82530
##       | 0.0000*
##

```

```

##      KUKY |    6.313404 -3.656522
##          |    0.0000*    0.0026*
##          |
##      LiFRLaw |    0.539206 -1.121281 -0.539826
##          |    1.0000    1.0000    1.0000
##          |
##      OmbuFlye |    7.526018  2.098278  3.927170  1.686430
##          |    0.0000*    0.3588    0.0009*    0.9171
##
## alpha = 0.05
## Reject Ho if p <= alpha
##
## Test for the significance of differences in subcorpus over PA3 :
##
##      Kruskal-Wallis rank sum test
##
## data: x and group
## Kruskal-Wallis chi-squared = 112.907, df = 4, p-value = 0
##
##
##                               Comparison of x by group
##                               (Bonferroni)
## Col Mean-|
## Row Mean |      CzCDC      FrBo      KUKY      LiFRLaw
## -----+-----
##      FrBo | -9.239165
##          |    0.0000*
##          |
##      KUKY | -1.300172  7.537538
##          |    1.0000    0.0000*
##          |
##      LiFRLaw | -3.023849 -1.612043 -2.799330
##          |    0.0250*    1.0000    0.0512
##          |
##      OmbuFlye | -4.182661  0.502797 -3.419066  1.703689
##          |    0.0003*    1.0000    0.0063*    0.8844
##
## alpha = 0.05
## Reject Ho if p <= alpha
##
## Test for the significance of differences in subcorpus over PA4 :
##
##      Kruskal-Wallis rank sum test
##
## data: x and group
## Kruskal-Wallis chi-squared = 36.3801, df = 4, p-value = 0
##
##
##                               Comparison of x by group
##                               (Bonferroni)
## Col Mean-|
## Row Mean |      CzCDC      FrBo      KUKY      LiFRLaw
## -----+-----
##      FrBo |  5.459549

```

```

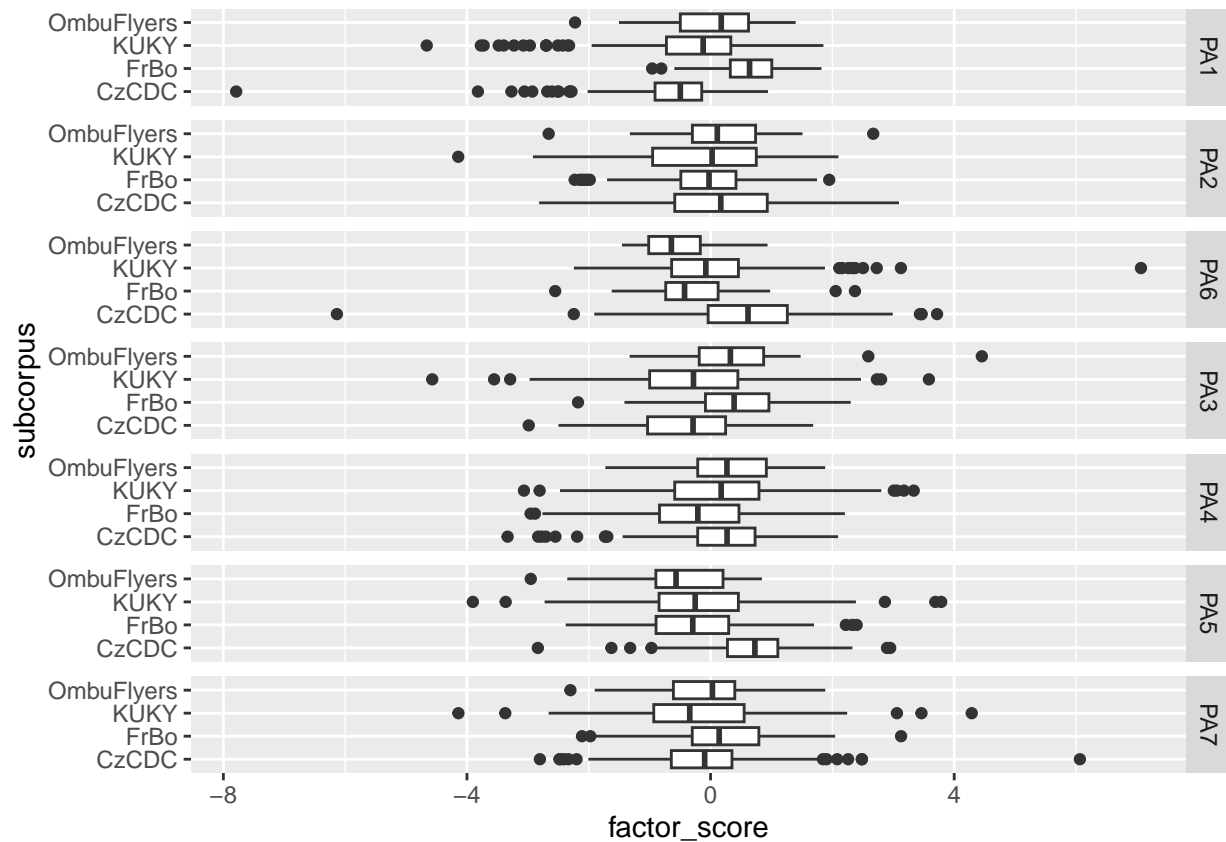
##          |      0.0000*
##
##      KUKY |      1.732943  -3.411845
##          |      0.8311      0.0065*
##
##  LiFRLaw |     -0.146970  -0.985287  -0.442916
##          |      1.0000      1.0000      1.0000
##
##  OmbuFlye |     -0.538009  -3.377899  -1.503636  -0.015445
##          |      1.0000      0.0073*      1.0000      1.0000
##
## alpha = 0.05
## Reject Ho if p <= alpha
##
## Test for the significance of differences in subcorpus over PA5 :
##
##      Kruskal-Wallis rank sum test
##
## data: x and group
## Kruskal-Wallis chi-squared = 169.6171, df = 4, p-value = 0
##
##
##                                Comparison of x by group
##                                (Bonferroni)
## Col Mean-|
## Row Mean |      CzCDC      FrBo      KUKY      LiFRLaw
## -----+-----
##      FrBo |      12.03428
##          |      0.0000*
##
##      KUKY |      9.587804  -1.289058
##          |      0.0000*      1.0000
##
##  LiFRLaw |      0.509819  -1.336300  -1.128601
##          |      1.0000      1.0000      1.0000
##
##  OmbuFlye |      7.022416   0.956708   1.594639   1.567093
##          |      0.0000*      1.0000      1.0000      1.0000
##
## alpha = 0.05
## Reject Ho if p <= alpha
##
## Test for the significance of differences in subcorpus over PA7 :
##
##      Kruskal-Wallis rank sum test
##
## data: x and group
## Kruskal-Wallis chi-squared = 30.7162, df = 4, p-value = 0
##
##
##                                Comparison of x by group
##                                (Bonferroni)
## Col Mean-|
## Row Mean |      CzCDC      FrBo      KUKY      LiFRLaw

```

```
## -----
##      FrBo | -3.966477
##           | 0.0007*
##
##      KUKY | 1.189282  5.123866
##           | 1.0000  0.0000*
##
##      LiFRLaw | -0.340818  0.267296 -0.543730
##           | 1.0000  1.0000  1.0000
##
##      OmbuFlye | -0.544032  1.497093 -1.205231  0.170711
##           | 1.0000  1.0000  1.0000  1.0000
##
## alpha = 0.05
## Reject Ho if p <= alpha
##
## p < 5e-2 found in: PA1 PA6 PA3 PA4 PA5 PA7
## p < 1e-2 found in: PA1 PA6 PA3 PA4 PA5 PA7
## p < 1e-3 found in: PA1 PA6 PA3 PA4 PA5 PA7
## p < 1e-4 found in: PA1 PA6 PA3 PA4 PA5 PA7
```

subcorpus wo/ LiFRLaw

```
analyze_distributions(
  data_factors_long %>% filter(subcorpus != "LiFRLaw"), "subcorpus"
)
```




```

##
## Test for the significance of differences in subcorpus over PA1 :
##
##   Kruskal-Wallis rank sum test
##
## data: x and group
## Kruskal-Wallis chi-squared = 324.9953, df = 3, p-value = 0
##
##
##                               Comparison of x by group
##                               (Bonferroni)
## Col Mean-|
## Row Mean |      CzCDC      FrBo      KUKY
## -----+-----
##   FrBo | -17.37448
##         |  0.0000*
##         |
##   KUKY | -5.087708  11.31941
##         |  0.0000*  0.0000*
##         |
## OmbuFlye | -4.539209  4.350595 -1.652060
##         |  0.0000*  0.0001*  0.5911
##
## alpha = 0.05
## Reject Ho if p <= alpha
##
## Test for the significance of differences in subcorpus over PA2 :
##
##   Kruskal-Wallis rank sum test
##
## data: x and group
## Kruskal-Wallis chi-squared = 7.6553, df = 3, p-value = 0.05
##
##
##                               Comparison of x by group
##                               (Bonferroni)
## Col Mean-|
## Row Mean |      CzCDC      FrBo      KUKY
## -----+-----
##   FrBo |  2.447210
##         |  0.0864
##         |
##   KUKY |  2.004739 -0.202682
##         |  0.2699  1.0000
##         |
## OmbuFlye | -0.089710 -1.359092 -1.211330
##         |  1.0000  1.0000  1.0000
##
## alpha = 0.05
## Reject Ho if p <= alpha
##
## Test for the significance of differences in subcorpus over PA6 :
##
##   Kruskal-Wallis rank sum test

```

```

##
## data: x and group
## Kruskal-Wallis chi-squared = 137.8128, df = 3, p-value = 0
##
##
##           Comparison of x by group
##           (Bonferroni)
## Col Mean-|
## Row Mean |      CzCDC      FrBo      KUKY
## -----+-----
##      FrBo |    10.83598
##           |    0.0000*
##           |
##      KUKY |    6.316190   -3.663846
##           |    0.0000*    0.0015*
##           |
## OmbuFlye |    7.539865    2.106923    3.939339
##           |    0.0000*    0.2107    0.0005*
##
## alpha = 0.05
## Reject Ho if p <= alpha
##
## Test for the significance of differences in subcorpus over PA3 :
##
##   Kruskal-Wallis rank sum test
##
## data: x and group
## Kruskal-Wallis chi-squared = 107.8981, df = 3, p-value = 0
##
##
##           Comparison of x by group
##           (Bonferroni)
## Col Mean-|
## Row Mean |      CzCDC      FrBo      KUKY
## -----+-----
##      FrBo |   -9.256635
##           |    0.0000*
##           |
##      KUKY |   -1.298220    7.556555
##           |    1.0000    0.0000*
##           |
## OmbuFlye |   -4.189325    0.505022   -3.426765
##           |    0.0002*    1.0000    0.0037*
##
## alpha = 0.05
## Reject Ho if p <= alpha
##
## Test for the significance of differences in subcorpus over PA4 :
##
##   Kruskal-Wallis rank sum test
##
## data: x and group
## Kruskal-Wallis chi-squared = 36.0837, df = 3, p-value = 0
##

```

```

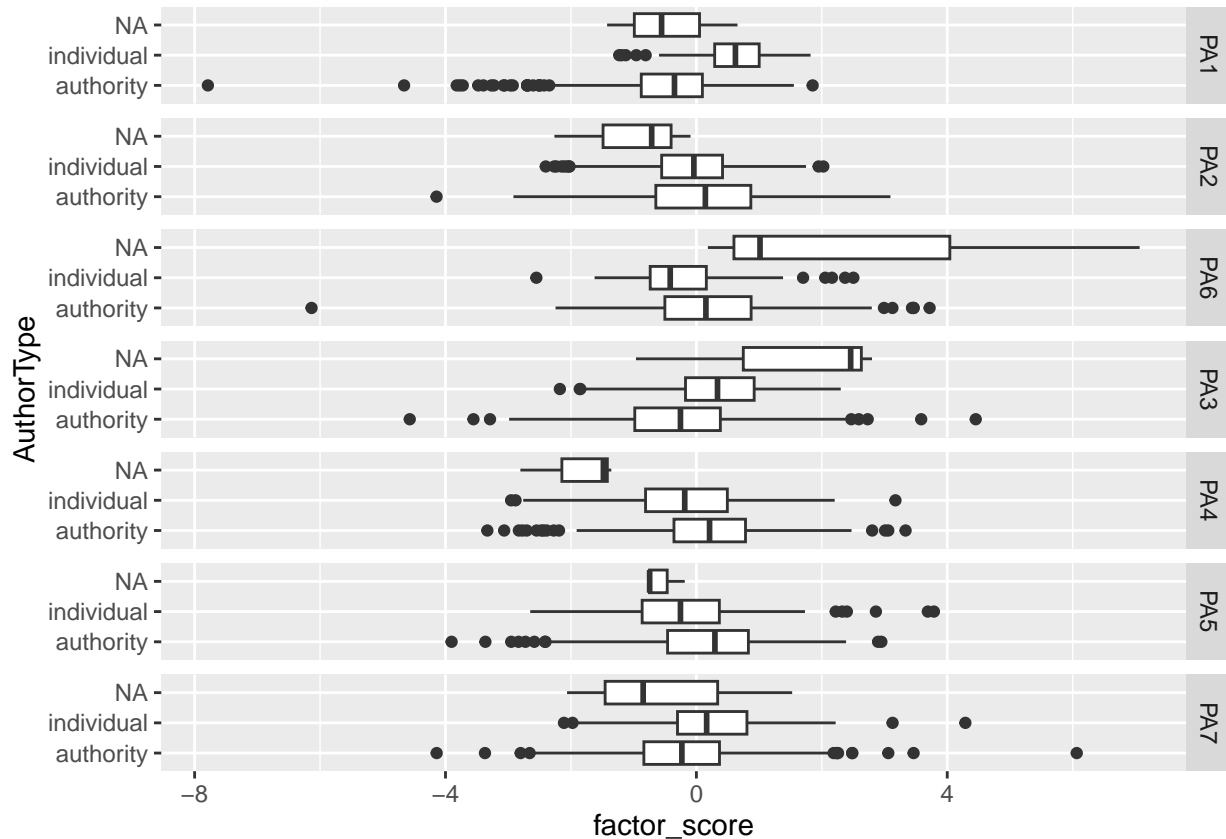
##
##                                     Comparison of x by group
##                                     (Bonferroni)
## Col Mean-|
## Row Mean |      CzCDC      FrBo      KUKY
## -----+-----
##      FrBo |      5.461216
##            |      0.0000*
##            |
##      KUKY |      1.734750  -3.411506
##            |      0.4967    0.0039*
##            |
## OmbuFlye |     -0.537587  -3.378330  -1.504230
##            |      1.0000    0.0044*    0.7951
##
## alpha = 0.05
## Reject Ho if p <= alpha
##
## Test for the significance of differences in subcorpus over PA5 :
##
##   Kruskal-Wallis rank sum test
##
## data: x and group
## Kruskal-Wallis chi-squared = 168.5035, df = 3, p-value = 0
##
##                                     Comparison of x by group
##                                     (Bonferroni)
## Col Mean-|
## Row Mean |      CzCDC      FrBo      KUKY
## -----+-----
##      FrBo |     12.01538
##            |      0.0000*
##            |
##      KUKY |      9.574393  -1.285257
##            |      0.0000*    1.0000
##            |
## OmbuFlye |      7.011861   0.955689   1.591681
##            |      0.0000*    1.0000    0.6687
##
## alpha = 0.05
## Reject Ho if p <= alpha
##
## Test for the significance of differences in subcorpus over PA7 :
##
##   Kruskal-Wallis rank sum test
##
## data: x and group
## Kruskal-Wallis chi-squared = 30.6296, df = 3, p-value = 0
##
##                                     Comparison of x by group
##                                     (Bonferroni)
## Col Mean-|

```

```
## Row Mean |      CzCDC      FrBo      KUKY
## -----|-----
##      FrBo |    -3.961805
##           |      0.0004*
##           |
##      KUKY |     1.188349     5.118335
##           |     1.0000     0.0000*
##           |
## OmbuFlye |    -0.542887     1.495845    -1.203573
##           |     1.0000     0.8082     1.0000
##
## alpha = 0.05
## Reject Ho if p <= alpha
##
## p < 5e-2 found in: PA1 PA6 PA3 PA4 PA5 PA7
## p < 1e-2 found in: PA1 PA6 PA3 PA4 PA5 PA7
## p < 1e-3 found in: PA1 PA6 PA3 PA4 PA5 PA7
## p < 1e-4 found in: PA1 PA6 PA3 PA4 PA5 PA7
```

AuthorType

```
analyze_distributions(data_factors_long, "AuthorType")
```



```
##
## Test for the significance of differences in AuthorType over PA1 :
##
## Kruskal-Wallis rank sum test
```

```

##
## data: x and group
## Kruskal-Wallis chi-squared = 300.0919, df = 1, p-value = 0
##
##
##                               Comparison of x by group
##                               (Bonferroni)
## Col Mean-|
## Row Mean |   authorit
## -----+-----
## individu |  -17.32316
##          |    0.0000*
##
## alpha = 0.05
## Reject Ho if p <= alpha
##
## Test for the significance of differences in AuthorType over PA2 :
##
##   Kruskal-Wallis rank sum test
##
## data: x and group
## Kruskal-Wallis chi-squared = 9.2401, df = 1, p-value = 0
##
##
##                               Comparison of x by group
##                               (Bonferroni)
## Col Mean-|
## Row Mean |   authorit
## -----+-----
## individu |    3.039749
##          |    0.0024*
##
## alpha = 0.05
## Reject Ho if p <= alpha
##
## Test for the significance of differences in AuthorType over PA6 :
##
##   Kruskal-Wallis rank sum test
##
## data: x and group
## Kruskal-Wallis chi-squared = 58.5159, df = 1, p-value = 0
##
##
##                               Comparison of x by group
##                               (Bonferroni)
## Col Mean-|
## Row Mean |   authorit
## -----+-----
## individu |    7.649569
##          |    0.0000*
##
## alpha = 0.05
## Reject Ho if p <= alpha
##

```

```

## Test for the significance of differences in AuthorType over PA3 :
##
##   Kruskal-Wallis rank sum test
##
## data: x and group
## Kruskal-Wallis chi-squared = 81.9629, df = 1, p-value = 0
##
##
##                               Comparison of x by group
##                               (Bonferroni)
## Col Mean-|
## Row Mean |   authorit
## -----+-----
## individu |  -9.053337
##          |    0.0000*
##
## alpha = 0.05
## Reject Ho if p <= alpha
##
## Test for the significance of differences in AuthorType over PA4 :
##
##   Kruskal-Wallis rank sum test
##
## data: x and group
## Kruskal-Wallis chi-squared = 30.2702, df = 1, p-value = 0
##
##
##                               Comparison of x by group
##                               (Bonferroni)
## Col Mean-|
## Row Mean |   authorit
## -----+-----
## individu |   5.501835
##          |    0.0000*
##
## alpha = 0.05
## Reject Ho if p <= alpha
##
## Test for the significance of differences in AuthorType over PA5 :
##
##   Kruskal-Wallis rank sum test
##
## data: x and group
## Kruskal-Wallis chi-squared = 39.5694, df = 1, p-value = 0
##
##
##                               Comparison of x by group
##                               (Bonferroni)
## Col Mean-|
## Row Mean |   authorit
## -----+-----
## individu |   6.290419
##          |    0.0000*
##

```

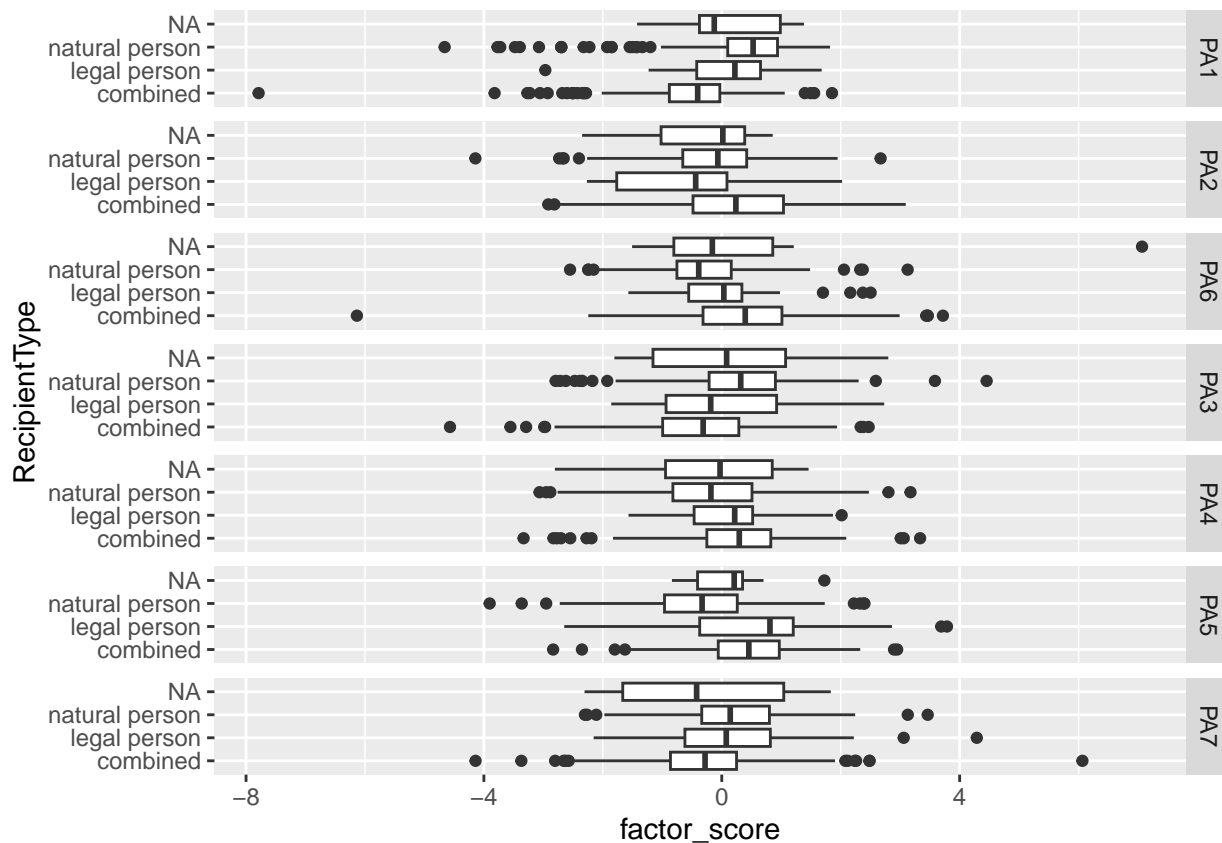
```

## alpha = 0.05
## Reject Ho if p <= alpha
##
## Test for the significance of differences in AuthorType over PA7 :
##
##   Kruskal-Wallis rank sum test
##
## data: x and group
## Kruskal-Wallis chi-squared = 40.9073, df = 1, p-value = 0
##
##
##                               Comparison of x by group
##                               (Bonferroni)
## Col Mean-|
## Row Mean |   authorit
## -----+-----
## individu |  -6.395879
##          |    0.0000*
##
## alpha = 0.05
## Reject Ho if p <= alpha
##
## p < 5e-2 found in: PA1 PA2 PA6 PA3 PA4 PA5 PA7
## p < 1e-2 found in: PA1 PA2 PA6 PA3 PA4 PA5 PA7
## p < 1e-3 found in: PA1 PA6 PA3 PA4 PA5 PA7
## p < 1e-4 found in: PA1 PA6 PA3 PA4 PA5 PA7

```

RecipientType

```
analyze_distributions(data_factors_long, "RecipientType")
```



```
##
## Test for the significance of differences in RecipientType over PA1 :
##
##   Kruskal-Wallis rank sum test
##
## data: x and group
## Kruskal-Wallis chi-squared = 235.2855, df = 2, p-value = 0
##
##
##           Comparison of x by group
##           (Bonferroni)
## Col Mean-|
## Row Mean |   combined   legal pe
## -----+-----
## legal pe |  -3.202351
##          |    0.0041*
##
## natural  | -15.33836 -2.168998
##          |    0.0000*    0.0902
##
## alpha = 0.05
## Reject Ho if p <= alpha
##
## Test for the significance of differences in RecipientType over PA2 :
##
##   Kruskal-Wallis rank sum test
##
```



```

## data: x and group
## Kruskal-Wallis chi-squared = 34.4591, df = 2, p-value = 0
##
##
##                               Comparison of x by group
##                               (Bonferroni)
## Col Mean-|
## Row Mean |    combined    legal pe
## -----+-----
## legal pe |    3.898285
##          |    0.0003*
##          |
## natural  |    5.079110  -2.144990
##          |    0.0000*    0.0959
##
## alpha = 0.05
## Reject Ho if p <= alpha
##
## Test for the significance of differences in RecipientType over PA6 :
##
##   Kruskal-Wallis rank sum test
##
## data: x and group
## Kruskal-Wallis chi-squared = 97.616, df = 2, p-value = 0
##
##
##                               Comparison of x by group
##                               (Bonferroni)
## Col Mean-|
## Row Mean |    combined    legal pe
## -----+-----
## legal pe |    1.873469
##          |    0.1830
##          |
## natural  |    9.879555    1.587947
##          |    0.0000*    0.3369
##
## alpha = 0.05
## Reject Ho if p <= alpha
##
## Test for the significance of differences in RecipientType over PA3 :
##
##   Kruskal-Wallis rank sum test
##
## data: x and group
## Kruskal-Wallis chi-squared = 88.5372, df = 2, p-value = 0
##
##
##                               Comparison of x by group
##                               (Bonferroni)
## Col Mean-|
## Row Mean |    combined    legal pe
## -----+-----
## legal pe |   -1.401806

```

```

##          |      0.4829
##          |
## natural  |  -9.396916  -1.893909
##          |      0.0000*      0.1747
##
## alpha = 0.05
## Reject Ho if p <= alpha
##
## Test for the significance of differences in RecipientType over PA4 :
##
##   Kruskal-Wallis rank sum test
##
## data: x and group
## Kruskal-Wallis chi-squared = 36.6854, df = 2, p-value = 0
##
##
##                               Comparison of x by group
##                               (Bonferroni)
## Col Mean-|
## Row Mean |   combined   legal pe
## -----+-----
## legal pe |   1.047412
##          |       0.8847
##          |
## natural  |   6.054595   1.074785
##          |   0.0000*    0.8474
##
## alpha = 0.05
## Reject Ho if p <= alpha
##
## Test for the significance of differences in RecipientType over PA5 :
##
##   Kruskal-Wallis rank sum test
##
## data: x and group
## Kruskal-Wallis chi-squared = 127.5444, df = 2, p-value = 0
##
##
##                               Comparison of x by group
##                               (Bonferroni)
## Col Mean-|
## Row Mean |   combined   legal pe
## -----+-----
## legal pe |   0.058011
##          |       1.0000
##          |
## natural  |  11.07741    3.841344
##          |   0.0000*    0.0004*
##
## alpha = 0.05
## Reject Ho if p <= alpha
##
## Test for the significance of differences in RecipientType over PA7 :
##

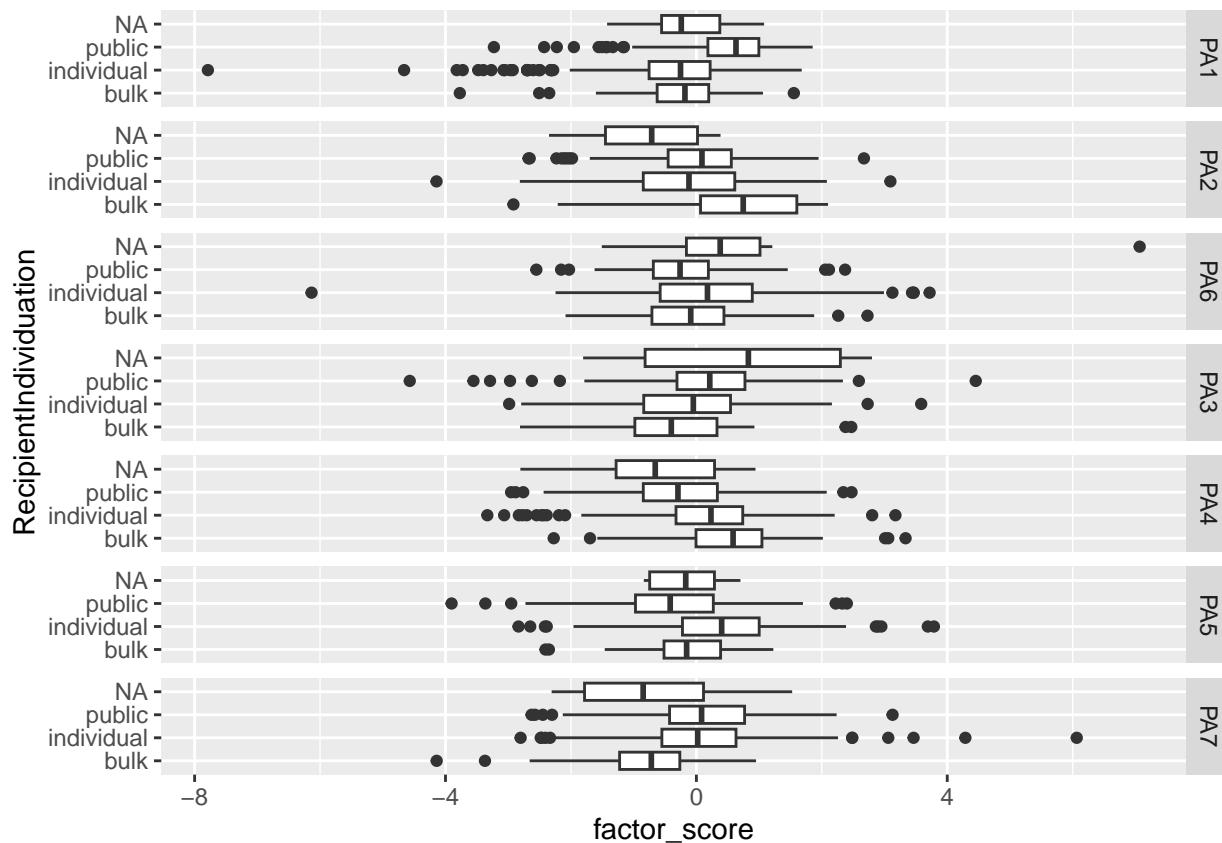
```

```
## Kruskal-Wallis rank sum test
##
## data: x and group
## Kruskal-Wallis chi-squared = 44.2699, df = 2, p-value = 0
##
##
## Comparison of x by group
## (Bonferroni)
## Col Mean-|
## Row Mean | combined legal pe
## -----+-----
## legal pe | -1.794855
##          | 0.2180
##          |
## natural | -6.636304 -0.525457
##          | 0.0000* 1.0000
##
## alpha = 0.05
## Reject Ho if p <= alpha
##
## p < 5e-2 found in: PA1 PA2 PA6 PA3 PA4 PA5 PA7
## p < 1e-2 found in: PA1 PA2 PA6 PA3 PA4 PA5 PA7
## p < 1e-3 found in: PA1 PA2 PA6 PA3 PA4 PA5 PA7
## p < 1e-4 found in: PA1 PA2 PA6 PA3 PA4 PA5 PA7
```

court decisions often with RecipientType = combined.

RecipientIndividuation

```
analyze_distributions(data_factors_long, "RecipientIndividuation")
```



```
##
## Test for the significance of differences in RecipientIndividuation over PA1 :
##
##   Kruskal-Wallis rank sum test
##
## data: x and group
## Kruskal-Wallis chi-squared = 209.5856, df = 2, p-value = 0
##
##
##               Comparison of x by group
##               (Bonferroni)
## Col Mean-|
## Row Mean |      bulk  individu
## -----+-----
## individu |    0.552940
##          |    1.0000
##          |
## public   |   -7.610655  -14.06096
##          |    0.0000*   0.0000*
##
## alpha = 0.05
## Reject Ho if p <= alpha
##
## Test for the significance of differences in RecipientIndividuation over PA2 :
##
##   Kruskal-Wallis rank sum test
##
```

```

## data: x and group
## Kruskal-Wallis chi-squared = 33.7947, df = 2, p-value = 0
##
##
##
## Comparison of x by group
## (Bonferroni)
## Col Mean-|
## Row Mean |      bulk   individu
## -----+-----
## individu |    5.741813
##          |    0.0000*
##          |
## public   |    4.258459   -2.452715
##          |    0.0001*    0.0425*
##
## alpha = 0.05
## Reject Ho if p <= alpha
##
## Test for the significance of differences in RecipientIndividuation over PA6 :
##
## Kruskal-Wallis rank sum test
##
## data: x and group
## Kruskal-Wallis chi-squared = 39.0551, df = 2, p-value = 0
##
##
##
## Comparison of x by group
## (Bonferroni)
## Col Mean-|
## Row Mean |      bulk   individu
## -----+-----
## individu |   -2.045441
##          |    0.1224
##          |
## public   |    1.596328    6.239990
##          |    0.3312    0.0000*
##
## alpha = 0.05
## Reject Ho if p <= alpha
##
## Test for the significance of differences in RecipientIndividuation over PA3 :
##
## Kruskal-Wallis rank sum test
##
## data: x and group
## Kruskal-Wallis chi-squared = 29.2184, df = 2, p-value = 0
##
##
##
## Comparison of x by group
## (Bonferroni)
## Col Mean-|
## Row Mean |      bulk   individu
## -----+-----
## individu |   -2.043038

```

```

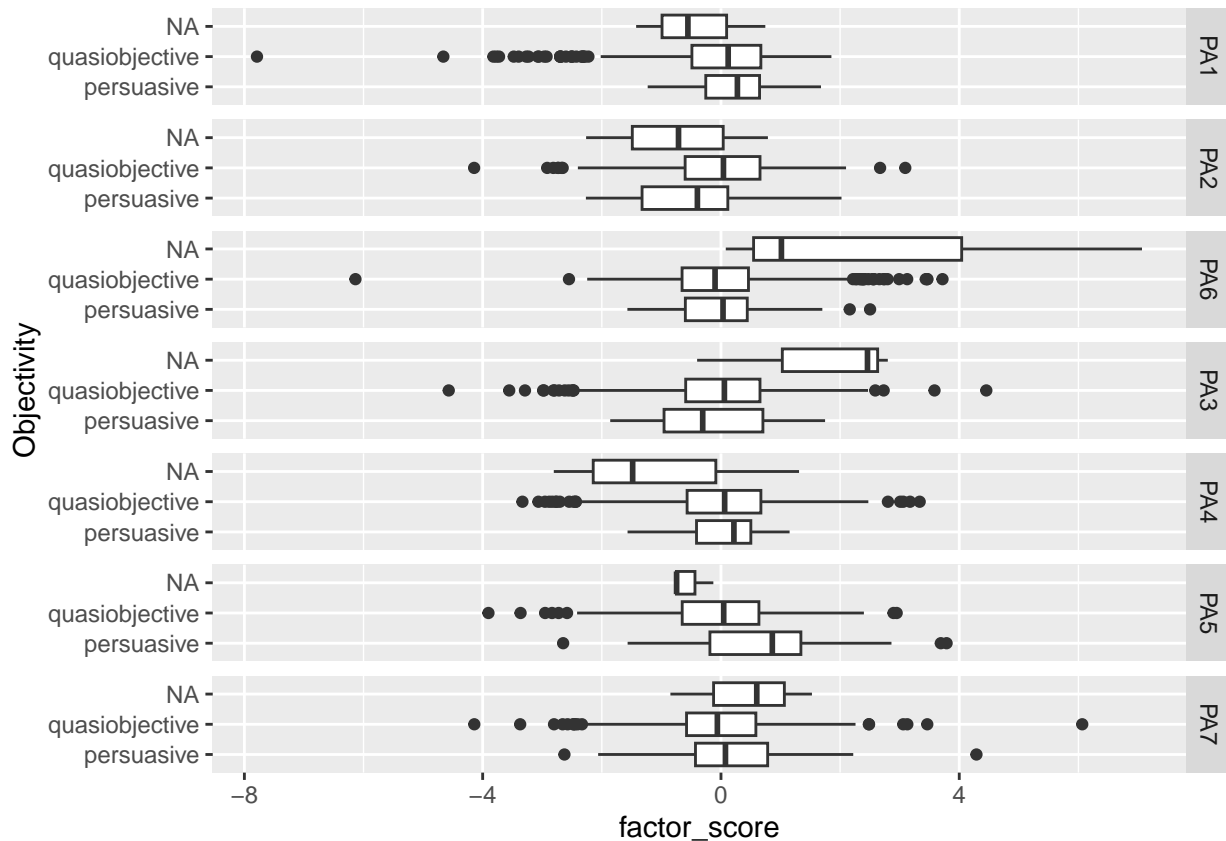
##          |      0.1231
##          |
## public | -4.487184 -4.249809
##          |      0.0000*      0.0001*
##
## alpha = 0.05
## Reject Ho if p <= alpha
##
## Test for the significance of differences in RecipientIndividuation over PA4 :
##
##   Kruskal-Wallis rank sum test
##
## data: x and group
## Kruskal-Wallis chi-squared = 58.2474, df = 2, p-value = 0
##
##
##                               Comparison of x by group
##                               (Bonferroni)
## Col Mean-|
## Row Mean |      bulk   individu
## -----+-----
## individu |    2.146907
##          |    0.0954
##          |
## public |    5.867168    6.451235
##          |    0.0000*    0.0000*
##
## alpha = 0.05
## Reject Ho if p <= alpha
##
## Test for the significance of differences in RecipientIndividuation over PA5 :
##
##   Kruskal-Wallis rank sum test
##
## data: x and group
## Kruskal-Wallis chi-squared = 100.7444, df = 2, p-value = 0
##
##
##                               Comparison of x by group
##                               (Bonferroni)
## Col Mean-|
## Row Mean |      bulk   individu
## -----+-----
## individu |   -4.029464
##          |    0.0002*
##          |
## public |    1.783526    9.946414
##          |    0.2235    0.0000*
##
## alpha = 0.05
## Reject Ho if p <= alpha
##
## Test for the significance of differences in RecipientIndividuation over PA7 :
##

```

```
## Kruskal-Wallis rank sum test
##
## data: x and group
## Kruskal-Wallis chi-squared = 50.2363, df = 2, p-value = 0
##
##
## Comparison of x by group
## (Bonferroni)
## Col Mean-|
## Row Mean |      bulk   individu
## -----+-----
## individu | -6.460242
##          |  0.0000*
##          |
## public   | -6.988232 -1.027106
##          |  0.0000*   0.9131
##
## alpha = 0.05
## Reject Ho if p <= alpha
##
## p < 5e-2 found in: PA1 PA2 PA6 PA3 PA4 PA5 PA7
## p < 1e-2 found in: PA1 PA2 PA6 PA3 PA4 PA5 PA7
## p < 1e-3 found in: PA1 PA2 PA6 PA3 PA4 PA5 PA7
## p < 1e-4 found in: PA1 PA2 PA6 PA3 PA4 PA5 PA7
```

Objectivity

```
analyze_distributions(data_factors_long, "Objectivity")
```



```
##
## Test for the significance of differences in Objectivity over PA1 :
##
##   Kruskal-Wallis rank sum test
##
## data: x and group
## Kruskal-Wallis chi-squared = 0.4589, df = 1, p-value = 0.5
##
##
##               Comparison of x by group
##               (Bonferroni)
## Col Mean-|
## Row Mean |   persuasi
## -----+-----
## quasiobj |   0.677452
##          |   0.4981
##
## alpha = 0.05
## Reject Ho if p <= alpha
##
## Test for the significance of differences in Objectivity over PA2 :
##
##   Kruskal-Wallis rank sum test
##
## data: x and group
## Kruskal-Wallis chi-squared = 4.2938, df = 1, p-value = 0.04
##
```



```

##
##                                     Comparison of x by group
##                                     (Bonferroni)
## Col Mean-|
## Row Mean |   persuasi
## -----+-----
## quasiobj |  -2.072146
##          |    0.0383*
##
## alpha = 0.05
## Reject Ho if p <= alpha
##
## Test for the significance of differences in Objectivity over PA6 :
##
##   Kruskal-Wallis rank sum test
##
## data: x and group
## Kruskal-Wallis chi-squared = 0.0013, df = 1, p-value = 0.97
##
##
##                                     Comparison of x by group
##                                     (Bonferroni)
## Col Mean-|
## Row Mean |   persuasi
## -----+-----
## quasiobj |  -0.035709
##          |    0.9715
##
## alpha = 0.05
## Reject Ho if p <= alpha
##
## Test for the significance of differences in Objectivity over PA3 :
##
##   Kruskal-Wallis rank sum test
##
## data: x and group
## Kruskal-Wallis chi-squared = 1.5825, df = 1, p-value = 0.21
##
##
##                                     Comparison of x by group
##                                     (Bonferroni)
## Col Mean-|
## Row Mean |   persuasi
## -----+-----
## quasiobj |  -1.257979
##          |    0.2084
##
## alpha = 0.05
## Reject Ho if p <= alpha
##
## Test for the significance of differences in Objectivity over PA4 :
##
##   Kruskal-Wallis rank sum test
##

```

```

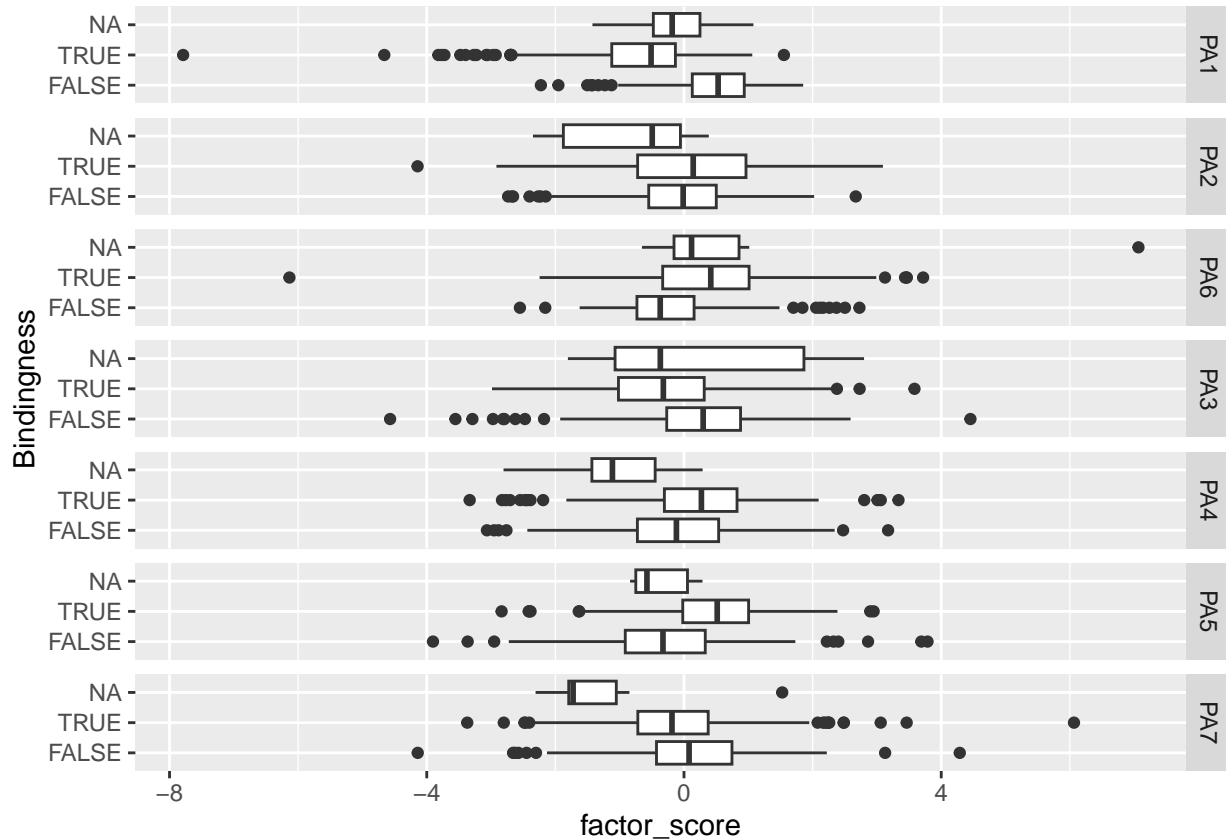
## data: x and group
## Kruskal-Wallis chi-squared = 0.0075, df = 1, p-value = 0.93
##
##
##                               Comparison of x by group
##                               (Bonferroni)
## Col Mean-|
## Row Mean |   persuasi
## -----+-----
## quasiobj |  -0.086722
##          |    0.9309
##
## alpha = 0.05
## Reject Ho if p <= alpha
##
## Test for the significance of differences in Objectivity over PA5 :
##
##   Kruskal-Wallis rank sum test
##
## data: x and group
## Kruskal-Wallis chi-squared = 7.8263, df = 1, p-value = 0.01
##
##
##                               Comparison of x by group
##                               (Bonferroni)
## Col Mean-|
## Row Mean |   persuasi
## -----+-----
## quasiobj |   2.797551
##          |   0.0051*
##
## alpha = 0.05
## Reject Ho if p <= alpha
##
## Test for the significance of differences in Objectivity over PA7 :
##
##   Kruskal-Wallis rank sum test
##
## data: x and group
## Kruskal-Wallis chi-squared = 0.366, df = 1, p-value = 0.55
##
##
##                               Comparison of x by group
##                               (Bonferroni)
## Col Mean-|
## Row Mean |   persuasi
## -----+-----
## quasiobj |   0.605013
##          |   0.5452
##
## alpha = 0.05
## Reject Ho if p <= alpha
##
## p < 5e-2 found in: PA2 PA5

```

```
## p < 1e-2 found in: PA5
## p < 1e-3 found in:
## p < 1e-4 found in:
```

Bindingness

```
analyze_distributions(data_factors_long, "Bindingness")
```



```
##
## Test for the significance of differences in Bindingness over PA1 :
##
##   Kruskal-Wallis rank sum test
##
## data: x and group
## Kruskal-Wallis chi-squared = 322.5625, df = 1, p-value = 0
##
##
##           Comparison of x by group
##           (Bonferroni)
## Col Mean-|
## Row Mean |      FALSE
## -----+-----
##   TRUE |   17.96002
##       |    0.0000*
##
## alpha = 0.05
## Reject Ho if p <= alpha
```

```

##
## Test for the significance of differences in Bindingness over PA2 :
##
##   Kruskal-Wallis rank sum test
##
## data: x and group
## Kruskal-Wallis chi-squared = 5.0063, df = 1, p-value = 0.03
##
##
##                               Comparison of x by group
##                               (Bonferroni)
## Col Mean-|
## Row Mean |      FALSE
## -----+-----
##      TRUE |  -2.237474
##           |    0.0253*
##
## alpha = 0.05
## Reject Ho if p <= alpha
##
## Test for the significance of differences in Bindingness over PA6 :
##
##   Kruskal-Wallis rank sum test
##
## data: x and group
## Kruskal-Wallis chi-squared = 94.9504, df = 1, p-value = 0
##
##
##                               Comparison of x by group
##                               (Bonferroni)
## Col Mean-|
## Row Mean |      FALSE
## -----+-----
##      TRUE |  -9.744250
##           |    0.0000*
##
## alpha = 0.05
## Reject Ho if p <= alpha
##
## Test for the significance of differences in Bindingness over PA3 :
##
##   Kruskal-Wallis rank sum test
##
## data: x and group
## Kruskal-Wallis chi-squared = 73.3375, df = 1, p-value = 0
##
##
##                               Comparison of x by group
##                               (Bonferroni)
## Col Mean-|
## Row Mean |      FALSE
## -----+-----
##      TRUE |   8.563733
##           |    0.0000*

```

```

##
## alpha = 0.05
## Reject Ho if p <= alpha
##
## Test for the significance of differences in Bindingness over PA4 :
##
##   Kruskal-Wallis rank sum test
##
## data: x and group
## Kruskal-Wallis chi-squared = 24.7338, df = 1, p-value = 0
##
##
##                               Comparison of x by group
##                               (Bonferroni)
## Col Mean-|
## Row Mean |      FALSE
## -----+-----
##    TRUE |  -4.973312
##         |    0.0000*
##
## alpha = 0.05
## Reject Ho if p <= alpha
##
## Test for the significance of differences in Bindingness over PA5 :
##
##   Kruskal-Wallis rank sum test
##
## data: x and group
## Kruskal-Wallis chi-squared = 126.2764, df = 1, p-value = 0
##
##
##                               Comparison of x by group
##                               (Bonferroni)
## Col Mean-|
## Row Mean |      FALSE
## -----+-----
##    TRUE |  -11.23727
##         |    0.0000*
##
## alpha = 0.05
## Reject Ho if p <= alpha
##
## Test for the significance of differences in Bindingness over PA7 :
##
##   Kruskal-Wallis rank sum test
##
## data: x and group
## Kruskal-Wallis chi-squared = 17.4925, df = 1, p-value = 0
##
##
##                               Comparison of x by group
##                               (Bonferroni)
## Col Mean-|
## Row Mean |      FALSE

```

```
## -----+-----
##      TRUE |    4.182400
##          |    0.0000*
##
## alpha = 0.05
## Reject Ho if p <= alpha
##
## p < 5e-2 found in: PA1 PA2 PA6 PA3 PA4 PA5 PA7
## p < 1e-2 found in: PA1 PA6 PA3 PA4 PA5 PA7
## p < 1e-3 found in: PA1 PA6 PA3 PA4 PA5 PA7
## p < 1e-4 found in: PA1 PA6 PA3 PA4 PA5 PA7
```

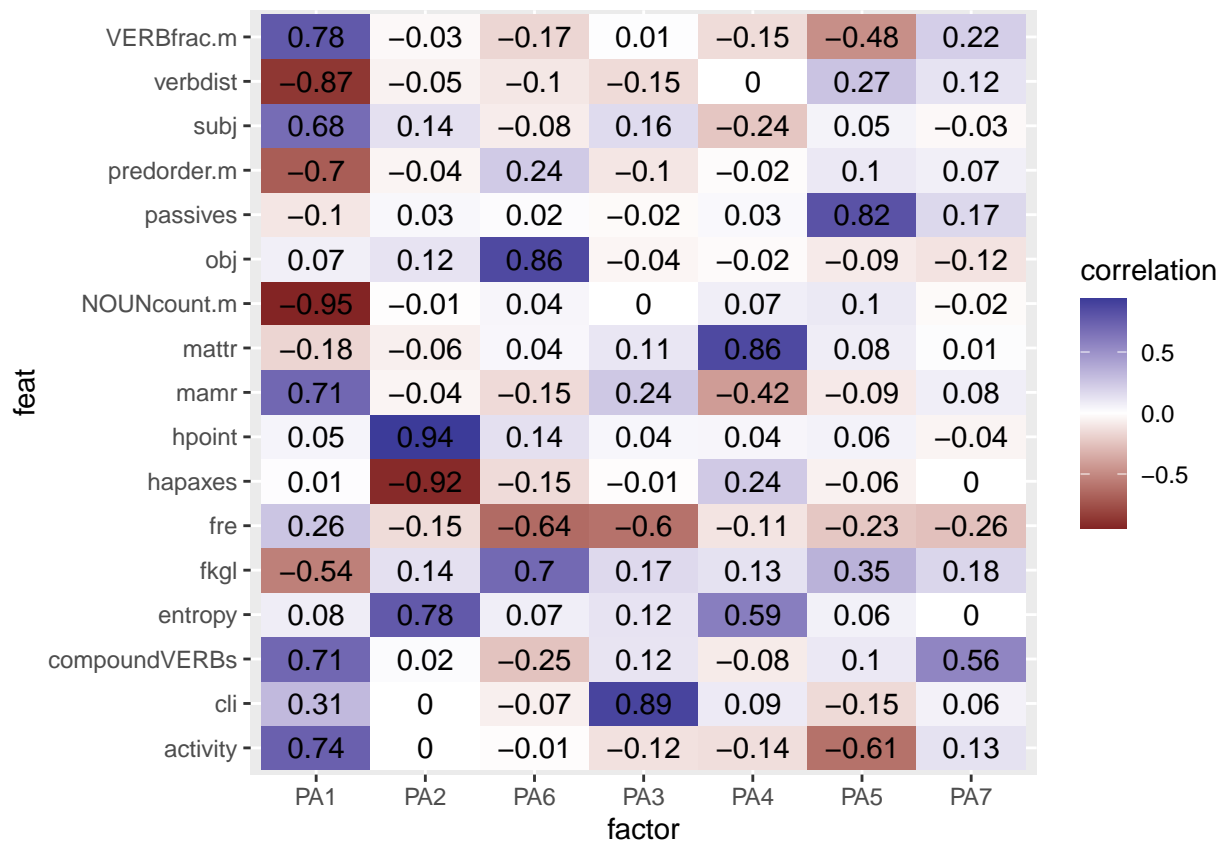
Feature-factor correlations

```
data_factors_longer <- data_factors_long %>%
  pivot_longer(
    abstractNOUNs:verbdist,
    names_to = "feat", values_to = "feat_value"
  )

data_factors_correlations <- data_factors_longer %>%
  group_by(feat, factor) %>%
  summarize(correlation = cor(feat_value, factor_score))
```

`summarise()` has grouped output by 'feat'. You can override using the
`.groups` argument.

```
data_factors_correlations %>%
  filter(feat %in% final_collist) %>%
  ggplot(aes(
    x = factor,
    y = feat,
    fill = correlation,
    label = round(correlation, 2)
  )) +
  geom_tile() +
  geom_text() +
  scale_fill_gradient2()
```



```
data_factors_correlations %>%
  filter(!(feat %in% final_collist)) %>%
  ggplot(aes(
    x = factor,
    y = feat,
    fill = correlation,
    label = round(correlation, 2)
  )) +
  geom_tile() +
  geom_text() +
  scale_fill_gradient2()
```

