

Appendix 5: Equi-Complexity Analyses

29 March, 2021

Session Info

Give the session info (reduced).

```
## [1] "R version 3.6.3 (2020-02-29)"  
## [1] "x86_64-pc-linux-gnu"
```

Load Packages

Load packages. If they are not installed yet on your local machine, use `install.packages()` to install them.

```
library(readr)  
library(MASS)  
library(tidyr)  
library(ggplot2)  
library(ggthemes)  
library(scales)  
library(plyr)  
library(rstatix)
```

Give the package versions.

```
## rstatix      plyr      scales ggthemes ggplot2      tidyr      MASS      readr  
## "0.6.0"     "1.8.6"     "1.1.1"     "0.5.3"     "3.3.3"     "1.1.2"     "7.3-53"     "1.4.0"
```

Load Data

Load results of all participants in the UD track directly from github repo by using the “readr” library. We here only use Track B as we have measures from different domains (morphology, syntax) in this track, while in Track A we have mainly morphological complexity measures.

```
#TRACK B (Universal Dependencies, UD)  
brunato.results <- read_csv("https://raw.githubusercontent.com/IWMLC/language-complexity-metrics/master/brunato.results.csv")  
coltekin.results <- read_csv("https://raw.githubusercontent.com/IWMLC/language-complexity-metrics/master/coltekin.results.csv")  
semenuks.results <- read_csv("https://raw.githubusercontent.com/IWMLC/language-complexity-metrics/master/semenuks.results.csv")  
sinemaki.results <- read_csv("https://raw.githubusercontent.com/IWMLC/language-complexity-metrics/master/sinemaki.results.csv")  
sozinova.results <- read_csv("https://raw.githubusercontent.com/IWMLC/language-complexity-metrics/master/sozinova.results.csv")
```

Load file with meta-information on the measures. This is slightly adapted from a file prepared by Katharina Ehret and Alice Blumenthal-Dramé in the context of the Interactive Workshop on Measuring Language Complexity (IWMLC 2019).

```
meta.info <- read_csv("https://raw.githubusercontent.com/IWMLC/language-complexity-metrics/master/meas
```

Data Pre-Processing

Create a single data frame merging results together using the `Reduce()` and `merge()` functions of base R.

```
# by default the merge() function uses columns with the same names
# to merge on, i.e. "id" and "language" in our case.
results <- Reduce(merge, list(brunato.results, coltekin.results, semenuks.results,
                             sinnemaki.results, sozinova.results))
```

Give some simple statistics for this data frame of results.

```
nrow(results) # i.e. number of different UD corpora
```

```
## [1] 63
```

```
length(unique(results$language)) # i.e. number of different languages
```

```
## [1] 44
```

```
unique(results$language) # output the language names
```

```
## [1] "Afrikaans"      "Arabic"          "Bulgarian"
## [4] "Catalan"        "Czech"           "Old Church Slavonic"
## [7] "Chinese"        "Danish"          "German"
## [10] "Greek"          "Estonian"        "English"
## [13] "Basque"         "Persian"         "Finnish"
## [16] "French"         "Gothic"          "Ancient Greek"
## [19] "Hebrew"         "Hindi"           "Croatian"
## [22] "Hungarian"      "Indonesian"      "Italian"
## [25] "Japanese"       "Korean"          "Latin"
## [28] "Latvian"        "Dutch"           "Norwegian"
## [31] "Polish"         "Portuguese"      "Romanian"
## [34] "Russian"        "Slovak"          "Slovenian"
## [37] "Spanish"        "Serbian"         "Swedish"
## [40] "Turkish"        "Uyghur"          "Ukrainian"
## [43] "Urdu"           "Vietnamese"
```

```
ncol(results)-2 # i.e. number of complexity measures
```

```
## [1] 27
```

Invert the values (by subtracting them from 1) for the measure “CR_inflection_accuracy”. Note that higher values in the original measure mean *lower* rather than higher complexity.

```
results$CR_inflection_accuracy <- 1-results$CR_inflection_accuracy
```

Center and scale all numerical columns to make them more commensurable.

```
# scale and add meta-information columns again
results.scaled <- cbind(results[1:2], scale(results[3:29]))
```

Remove certain measures. To include all measures, this code can just be commented out. In Track B, some measures given by the same team have strong positive correlations, e.g. the number of tokens in a sentence (BV_n_tokens) and the average number of tokens per clause (BV_avg_token_per_clause). We hence just keep one of the strongly correlated measures to not inflate the number of strongly correlated data points.

Also there are measures with many NAs in Track B, i.e. “SI_double_dl”, “SI_head_dl”, “SI_zero_dl”, which are removed here.

```
# Remove measures in Track B
results.scaled <- results.scaled[ , -which(names(results.scaled) %in%
                                           c("BV_avg_max_depth", "BV_avg_token_per_clause",
                                             "SI_double_dl", "SI_head_dl", "SI_zero_dl"))]

nrow(results.scaled)
```

```
## [1] 63
```

Transform data frames from wide format to long format (this is necessary for later plotting and analyses by columns rather than rows). For later comparison we now have one dataframe in which there are still some NAs for certain languages and measures (i.e. Vietnamese and Turkish), and one dataframe where these languages are removed.

```
results.long <- gather(results.scaled, key = measure, value = value, BV_n_tokens:SBS_DER)
```

Remove rows which contain NAs.

```
results.long <- results.long[complete.cases(results.long), ]
nrow(results.long)
```

```
## [1] 1380
```

Add meta-information on complexity measures.

```
results.long <- merge(results.long, meta.info[, 2:4], by = "measure")
```

Generate data frames for subdomains (morphology, syntax). This can be used for comparison with aggregated results.

```
results.morph <- results.long[results.long$domain == "morphology", ]
results.syntax <- results.long[results.long$domain == "syntax", ]
```

Density Distributions

Plot density distributions of complexity measurements by language. Individual measurements for each complexity measure (and different corpora if available) are plotted as dots. The central value (0) is indicated by a vertical dotted line for visual reference.

Create data frame with both domains + “overall”, this is necessary for the plots below.

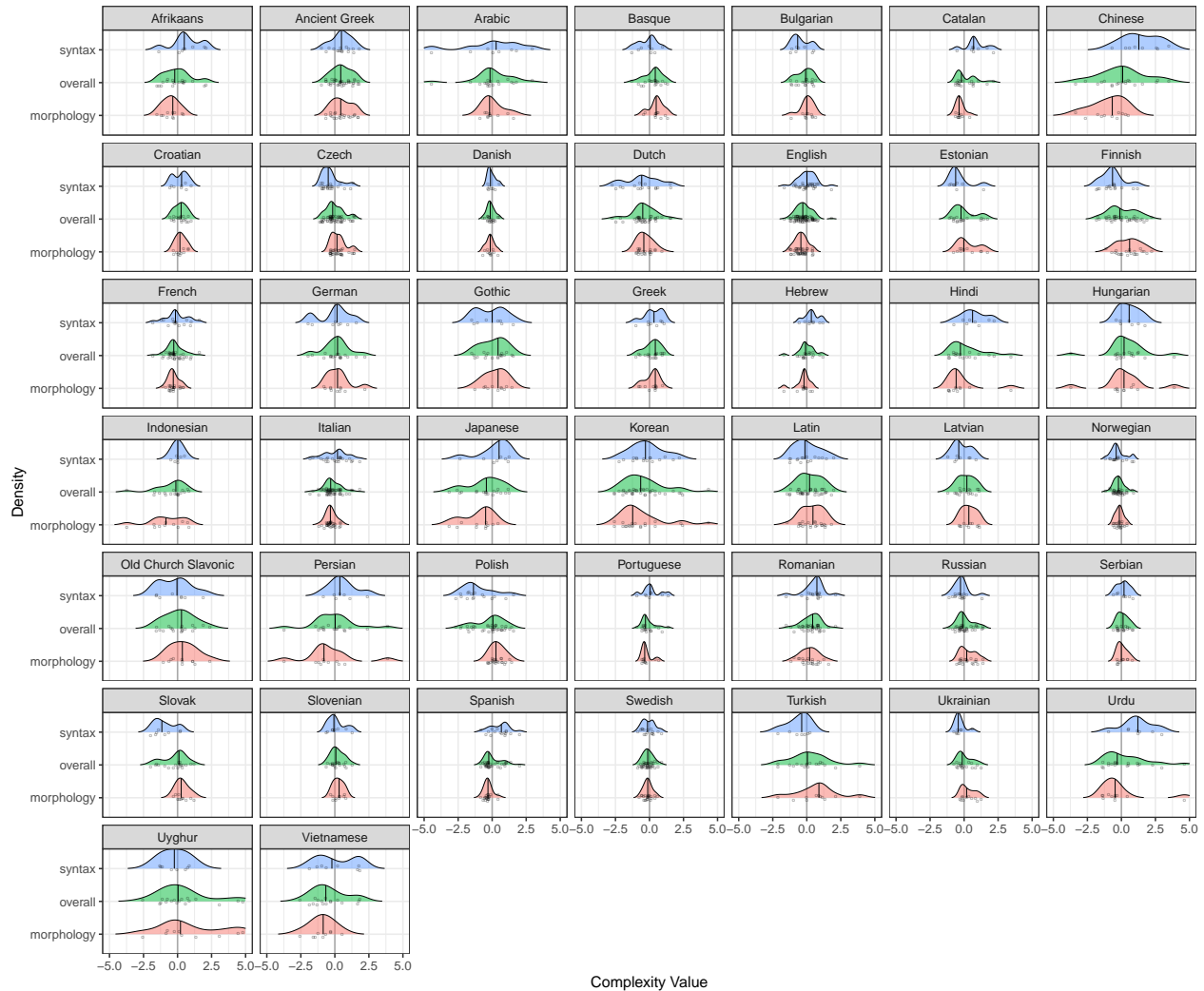
```
results.overall <- results.long
results.overall$domain <- rep("overall", times = nrow(results.long))
results.plot <- rbind(results.overall, results.long)
```

Plot density distributions with indication of median (mean) values.

```
density.plot <- ggplot(results.plot, aes(x = value, y = domain, fill = domain)) +
  geom_vline(aes(xintercept = 0), color = "darkgrey") +
  stat_density_ridges(quantile_lines = TRUE, quantiles = 0.5,
                      rel_min_height = 0.01, scale = 0.6, alpha = 0.5,
                      jittered_points = TRUE, point_shape = "o", point_size = 1,
                      size = 0.25, position = position_points_jitter(height = 0.1)) +
  #geom_vline(data = med, aes(xintercept = grp.median), linetype = "dashed") +
  facet_wrap(~ language) +
  xlim(-5, 5) +
```

```
labs(x = "Complexity Value", y = "Density") +
theme_bw() +
theme(legend.position = "none")
print(density.plot)
```

Warning: Removed 4 rows containing non-finite values (stat_density_ridges).



Save figure to file.

```
ggsave("Figures/EquiCompl/density_plot.pdf", density.plot,
       dpi = 300, scale = 1, width = 12, height = 10, device = cairo_pdf)
```

Statistical Tests

Run statistical tests to assess whether the aggregate complexity distributions for certain pairs of languages differ significantly from one another. Note that for this sample of 44 languages there are $44 \cdot (44-1) / 2 = 946$ possible pairwise comparisons.

Overview of median values

Get mean, median, and standard deviation values.

```
# get median value for each language
med <- ddply(results.long, "language", summarise, grp.median = median(value))
# get mean value for each language
mu <- ddply(results.long, "language", summarise, grp.mean = mean(value))
# get standard deviation for each language
sdev <- ddply(results.long, "language", summarise, grp.sdev = sd(value))
```

Give an overview of languages with highest and lowest median complexity values.

```
stats.df <- cbind(mu, med[, 2], sdev[, 2])
colnames(stats.df) <- c("language", "mu", "med", "sdev")
stats.df.sorted <- stats.df[order(-stats.df$med),]
# round values to two decimal places, the "-1" excludes column 1
stats.df.sorted[, -1] <- round(stats.df.sorted[, -1], 2)
print(stats.df.sorted)
```

##	language	mu	med	sdev
## 2	Ancient Greek	0.49	0.43	0.74
## 17	Gothic	0.08	0.43	0.95
## 33	Romanian	0.34	0.43	0.74
## 18	Greek	0.22	0.43	0.60
## 4	Basque	0.25	0.43	0.69
## 29	Old Church Slavonic	0.15	0.29	1.11
## 8	Croatian	0.22	0.26	0.45
## 26	Latin	0.23	0.20	0.90
## 27	Latvian	0.13	0.20	0.65
## 16	German	0.08	0.20	0.99
## 21	Hungarian	0.33	0.20	1.46
## 35	Serbian	0.10	0.12	0.41
## 43	Uyghur	0.80	0.12	2.48
## 36	Slovak	-0.21	0.10	0.90
## 7	Chinese	0.05	0.09	1.77
## 37	Slovenian	0.20	0.08	0.51
## 31	Polish	-0.21	0.06	1.11
## 40	Turkish	0.21	0.05	1.46
## 30	Persian	-0.03	0.03	1.61
## 5	Bulgarian	-0.17	-0.09	0.59
## 19	Hebrew	0.00	-0.09	0.62
## 34	Russian	0.07	-0.11	0.63
## 14	Finnish	0.06	-0.12	1.05
## 22	Indonesian	-0.46	-0.12	1.11
## 39	Swedish	-0.10	-0.13	0.40
## 41	Ukrainian	0.04	-0.14	0.57
## 10	Danish	-0.10	-0.14	0.31
## 3	Arabic	0.04	-0.16	1.53
## 9	Czech	0.02	-0.16	0.66
## 6	Catalan	0.19	-0.20	0.81
## 1	Afrikaans	-0.02	-0.20	1.02
## 28	Norwegian	-0.19	-0.22	0.43
## 13	Estonian	0.00	-0.22	0.86
## 38	Spanish	0.05	-0.25	0.67

```
## 20          Hindi  0.18 -0.27 1.24
## 15          French -0.20 -0.28 0.64
## 32    Portuguese -0.07 -0.29 0.57
## 12          English -0.23 -0.29 0.59
## 23          Italian -0.17 -0.31 0.68
## 42          Urdu   0.36 -0.31 1.62
## 24          Japanese -0.52 -0.43 1.30
## 11          Dutch  -0.42 -0.49 0.93
## 25          Korean -0.26 -0.64 1.80
## 44    Vietnamese -0.45 -0.66 1.29
```

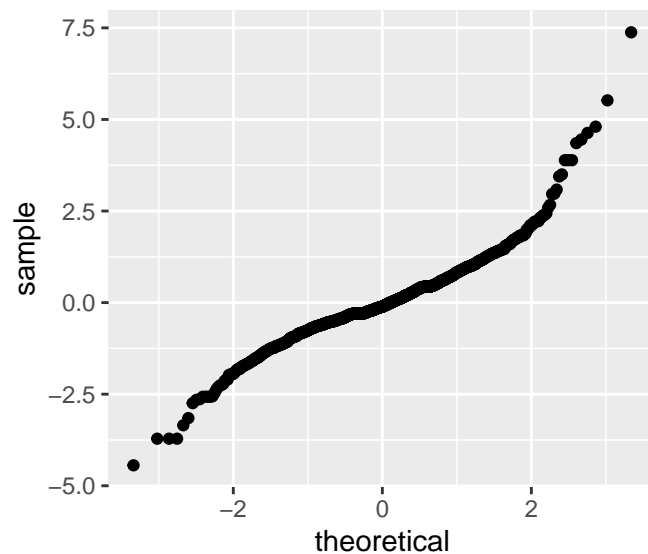
Output data frame as csv file.

```
write.csv(stats.df.sorted, file = "Tables/descriptiveStats.csv", row.names = F)
```

Normality

Check normality of data points by QQ-plot.

```
ggplot(results.long, aes(sample = value)) +
  stat_qq()
```



Choose statistical tests

Select a statistical test: Since there are some deviations from normality visible in the QQ-Plot above, we here choose a Wilcoxon test. If we supply two data vectors, then by default the command `wilcox.test()` runs a Wilcoxon rank sum test (for unpaired samples), and with “paired = T” a Wilcoxon signed rank test. Note that while the same measurement procedures were used here across different languages (and corresponding text samples) to assess different types of complexity, there are sometimes NAs in the original data. We thus have to consider the resulting vectors “unpaired”. Note that `pairwise.wilcox.test()` is a function of the R-core stats package which runs multiple tests, i.e. for all groups in the “language” column in our case.

P-value adjustment for multiple comparisons: In case of multiple testing, we should account for the fact that the likelihood of finding a significant result by chance increases with the number of statistical tests. One of the most conservative methods to account for this is the so-called Bonferroni correction, i.e. multiplying the p-values with the number of tests. This method is appropriate when tests are independent of one another

(MacDonald 2014, p. 254-260). Since we here run pairwise tests by languages, our tests are not independent (the same language is tested against others multiple times). We therefore apply the so-called Holm-Bonferroni method, which is less conservative. It does not assume independence between tests (see the descriptions in the vignette invoked by the command “?p.adjust()”).

Tests for all measures (morphology and syntax)

```
# we add some random noise here to the value vector with
# the function jitter(), since we otherwise get warnings due to ties in the data
p.values <- pairwise.wilcox.test(jitter(results.long$value), results.long$language,
                                paired = F, p.adjust.method = "holm")
# print(p.values)
# get dataframe with pairs of languages where p < 0.05
m <- p.values$p.value
indices <- which(m < 0.05, arr.ind = T)
v1 <- rownames(m)[indices[, "row"]]
v2 <- colnames(m)[indices[, "col"]]
df <- cbind(v1, v2)
print(df)
```

```
##      v1      v2
## [1,] "Dutch"   "Ancient Greek"
## [2,] "English" "Ancient Greek"
## [3,] "French"  "Ancient Greek"
## [4,] "Italian" "Ancient Greek"
## [5,] "Norwegian" "Ancient Greek"
## [6,] "Romanian" "English"
```

Tests for morphological complexity measures

```
p.values.morph <- pairwise.wilcox.test(jitter(results.morph$value), results.morph$language,
                                       paired = F, p.adjust.method = "holm")
# print(p.values.morph)
# we add some random noise here to the value vector with
# the function jitter(), since we otherwise get warnings due to ties in the data
# get dataframe with pairs of languages where p < 0.05
m <- p.values.morph$p.value
indices <- which(m < 0.05, arr.ind = T)
v1 <- rownames(m)[indices[, "row"]]
v2 <- colnames(m)[indices[, "col"]]
df <- cbind(v1, v2)
print(df)
```

```
##      v1      v2
## [1,] "English" "Ancient Greek"
## [2,] "Italian" "Ancient Greek"
## [3,] "Spanish" "Ancient Greek"
## [4,] "English" "Basque"
## [5,] "Italian" "Basque"
## [6,] "Polish"  "Catalan"
## [7,] "English" "Czech"
## [8,] "French"  "Czech"
```

```
## [9,] "Italian" "Czech"
## [10,] "Japanese" "Czech"
## [11,] "Spanish" "Czech"
## [12,] "Finnish" "English"
## [13,] "Polish" "English"
## [14,] "Russian" "English"
## [15,] "Slovak" "English"
## [16,] "Polish" "French"
## [17,] "Polish" "Italian"
## [18,] "Polish" "Japanese"
## [19,] "Spanish" "Polish"
```

Tests for syntactic complexity measures

```
p.values.syntax <- pairwise.wilcox.test(jitter(results.syntax$value), results.syntax$language,
    paired = F, p.adjust.method = "holm")
# print(p.values.syntax)
# we add some random noise here to the value vector with
# the function jitter(), since we otherwise get warnings due to ties in the data
m <- p.values.syntax$p.value
indices <- which(m < 0.05, arr.ind = T)
v1 <- rownames(m)[indices[, "row"]]
v2 <- colnames(m)[indices[, "col"]]
df <- cbind(v1, v2)
print(df)
```

```
##      v1 v2
```

Effect Size

Statistical significance is only one part of the story. For instance, a difference in complexity values might be statistically significant, but so small that it is negligible for any theorizing. In fact, it is sometimes argued that effect sizes – rather than p-values – should be the aim of statistical inquiry (Cahusac 2020, p. 12-15). An overview of effect size measures per statistical test is given in Patil (2020). In conjunction with the Wilcoxon rank sum test we here use the statistic *r* as an effect size measure (i.e. function `wilcox_effsize()` of the “rstatix” package). It runs from 0 to 1. Values from 0.10 to 0.3 are typically considered small effects, 0.3 to 0.5 moderate effects, and ≥ 0.5 large effects.

For all measures

```
effect.sizes <- wilcox_effsize(results.long, value ~ language, paired = F)
#print(effect.sizes)
```

For morphology

```
effect.sizes.morph <- wilcox_effsize(results.morph, value ~ language, paired = F)
#print(effect.sizes.morph)
```


For syntax

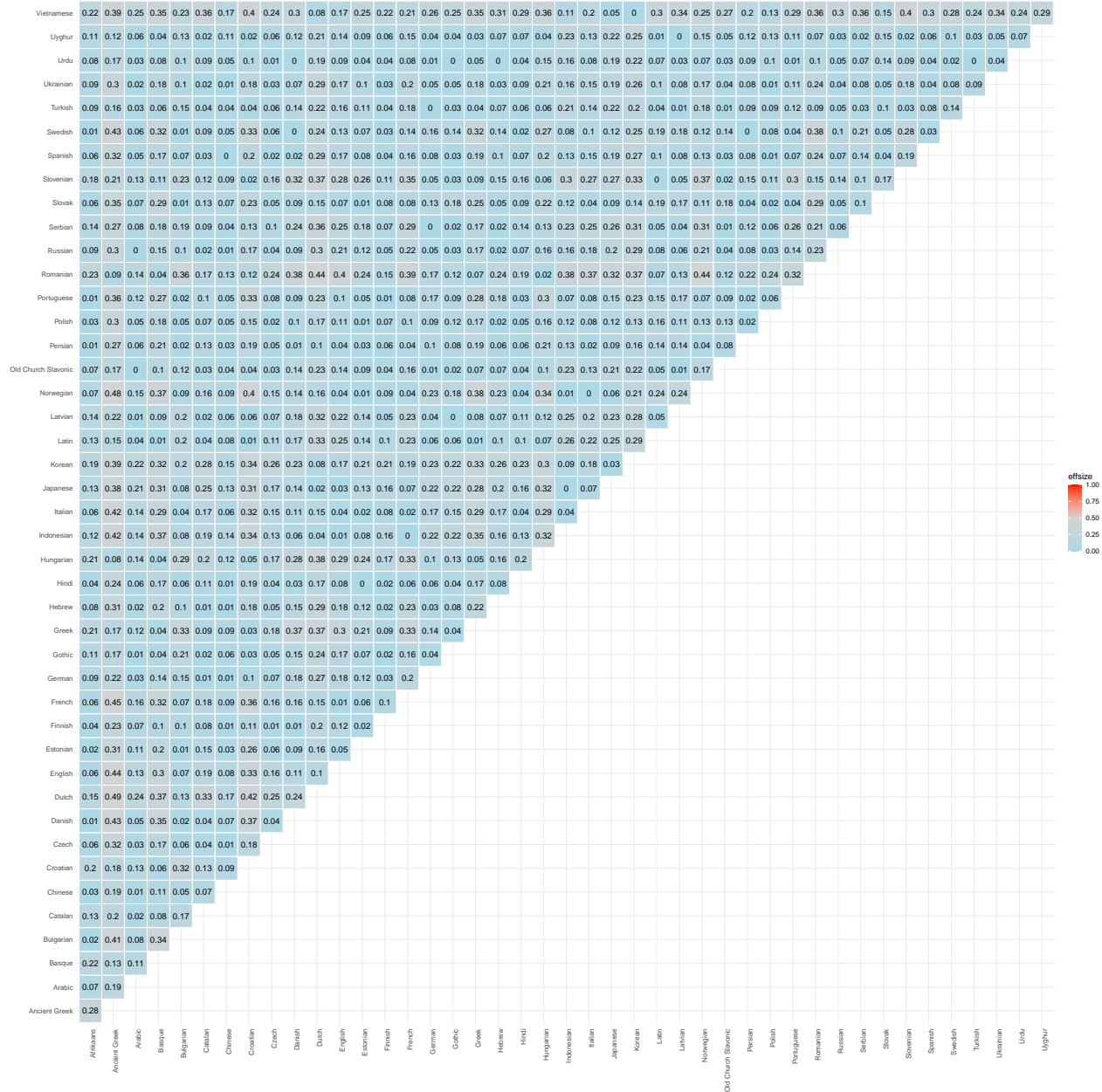
```
effect.sizes.syntax <- wilcox_effsize(results.syntax, value ~ language, paired = F)
#print(effect.sizes.syntax)
```

Effect Size Heatmap

Plot a heatmap with effect sizes to get a better overview.

For all measures

```
effect.sizes.plot <- ggplot(as.data.frame(effect.sizes), aes(group1, group2)) +
  geom_tile(aes(fill = effsize), color = "white") +
  scale_fill_gradient2(low = "light blue", mid = "light grey", high = "red",
    midpoint = 0.5, limit = c(0,1)) +
  geom_text(aes(label = round(effsize, 2))) +
  labs(x = "", y = "") +
  theme_minimal() +
  theme(axis.text.x = element_text(angle = 90, hjust = 1))
effect.sizes.plot
```



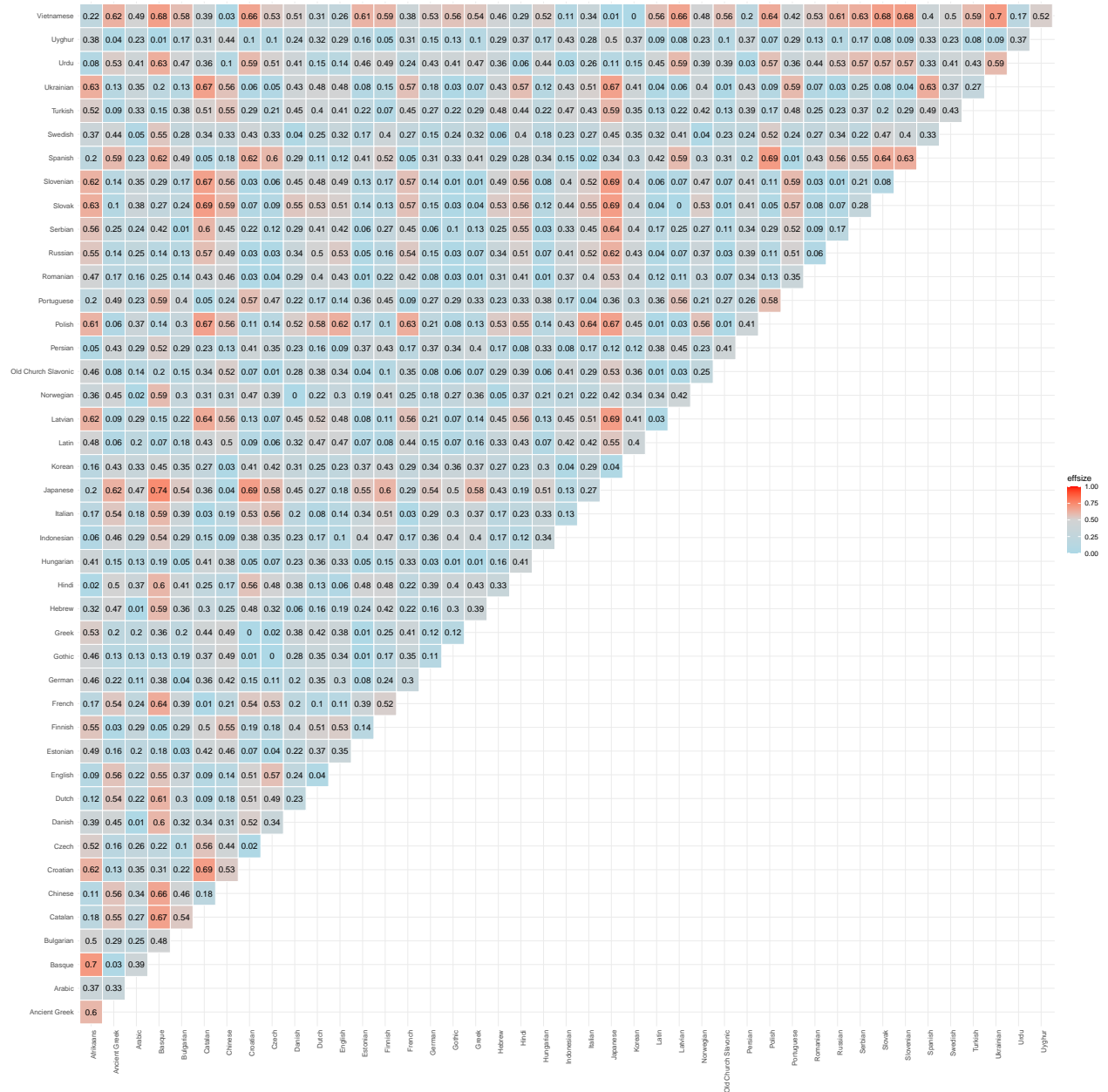
Save figure to file.

```
#ggsave("Figures/EquiCompl/effectSize_plot.pdf", effect.sizes.plot,
#       dpi = 300, scale = 1, width = 20, height = 20, device = cairo_pdf)
```

For morphology

```
effect.sizes.plot <- ggplot(as.data.frame(effect.sizes.morph), aes(group1, group2)) +
  geom_tile(aes(fill = effsize), color = "white") +
  scale_fill_gradient2(low = "light blue", mid = "light grey", high = "red",
    midpoint = 0.5, limit = c(0,1)) +
  geom_text(aes(label = round(effsize, 2))) +
  labs(x = "", y = "") +
```

```
theme_minimal() +
theme(axis.text.x = element_text(angle = 90, hjust = 1))
effect.sizes.plot
```



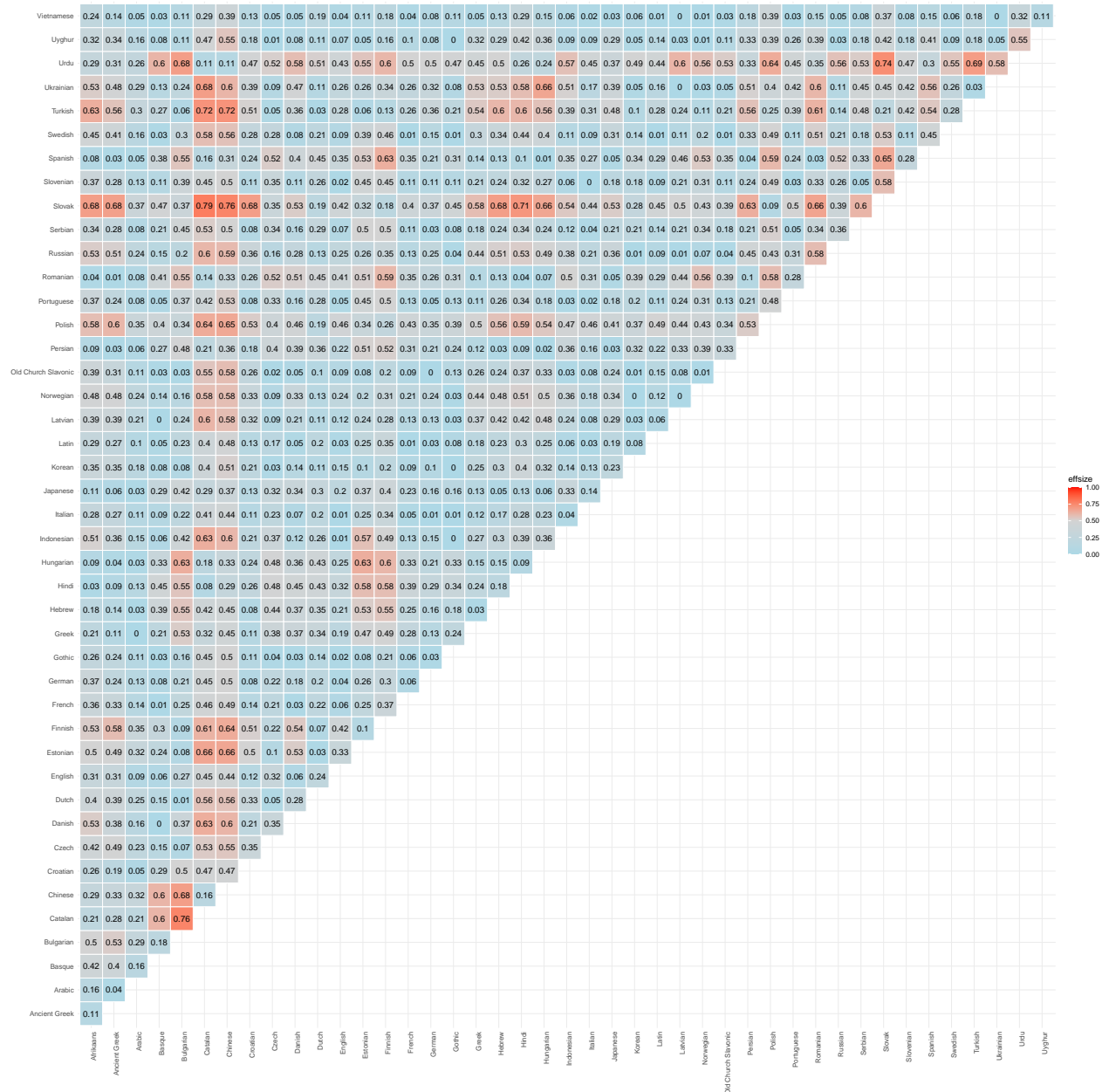
For syntax

```
effect.sizes.plot <- ggplot(as.data.frame(effect.sizes.syntax), aes(group1, group2)) +
  geom_tile(aes(fill = effsize), color = "white") +
  scale_fill_gradient2(low = "light blue", mid = "light grey", high = "red",
    midpoint = 0.5, limit = c(0,1)) +
  geom_text(aes(label = round(effsize, 2))) +
  labs(x = "", y = "") +
```

```

theme_minimal() +
theme(axis.text.x = element_text(angle = 90, hjust = 1))
effect.sizes.plot

```



Interpretation:

We find very little evidence for systematic differences (i.e. statistically significant differences with moderate to high effect sizes) in the aggregate complexities of the 44 languages investigated here. In fact, there are only five pairs of languages out of 946 for which we find statistically significant location shifts in the overall complexity distributions. These mostly involve Ancient Greek compared to modern day languages (English, Dutch, Norwegian, and Italian). A further significant difference we find between English and Romanian. While these results certainly depend on the number of data points (i.e. measurements) available per language,

it is clearly visible in the effect size matrices, that for morphology and syntax separately we find sometimes considerable differences, while for the aggregated measures there are generally lower effect sizes.

So, given the data, methods, and languages in this meta study, there is strong evidence that languages have a tendency to be equi-complex, if different dimensions of complexity are aggregated.

References

Cahusac, P. M. B. (2021). Evidence-based statistics. John Wiley & Sons.

McDonald, J.H. (2014). Handbook of Biological Statistics (3rd ed.). Sparky House Publishing, Baltimore, Maryland. online at <http://www.biostathandbook.com>

Patil, I. (2020). Test and effect size details. online at https://cran.r-project.org/web/packages/statsExpressions/vignettes/stats_details.html.