

The Dutch Diminutive: Between Inflection and Derivation

Analysis Script

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0. Important notice

This script is the only one you should need to run in order to replicate the results of the study. While “preprocessing.Rmd” relies on the externally-accessed DLP2 files in order to build the experimental dataset in the first place, here the dataset is already assembled and ready for final data transformations and subsequent analysis. If you’re looking to get a full picture of the pipeline and account for every data-related step within this project, feel free to peek into the preprocessing script. Otherwise, you should be good to go!

1. Import the necessary R packages

```
library(dplyr) # For data cleanup and transformations
library(readr) # For more straightforward ways to import/export data
library(lme4) # For mixed-effects linear regression modelling
library(car) # For alternative options when it comes to plots and regressions
library(ggplot2) # For a more comprehensive way of plotting data
library(ggpubr) # For including statistical values in plots
library(sjPlot) # For plotting interaction effects
library(sjmisc) # Auxiliary library for sjPlot
library(effsize) # For Cohen's d, etc.
library(afex) # For p-values in lmer summaries
library(MuMIn) # For extracting R-squared values from lmers
options(scipen = 999) # For easier interpretability of the slopes
```

2. Import the experimental dataset, perform some final cleanup

```
trialdata <- read_csv("../corpus/trialdata.csv", show_col_types = FALSE)
# Move all relevant columns to the left for better readability
trialdata <- select(trialdata,
  "spelling": "dec_criterion",
  "rtC": "rateC",
  "Length": "Colt_Nphon",
  "item",
  "participant",
  "lower": "rateR",
  "rtI": "zrateI",
  "acc.mean": "zrateI.sd"
```

```

)
# Filter out the irrelevant columns based on theory-supported decisions
# NOTE: Done here so variables could be reintroduced at will if need be
trialdata <- select(trialdata,
  -"N_phonemes",
  # OLD20 chosen as the neighbourhood var: filter out the rest
  -"Colt_N",
  -"PLD30",
  -"Colt_Nphon",
  # RTs chosen as the dependent var; filter out the rest,
  # do the centering and z-Transforming within the script;
  # filter out the pre-existing variables
  -"lower",
  -"upper",
  -"rtR",
  -"rateR",
  -"rtI",
  -"rateI",
  -"zrtC",
  -"zrateC",
  -"zrtI",
  -"zrateI",
  -"rtC.mean",
  -"rtC.sd",
  -"rateC.mean",
  -"rateC.sd",
  -"zrtC.mean",
  -"zrtC.sd",
  -"zrateC.mean",
  -"zrateC.sd",
  -"rtI.mean",
  -"rtI.sd",
  -"rateI.mean",
  -"rateI.sd",
  -"zrtI.mean",
  -"zrtI.sd",
  -"zrateI.mean",
  -"zrateI.sd"
)

```

3. Run sanity checks

```

# Make sure the response variable looks fine
summary(trialdata$rtC) # Seems some responses are unreasonably long

```

```

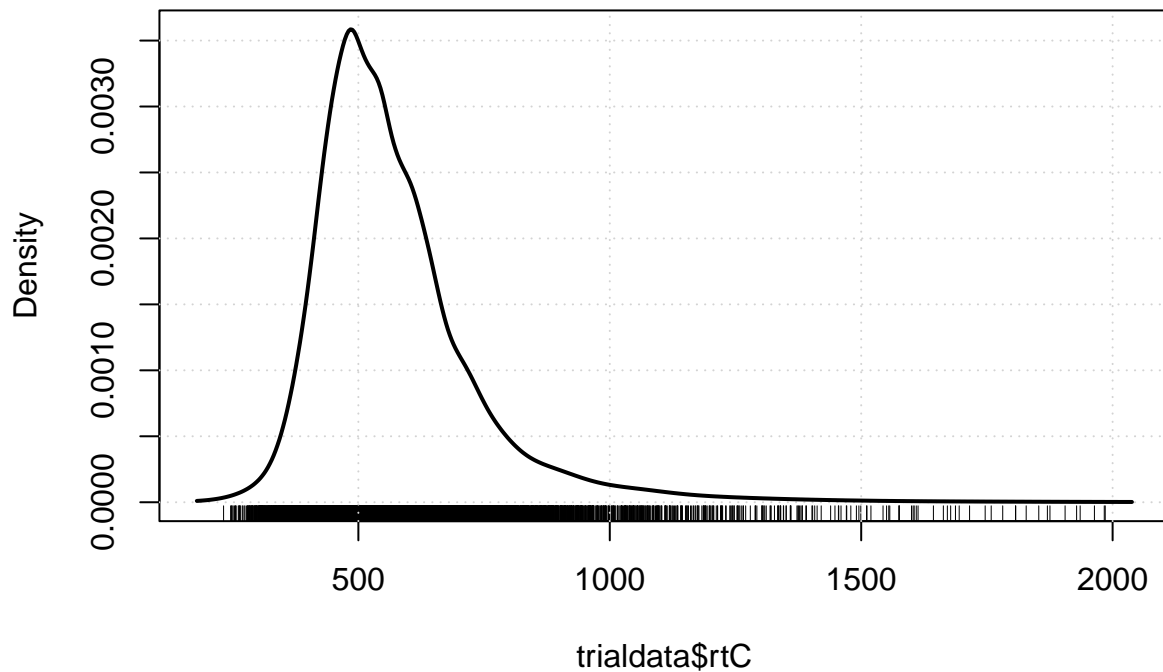
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##    232.0   466.5   540.0   574.3   637.2  1985.3

```

```

densityPlot(trialdata$rtC) # Few past 1000, even fewer past 1500

```



```
cat(
  "Only", NROW(filter(trialdata, rtC > 1500)), "observations past 1500 \n",
  "Only", NROW(filter(trialdata, rtC > 1250)), "observations past 1250 \n",
  "Only", NROW(filter(trialdata, rtC > 1000)), "observations past 1000 \n"
)
```

```
## Only 37 observations past 1500
## Only 103 observations past 1250
## Only 320 observations past 1000
```

```
# Need to subset by some number; 1250 as the sweet spot.
# NOTE: not subsetting the data here leads to an pretty awful skew in model
# residuals; seems not even log-transforming the rt value is enough to
# eliminate the effect of these more extreme values.
trialdata <- filter(trialdata, rtC < 1250)

# Compare number of rows per diminutive condition
trialdata <- mutate(trialdata, dim_type=factor(dim_type))
summary(trialdata$dim_type)
```

```
## both deriv infl
## 1461 4773 5012
```

```
# Check distributions of all relevant predictors
trialdata %>% select("SUBTLEX2",
                    "Length",
                    "Nsyl",
                    "nmorph",
                    "OLD20",
                    "Concreteness",
                    "AoA",
                    "Word_prevalence1") %>% summary()
```

```
##      SUBTLEX2      Length      Nsyl      nmorph
## Min.   :    0.0   Min.   : 5.000   Min.   :2.00   Min.   :2.000
## 1st Qu.:   32.0   1st Qu.: 6.000   1st Qu.:2.00   1st Qu.:2.000
## Median :  104.0   Median : 8.000   Median :3.00   Median :3.000
## Mean   :   740.2   Mean   : 8.251   Mean   :2.65   Mean   :2.928
## 3rd Qu.:  268.0   3rd Qu.:10.000   3rd Qu.:3.00   3rd Qu.:3.000
## Max.   :59247.0   Max.   :16.000   Max.   :5.00   Max.   :5.000
##      OLD20      Concreteness      AoA      Word_prevalence1
## Min.   :1.000   Min.   :1.733   Min.   : 3.750   Min.   :0.561
## 1st Qu.:1.700   1st Qu.:3.143   1st Qu.: 6.500   1st Qu.:2.212
## Median :1.900   Median :4.000   Median : 7.722   Median :2.504
## Mean   :2.402   Mean   :3.794   Mean   : 7.944   Mean   :2.434
## 3rd Qu.:3.350   3rd Qu.:4.571   3rd Qu.: 9.333   3rd Qu.:2.765
## Max.   :6.050   Max.   :5.000   Max.   :13.950   Max.   :3.213
```

```
# Check for correlations using Pearson's R
cat(
  "SUBTLEX2~Length =", cor(trialdata$SUBTLEX2, trialdata$Length), "\n",
  "Length~Nsyl =", cor(trialdata$Length, trialdata$Nsyl), "\n",
  "Length~nmorph =", cor(trialdata$Length, trialdata$nmorph), "\n",
  "Nsyl~nmorph =", cor(trialdata$Nsyl, trialdata$nmorph), "\n",
  "Length~OLD20 =", cor(trialdata$Length, trialdata$OLD20), "\n",
  "nmorph~OLD20 =", cor(trialdata$nmorph, trialdata$OLD20), "\n",
  "Nsyl~OLD20 =", cor(trialdata$Nsyl, trialdata$OLD20)
)
```

```
## SUBTLEX2~Length = -0.1234078
## Length~Nsyl = 0.868184
## Length~nmorph = 0.5716233
## Nsyl~nmorph = 0.5525361
## Length~OLD20 = 0.8893472
## nmorph~OLD20 = 0.5888254
## Nsyl~OLD20 = 0.8008714
```

```
# Get mean r-value for all intercorrelations
meanrcorr <- c(cor(trialdata$Nsyl, trialdata$Length),
               cor(trialdata$Nsyl, trialdata$nmorph),
               cor(trialdata$Nsyl, trialdata$OLD20),
               cor(trialdata$Length, trialdata$nmorph),
               cor(trialdata$Length, trialdata$OLD20),
               cor(trialdata$Length, trialdata$Nsyl),
               cor(trialdata$OLD20, trialdata$Length),
```

```

cor(trialdata$OLD20, trialdata$nmorph),
cor(trialdata$OLD20, trialdata$Nsyl),
cor(trialdata$nmorph, trialdata$Length),
cor(trialdata$nmorph, trialdata$OLD20),
cor(trialdata$nmorph, trialdata$Nsyl))
mean(meanrcorr)

```

```
## [1] 0.7118979
```

```

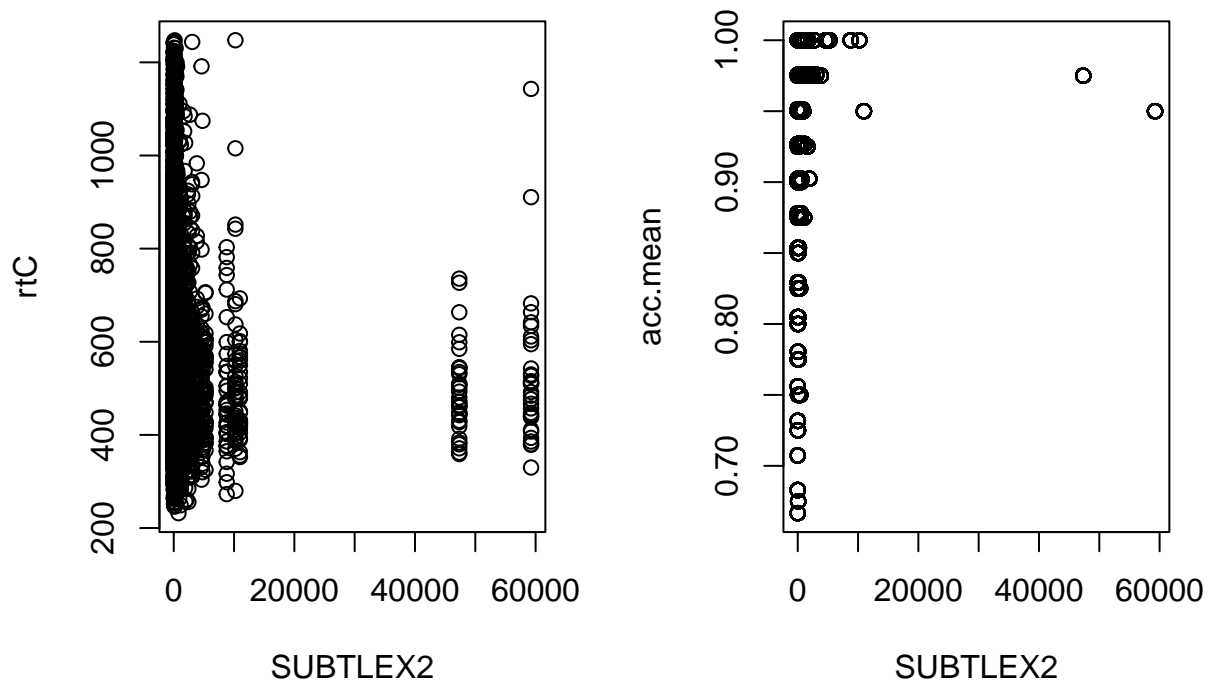
# Both length and morpheme count pretty highly correlated with syllable count;
# Keeping Nsyl has much less of a theoretical reason and might impact the
# effects of the other two predictors; exclude it from the analysis.
trialdata <- select(trialdata, ~Nsyl)

```

```

# There's only two items past the 11000 mark
par(mfrow = c(1, 2))
with(trialdata, plot(SUBTLEX2, rtC))
with(trialdata, plot(SUBTLEX2, acc.mean))

```



```

# Find out what they are
trialdata %>%
  select("spelling", "SUBTLEX2") %>%
  distinct() %>%
  arrange(desc(SUBTLEX2)) %>%
  head()

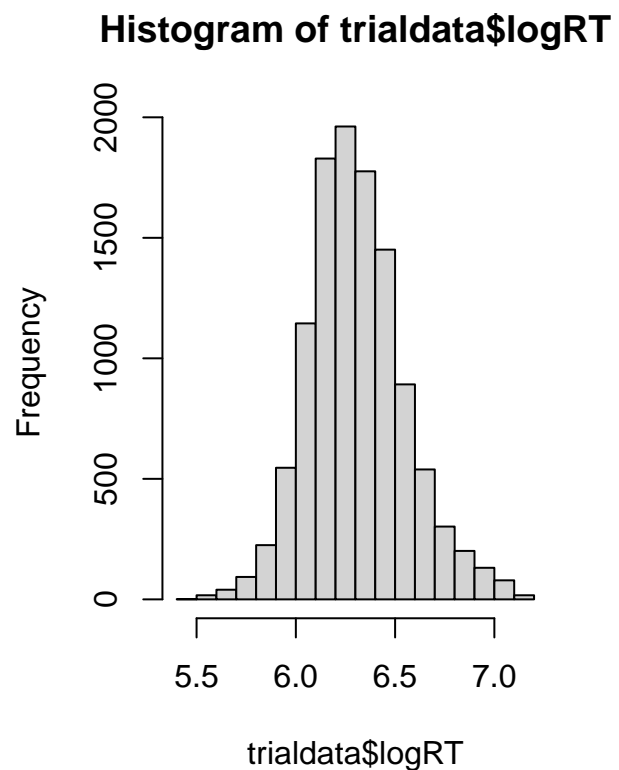
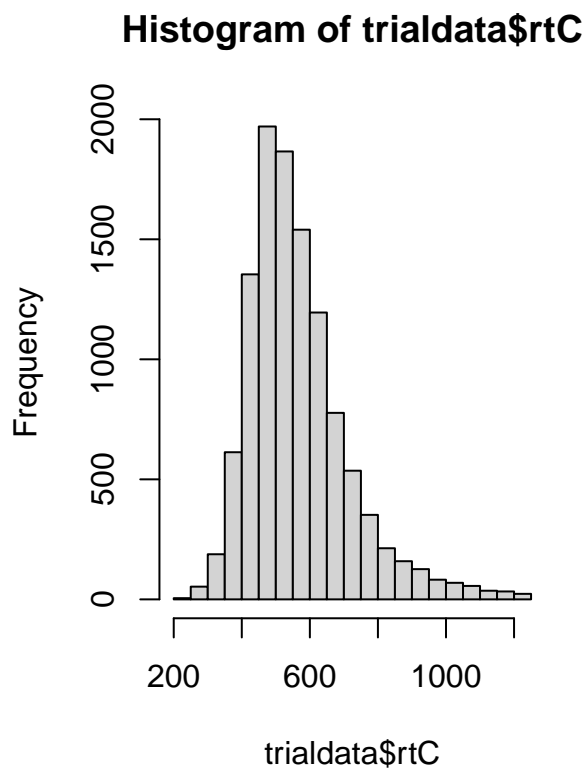
```

```
## # A tibble: 6 x 2
##   spelling SUBTLEX2
##   <chr>      <dbl>
## 1 beetje    59247
## 2 meisje    47345
## 3 liefje    10969
## 4 grapje    10226
## 5 feestje    8787
## 6 drankje    5265
```

*# "beetje" and "meisje" both have egregiously extreme freq values;
all the more reason to use Zipf-vals (See SUBTLEX-UK by Van Heuven et al., 2014)*

4. Finalise fine preprocessing

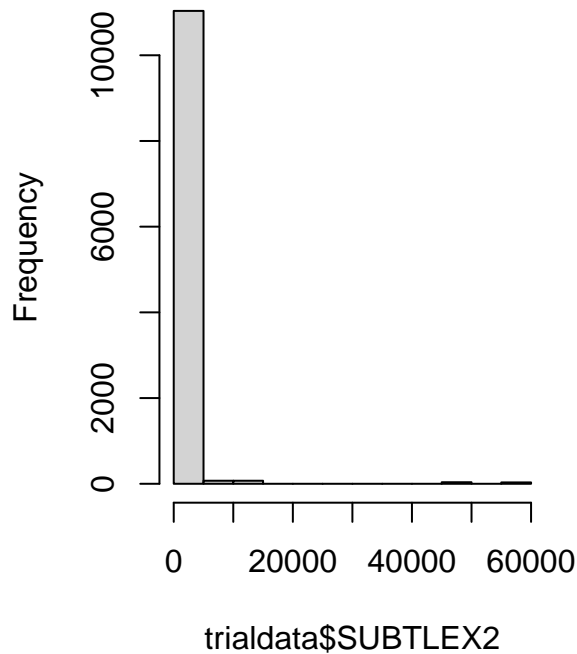
```
# Log-transform reaction times using the base logarithm (see Winter 2019)
trialdata$logRT <- log(trialdata$rtC)
par(mfrow = c(1, 2))
hist(trialdata$rtC)
hist(trialdata$logRT)
```



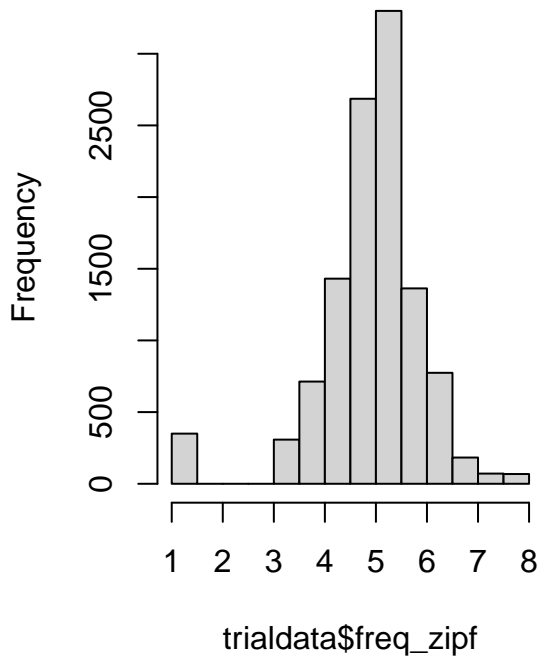
```
# Zipf-values for frequency (see Van Heuven et al., 2014)
trialdata$freq_zipf <- log10(trialdata$SUBTLEX2+0.01)+3
```

```
par(mfrow = c(1, 2))
hist(trialdata$SUBTLEX2)
hist(trialdata$freq_zipf)
```

Histogram of trialdata\$SUBTLEX2



Histogram of trialdata\$freq_zipf



```
# Standardise all the relevant predictors for an easier comparison of effect size
trialdata <- mutate(trialdata,
  zipf_z = scale(freq_zipf),
  len_z = scale(length),
  nmorph_z = scale(nmorph),
  old_z = scale(OLD20),
  conc_z = scale(Concreteness),
  aoa_z = scale(AoA),
  # Word prevalence already standardised, just center
  wp_z = scale(Word_prevalence1, scale = FALSE))

# Optional step: exclude the non-core diminutive items first,
# i.e. the ones with multiple ways to parse.
# NOTE: make sure to change contrasts below!
trialboth <- trialdata # for exploring later
trialdata <- filter(trialdata, dim_type != "both")
```

5. Descriptive Statistics

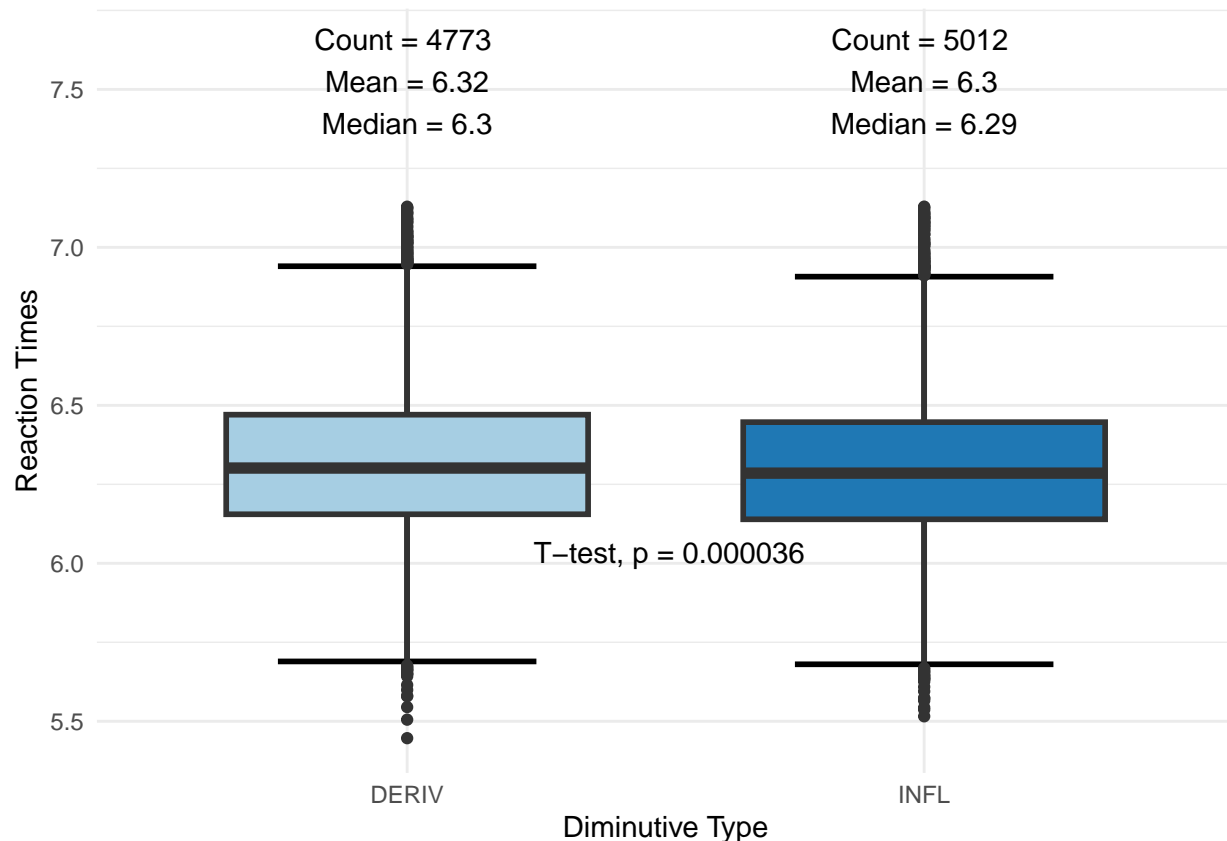
```
# Get means for the diminutives
trialdata %>% group_by(dim_type) %>%
  summarize(M = mean(rtC), SD = sd(rtC))
```

```
## # A tibble: 2 x 3
##   dim_type      M      SD
##   <fct>      <dbl> <dbl>
## 1 deriv      574.  150.
## 2 infl      562.  147.
```

```
trialdata %>% group_by(dim_type) %>%
  summarize(M = mean(logRT), SD = sd(logRT))
```

```
## # A tibble: 2 x 3
##   dim_type      M      SD
##   <fct>      <dbl> <dbl>
## 1 deriv      6.32 0.245
## 2 infl      6.30 0.243
```

```
# Make a plot with all the relevant statistics, throw in a t-test as well
trialdata %>% ggplot(aes(x = dim_type, y = logRT, fill = dim_type)) +
  stat_boxplot(geom = 'errorbar', linewidth=1, width=.5) +
  geom_boxplot(lwd=1, width=.7, show.legend = FALSE) + theme_minimal() +
  labs(
    x = "Diminutive Type",
    y = "Reaction Times",
  ) +
  scale_x_discrete(labels=c('DERIV', 'INFL')) +
  stat_summary(fun.data = get_box_stats, geom = "text", hjust = 0.5, vjust = 0.9) +
  scale_fill_brewer(palette = "Paired") +
  stat_compare_means(method="t.test", label.y = 6.0, label.x = 1.35)
```

```
# Save the plot for later
ggsave("../figures/dim_box.png", width = 6, height = 4)
```

6. Inferential Statistics

Here, we will finally handle some tests that will let us draw conclusions from the sample about the population at large. We start with assigning contrasts, then run a simple t-test and then move on to modelling.

6.1. Contrasts and t-tests

The next two code chunks handle the contrast coding; they are mutually exclusive depending on the decision to include observations with “both” as a value for `dim_type`. In order to switch between them, go to the chunk options and specify `eval=FALSE` to stop the script from running the code and `include=FALSE` to prevent the code from being included in the final knitted document.

The motivation for sum-coding between “deriv” and “infl” is taken from Winter 2019, where it is argued that sum-coding is better suited for mixed-effects models with interactions and random effects; additionally, sum-coding is argued to make the coefficients easier to interpret.

```
# Sum-coding for a purely deriv/infl dataset (see above)
contrasts(trialdata$dim_type) <- contr.sum(2)
contrasts(trialdata$dim_type)
```

```
##      [,1]
```

```
## deriv    1
## infl    -1
```

```
t.test(rtC ~ dim_type, data = trialdata)
```

```
##
## Welch Two Sample t-test
##
## data:  rtC by dim_type
## t = 3.9364, df = 9731.1, p-value = 0.00008329
## alternative hypothesis: true difference in means between group deriv and group infl is not equal to 0
## 95 percent confidence interval:
##    5.935466 17.710467
## sample estimates:
## mean in group deriv  mean in group infl
##           574.2418           562.4188
```

```
t.test(logRT ~ dim_type, data = trialdata)
```

```
##
## Welch Two Sample t-test
##
## data:  logRT by dim_type
## t = 4.1361, df = 9751.9, p-value = 0.00003562
## alternative hypothesis: true difference in means between group deriv and group infl is not equal to 0
## 95 percent confidence interval:
##    0.01073313 0.03007119
## sample estimates:
## mean in group deriv  mean in group infl
##           6.322096           6.301694
```

```
cohen.d(rtC ~ dim_type, data = trialdata)
```

```
##
## Cohen's d
##
## d estimate: 0.07965868 (negligible)
## 95 percent confidence interval:
##    lower    upper
## 0.03999865 0.11931871
```

```
cohen.d(logRT ~ dim_type, data = trialdata)
```

```
##
## Cohen's d
##
## d estimate: 0.08366724 (negligible)
## 95 percent confidence interval:
##    lower    upper
## 0.04400559 0.12332889
```

6.2. Modelling

The formula for the experimental model closely follows the formula reported in the DLP2 paper, with the addition of two predictors:

- a. `dim_type`, a factor with values “deriv” and “infl” (possibly “both” for the expanded dataset)
- b. `nmorph`, a numeric with values reflecting the (observable and theoretically motivated) morpheme count in the structure of each wordform: assuming full decomposition, every word is broken down to the most primitive units (= morphemes), so it logically follows that the more morphemes a wordform consists of, the more there is to break down and recompose, and the more time it should take to recognize a word.

Note the absence of two predictors reported for the DLP2 model, namely `Nsyl` and `Length`. The justification for both is the high degree of correlation between `Length`, `Nsyl`, `nmorph` and `OLD20` as explanatory variables that all in some ways have to deal with length. `Nsyl`, the number of syllables, was excluded first in favour of the more theoretically relevant `nmorph`. Dropping length was a tough decision that was ultimately made after some stepwise modelling to establish which of the two factors, length or `OLD20`, would contribute more to explaining the variance in the dataset.

The final formula of the model is therefore this (see “`mod_full`” below):

RT* ~ Diminutive TypeFrequency + Morpheme count + OLD20 ratings + Concreteness + Age of acquisition + Word prevalence + Varying intercepts by participant and by item

```
# Run the base model with only frequency and random intercepts
# Mention including the participant and item intercepts as the
# motivation to satisfy the independence assumption (Winter 2019, Ch.14)
mod_base <- lmer(logRT ~ zipf_z +
                 (1|participant) +
                 (1|item), data = trialdata, REML = TRUE)
summary(mod_base) # Make sure the frequency findings aren't wildly off
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: logRT ~ zipf_z + (1 | participant) + (1 | item)
## Data: trialdata
##
## REML criterion at convergence: -4382.8
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.0186 -0.6652 -0.1257  0.5158  5.3901
##
## Random effects:
## Groups      Name                Variance Std.Dev.
## item        (Intercept)  0.002922  0.05405
## participant (Intercept)  0.020267  0.14236
## Residual                    0.034708  0.18630
## Number of obs: 9785, groups: item, 270; participant, 81
##
## Fixed effects:
##              Estimate Std. Error    df t value      Pr(>|t|)
## (Intercept)   6.311948   0.016270 86.832963  388.0 <0.0000000000000002 ***
## zipf_z        -0.049475   0.003584 271.628542 -13.8 <0.0000000000000002 ***
```

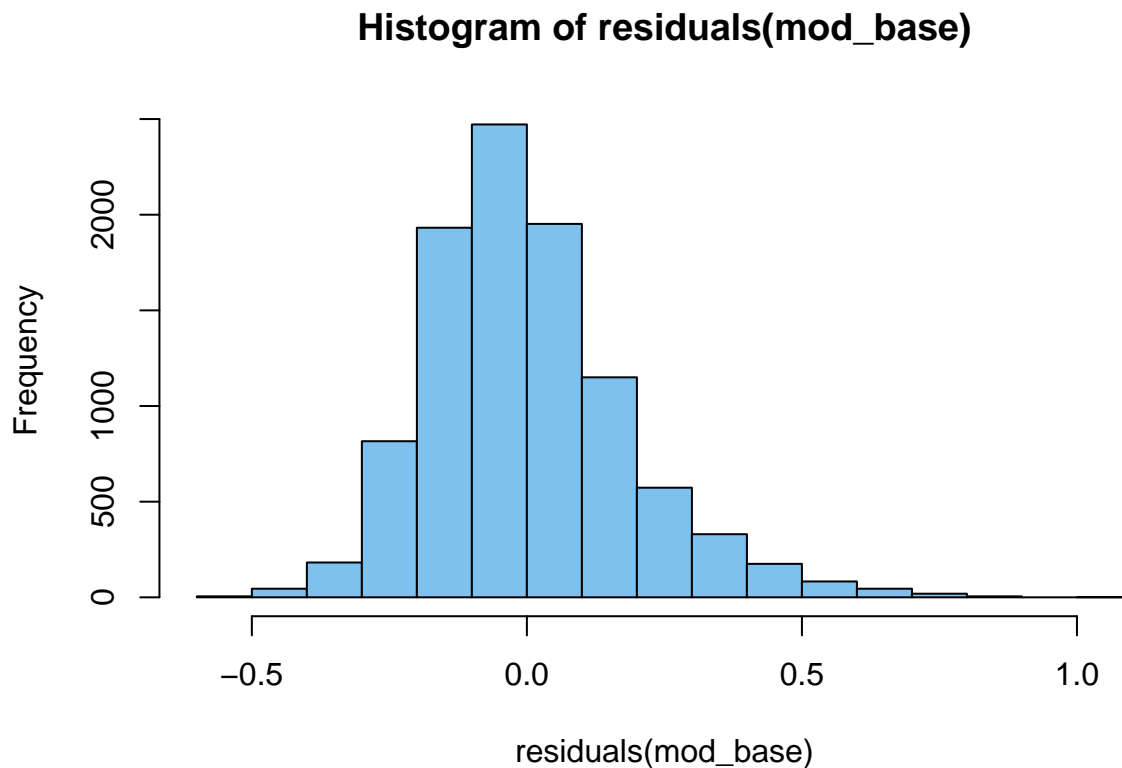
```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##      (Intr)
## zipf_z 0.016
```

```
r.squaredGLMM(mod_base)
```

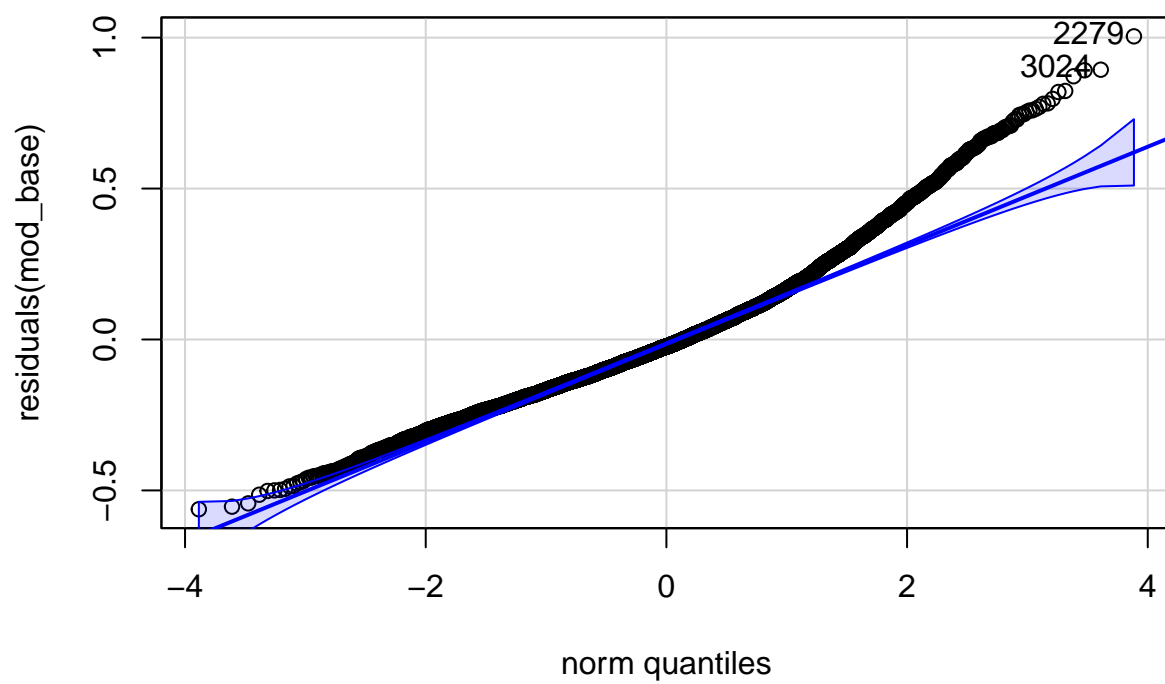
```
## Warning: 'r.squaredGLMM' now calculates a revised statistic. See the help page.
```

```
##           R2m      R2c
## [1,] 0.04335228 0.426511
```

```
hist(residuals(mod_base), col = 'skyblue2') # Plot 1, histogram
```

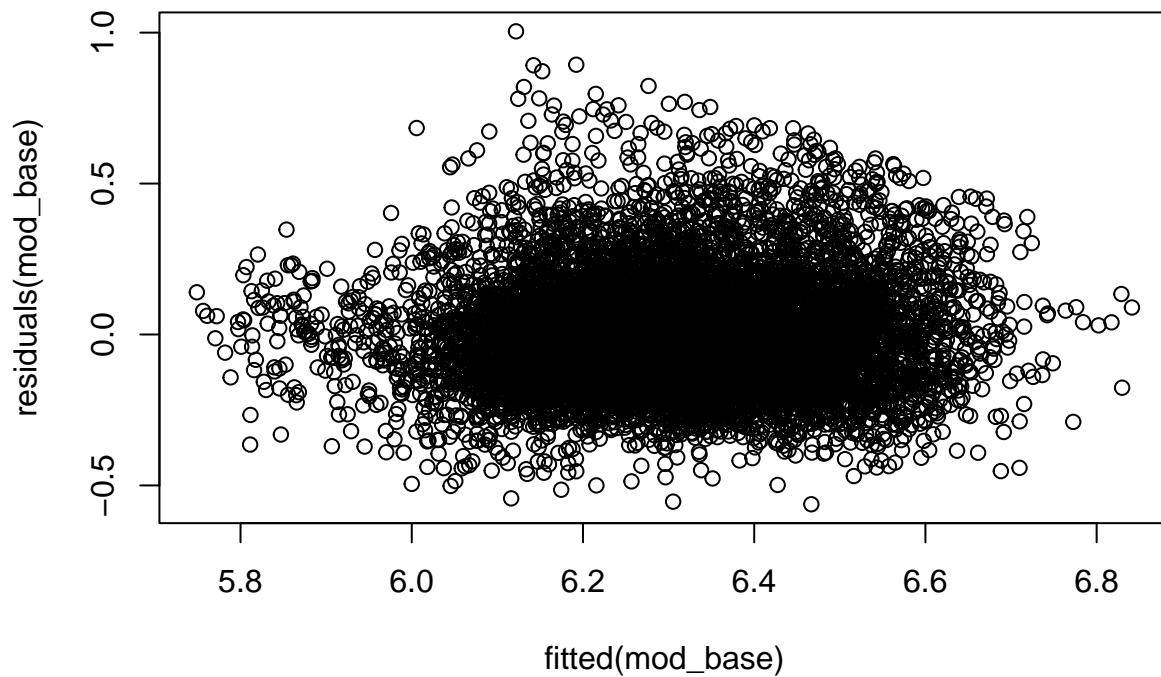


```
qqPlot(residuals(mod_base)) # Plot 2, Q-Q plot
```



```
## [1] 2279 3024
```

```
plot(fitted(mod_base), residuals(mod_base)) # Plot 3, residual plot
```



```
# Run the full model
mod_full <- lmer(logRT ~
  dim_type*zipf_z +
  nmorph_z +
  old_z +
  conc_z +
  aoa_z +
  wp_z +
  (1|participant) +
  (1|item), data = trialdata)
summary(mod_full)

## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: logRT ~ dim_type * zipf_z + nmorph_z + old_z + conc_z + aoa_z +
##      wp_z + (1 | participant) + (1 | item)
##      Data: trialdata
##
## REML criterion at convergence: -4416.3
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.2041 -0.6637 -0.1245  0.5150  5.3553
##
## Random effects:
##      Groups      Name      Variance Std.Dev.
```

```

## item (Intercept) 0.001819 0.04265
## participant (Intercept) 0.020229 0.14223
## Residual 0.034707 0.18630
## Number of obs: 9785, groups: item, 270; participant, 81
##
## Fixed effects:
## Estimate Std. Error df t value Pr(>|t|)
## (Intercept) 6.310523 0.016134 84.355623 391.133 < 0.0000000000000002
## dim_type1 -0.005078 0.005868 253.985383 -0.865 0.387658
## zipf_z -0.023645 0.004318 262.209924 -5.476 0.0000001017
## nmorph_z 0.003501 0.006833 253.955012 0.512 0.608858
## old_z 0.019665 0.005019 252.299591 3.918 0.000115
## conc_z 0.001979 0.003730 254.785559 0.531 0.596199
## aoa_z 0.017054 0.004413 252.592626 3.865 0.000141
## wp_z -0.047086 0.008497 262.656860 -5.542 0.0000000728
## dim_type1:zipf_z 0.006822 0.003124 270.076236 2.184 0.029825
##
## (Intercept) ***
## dim_type1
## zipf_z ***
## nmorph_z
## old_z ***
## conc_z
## aoa_z ***
## wp_z ***
## dim_type1:zipf_z *
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
## (Intr) dm_ty1 zipf_z nmorph_ old_z conc_z aoa_z wp_z
## dim_type1 -0.011
## zipf_z 0.006 -0.220
## nmorph_z 0.019 -0.796 0.221
## old_z -0.022 0.492 0.145 -0.665
## conc_z 0.004 0.100 0.305 0.040 -0.017
## aoa_z 0.007 -0.096 0.232 0.006 -0.194 0.319
## wp_z 0.012 0.128 -0.455 -0.118 -0.163 -0.181 0.289
## dm_ty1:zp_ 0.007 0.118 -0.112 -0.062 0.026 0.108 0.035 0.072

```

```
Anova(mod_full)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
```

```
##
```

```
## Response: logRT
```

```

## Chisq Df Pr(>Chisq)
## dim_type 1.2766 1 0.2585384
## zipf_z 27.7154 1 0.00000014054 ***
## nmorph_z 0.2625 1 0.6084128
## old_z 15.3514 1 0.00008925600 ***
## conc_z 0.2815 1 0.5957365
## aoa_z 14.9372 1 0.0001111 ***
## wp_z 30.7096 1 0.00000002997 ***
## dim_type:zipf_z 4.7697 1 0.0289649 *

```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

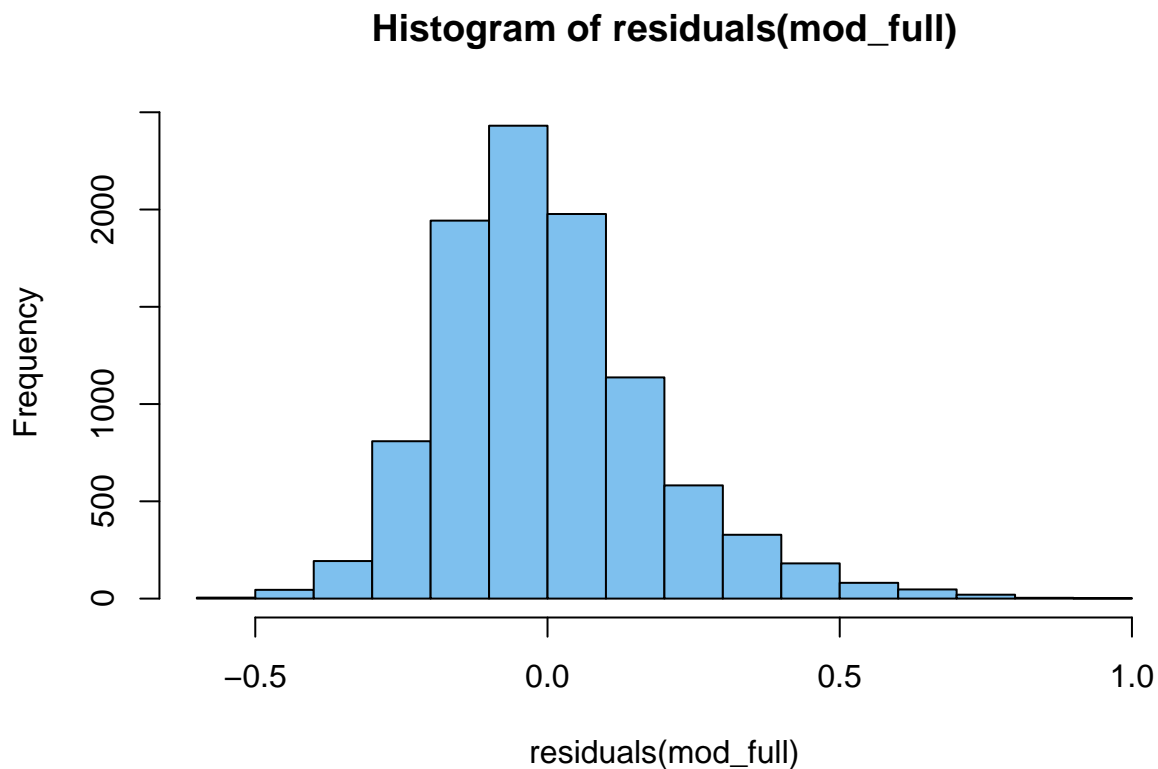
```
r.squaredGLMM(mod_full) # Fixed effects: 6.1%; Fixed+Random: 44%
```

```
##           R2m           R2c
## [1,] 0.06160806 0.4261597
```

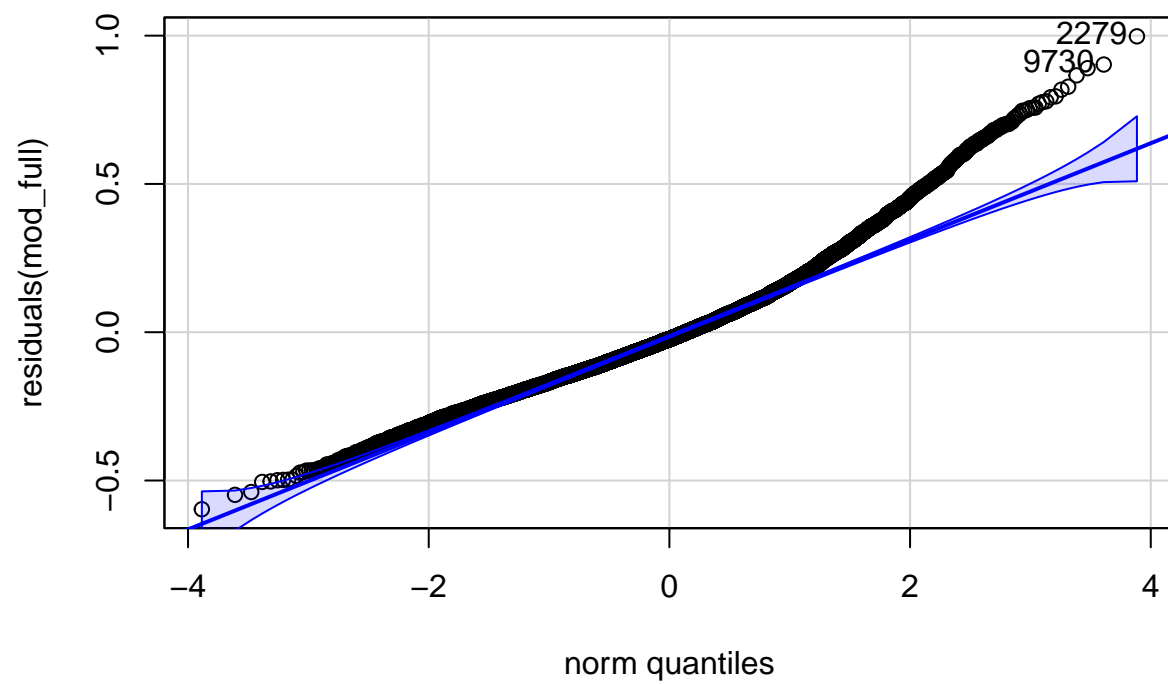
```
vif(mod_full) # Get variance inflation factors to check for collinearity
```

```
##           dim_type           zipf_z           nmorph_z           old_z           conc_z
##           3.258718           2.011141           4.942687           2.581457           1.408611
##           aoa_z           wp_z dim_type:zipf_z
##           1.850146           1.710761           1.048726
```

```
# Plots not ideal, but not as grossly off as before
hist(residuals(mod_full), col = 'skyblue2') # Plot 1, histogram
```

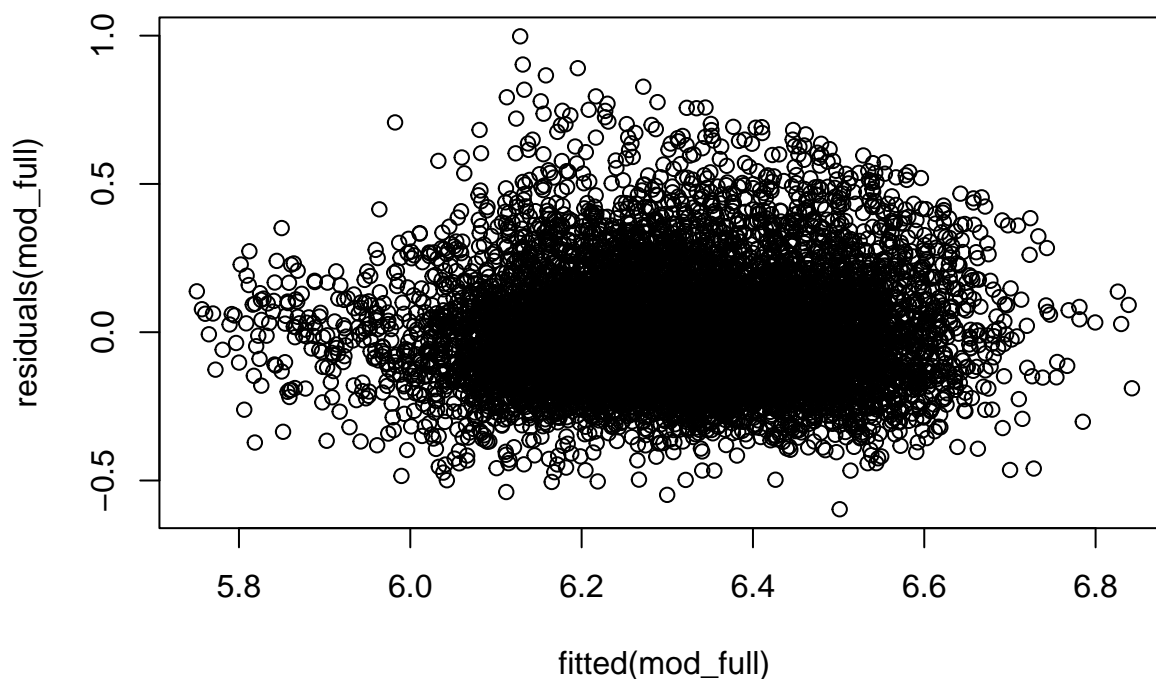


```
qqPlot(residuals(mod_full)) # Plot 2, Q-Q plot
```

```
## [1] 2279 9730
```

```
plot(fitted(mod_full), residuals(mod_full)) # Plot 3, residual plot
```



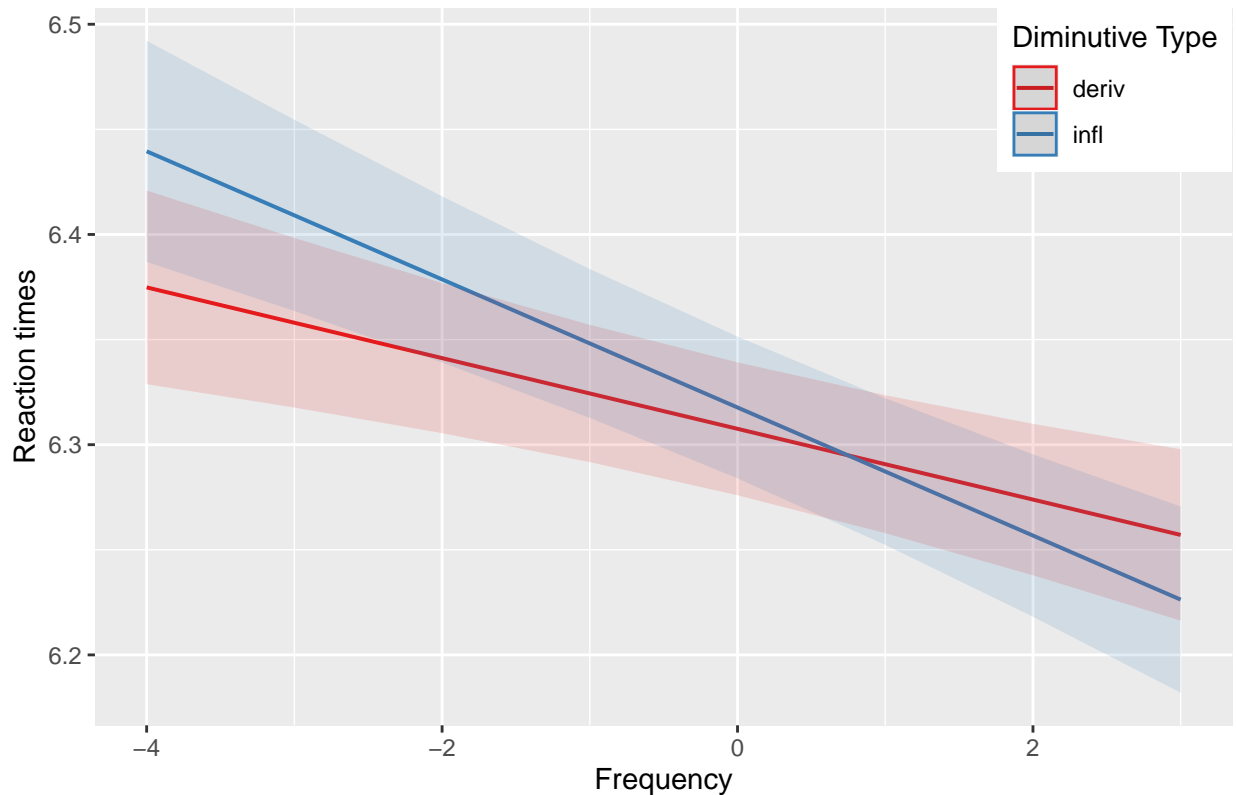
```
fixef(mod_full)
```

```
##      (Intercept)      dim_type1      zipf_z      nmorph_z
##      6.310523358    -0.005077955   -0.023645292    0.003500633
##      old_z      conc_z      aoa_z      wp_z
##      0.019664597    0.001979143    0.017053829   -0.047085511
## dim_type1:zipf_z
##      0.006821796
```

```
table_fixed <- as.data.frame(round(summary(mod_full)$coefficients, 4))
print(table_fixed)
```

```
##      Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)      6.3105      0.0161  84.3556 391.1326  0.0000
## dim_type1      -0.0051      0.0059 253.9854  -0.8654  0.3877
## zipf_z      -0.0236      0.0043 262.2099  -5.4762  0.0000
## nmorph_z      0.0035      0.0068 253.9550   0.5123  0.6089
## old_z      0.0197      0.0050 252.2996   3.9181  0.0001
## conc_z      0.0020      0.0037 254.7856   0.5305  0.5962
## aoa_z      0.0171      0.0044 252.5926   3.8649  0.0001
## wp_z      -0.0471      0.0085 262.6569  -5.5416  0.0000
## dim_type1:zipf_z  0.0068      0.0031 270.0762   2.1840  0.0298
```

```
# Include an interaction plot for easier interpretability
plot_model(mod_full, type = "pred",
           terms = c("zipf_z", "dim_type"),
           title = "",
           legend.title = "Diminutive Type") +
theme_minimal() +
legend_style(inside=TRUE, pos="top right") +
labs(x = "Frequency", y = "Reaction times")
```



```
# And save it
ggsave("../figures/mod_int.png", width = 6, height = 4)
```

6.3. An exploratory look into the “both” group

The motivation for Helmert-coding between “deriv”, “infl”, and “both” is simple: for wordforms with either “deriv” or “infl”, a single decomposition pipeline is proposed. Assuming structural differences, recognizing either is the same type of operation being performed in a different location in the structure. Compare with “both”, where the decomposition apparatus presumably pursues both leads at once; therefore, this should be reflected in the coding as such:

- First, compare the differences between deriv and infl (either x or y)
- Then, compare their average RTs to both (x and y at the same time)