05 CSI online typing APPENDIX: Plotting and analysis with manual classification

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Load packages

```
library(dplyr)
```

```
##
## Attaching package: 'dplyr'
```

```
## The following objects are masked from 'package:stats':
##
##     filter, lag
```

```
## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```
library(tidyr)
library(lme4)
```

```
## Loading required package: Matrix
```

```
##
## Attaching package: 'Matrix'
```

```
## The following objects are masked from 'package:tidyr':
##
##     expand, pack, unpack
```

```
library(lmerTest)
```

```
##
## Attaching package: 'lmerTest'
## The following object is masked from 'package:lme4':
##
##     lmer
```

```
## The following object is masked from 'package:stats':
##
##     step
```

```
library(Rmisc)
```

```
## Loading required package: lattice
```

```
## Loading required package: plyr
```

```
## ------------------------------------------------------------------------------
```

```
## You have loaded plyr after dplyr - this is likely to cause problems.
## If you need functions from both plyr and dplyr, please load plyr first, then dpl
yr:
## library(plyr); library(dplyr)
```

```
## ------------------------------------------------------------------------------
```

```
##
## Attaching package: 'plyr'
```

```
## The following objects are masked from 'package:dplyr':
##
##     arrange, count, desc, failwith, id, mutate, rename, summarise,
##     summarize
```

```
library(Cairo)
#library(strengejacke)
library(ggplot2)
library(sjPlot)

options(scipen=999)

rm(list = ls())
options( "encoding" = "UTF-8" )
set.seed(99)
```

Load and preprocess data

```
# input
#input = "data_long_final.csv"
input = "data_long_anonymous.csv"
classification_type = "manual" # select "manual" or "automatic"

# load data
df <- read.csv(here::here("data", input))
```

Check amount of participants and trials

```
# no. of participants:
length(unique(df$subject))
```

```
## [1] 30
```

```
# no. of trials is 160 per participant?
nrow(df) == 160 * length(unique(df$subject))
```

```
## [1] TRUE
```

Factorize columns

```
# factorize columns
is.numeric(df$timing.01)
```

```
## [1] TRUE
```

```
df$PosOr <- as.factor(df$PosOr)
df$subject <- as.factor(df$subject)
```

Select correct classification column

```
if(classification_type == "automatic") {
  df$answercode <- df$answer_auto_jaro
  df$correct <- df$correct_auto_jaro
} else if(classification_type == "manual") {
  df$answercode <- df$answercode
  df$correct <- df$correct_manual
} else {
  print("Select a correct type!")
}
```

```
as.data.frame(table(df$correct, df$answercode)) %>% filter(Freq != 0)
```

```
##   Var1                  Var2 Freq
## 1    1          almostcorrect  772
## 2    0  backspace_space_enter   25
## 3    1                correct 3520
## 4    0 first_letter_incorrect  192
## 5    0                   isna  153
## 6    0      semantic_relation  115
## 7    0            shift_start   10
## 8    0        unrelated_other   13
```

```
as.data.frame(table(df$correct, df$answercode)) %>% filter(Freq != 0) %>%
  mutate(Percentage = case_when(Var1 == 1 ~ Freq/sum(df$correct == 1),
                                Var1 == 0 ~ Freq/sum(df$correct == 0)))
```

```
##   Var1                  Var2 Freq Percentage
## 1    1          almostcorrect  772 0.17986952
## 2    0  backspace_space_enter   25 0.04921260
## 3    1                correct 3520 0.82013048
## 4    0 first_letter_incorrect  192 0.37795276
## 5    0                   isna  153 0.30118110
## 6    0      semantic_relation  115 0.22637795
## 7    0            shift_start   10 0.01968504
## 8    0        unrelated_other   13 0.02559055
```

```
# raw
table(df$correct)
```

```
##
##    0    1
##  508 4292
```

```
# in percent
round(table(df$correct)/nrow(df)*100,2)
```

```
##
##     0     1
## 10.58 89.42
```

```
## How many correct/incorrect non-filler trials?
table(df$correct[df$category != "Filler"])
```

```
##
##    0    1
##  413 3187
```

Show amount of incorrect trials per ordinal position (excluding fillers):

```
## How many correct/incorrect non-filler trials per ordinal position?
table(df$PosOr[df$category != "Filler" & df$correct == 0],
      df$correct[df$category != "Filler" & df$correct == 0])
```

```
##
##       0
##   1 73
##   2 84
##   3 79
##   4 83
##   5 94
```

Drop incorrect trials:

```
df <- df %>% filter(df$correct == 1)
```

Plotting

Make plots suitable for APA format, font sizes can be adjusted

```
apatheme <- theme_bw()+
  theme(plot.title=element_text(family="Arial",size=22,hjust = .5),
        panel.grid.major=element_blank(), panel.grid.minor=element_blank(),
        panel.border=element_blank(),axis.line=element_line(),
        text=element_text(family="Arial",size=16))
```

Descriptives

```
(means_final<- df %>%
   filter(category != "Filler") %>%
   Rmisc::summarySEwithin(.,"timing.01",idvar = "subject",
                          withinvars = "PosOr", na.rm = T))
```

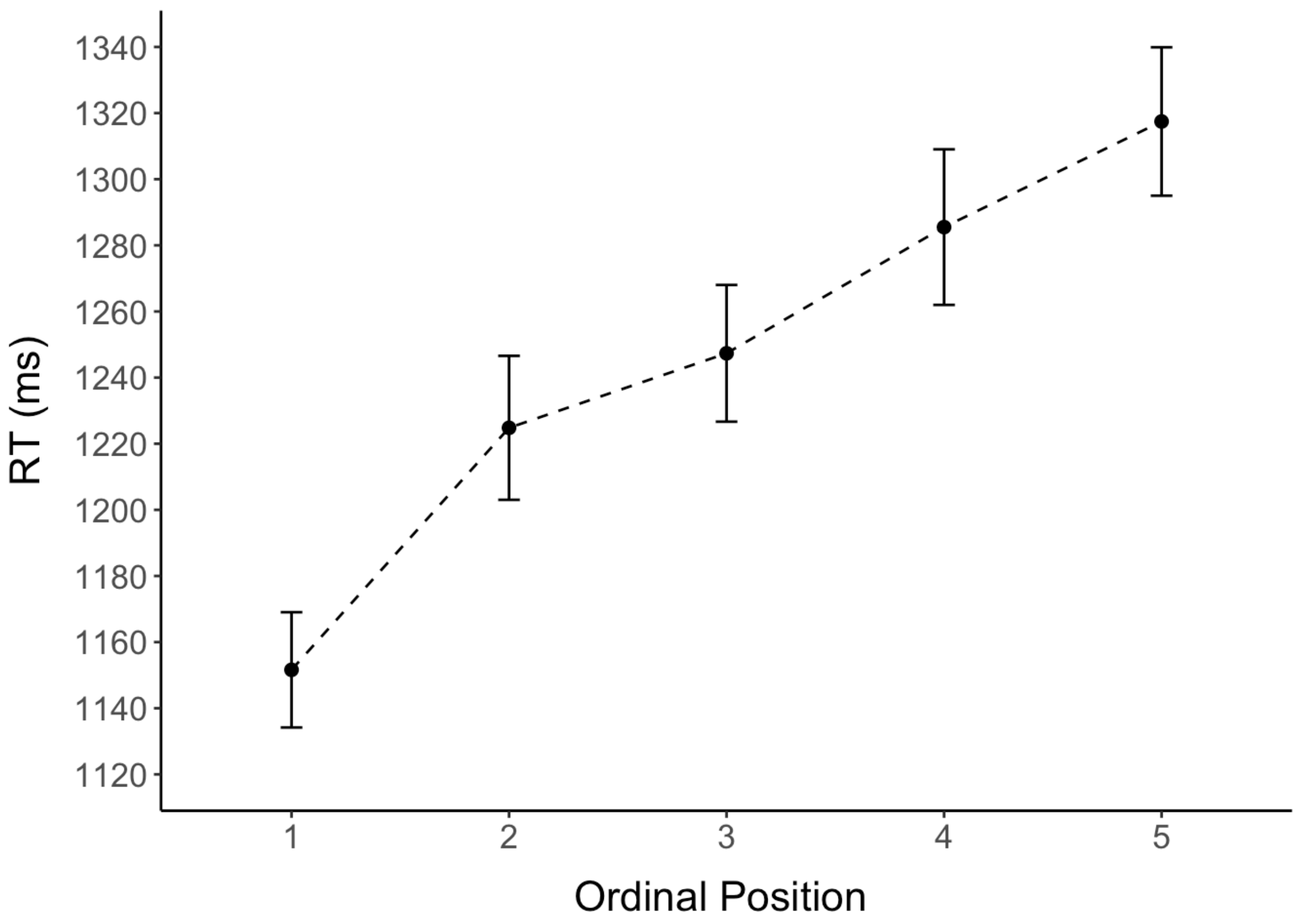
```
##   PosOr   N timing.01       sd       se       ci
## 1     1 647  1151.609 443.3882 17.43139 34.22902
## 2     2 636  1224.805 549.0747 21.77223 42.75427
## 3     3 641  1247.348 523.4455 20.67485 40.59875
## 4     4 637  1285.511 593.8831 23.53050 46.20687
## 5     5 626  1317.456 561.4240 22.43902 44.06499
```

```
# Export as word file
library(flextable)
huxt_word <- huxtable::huxtable(means_final)
huxt_word <- huxtable::set_number_format(huxt_word, round(2))
huxtable::quick_docx(huxt_word,
                     file = here::here("results", "tables",
                                       "CSI_online_typing__APPENDIX_RT_summary.docx
"),
                                       open = FALSE)
```

RTs by ordinal position

Line graph (only correct trials, without fillers)

```
(plot_rt <- means_final %>%
    ggplot(., aes(x=PosOr, y=timing.01)) +
    geom_point(size = 2)+
    stat_summary(fun=mean,  geom="line", size = 0.5, group = 1, linetype = "dashed"
) +
    geom_errorbar(aes(ymin=timing.01-se, ymax=timing.01+se), width =.1) +
    apatheme+
    scale_y_continuous(limits = c(1120, 1340), breaks =seq(1120,1340, by = 20)) +
                       #breaks = c(1100, 1150, 1200, 1250, 1300, 1350)) +
    labs(x="Ordinal Position ",y ="RT (ms)") +
    theme(
    axis.title.y = element_text(margin = margin(0,10,0,0)),
    axis.title.x = element_text(margin = margin(10,0,0,0))))
```

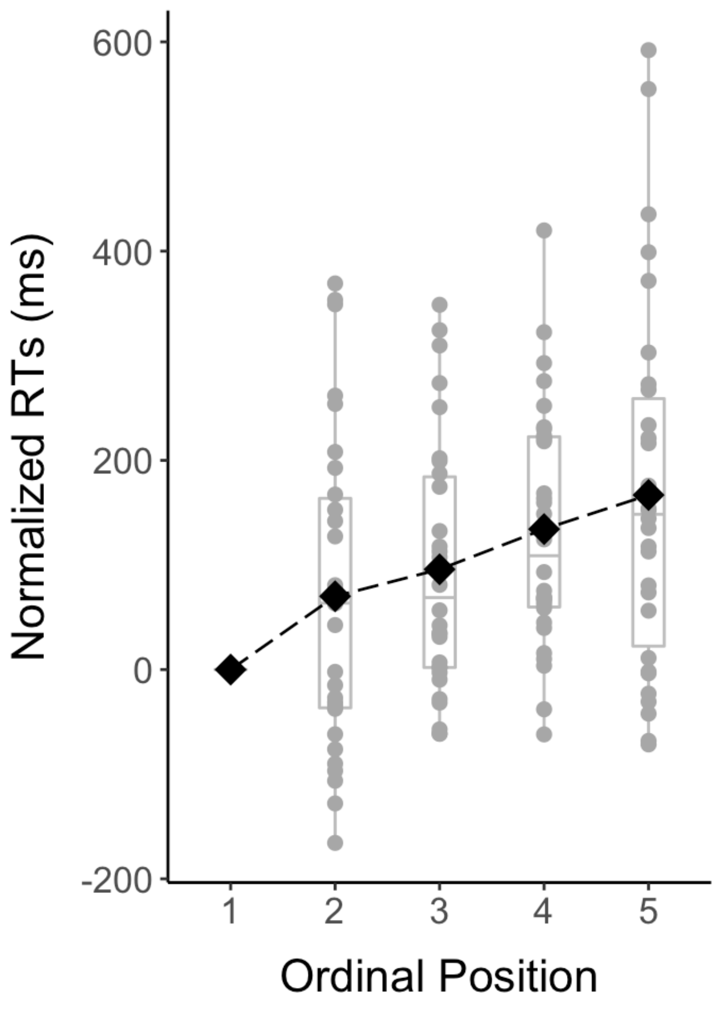


Normalized boxplot

```
means_subject <- df %>%
   filter(category != "Filler") %>%
   summarySEwithin(.,"timing.01",withinvars = c("subject","PosOr"))
(means_subject <- means_subject %>%
  group_by(subject) %>%
  dplyr::mutate(timing.01_norm = timing.01 - first(timing.01)))
```

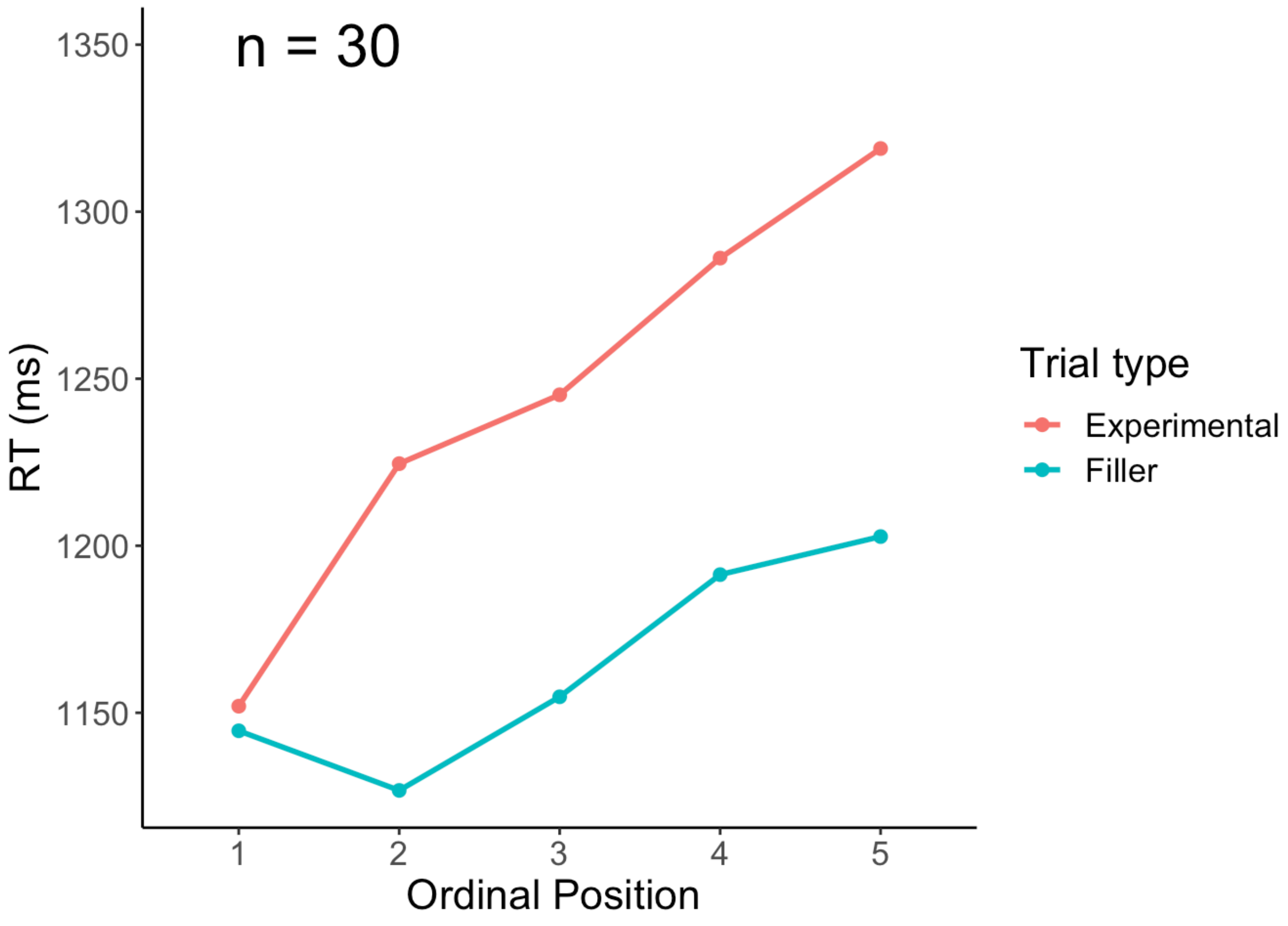
```
## # A tibble: 150 x 8
## # Groups:   subject [30]
##    subject PosOr     N timing.01    sd    se    ci timing.01_norm
##    <fct>   <fct> <dbl>     <dbl> <dbl> <dbl> <dbl>          <dbl>
##  1 1       1        24     1127.  250.  51.1  106.             0
##  2 1       2        22     1269.  325.  69.3  144.           142.
##  3 1       3        22     1240.  277.  59.1  123.           113.
##  4 1       4        24     1348.  491. 100.   207.           221.
##  5 1       5        24     1526.  586. 120.   247.           399.
##  6 2       1        23     1030   332.  69.2  144.             0
##  7 2       2        22     1073.  478. 102.   212.            42.5
##  8 2       3        23     1087.  470.  97.9  203.            56.7
##  9 2       4        21     1098.  538. 117.   245.            68.3
## 10 2       5        24      962.  260.  53.0  110.           -68.1
## # … with 140 more rows
```

```
(boxplot <-
  ggplot() +

  ## boxplot
  geom_boxplot(data=means_subject, aes(x = PosOr,y =timing.01_norm),
               colour = "grey", width = 0.3,fatten = 1)+
  ### individual means
  geom_jitter(data=means_subject, aes(x = PosOr,y =timing.01_norm),
              position = position_dodge(0.6),
              shape=19,color = "dark grey", size=2)+
  ### group means
  stat_summary(data=means_subject, aes(x = PosOr,y =timing.01_norm),
               fun=mean, geom="point",colour = "black", shape=18, size=5)+
  ### line
  stat_summary(data=means_subject, aes(x = PosOr,y =timing.01_norm),
               fun=mean, geom="line",colour = "black", linetype = "longdash", group
= 1)+

  ## other stuff
  #scale_y_continuous(breaks = seq(600, 1300, by = 50))+
  labs(x="Ordinal Position",y ="Normalized RTs (ms)")+
  apatheme +
  theme(
    axis.title.y = element_text(margin = margin(0,10,0,0)),
    axis.title.x = element_text(margin = margin(10,0,0,0))) +
  coord_equal(ratio = 1/100))
```



CONTROL: with fillers

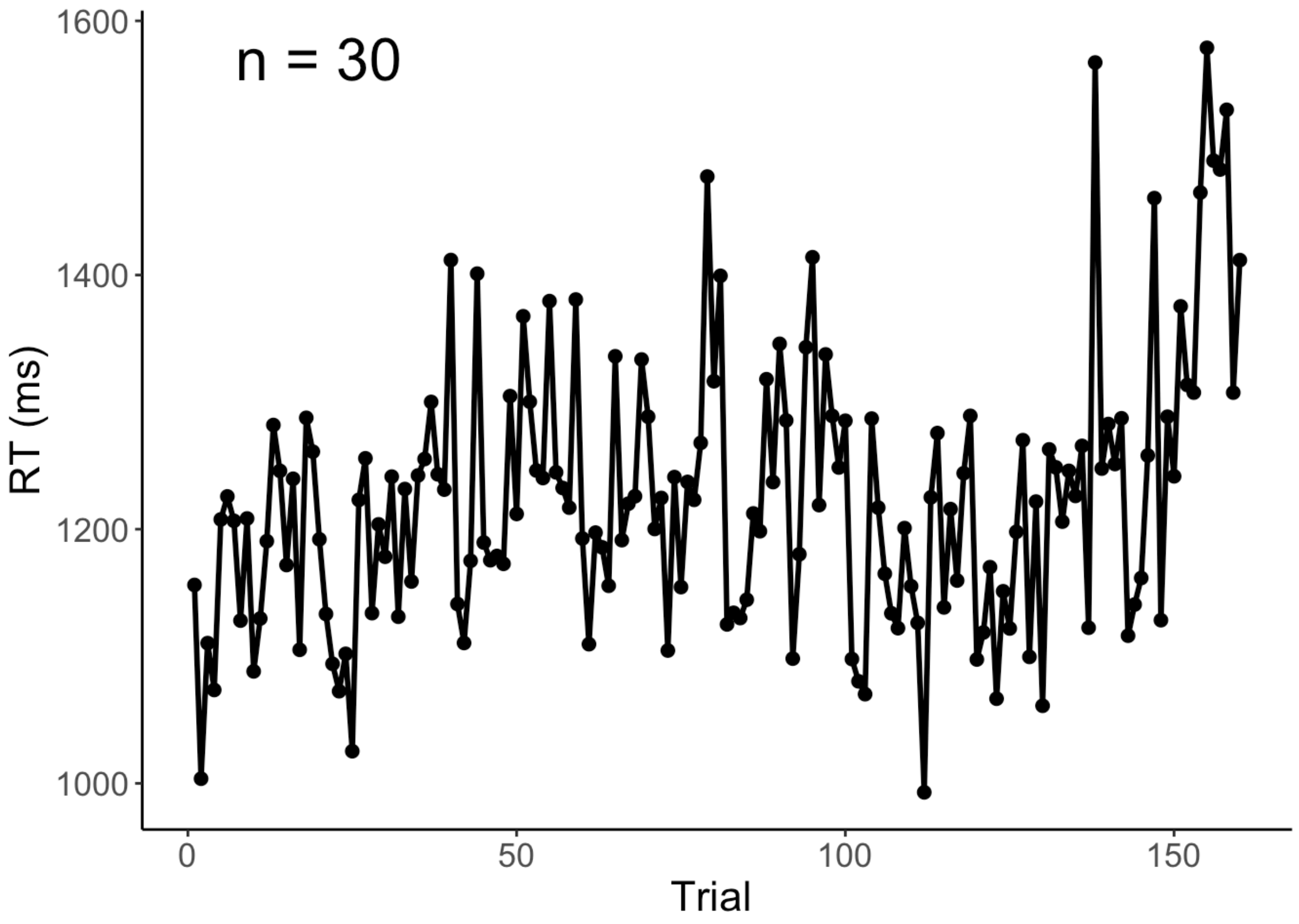
```
(plot_rt_fillers <- df %>%
    mutate(kind = case_when(category == "Filler" ~"Filler",
                         category != "Filler" ~"Experimental")) %>%
    ggplot(., aes(x=PosOr, y=timing.01, group=kind, color=kind)) +
    stat_summary(fun=mean,  geom="point", size = 2)+
    stat_summary(fun=mean,  geom="line", size = 1) +
    apatheme+
    labs(x="Ordinal Position ",y ="RT (ms)", color = "Trial type")+
  annotate(geom="text", x=1.5, y=1350, label="n = 30",
           color="black", size = 8))
```



Control: Plot RTs accross the experiment

All correct trials (including fillers)

```
(plot_RTs_all <- ggplot(data=df, aes(x=trial, y=timing.01)) +
  stat_summary(fun=mean,  geom="point", size = 2)+
  stat_summary(fun=mean,  geom="line", size = 1) +
  apatheme+
  labs(x="Trial ",y ="RT (ms)")+
  annotate(geom="text", x=20, y=1570, label="n = 30",
           color="black", size = 8))
```



Check distribution of data

Are the data normally distributed or does a gamma distribution fit the data better?

Subset data to correct trials only and exclude fillers

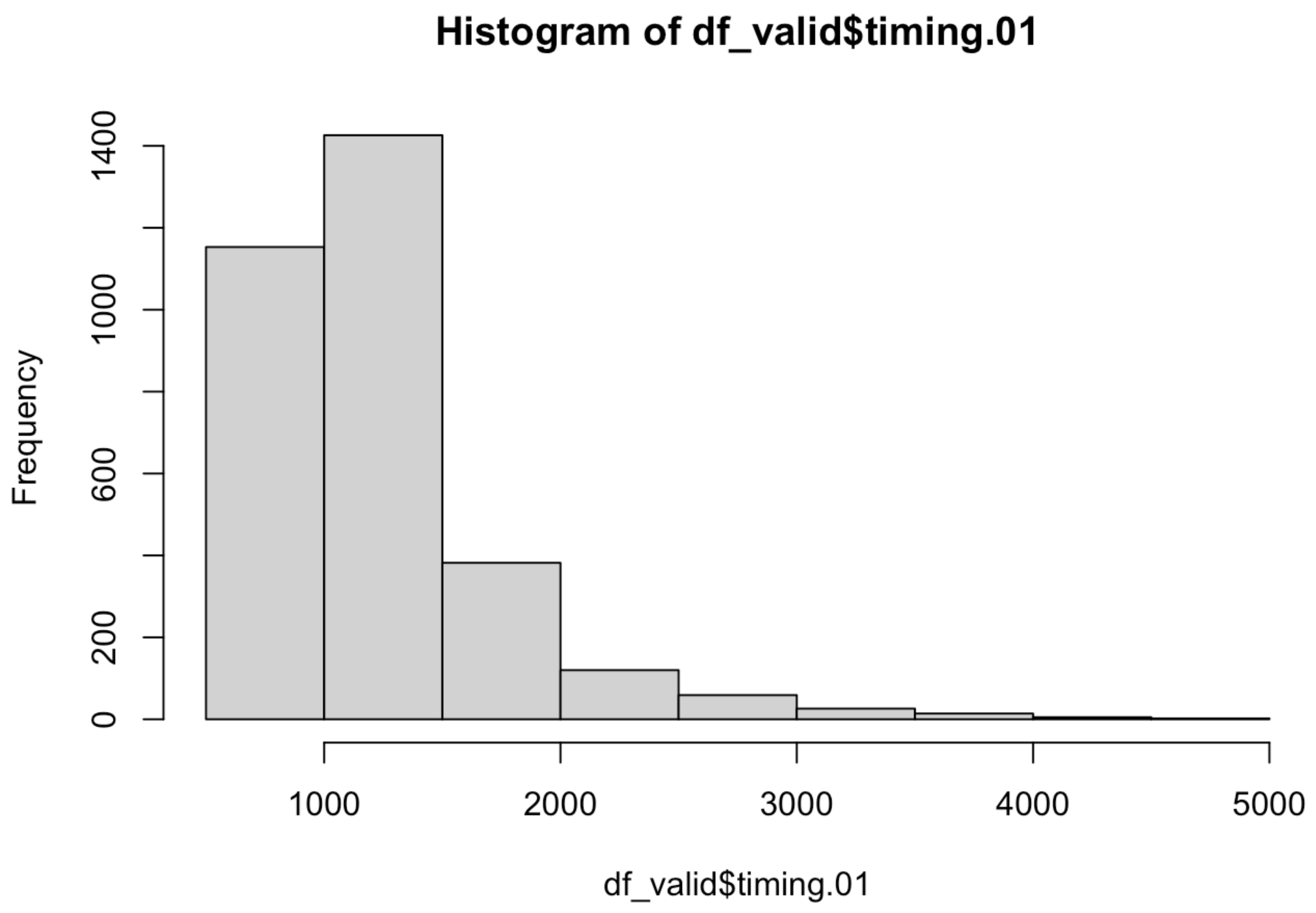
```
df_valid <- df %>% filter(category != "Filler") %>%
  filter(correct == 1) %>% droplevels()
```

Center predictor variable

```
df_valid$PosOr.cont <- scale(as.numeric(as.character(df_valid$PosOr)),
                                        center = T, scale = F)
# table(df_valid$PosOr.cont)
# mean(df_valid$PosOr.cont)
```

Histogram of the reaction time data

```
hist(df_valid$timing.01)
```



Check fit of normal vs gamma distribution in histograms, q-q-plots and using objective criteria:
1) Fit normal and gamma distributions to the reaction time data

```
library(fitdistrplus)
```

```
## Loading required package: MASS
```

```
##
## Attaching package: 'MASS'
```

```
## The following object is masked from 'package:dplyr':
##
##     select
```

```
## Loading required package: survival
```

```
fit.normal<- fitdist(df_valid$timing.01, distr = "norm", method = "mle")
summary(fit.normal)
```

```
## Fitting of the distribution ' norm ' by maximum likelihood
## Parameters :
##      estimate Std. Error
## mean 1244.812   8.865251
## sd    500.474   6.268567
## Loglikelihood:  -24331.13   AIC:  48666.27   BIC:  48678.4
## Correlation matrix:
##      mean sd
## mean    1  0
## sd      0  1
```

```
#plot(fit.normal)
```

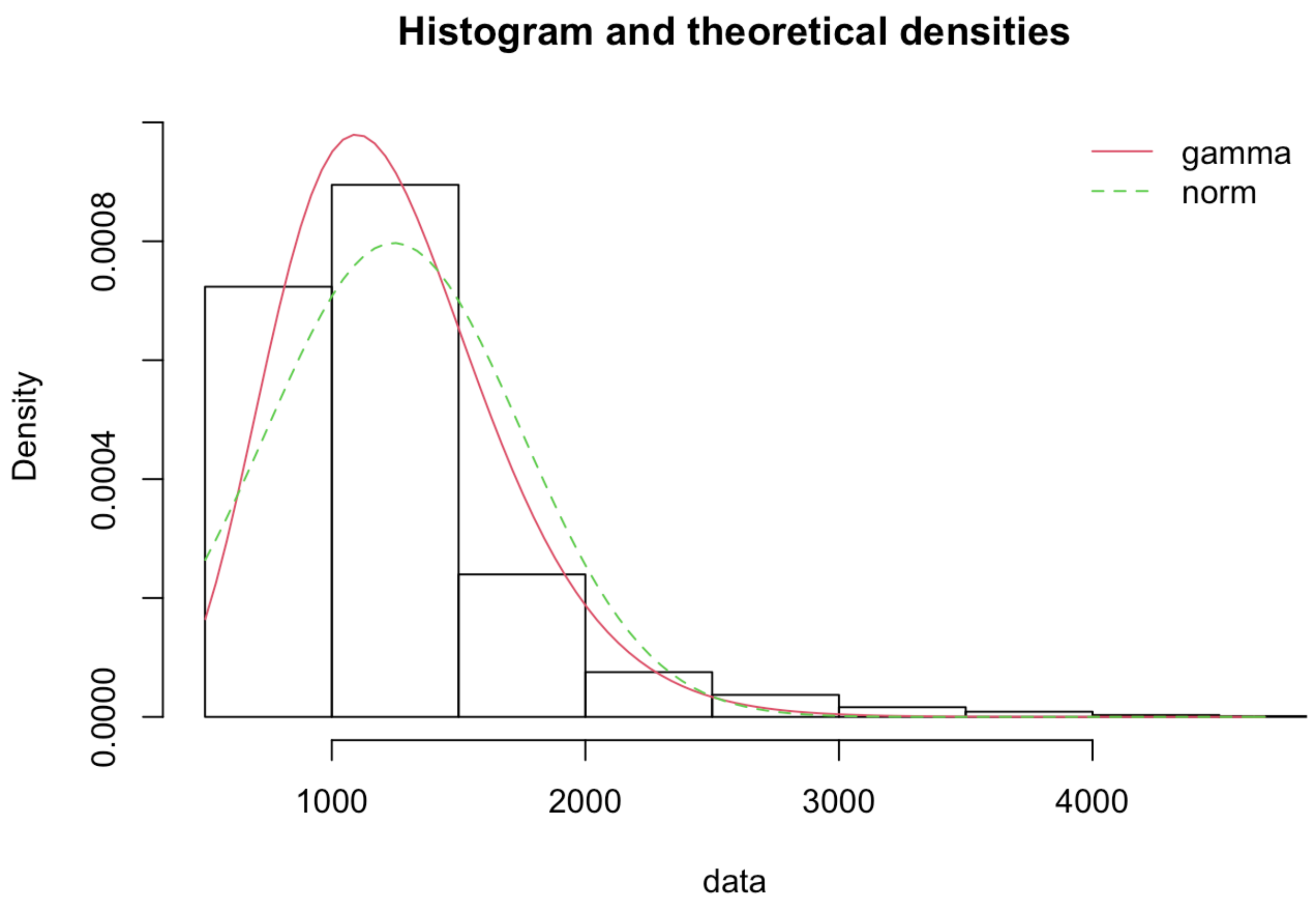
```
fit.gamma <- fitdist(df_valid$timing.01, distr = "gamma", method = "mle")
summary(fit.gamma)
```

```
## Fitting of the distribution ' gamma ' by maximum likelihood
## Parameters :
##          estimate   Std. Error
## shape 8.419774650 0.1695036366
## rate  0.006763458 0.0001371497
## Loglikelihood:  -23710.19   AIC:  47424.38   BIC:  47436.52
## Correlation matrix:
##           shape      rate
## shape 1.0000000 0.9557166
## rate  0.9557166 1.0000000
```

```
#plot(fit.gamma)
```

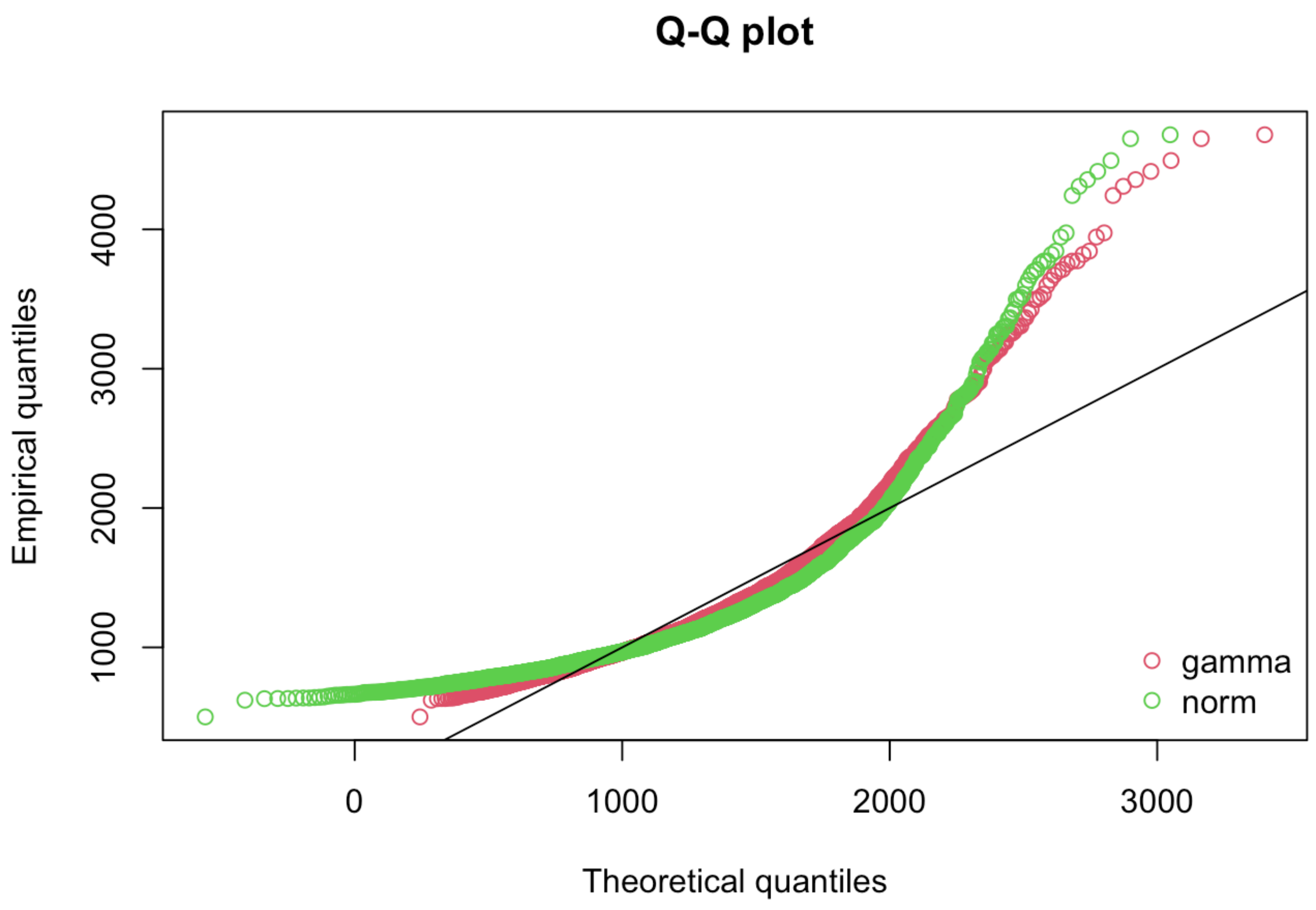
2. Compare the fit of the two distributions
   Visually compare fit of both distributions in histogram

```
denscomp(list(fit.gamma, fit.normal))
```



Visually compare fit of both distributions in Q-Q-plots

```
qqcomp(list(fit.gamma, fit.normal))
```



Compare information criteria

```
gofstat(list(fit.gamma, fit.normal),
        fitnames = c("Gamma", "Normal"))
```

```
## Goodness-of-fit statistics
##                                    Gamma     Normal
## Kolmogorov-Smirnov statistic  0.09601246   0.143611
## Cramer-von Mises statistic   11.68311163  27.368833
## Anderson-Darling statistic   70.47206277 158.559608
##
## Goodness-of-fit criteria
##                                   Gamma   Normal
## Akaike's Information Criterion 47424.38 48666.27
## Bayesian Information Criterion 47436.52 48678.40
```

Conclusion: Both the visual inspection and the objective criteria suggest that a gamma distribution fits the data better (although not that well). Therefore, we fit a Gamma distribution in a GLMM with the continuous predictor ordinal position (Pos.cont), the factorial predictor (experiment), and their interaction. We compute the maximal random effects structure.

Inferential analyses: GLMM (Gamma distribution) with ordinal position as a

continuous predictor

```
m1 <- glmer(timing.01 ~ PosOr.cont +
               (PosOr.cont|subject) +(PosOr.cont|category),
             data = df_valid,
            family =Gamma(link ="identity"),
            control=glmerControl(optimizer = "bobyqa"))
summary(m1)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: Gamma  ( identity )
## Formula: timing.01 ~ PosOr.cont + (PosOr.cont | subject) + (PosOr.cont |
##     category)
##    Data: df_valid
## Control: glmerControl(optimizer = "bobyqa")
##
##      AIC      BIC   logLik deviance df.resid
##  46676.9  46731.5 -23329.4  46658.9     3178
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.5341 -0.5803 -0.2605  0.2551  8.4390
##
## Random effects:
##  Groups   Name        Variance  Std.Dev. Corr
##  subject  (Intercept) 8209.9951 90.6090
##           PosOr.cont   660.5950 25.7020  -0.02
##  category (Intercept) 9785.2051 98.9202
##           PosOr.cont   468.2029 21.6380  0.25
##  Residual                0.1284  0.3583
## Number of obs: 3187, groups:  subject, 30; category, 24
##
## Fixed effects:
##             Estimate Std. Error t value             Pr(>|z|)
## (Intercept) 1296.048     12.264 105.677 < 0.0000000000000002 ***
## PosOr.cont    42.320      7.213   5.867         0.00000000442 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##            (Intr)
## PosOr.cont 0.057
```

```r
# save model output
tab_model(m1,transform = NULL,
          show.re.var = F, show.stat = T,show.r2 = F,show.icc = F,
          title = "GLMM (Gamma distribution) with continuous predictor",
          pred.labels = c("(Intercept)", "Ordinal Position"),
          dv.labels = "Typing Onset Latency",
          #string.pred = "",
          string.stat = "t-Value",
          file = here::here("results", "tables", "CSI_online_typing_APPENDIX_glmm_c
ont.html"))
```

GLMM (Gamma distribution) with continuous predictor

	Typing Onset Latency			
Predictors	*Estimates*	*CI*	*t-Value*	*p*
(Intercept)	1296.05	1272.01 – 1320.09	105.68	**<0.001**
Ordinal Position	42.32	28.18 – 56.46	5.87	**<0.001**
N $_{subject}$	30			
N $_{category}$	24			
Observations	3187			