

06 CSI online typing: Comparison to verbal naming

Kirsten Stark 22 Mai, 2021

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
## 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 data

Load data from both the verbal online CSI experiment and the typing online CSI experiment.

Load typing data

```
df_typing <- read.csv(here::here("data", "data_long_anonymous.csv"))
```

Select classification type (as in script 05)

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

Load verbal data

```
load(here::here("data", "verbal_CSI", "CSI_online_verbal_df_full.RData")
df_verbal <- df_full
```

Combine both data frames into one

1. Subset relevant columns and give identical names

```
df_typing <- df_typing %>%
  dplyr::select(subject, item, category, timing.01, Pos0r, correct) %>%
  dplyr::rename(RT = timing.01, Pos = Pos0r) %>%
  mutate(experiment = "typing")
```

```
df_verbal <- df_verbal %>%
  dplyr::select(VP, Item, subcat, VOT, correct, Pos) %>%
  dplyr::rename(subject = VP, item = Item, category = subcat, RT = VOT)
```

```
mutate(experiment = "verbal")
```

2. Give subjects from both experiments different names

```
df_typing <- df_typing %>% mutate(subject = subject + 200)
df_verbal <- df_verbal %>% mutate(subject = subject + 100)
```

3. Put columns into correct format

```
df_typing <- df_typing %>%
  mutate(subject = as.factor(subject)) %>%
  mutate(item = as.character(item)) %>%
  mutate(category = as.factor(category)) %>%
  mutate(RT = as.numeric(RT)) %>%
  mutate(Pos = as.numeric(Pos)) %>%
  mutate(experiment = factor(experiment, levels = c("verbal", "typing")))

df_verbal <- df_verbal %>%
  mutate(subject = as.factor(subject)) %>%
  mutate(item = as.character(item)) %>%
  mutate(category = as.factor(category)) %>%
  mutate(RT = as.numeric(RT)) %>%
  mutate(Pos = as.numeric(Pos)) %>%
  mutate(experiment = factor(experiment, levels = c("verbal", "typing")))
```

4. Bind both data frames into one

```
df <- bind_rows(df_typing, df_verbal)
```

5. Give identical category names in both experiments

```
df <- df %>% dplyr::mutate(category = case_when(category == "Buero" ~ '
  category == "Gebaeude" ~ "Gebäude",
  category == "Gemuese" ~ "Gemüse",
  category ==
    "Koerperteile" ~ "Körperteile",
  category == "Kueche" ~ "Küche",
  category ==
    "Suessigkeiten" ~ "Süssigkeiten",
  category ==
    "Trinkgefaessee" ~ "Trinkgefässe",
  category == "Voegel" ~ "Vögel",
  TRUE ~ as.character(category))) %>%
```

```
mutate(category == as.factor(category)) %>% droplevels()
table(df$category)
```

```
##
## Aufbewahrung    Bauernhof    Blumen    Büro    Filler
##          300          300          300          300          1200
##      Filler2    Fische    Gebäude    Gemüse    Heimwerker
##          600          300          300          300          300
##      Insekten  Instrumente    Jacken    Kochen    Körperteile
##          300          300          300          300          300
##      Obst    Raubtiere    Schmuck    Sitzen    Strasse Sü:
##          300          300          300          300          300
## Trinkgefäße    Vögel    Wasser
##          300          300          300
```

5. Drop filler trials

```
df <- df %>% filter(category != "Filler" &
                    category != "Filler1" & category != "Filler2") %>%
  droplevels()
```

6. Drop incorrect trials

```
df <- df %>% filter(!is.na(correct) & correct != 0) %>%
  dplyr::select(-correct) %>%
  droplevels()
```

7. Export combined data frame for post-hoc power plot

```
write.csv(df, here::here("data", "CSI_online_combined.csv"))
```

Descriptives

```
(descriptives <- df %>%
  Rmisc::summarySEwithin(., "RT", idvar = "subject",
                        withinvars = "Pos",
                        betweenvars = "experiment",
                        na.rm = T))
```

```
## Automatically converting the following non-factors to factors: Pos
```

##	experiment	Pos	N	RT	sd	se	ci
## 1	verbal	1	670	1051.558	273.0161	10.54753	20.71025
## 2	verbal	2	651	1078.679	293.7729	11.51387	22.60887
## 3	verbal	3	662	1110.344	307.4410	11.94903	23.46264
## 4	verbal	4	650	1108.178	308.8411	12.11374	23.78686
## 5	verbal	5	631	1172.052	335.0839	13.33948	26.19522
## 6	typing	1	645	1009.955	444.1659	17.48902	34.34238
## 7	typing	2	633	1085.806	553.3236	21.99264	43.18749
## 8	typing	3	638	1105.610	525.8232	20.81754	40.87930
## 9	typing	4	637	1143.374	593.4891	23.51489	46.17622
## 10	typing	5	625	1174.959	562.0187	22.48075	44.14708

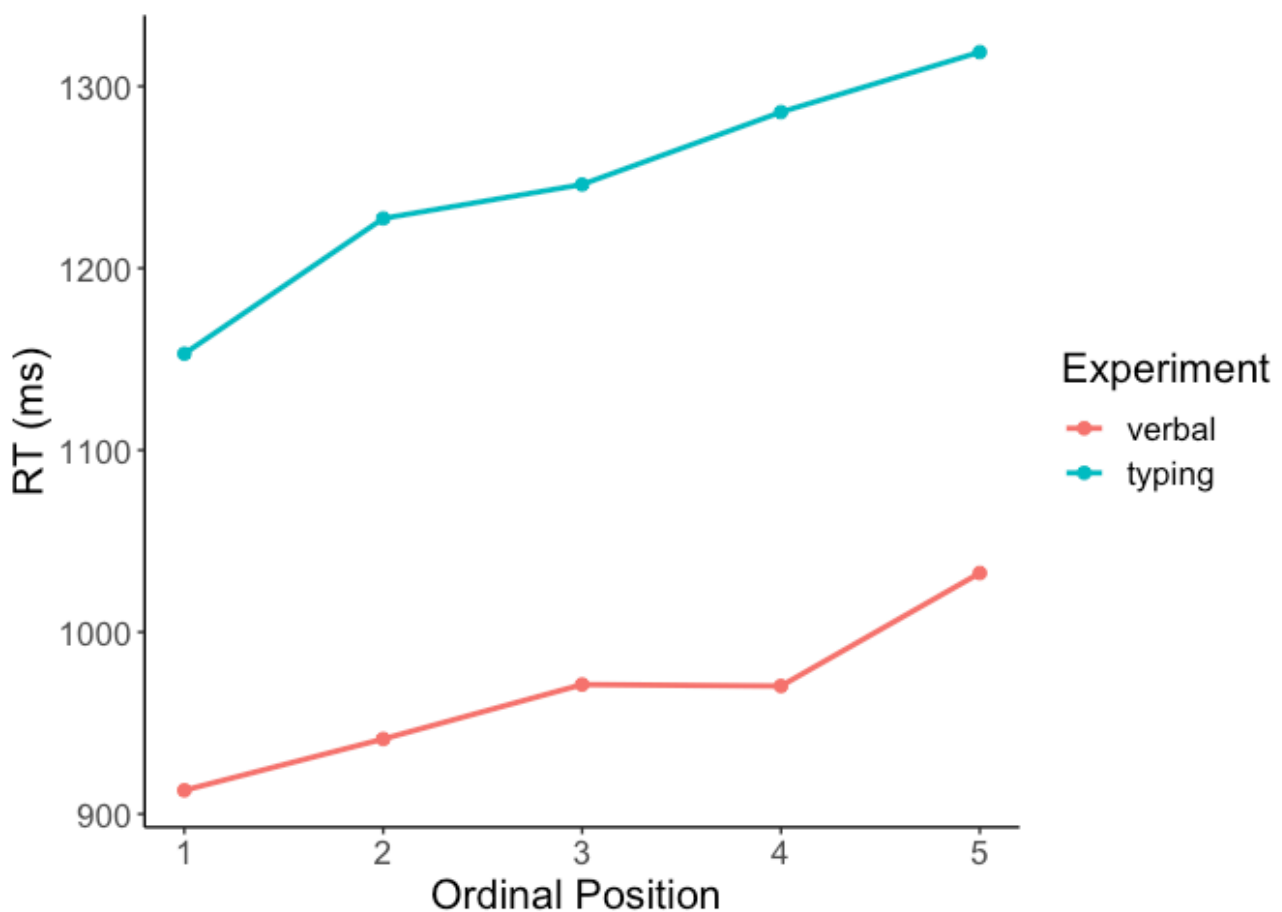
Plotting

Make plots suitable for APA format

```
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))
```

Plot RTs by ordinal position for both experiments

```
(plot <- df %>%  
  ggplot(., aes(x=Pos, y=RT,  
               group=experiment, color=experiment)) +  
  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 = "Experiment"))
```



```
filename <- "CSI_online_exp_comparison_plot_rt.pdf"
ggsave(plot, filename =
  here::here("results", "figures", filename),
  width = 18, height = 12, units = "cm",
  dpi = 300, device = cairo_pdf)
embedFonts(file = here::here("results", "figures", filename))
```

Set contrasts and convert continuous predictor variable

1. Set contrasts: Sliding difference contrast for factor experiment
Subsequent factor levels are being compared to each other, i.e. verbal-typing, the intercept being the grand mean.

```
# define sliding difference contrast for factor experiment:
# contrast is verbal - typing, intercept being the grand mean
levels(df$experiment)
```

```
## [1] "verbal" "typing"
```

```
contrasts(df$experiment) <- MASS::contr.sdif(2)
```

2. Center the continuous predictor variable position around zero (ordinal contrast with five levels)

```
df$Pos.cont <- scale(as.numeric(as.character(df$Pos)),  
                     center = T, scale = F)
```

```
# table(df$Pos.cont)
```

```
# mean(df$Pos.cont)
```

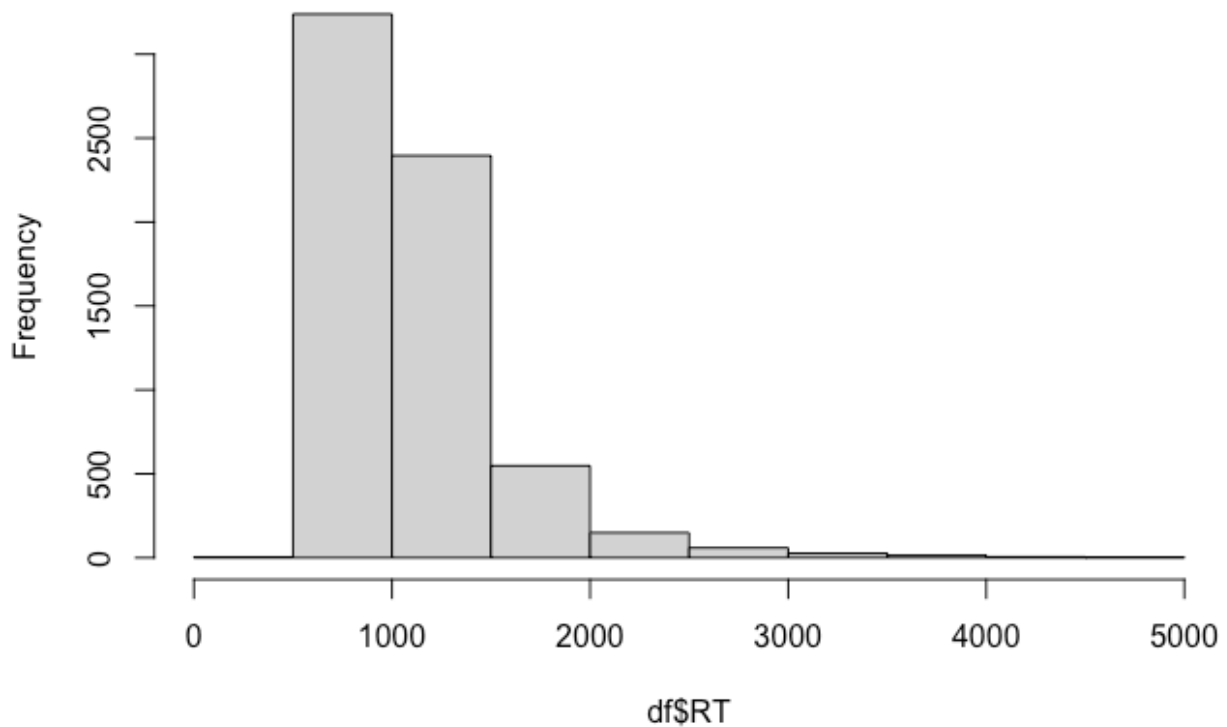
Check distribution of data

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

Histogram of the reaction time data

```
hist(df$RT)
```


Histogram of df\$RT



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<- fitdistr(df$RT, distr = "norm", method = "mle")  
summary(fit.normal)
```

```
## Fitting of the distribution ' norm ' by maximum likelihood
## Parameters :
##      estimate Std. Error
## mean 1103.4596   5.389018
## sd   432.5251   3.810561
## Loglikelihood: -48241.43   AIC:  96486.85   BIC:  96500.39
## Correlation matrix:
##      mean sd
## mean    1  0
## sd      0  1
```

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

```
fit.gamma <- fitdist(df$RT, distr = "gamma", method = "mle")
summary(fit.gamma)
```

```
## Fitting of the distribution ' gamma ' by maximum likelihood
## Parameters :
##      estimate   Std. Error
## shape 8.714704899 0.1288279543
## rate  0.007897942 0.0001182167
## Loglikelihood: -47047.64   AIC:  94099.27   BIC:  94112.81
## Correlation matrix:
##      shape      rate
## shape 1.0000000 0.9607663
## rate  0.9607663 1.0000000
```

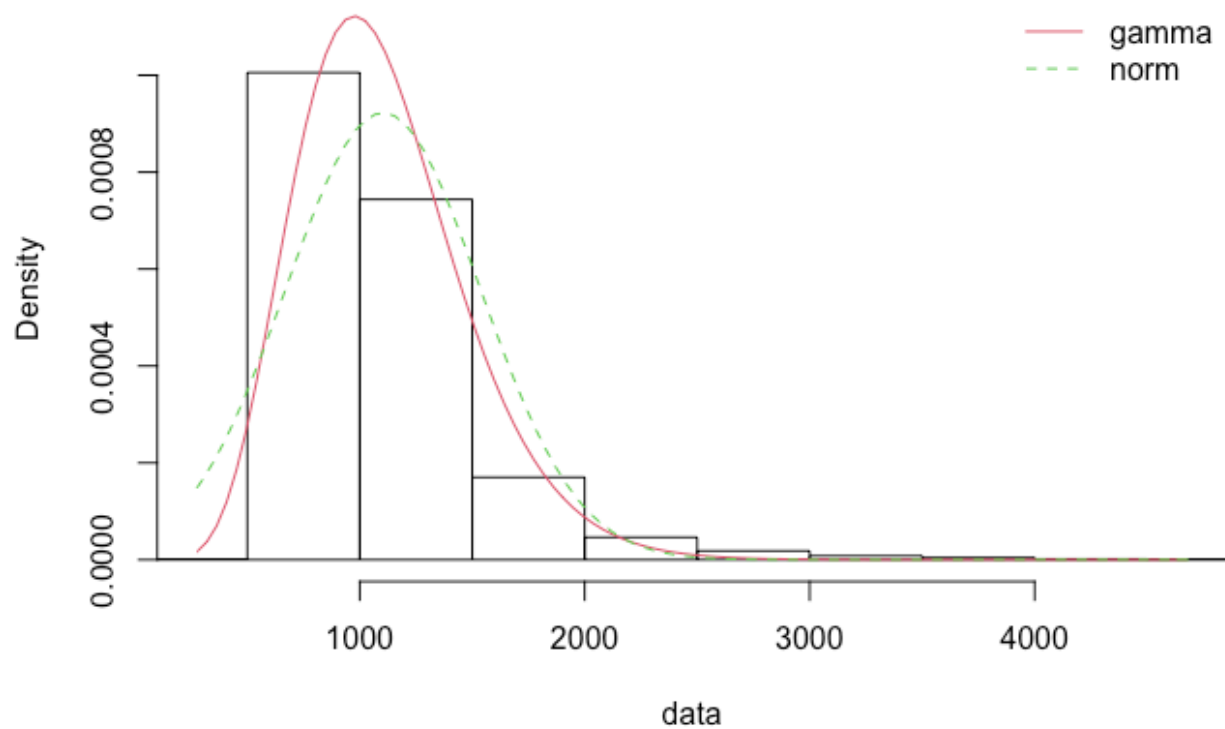
```
#plot(fit.gamma)
```

2. Compare the fit of the two distributions

Visually compare fit of both distributions in histogram

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

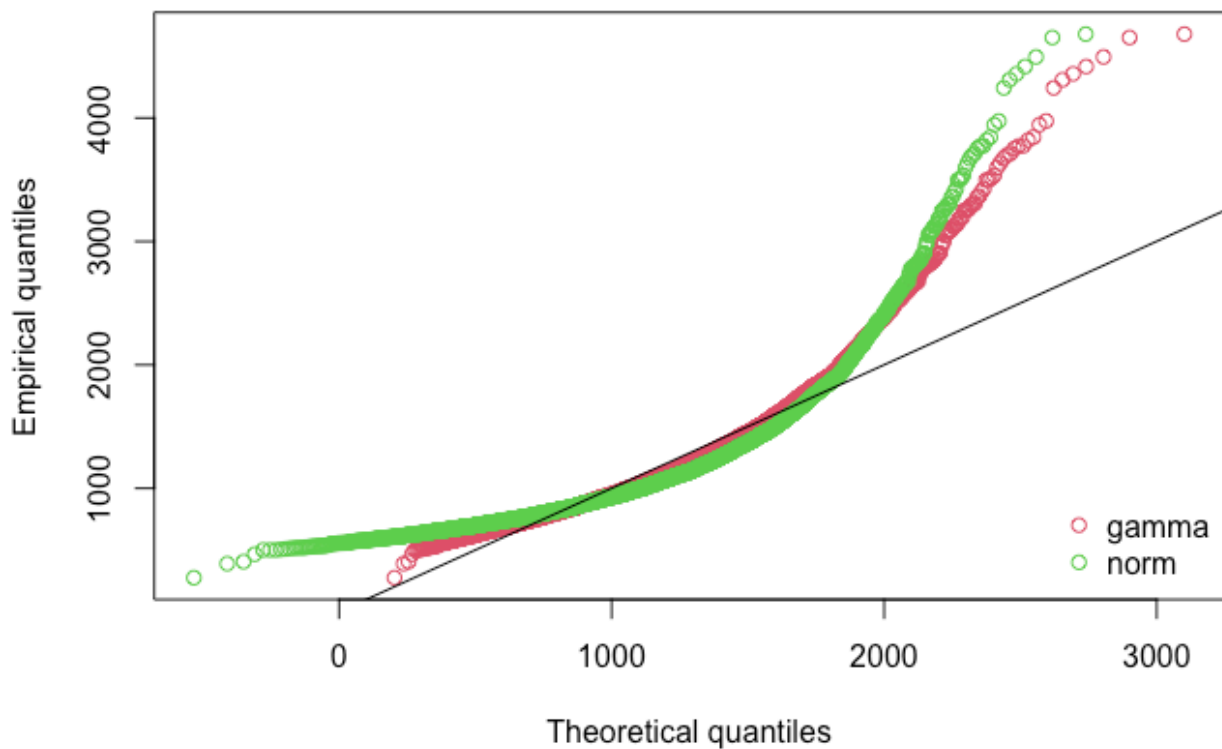
Histogram and theoretical densities



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

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

Q-Q plot



Compare information criteria

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

```
## Goodness-of-fit statistics
##
##      Gamma      Normal
## Kolmogorov-Smirnov statistic  0.08526673  0.1349558
## Cramer-von Mises statistic   16.64374270  45.0123565
## Anderson-Darling statistic  100.97376437 263.8788753
##
## Goodness-of-fit criteria
##
##      Gamma      Normal
## Akaike's Information Criterion 94099.27 96486.85
## Bayesian Information Criterion 94112.81 96500.39
```

Conclusion: Both the visual inspection and the objective criteria suggest that a gamma distribution fits the data better. 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.

Interferential statistics: GLMM with predictors Pos.cont and experiment

```
m1 <- afex::lmer_alt(RT ~ Pos.cont*experiment +  
  (Pos.cont||subject) +(Pos.cont*experiment||category),  
  data = df,  
  family =Gamma(link ="identity"),  
  control=glmerControl(optimizer = "bobyqa", optCtrl = list(r
```

```
## Registered S3 methods overwritten by 'car':  
##   method                                from  
##   influence.merMod                      lme4  
##   cooks.distance.influence.merMod      lme4  
##   dfbeta.influence.merMod              lme4  
##   dfbetas.influence.merMod             lme4
```

```
summary(m1)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace  
##   Approximation) [glmerMod]  
##   Family: Gamma ( identity )  
## Formula: RT ~ Pos.cont * experiment + (1 + re1.Pos.cont || subject)  
##          (1 + re2.Pos.cont + re2.experiment2.1 + re2.Pos.cont_by_experim  
##          category)  
##   Data: data  
## Control: glmerControl(optimizer = "bobyqa", optCtrl = list(maxfun =  
##  
##          AIC      BIC    logLik deviance df.resid  
##  91500.8  91575.3 -45739.4  91478.8     6431  
##  
## Scaled residuals:  
##      Min       1Q   Median       3Q      Max  
## -2.0610 -0.6089 -0.2349  0.3176  9.4786  
##  
## Random effects:  
##   Groups      Name                                Variance Std.Dev.  
##  subject    (Intercept)                        5632.0470  75.0470  
##  subject.1  re1.Pos.cont                        418.1712  20.4492  
##  category   (Intercept)                        4510.9510  67.1636
```

```
## category.1 re2.Pos.cont 247.0792 15.7188
## category.2 re2.experiment2.1 4224.1364 64.9934
## category.3 re2.Pos.cont_by_experiment2.1 502.1754 22.4093
## Residual 0.0988 0.3143
## Number of obs: 6442, groups: subject, 60; category, 24
##
## Fixed effects:
## Estimate Std. Error t value Pr(>
## (Intercept) 1153.267 4.780 241.287 < 0.0000000000000000e+000
## Pos.cont 34.353 4.735 7.256 0.0000000000000000e+000
## experiment2-1 289.641 4.839 59.850 < 0.0000000000000000e+000
## Pos.cont:experiment2-1 11.365 7.184 1.582 0.0614111111111111e+000
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
## (Intr) Ps.cnt exp2-1
## Pos.cont 0.177
## expermnt2-1 -0.221 -0.193
## Ps.cnt:x2-1 -0.278 -0.161 0.115

# 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)",
          pred.labels = c("(Intercept)", "Ordinal Position",
                          "Experiment", "(Ordinal Position) x
                          \n (Experiment)"),
          wrap.labels = 10,
          dv.labels = "Typing Onset Latency",
          #string.pred = "",
          string.stat = "t-Value",
          file = here::here("results", "tables",
                           "CSI_online_experiment_comparison_glmm_cont"))
```

GLMM (Gamma distribution)

	Typing Onset Latency			
Predictors	Estimates	CI	t-Value	p
(Intercept)	1153.27	1143.90 – 1162.64	241.29	<0.001

Ordinal Position	34.35	25.07 – 43.63	7.26	<0.001
Experiment	289.64	280.16 – 299.13	59.85	<0.001
(Ordinal Position) x (Experiment)	11.37	-2.71 – 25.44	1.58	0.114
N _{subject}	60			
N _{category}	24			
Observations	6442			