

# Effects of stimulus emotional content on gaze pattern: an eye-tracking study

Code and analyses

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## Descripción

This document contains all code, and step by step explanations for all analyses, figures and tables (including supplementary figures and tables) for:

Castellanos-Chacón, A., Leongómez, J. D., & Vásquez-Amézquita, M. (in prep). *Effects of stimulus emotional content on gaze pattern: an eye-tracking study*.

Data available from the Open Science Framework (OSF): <https://doi.org/10.XXXXXX/OSF.IO/XXXXX>. All analyses were planned by Andrés Castellanos-Chacón, Milena Vásquez-Amézquita and Juan David Leongómez. This document and its underlying code were created in R Markdown by Andrés Castellanos-Chacón using L<sup>A</sup>T<sub>E</sub>X.

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# 1 Preliminaries

## 1.1 Load packages

This file was created using `knitr` (Xie, 2014), mostly using `tidyverse` (Wickham et al., 2019) syntax. As such, data wrangling was mainly done using packages such as `dplyr` (Wickham et al., 2022), and most figures were created or modified using `ggplot2` (Wickham, 2016). Tables were created using `knitr::kable` and `kableExtra` (Zhu, 2020). The database was loaded with the `readxl` package (Wickham & Bryan, 2021).

Linear mixed models were fitted using `lmerTest` (Kuznetsova et al., 2017), assumptions were performed using `performance` (Lüdecke et al., 2021), contrasts and interactions were explored using `emmeans` (Lenth, 2022). The `broom` package (Robinson, 2020) was used to convert data into tibble type.

The `ggbpusr` (Kassambara, 2023) package, which allows the use of specialized tools, was used to create the graphs. The `gtools` (Bolker et al., 2022) package helped us to obtain the p-values, to create the significance bars in the graphs, together with the `tidyrr` (Wickham et al., 2023) package that helped us to organize the information in the post hoc results tables.

To generate Bootstrap, the `boot` (Canty & Ripley, 2022) package was used to generate resampling and the `lmeresampler` (Loy et al., 2023) package to generate Bootstrap with mixed linear models.

Used packages also include `osfr` (Wolen et al., 2020) to download and open data files directly from the Open Science Framework ([OSF](#)), using the `osf_retrieve_file` and `osf_download` functions.

All packages used in this file can be directly installed from the Comprehensive R Archive Network ([CRAN](#)).

```
library(tidyverse)
library(dplyr)
library(lmerTest)
library(performance)
library(readxl)
library(emmeans)
library(kableExtra)
library(broom)
```

```
library(ggpubr)
library(gtools)
library(tidyr)
library(lmeresampler)
library(boot)
```

## 1.2 Custom functions

### 1.2.1 pval.stars

This function takes p-values and adds starts to represent significance levels.

```
pval.stars <- function(pvals) {
  ifelse(pvals < 0.0001,
         "****",
         ifelse(pvals < 0.001,
                "***",
                ifelse(pvals < 0.01,
                       "**",
                       ifelse(pvals < 0.05,
                              "*", NA))))
}
```

## 1.3 Load and wrangle data

### 1.3.1 Load data base.

The first thing we do is to load the database and save it in a variable that we will call ‘bd’. After that, we will check all the variables that are identified as ‘character’ and we will convert them into ‘factor’ type. And we will reorder the levels leaving the Neutral stimuli first, followed by the Control, positive and negative stimuli.

```
bd <- read_excel("Data/Datos1.xlsx") |>
  mutate(across(where(is.character), as.factor)) |>
  rename(stimulus_content=tipo_estimulos) |>
  rename(Gender=sexo) |>
  mutate(stimulus_content = fct_relevel(stimulus_content,
                                         "Negative",
                                         "Positive",
                                         "Neutral",
                                         "Control" ))
```

### 1.3.2 Calculate first fixation count data

This formula takes the values of the first fixation column and stores them in a variable so as not to repeat values due to the vertical database being handled.

```
pf <- bd |>
  group_by(Participant, primeta_fix) |>
  count(primeta_fix, .drop = FALSE) |>
  mutate(n = n/4) |>
  mutate(Gender = ifelse(grepl("H", Participant),
                        "Male", "Female")) |>
  mutate(primeta_fix = fct_relevel(primeta_fix,
                                   "Negative",
                                   "Positive",
                                   "Neutral",
                                   "Control" ))
```

## 2 Linear Mixed Models (LMM)

Linear model is an approach for modeling the relationship between n independent observations with one or more explanatory variables (Pusponegoro et al., 2017).

Pusponegoro, N. H., Notodiputro, K. A., & Sartono, B. (2017). Linear mixed model for analyzing longitudinal data: A simulation study of children growth differences. Procedia computer science, 116, 284-291.https://doi.org/10.1016/j.procs.2017.10.071

### 2.1 Time to first fixation

The time to first fixation is understood as the participant's latency to the first stimulus, once the competing stimuli are presented. Previously, a cross has been presented so that the participant fixates his gaze on the center of the screen and has the same probability of seeing any stimulus.

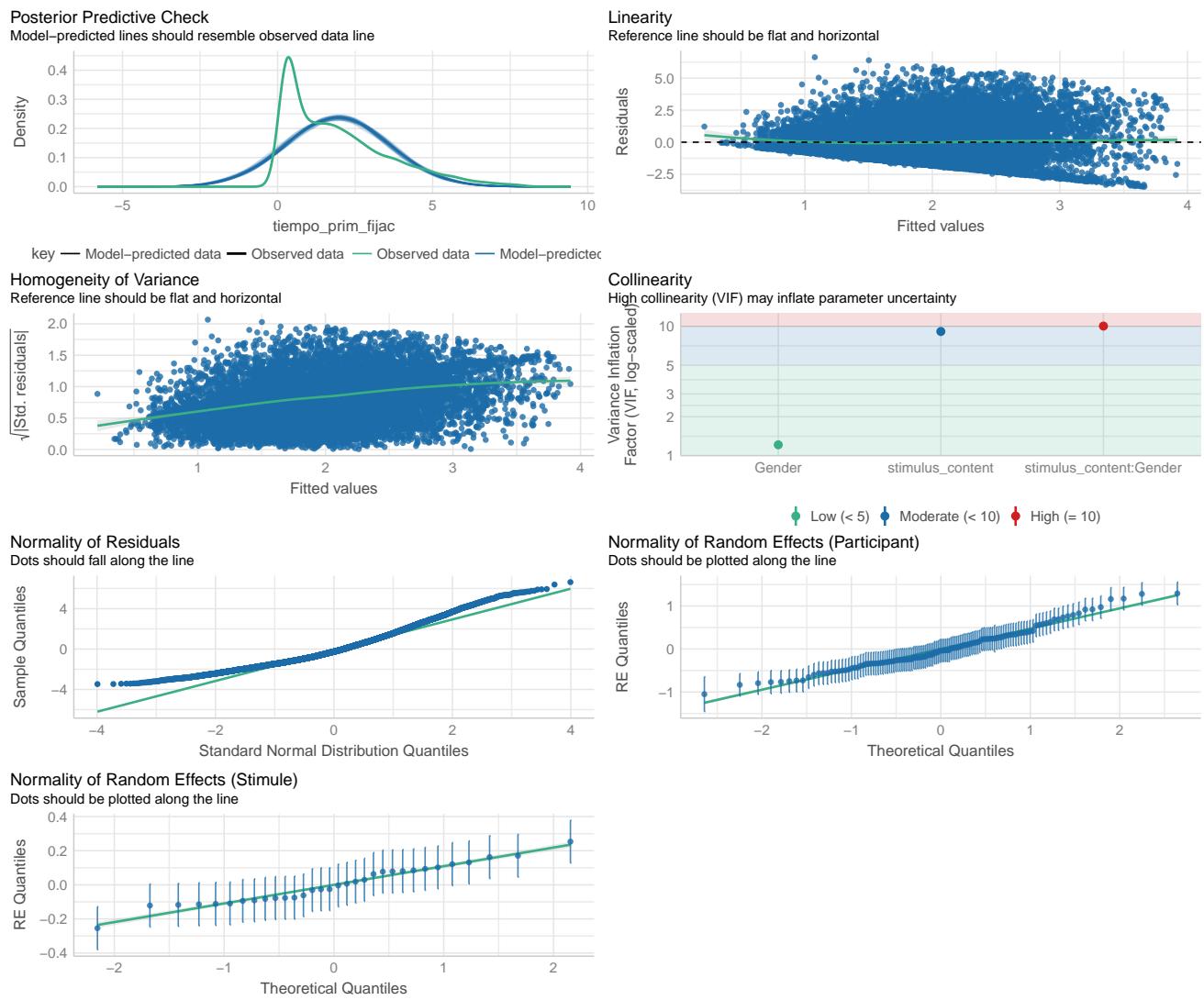
#### 2.1.1 Fit model

For the first model, the time to first fixation will be predicted by means of the variables, type of stimulus and its interaction with the participant's gender. Additionally, there are random intercepts such as the participant and the stimulus. This means that each participant and each stimulus is expected to have its own effect on the response variable, rather than having a constant effect in all cases.

```
mod1 <- lmer(tiempo_prim_fijac ~ stimulus_content * Gender +
              (1 | Participant) +
              (1 | Stimule),
              data = bd)
```

**2.1.1.1 Model assumptions** The following functions ‘check\_model()’, ‘check\_distribution()’, and ‘check\_normality()’ are used to evaluate the quality of fit and distribution of residuals in a statistical model. For example, check\_model() could provide a visualization of residuals and diagnose problems such as heteroscedasticity or bias in the model. check\_distribution() could provide a visualization of the distribution of residuals and diagnose problems such as deviation from normality or outliers. check\_normality() could provide a normality test for the residuals of the model and evaluate whether normality assumptions are met.

```
check_model(mod1)
```



```
dist_checkmod1 <- check_distribution(mod1)
kable(data.frame(dist_checkmod1),
      digits = 2, booktabs = TRUE,
      caption = "Distribution of residuals model 1") %>%
  kable_styling(latex_options = c("HOLD_position"))
```

**Table S1.** Distribution of residuals model 1

Distribution	p_Residuals	p_Response
bernelloulli	0.00	0.00
beta	0.00	0.00
beta-binomial	0.00	0.00
binomial	0.00	0.00
cauchy	0.41	0.00
chi	0.00	0.00
exponential	0.00	0.00
F	0.00	0.00
gamma	0.06	0.00
half-cauchy	0.00	0.00
inverse-gamma	0.00	0.00
lognormal	0.00	0.00
neg. binomial (zero-infl.)	0.00	0.00
negative binomial	0.00	0.00
normal	0.47	0.00
pareto	0.00	0.00
poisson	0.00	0.00
poisson (zero-infl.)	0.00	0.00
tweedie	0.03	0.97
uniform	0.00	0.00
weibull	0.03	0.03

```
check_normality(mod1)
```

```
## Warning: Non-normality of residuals detected (p < .001).
```

**2.1.1.2 Summary model** To obtain a summary of model 1, the ‘summary’ function was used, which provides a summary of the coefficients of model 1, along with the standard deviation, t-value, and associated p-value for each coefficient. Similarly, the ‘anova’ function returns an ANOVA table with information on the variance decomposition of model 1, sum of squares, degrees of freedom, and associated F-statistics. Finally, the ‘r2\_nakagawa’ function is used to calculate the pseudo R-squared proposed by Nakagawa & Schielzeth (2013) for mixed-effects models. The pseudo R-squared is used to evaluate the goodness of fit of a model and is interpreted similarly to an R-squared in standard linear models.

```
anova.mod1 <- anova(mod1)
anova.mod1 <- as.data.frame(anova.mod1) |>
  rownames_to_column() |>
  mutate_at("rowname", str_replace_all, ":" , " × ") |>
  mutate_at("rowname", str_replace_all, "stimulus_content",
            "Stimulus content") |>
  rename( Effect = rowname) |>
  kable(digits = 2, booktabs = TRUE,
        align = c("l", "l", rep("c", 4)), caption = "Effect of Stimulus
Content and Participant's Gender on Time to First Fixation (TFF)",
        escape = FALSE) |>
  kable_styling(latex_options = c("hold_position"))
anova.mod1
```

```
sum.mod1 <- summary(mod1)

sum.mod1_df <- as.data.frame(sum.mod1$coefficients) |>
  rownames_to_column() |>
```

**Table S2.** Effect of Stimulus Content and Participant's Gender on Time to First Fixation (TFF)

Effect	Sum Sq	Mean Sq	NumDF	DenDF	F value	Pr(>F)
Stimulus content	1349.46	449.82	3	15156.24	186.43	0.00
Gender	0.34	0.34	1	119.17	0.14	0.71
Stimulus content × Gender	3.84	1.28	3	15156.00	0.53	0.66

```

mutate_at("rowname", str_replace_all, ":" , " × ") |>
mutate_at("rowname", str_replace_all, "stimulus_contentControl",
          "Stimulus content [Control]")|>
mutate_at("rowname", str_replace_all, "stimulus_contentPositive",
          "Stimulus content [Positive]")|>
mutate_at("rowname", str_replace_all, "stimulus_contentNeutral",
          "Stimulus content [Neutral]")|>
mutate_at("rowname", str_replace_all, "GenderMale",
          "Gender [Male]") |>
rename( Effect = rowname)|>
kable(digits = 2, booktabs = TRUE,
      align = c("l", "l", rep("c", 4)),
      caption = "Time to First Fixation (TFF) by stimulus content, gender
and the interaction between stimulus content and gender",
      escape = FALSE) |>
kable_styling(latex_options = c("HOLD_position"))

sum.mod1_df

```

**Table S3.** Time to First Fixation (TFF) by stimulus content, gender and the interaction between stimulus content and gender

Effect	Estimate	Std. Error	df	t value	Pr(> t )
(Intercept)	1.57	0.08	192.55	20.06	0.00
Stimulus content [Positive]	0.29	0.05	15155.58	5.74	0.00
Stimulus content [Neutral]	0.46	0.05	15155.89	9.04	0.00
Stimulus content [Control]	0.79	0.05	15155.81	15.46	0.00
Gender [Male]	-0.05	0.10	175.10	-0.47	0.64
Stimulus content [Positive] × Gender [Male]	0.01	0.07	15155.99	0.21	0.83
Stimulus content [Neutral] × Gender [Male]	-0.02	0.07	15156.42	-0.34	0.74
Stimulus content [Control] × Gender [Male]	0.06	0.07	15156.39	0.89	0.37

```

r2mod1 <- r2_nakagawa(mod1)
r2_tblmod1 <- as_tibble(r2mod1)
kable(r2_tblmod1, format = "markdown", booktabs =TRUE,
      align = "c", caption = "R model 1",
      escape = FALSE) %>%
kable_styling(latex_options = c("HOLD_position"))

```

**Table S4.** R model 1

R2_conditional	R2_marginal
0.1279185	0.0322227

**2.1.1.3 Estimated marginal means** Taking into account the obtained results, in the ANOVA-type table, where significant values for the stimulus content variable are observed, post-hoc tests are performed and the contrast

between variables is presented.

```
mcm1 <- emmeans(mod1, pairwise ~ stimulus_content)

mcm1_emmeans <- tibble(data.frame(mcm1$emmeans)) |>
  rename(tiempo_prim_fijac = emmean) |>
  select(-df)

contrasts_df1 <- as.data.frame(mcm1$contrasts) |>
  select(-df)

kable(contrasts_df1, digits = 5, booktabs = TRUE,
      align = "c", caption = "contrasts between variables, according to the
      content of the stimulus of model 1") %>%
  kable_styling(latex_options = "HOLD_position",
                font_size = 12,
                full_width = FALSE)
```

**Table S5.** contrasts between variables, according to the content of the stimulus of model 1

contrast	estimate	SE	z.ratio	p.value
Negative - Positive	-0.30104	0.03543	-8.49568	0.00000
Negative - Neutral	-0.45151	0.03547	-12.72862	0.00000
Negative - Control	-0.82608	0.03556	-23.22999	0.00000
Positive - Neutral	-0.15047	0.03552	-4.23624	0.00013
Positive - Control	-0.52504	0.03561	-14.74463	0.00000
Neutral - Control	-0.37458	0.03564	-10.50886	0.00000

## 2.1.2 Figure

Finally, for this model 1, a figure is shown in which the time for the first fixation is observed according to the content of the stimulus and the respective differences between the variables are presented.

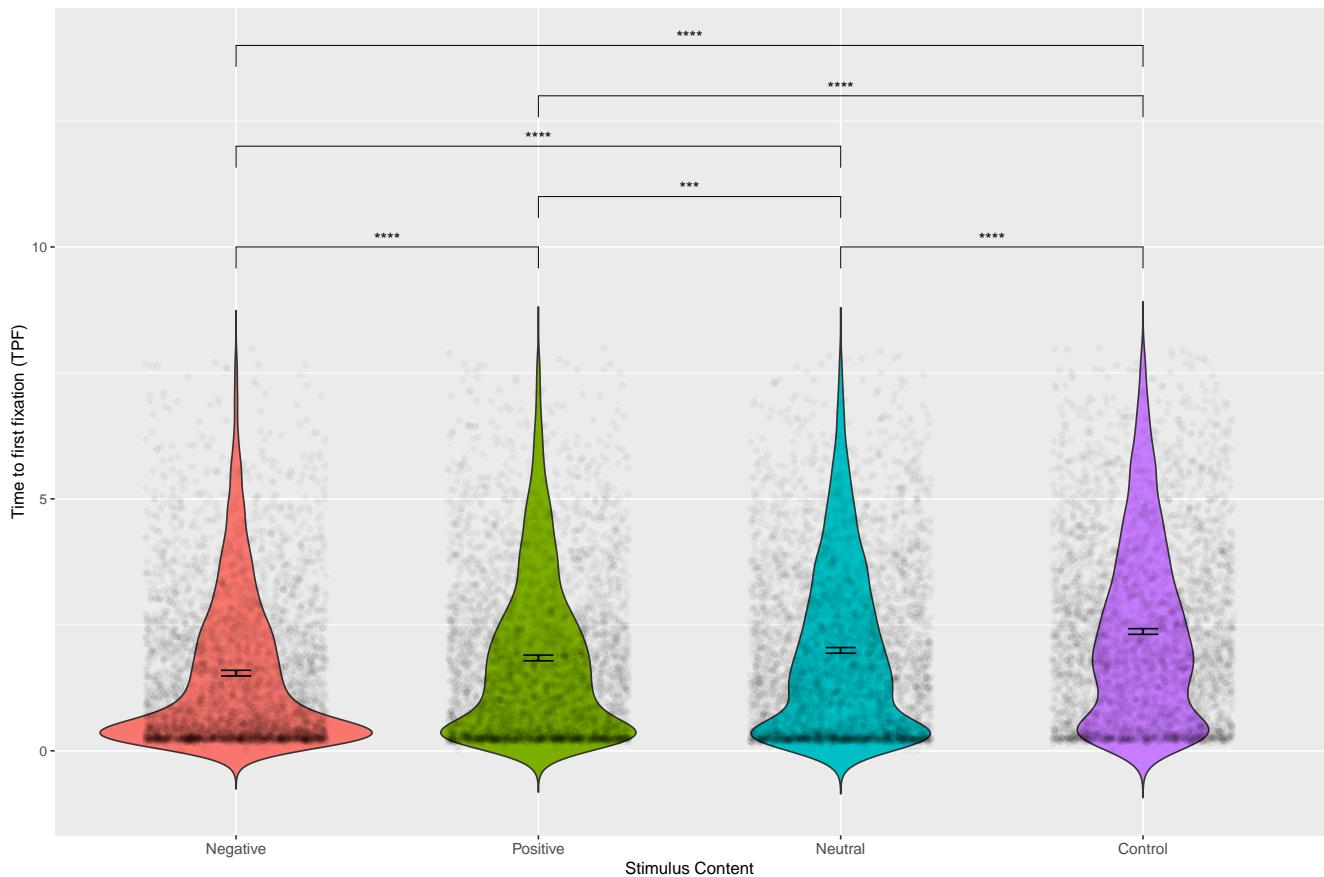
```
tbl.contrasts_df1 <- contrasts_df1 %>%
  mutate(.y. = "tiempo_prim_fijac") %>%
  separate_wider_delim(contrast, " - ",
                        names = c("group1", "group2")) %>%
  select(7, 1:6) %>%
  mutate(p.signif = pval.stars(p.value))

ggplot(bd, aes(x=stimulus_content,
                y=tiempo_prim_fijac)) +
  geom_violin(trim = FALSE,
              aes(fill = stimulus_content)) +
  geom_jitter(alpha = 0.04, width = 0.3) +
  geom_errorbar(data = mcm1_emmeans,
                mapping =
                aes(ymin = tiempo_prim_fijac-SE,
                    ymax = tiempo_prim_fijac+SE),
                colour = "black", width = 0.1) +
  geom_point(data = mcm1_emmeans,
              shape = 50, size = 1,
              color = "black", fill = "white") +
  stat_pvalue_manual(tbl.contrasts_df1,
```

```

            label = "p.signif",
            y.position = c(10, 12, 14, 11, 13, 10)) +
  labs(x = "Stimulus Content",
       y = "Time to first fixation (TPF)",
       fill = " ") +
  theme(axis.text.x = element_text(size = 10))+
  guides(fill = FALSE)

```



**Figure S1.** Dimension between the emotional content of the stimulus, images with negative, positive, neutral and control emotional content, see Table S5, where the contrasts between each dimension are observed. In all cases, significant effects are represented with lines and stars: \* $p < .05$ , \*\* $p < .01$ , \*\*\* $p < .001$ , \*\*\*\* $p < .0001$ .

### 2.1.3 Bootstrap

Considering that the model did not behave normally, the distribution was estimated using Bootstrap. The bootstrap method is used to generate multiple samples of data from the original sample and, from them, obtain a sampling distribution of the statistic of interest, which allows estimating the variability and uncertainty associated with the statistic of interest, in this case the Time to first fixation (TPF).

```

set.seed(824)

B <- 10000
mod1_boot <- bootstrap(mod1, .f = fixef, type = "residual", B = B)
matriz_mod1 <- as.matrix(mod1_boot$stats)

columnas_a_convertir <- c("observed", "rep.mean", "se", "bias")

boots_mod1_table <- as.data.frame(matriz_mod1) |>

```

```

mutate_at("term", str_replace_all, ":" , " × ") |>
  mutate_at("term", str_replace_all, "stimulus_contentControl",
    "Stimulus content [Control]")|>
  mutate_at("term", str_replace_all, "stimulus_contentPositive",
    "Stimulus content [Positive]")|>
  mutate_at("term", str_replace_all, "stimulus_contentNeutral",
    "Stimulus content [Neutral]")|>
  mutate_at("term", str_replace_all, "GenderMale",
    "Gender [Male]")|>
  mutate(across(all_of(columnas_a_convertir), as.numeric))

bootstrap_mod1 <- as.data.frame(confint(mod1_boot,
                                         type = "basic")) |>
  mutate_at("term", str_replace_all, ":" , " × ") |>
  mutate_at("term", str_replace_all, "stimulus_contentControl",
    "Stimulus content [Control]")|>
  mutate_at("term", str_replace_all, "stimulus_contentPositive",
    "Stimulus content [Positive]")|>
  mutate_at("term", str_replace_all, "stimulus_contentNeutral",
    "Stimulus content [Neutral]")|>
  mutate_at("term", str_replace_all, "GenderMale",
    "Gender [Male]")

orden_deseado <- c("(Intercept)",
  "Stimulus content [Positive]",
  "Stimulus content [Neutral]",
  "Stimulus content [Control]" ,
  "Gender [Male]",
  "Stimulus content [Positive] × Gender [Male]",
  "Stimulus content [Neutral] × Gender [Male]",
  "Stimulus content [Control] × Gender [Male]")

unidas_mod1 <- merge(boots_mod1_table, bootstrap_mod1, by = "term")|>
  select(-estimate, -type, -level)

unidas_mod1 <- arrange(unidas_mod1,
  match(term, orden_deseado)) |>
  kable(digits = 4, booktabs = TRUE,
  align = c("l", "l", rep("c", 4)),
  caption = "Bootstrap estimated values of model 1",
  escape = FALSE) |>
  kable_styling(latex_options = c("HOLD_position"))

unidas_mod1

```

**Table S6.** Bootstrap estimated values of model 1

term	observed	rep.mean	se	bias	lower	upper
(Intercept)	1.5664	1.5666	0.0594	0.0002	1.4494	1.6826
Stimulus content [Positive]	0.2936	0.2934	0.0511	-0.0002	0.1920	0.3947
Stimulus content [Neutral]	0.4634	0.4631	0.0512	-0.0003	0.3635	0.5648
Stimulus content [Control]	0.7945	0.7941	0.0510	-0.0003	0.6957	0.8945
Gender [Male]	-0.0486	-0.0493	0.1029	-0.0006	-0.2504	0.1538
Stimulus content [Positive] × Gender [Male]	0.0148	0.0156	0.0709	0.0008	-0.1246	0.1526
Stimulus content [Neutral] × Gender [Male]	-0.0238	-0.0226	0.0704	0.0012	-0.1650	0.1109
Stimulus content [Control] × Gender [Male]	0.0632	0.0643	0.0703	0.0011	-0.0786	0.1985

## 2.2 First fixation duration

It is a measure of early attention and its objective is to capture the total time a person spends looking at a stimulus the first time he/she directs his/her gaze to the target.

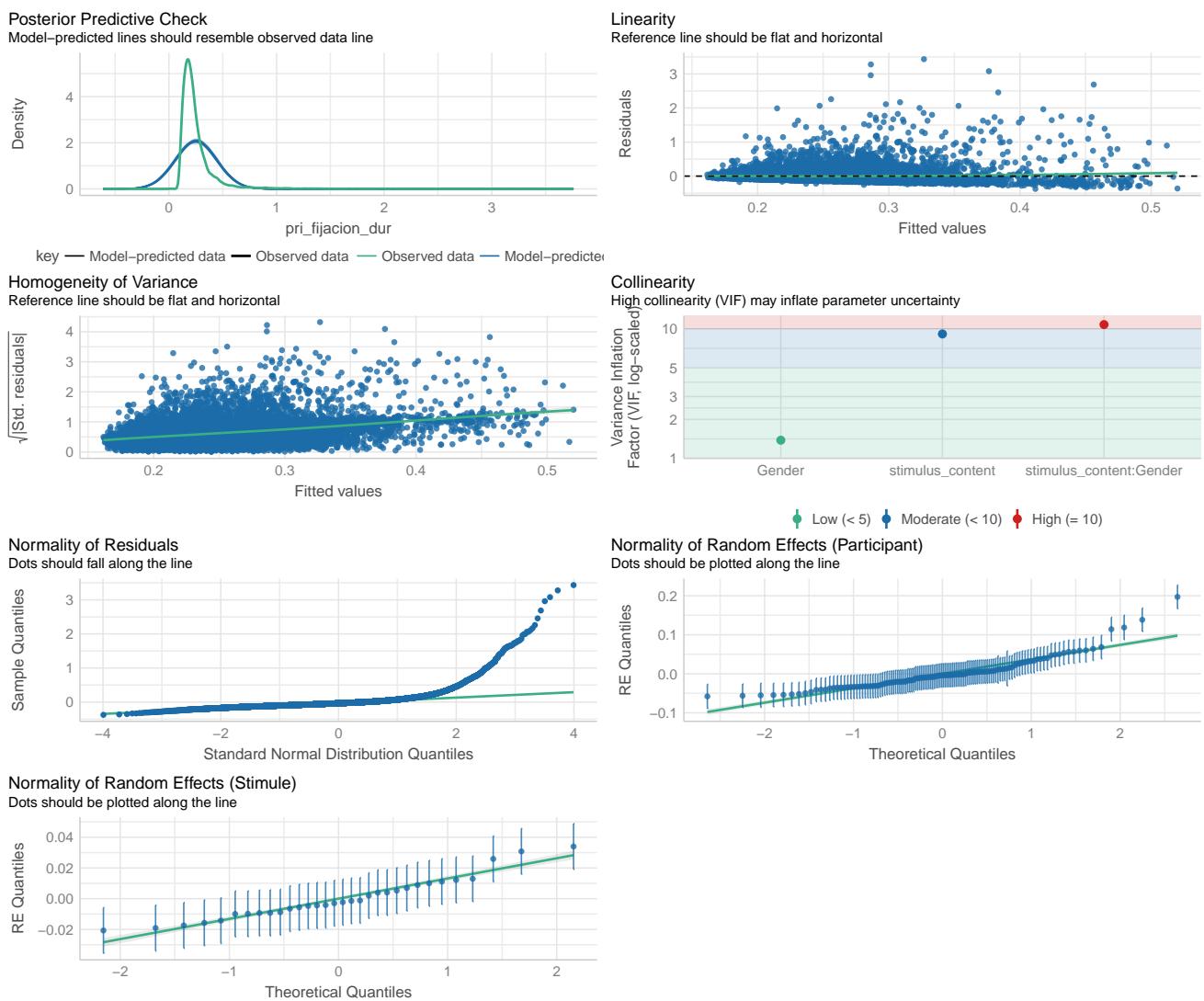
### 2.2.1 Fit model

For the second model, the First fixation duration will be predicted by the variables stimulus type and its interaction with the participant's gender. In addition, there are random intercepts such as participant and stimulus. This means that each participant and stimulus is expected to have its own effect on the response variable, rather than having a constant effect in all cases.

```
mod2 <- lmer(pri_fijacion_dur ~
  stimulus_content * Gender +
  (1 | Participant) +
  (1 | Stimule),
  data = bd)
```

**2.2.1.1 Model assumptions** The following functions ‘check\_model()’, ‘check\_distribution()’, and ‘check\_normality()’ are used to evaluate the quality of fit and distribution of residuals in a statistical model. For example, check\_model() could provide a visualization of residuals and diagnose problems such as heteroscedasticity or bias in the model. check\_distribution() could provide a visualization of the distribution of residuals and diagnose problems such as deviation from normality or outliers. check\_normality() could provide a normality test for the residuals of the model and evaluate whether normality assumptions are met.

```
check_model(mod2)
```



```
dist_checkmod2 <- check_distribution(mod2)
  kable(data.frame(dist_checkmod2),
  digits = 2, booktabs = TRUE,
  caption = "Distribution of residuals model 2") %>%
  kable_styling(latex_options = c("HOLD_position"))
```

**Table S7.** Distribution of residuals model 2

Distribution	p_Residuals	p_Response
bernoulli	0.00	0.03
beta	0.00	0.06
beta-binomial	0.03	0.00
binomial	0.00	0.06
cauchy	0.75	0.00
chi	0.00	0.00
exponential	0.03	0.06
F	0.00	0.00
gamma	0.03	0.00
half-cauchy	0.00	0.00
inverse-gamma	0.03	0.47
lognormal	0.00	0.00
neg. binomial (zero-infl.)	0.00	0.00
negative binomial	0.00	0.00
normal	0.12	0.00
pareto	0.00	0.00
poisson	0.00	0.03
poisson (zero-infl.)	0.00	0.06
tweedie	0.00	0.22
uniform	0.00	0.00
weibull	0.00	0.00

```
check_normality(mod2)
```

```
## Warning: Non-normality of residuals detected (p < .001).
```

**2.2.1.2 Summary model** To obtain a summary of model 2, the ‘summary’ function was used, which provides a summary of the coefficients of model 2, along with the standard deviation, t-value and associated p-value for each coefficient. Similarly, the ‘anova’ function returns an ANOVA table with information on the variance decomposition of model 2, sum of squares, degrees of freedom and associated F-statistics. Finally, the function ‘r2\_nakagawa’ is used to compute the pseudo R-squared proposed by Nakagawa & Schielzeth (2013) for mixed effects models. The pseudo R-squared is used to assess the goodness-of-fit of a model and is interpreted similarly to an R-squared in standard linear models.

```
anova.mod2 <- anova(mod2)

anova.mod2 <- as.data.frame(anova.mod2) |>
  rownames_to_column() |>
  mutate_at("rowname", str_replace_all, ":", " × ") |>
  mutate_at("rowname", str_replace_all, "stimulus_content",
            "Stimulus content")|>
  rename( Effect = rowname)|>
  kable(digits = 2, booktabs = TRUE,
        align = c("l", "l", rep("c", 4)),
        caption = "Effect of Stimulus
Content and Participant's Gender on Duration of first
Fixation (dff)",
        escape = FALSE)|>
  kable_styling(latex_options = c("hold_position"))
```

```
anova.mod2
```

**Table S8.** Effect of Stimulus Content and Participant's Gender on Duration of first Fixation (DFF)

Effect	Sum Sq	Mean Sq	NumDF	DenDF	F value	Pr(>F)
Stimulus content	5.38	1.79	3	15157.50	53.09	0.00
Gender	0.06	0.06	1	120.07	1.71	0.19
Stimulus content × Gender	0.06	0.02	3	15157.27	0.55	0.65

```
sum.mod2 <- summary(mod2)

sum.mod2_df <- as.data.frame(sum.mod2$coefficients) |>
  rownames_to_column() |>
  mutate_at("rowname", str_replace_all, ":" , " × ") |>
  mutate_at("rowname", str_replace_all,
            "stimulus_contentControl",
            "Stimulus content [Control]") |>
  mutate_at("rowname", str_replace_all,
            "stimulus_contentPositive",
            "Stimulus content [Positive]") |>
  mutate_at("rowname", str_replace_all,
            "stimulus_contentNeutral",
            "Stimulus content [Neutral]") |>
  mutate_at("rowname", str_replace_all,
            "GenderMale",
            "Gender [Male]") |>
  rename(Effect = rowname) |>
  kable(digits = 2, booktabs = TRUE,
        align = c("l", "l", rep("c", 4)),
        caption = "Duration of first
Fixation (DFF) by stimulus content,
gender and the interaction
between stimulus contentand gender",
        escape = FALSE) |>
  kable_styling(latex_options = c("HOLD_position"))

sum.mod2_df
```

**Table S9.** Duration of first Fixation (DFF) by stimulus content, gender and the interaction between stimulus contentand gender

Effect	Estimate	Std. Error	df	t value	Pr(> t )
(Intercept)	0.25	0.01	236.27	32.61	0.00
Stimulus content [Positive]	0.00	0.01	15156.58	-0.44	0.66
Stimulus content [Neutral]	0.01	0.01	15157.12	1.46	0.14
Stimulus content [Control]	0.04	0.01	15156.96	7.00	0.00
Gender [Male]	-0.01	0.01	228.74	-1.16	0.25
Stimulus content [Positive] × Gender [Male]	0.00	0.01	15157.24	0.37	0.71
Stimulus content [Neutral] × Gender [Male]	-0.01	0.01	15157.93	-0.68	0.50
Stimulus content [Control] × Gender [Male]	0.00	0.01	15157.84	0.50	0.62

```
r2mod2 <- r2_nakagawa(mod2)
r2_tblmod2 <- as_tibble(r2mod2)
kable(r2_tblmod2,
```

```

format = "markdown",
booktabs =TRUE,
align = "c", caption = "R model 2",
escape = FALSE) %>%
kable_styling(latex_options = c("HOLD_position"))

```

**Table S10.** *R model 2*

R2_conditional	R2_marginal
0.0674736	0.010673

**2.2.1.3 Estimated marginal means** Taking into account the obtained results, in the ANOVA-type table, where significant values for the stimulus content variable are observed, post-hoc tests are performed and the contrast between variables is presented.

```

mcm2 <- emmeans(mod2, pairwise ~ stimulus_content)

mcm2_emmeans <- tibble(data.frame(mcm2$emmeans)) |>
  rename(pri_fijacion_dur = emmean) |>
  select(-df)

contrasts_df2 <- as.data.frame(mcm2$contrasts) |>
  select(-df)

kable(contrasts_df2, digits = 5,
  booktabs =TRUE,
  align = "c",
  caption = "Contrasts between variables, according to the
content of the stimulus of model 2") %>%
kable_styling(latex_options = "HOLD_position",
  font_size = 12,
  full_width = FALSE)

```

**Table S11.** *Contrasts between variables, according to the content of the stimulus of model 2*

contrast	estimate	SE	z.ratio	p.value
Negative - Positive	0.00110	0.00419	0.26267	0.99366
Negative - Neutral	-0.00601	0.00420	-1.43223	0.47911
Negative - Control	-0.04467	0.00421	-10.61448	0.00000
Positive - Neutral	-0.00711	0.00420	-1.69234	0.32767
Positive - Control	-0.04577	0.00421	-10.86143	0.00000
Neutral - Control	-0.03866	0.00422	-9.16443	0.00000

## 2.2.2 Figure

Finally, for this model 2, a figure is shown in which the time for First fixation duration is observed according to the content of the stimulus and the respective differences between the variables are presented.

```

tbl.contrasts_df2 <- contrasts_df2 %>%
  mutate(.y. = "pri_fijacion_dur") %>%
  separate_wider_delim(contrast, " - ",
    names = c("group1", "group2")) %>%
  select(7, 1:6) %>%

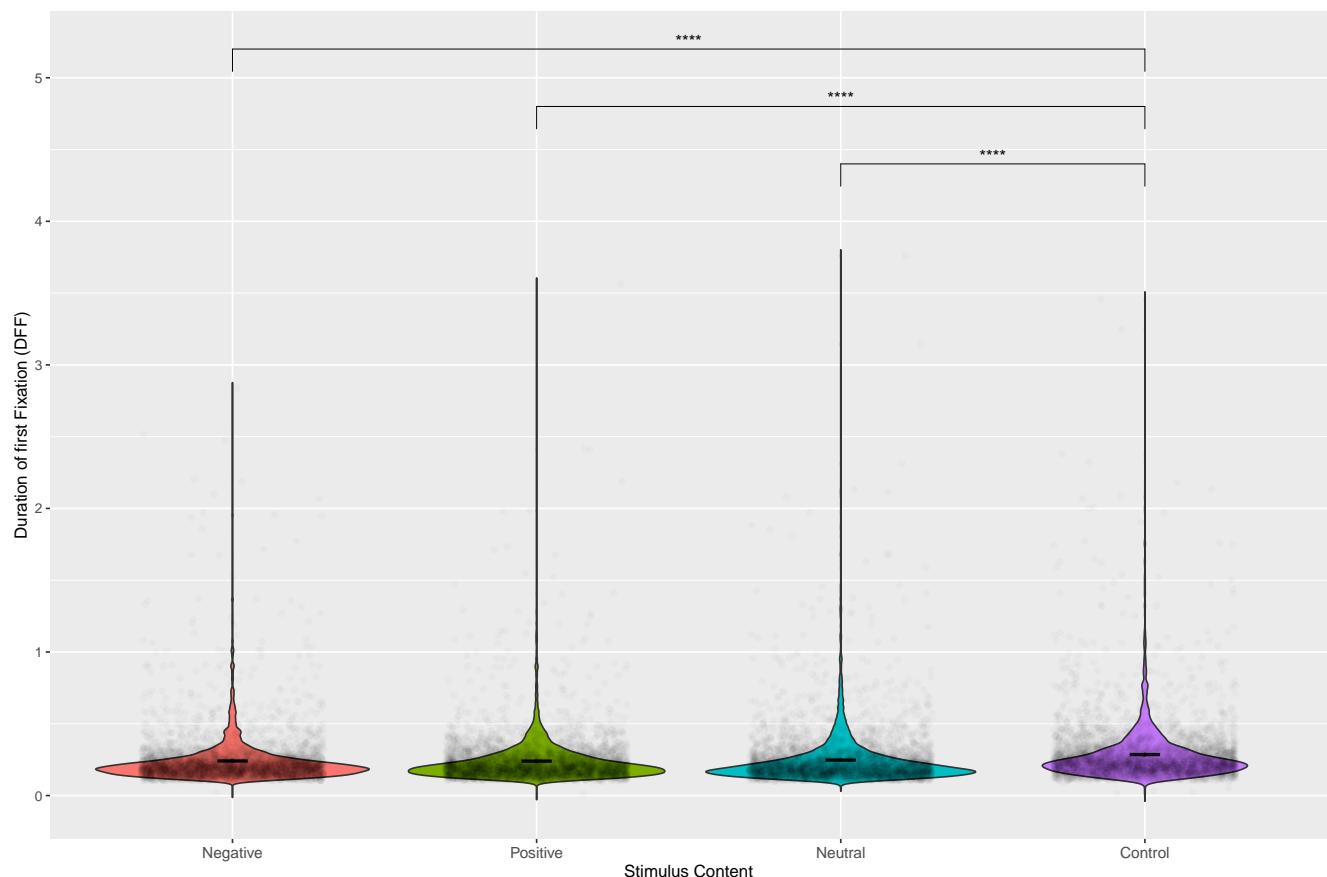
```

```

mutate(p.signif = pval.stars(p.value))

ggplot(bd, aes(x=stimulus_content,
                y=pri_fijacion_dur)) +
  geom_violin(trim = FALSE,
              aes(fill = stimulus_content)) +
  geom_jitter(alpha = 0.02, width = 0.3) +
  geom_errorbar(data = mcm2_emmeans,
                 mapping =
                 aes(ymin = pri_fijacion_dur-SE,
                     ymax = pri_fijacion_dur+SE),
                 colour = "black", width = 0.1) +
  geom_point(data = mcm2_emmeans,
             shape = 50, size = 1,
             color = "black", fill = "white") +
  stat_pvalue_manual(tbl.contrasts_df2,
                     label = "p.signif",
                     y.position = c(2.5, 4.2, 5.2, 3.9, 4.8, 4.4)) +
  labs(x = "Stimulus Content",
       y = "Duration of first Fixation (DFF)",
       fill = " ")
  theme(axis.text.x = element_text(size = 10))+
  guides(fill = FALSE)

```



**Figure S2.** Dimension between the emotional content of the stimulus, images with negative, positive, neutral and control emotional content, see Table S11, where the contrasts between each dimension are observed. In all cases, significant effects are represented with lines and stars: \* $p < .05$ , \*\* $p < .01$ , \*\*\* $p < .001$ , \*\*\*\* $p < .0001$ .

### 2.2.3 Bootstrap

Considering that the model did not behave normally, the distribution was estimated using Bootstrap. The bootstrap method is used to generate multiple samples of data from the original sample and, from them, obtain a sampling distribution of the statistic of interest, which allows estimating the variability and uncertainty associated with the statistic of interest, in this case the Duration of first Fixation (DFF).

```
set.seed(824)
B <- 10000

mod2_boot <- bootstrap(mod2, .f = fixef, type = "residual", B = B)
matriz_mod2 <- as.matrix(mod2_boot$stats)

columnas_a_convertir <- c("observed", "rep.mean", "se", "bias")

boots_mod2_table <- as.data.frame(matriz_mod2) |>
  mutate_at("term", str_replace_all, ":" , " × ") |>
  mutate_at("term", str_replace_all, "stimulus_contentControl",
            "Stimulus content [Control]")|>
  mutate_at("term", str_replace_all, "stimulus_contentPositive",
            "Stimulus content [Positive]")|>
  mutate_at("term", str_replace_all, "stimulus_contentNeutral",
            "Stimulus content [Neutral]")|>
  mutate_at("term", str_replace_all, "GenderMale",
            "Gender [Male]")|>
  mutate(across(all_of(columnas_a_convertir), as.numeric))

bootstrap_mod2 <- as.data.frame(confint(mod2_boot,
                                         type = "basic")) |>
  mutate_at("term", str_replace_all, ":" , " × ") |>
  mutate_at("term", str_replace_all, "stimulus_contentControl",
            "Stimulus content [Control]")|>
  mutate_at("term", str_replace_all, "stimulus_contentPositive",
            "Stimulus content [Positive]")|>
  mutate_at("term", str_replace_all, "stimulus_contentNeutral",
            "Stimulus content [Neutral]")|>
  mutate_at("term", str_replace_all, "GenderMale",
            "Gender [Male]")

unidas_mod2 <- merge(boots_mod2_table, bootstrap_mod2, by = "term")|>
  select(-estimate, -type, -level)

unidas_mod2 <- arrange(unidas_mod2,
                       match(term, orden_deseado)) |>
  kable(digits = 4, booktabs = TRUE,
        align = c("l", "l", rep("c", 4)),
        caption = "Bootstrap estimated values of model 2",
        escape = FALSE) |>
  kable_styling(latex_options = c("HOLD_position"))

unidas_mod2
```

**Table S12.** Bootstrap estimated values of model 2

term	observed	rep.mean	se	bias	lower	upper
(Intercept)	0.2465	0.2466	0.0058	0e+00	0.2351	0.2580
Stimulus content [Positive]	-0.0027	-0.0026	0.0060	1e-04	-0.0144	0.0091
Stimulus content [Neutral]	0.0088	0.0089	0.0060	0e+00	-0.0028	0.0207
Stimulus content [Control]	0.0426	0.0427	0.0060	1e-04	0.0310	0.0542
Gender [Male]	-0.0113	-0.0114	0.0097	-1e-04	-0.0299	0.0078
Stimulus content [Positive] × Gender [Male]	0.0031	0.0031	0.0083	0e+00	-0.0132	0.0192
Stimulus content [Neutral] × Gender [Male]	-0.0057	-0.0056	0.0083	0e+00	-0.0218	0.0105
Stimulus content [Control] × Gender [Male]	0.0042	0.0041	0.0083	-1e-04	-0.0123	0.0206

## 2.3 First fixation count

It is a measure of early attention, in which the way it is measured is by counting the number of times a stimulus was first seen in competition with other stimuli.

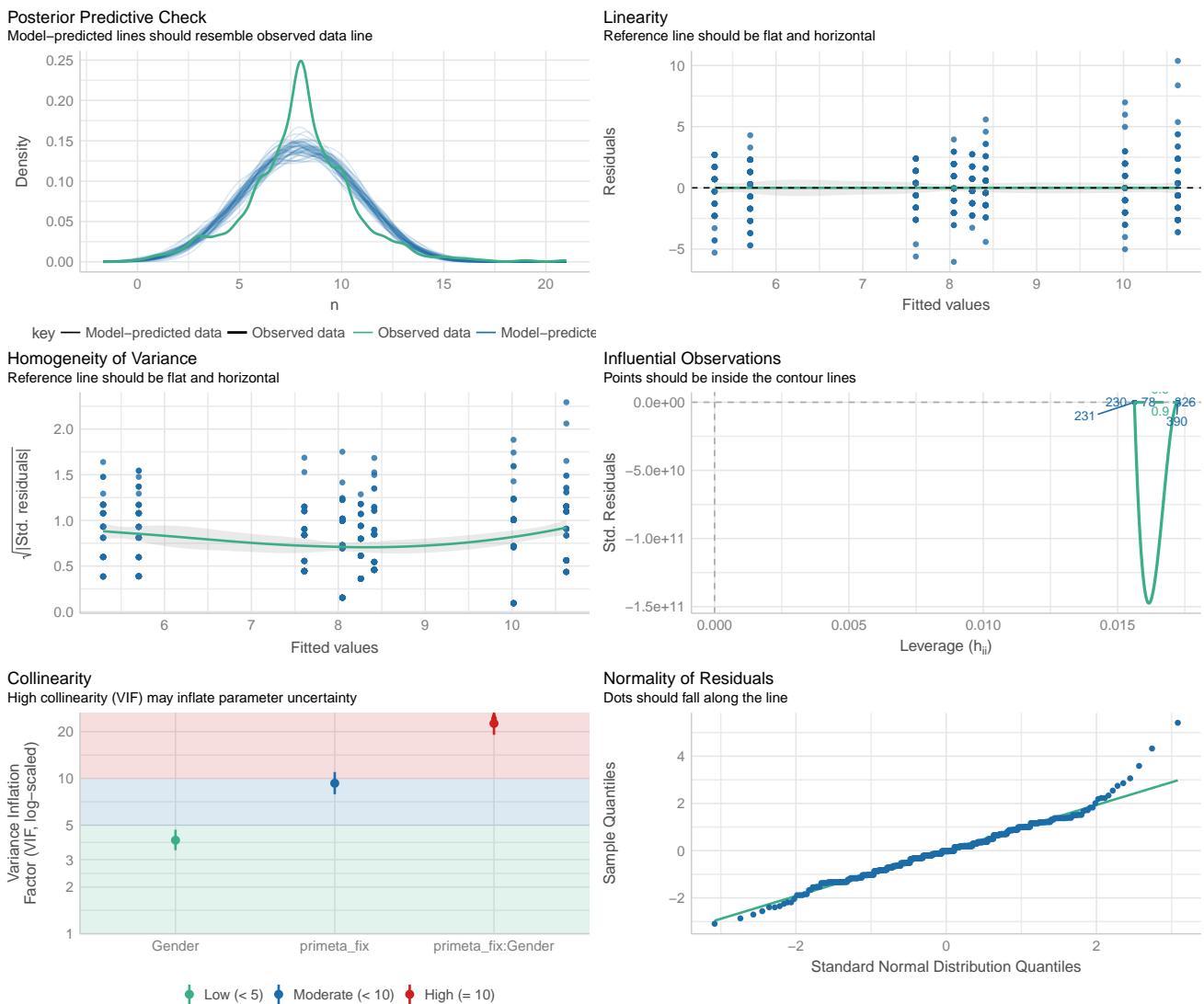
### 2.3.1 Fit model

For the third model, it is a linear regression to predict the number of first fixations through the variables stimulus type and its interaction with the participant's gender.

```
mod3 <- lm(n ~ primeta_fix * Gender, data = pf)
```

**2.3.1.1 Model assumptions** To obtain a summary of model 3, the ‘summary’ function was used, which provides a summary of the coefficients of model 3, along with the standard deviation, t-value and associated p-value for each coefficient. Similarly, the ‘anova’ function returns an ANOVA table with information on the variance decomposition of model 3, sum of squares, degrees of freedom and associated F-statistics.

```
check_model(mod3)
```



```
dist_checkmod3 <- check_distribution(mod3)
kable(data.frame(dist_checkmod3),
      digits = 2, booktabs = TRUE,
      caption = "Distribution of residuals model 3") %>%
  kable_styling(latex_options = c("HOLD_position"))
```

**Table S13.** Distribution of residuals model 3

Distribution	p_Residuals	p_Response
bernoulli	0.00	0.00
beta	0.00	0.00
beta-binomial	0.03	0.12
binomial	0.00	0.44
cauchy	0.22	0.00
chi	0.00	0.00
exponential	0.00	0.00
F	0.00	0.00
gamma	0.00	0.00
half-cauchy	0.00	0.00
inverse-gamma	0.00	0.00
lognormal	0.00	0.00
neg. binomial (zero-infl.)	0.00	0.06
negative binomial	0.09	0.09
normal	0.47	0.00
pareto	0.00	0.00
poisson	0.03	0.25
poisson (zero-infl.)	0.00	0.03
tweedie	0.16	0.00
uniform	0.00	0.00
weibull	0.00	0.00

```
check_normality(mod3)
```

```
## Warning: Non-normality of residuals detected (p < .001).
```

**2.3.1.2 Summary model** To obtain a summary of model 3, the ‘summary’ function was used, which provides a summary of the coefficients of model 3, along with the standard deviation, t-value, and associated p-value for each coefficient. Similarly, the ‘anova’ function returns an ANOVA table with information on the variance decomposition of model 3, sum of squares, degrees of freedom, and associated F-statistics.

```
anova.mod3 <- as.data.frame(car::Anova(mod3, type = 3)) |>
  rownames_to_column() |>
  mutate_at("rowname", str_replace_all, ":" , " × ") |>
  mutate_at("rowname", str_replace_all, "primeta_fix",
           "Stimulus content") |>
  rename( Effect = rowname) |>
  kable(digits = 2, booktabs = TRUE,
        align = c("l", "l", rep("c", 4)),
        caption = "Effect of Stimulus Content and Participant's Gender on First Fixation Count (FFC)",
        escape = FALSE) |>
  kable_styling(latex_options = c("hold_position"))

anova.mod3
```

```
sum.mod3 <- summary(mod3)
sum.mod3_df <- as.data.frame(sum.mod3$coefficients) |>
  rownames_to_column() |>
  mutate_at("rowname", str_replace_all, ":" , " × ") |>
  mutate_at("rowname", str_replace_all,
```

**Table S14.** Effect of Stimulus Content and Participant's Gender on First Fixation Count (FFC)

Effect	Sum Sq	Df	F value	Pr(>F)
(Intercept)	5820.02	1	1472.92	0.00
Stimulus content	674.81	3	56.93	0.00
Gender	11.24	1	2.84	0.09
Stimulus content × Gender	37.41	3	3.16	0.02
Residuals	1896.64	480		

```

"primeta_fixControl",
"Stimulus content [Control])|>
mutate_at("rowname", str_replace_all,
"primeta_fixPositive",
"Stimulus content [Positive])|>
mutate_at("rowname", str_replace_all,
"primeta_fixNeutral",
"Stimulus content [Neutral])|>
mutate_at("rowname", str_replace_all,
"GenderMale",
"Gender [Male]) |>
rename( Effect = rowname)|>
kable(digits = 2, booktabs = TRUE,
align = c("l", "l", rep("c", 4)),
caption = "First Fixation Count (FFC)
by stimylus content,
gender and the interaction
between stimulus contentand gender", escape = FALSE) |>
kable_styling(latex_options = c("HOLD_position"))

sum.mod3_df

```

**Table S15.** First Fixation Count (FFC) by stimylus content, gender and the interaction between stimulus contentand gender

Effect	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	10.02	0.26	38.38	0.00
Stimulus content [Positive]	-1.60	0.37	-4.34	0.00
Stimulus content [Neutral]	-1.76	0.37	-4.76	0.00
Stimulus content [Control]	-4.72	0.37	-12.80	0.00
Gender [Male]	0.61	0.36	1.69	0.09
Stimulus content [Positive] × Gender [Male]	-1.41	0.51	-2.77	0.01
Stimulus content [Neutral] × Gender [Male]	-0.82	0.51	-1.61	0.11
Stimulus content [Control] × Gender [Male]	-0.20	0.51	-0.39	0.70

**2.3.1.3 Estimated marginal means** Taking into account the results obtained in the ANOVA table, where significant values are observed for the stimulus content variable, but also for the interaction between stimulus content and gender, post-hoc tests were performed and the contrast between variables is presented.

```

mcm3 <- emmeans(mod3, pairwise ~ primeta_fix * Gender)

mcm3_emmeans <- tibble(data.frame(mcm3$emmeans)) |>
  rename(primeria_fij = emmean)|>
  select(-df)

```

```

contrasts_df3 <- as.data.frame(mcm3$contrasts) |>
  select(-df)

kable(contrasts_df3, digits = 5,
      booktabs =TRUE,
      align = "c",
      caption = "Contrasts between variables, according to the
      content of the stimulus of model 3") %>%
  kable_styling(latex_options = "HOLD_position",
                font_size = 12,
                full_width = FALSE)

```

**Table S16.** *Contrasts between variables, according to the content of the stimulus of model 3*

contrast	estimate	SE	t.ratio	p.value
Negative Female - Positive Female	1.60345	0.36912	4.34392	0.00045
Negative Female - Neutral Female	1.75862	0.36912	4.76430	0.00007
Negative Female - Control Female	4.72414	0.36912	12.79822	0.00000
Negative Female - Negative Male	-0.60776	0.36037	-1.68649	0.69611
Negative Female - Positive Male	2.40787	0.36037	6.68166	0.00000
Negative Female - Neutral Male	1.97037	0.36037	5.46763	0.00000
Negative Female - Control Male	4.31412	0.36037	11.97137	0.00000
Positive Female - Neutral Female	0.15517	0.36912	0.42038	0.99989
Positive Female - Control Female	3.12069	0.36912	8.45430	0.00000
Positive Female - Negative Male	-2.21121	0.36037	-6.13594	0.00000
Positive Female - Positive Male	0.80442	0.36037	2.23220	0.33431
Positive Female - Neutral Male	0.36692	0.36037	1.01817	0.97162
Positive Female - Control Male	2.71067	0.36037	7.52191	0.00000
Neutral Female - Control Female	2.96552	0.36912	8.03392	0.00000
Neutral Female - Negative Male	-2.36638	0.36037	-6.56654	0.00000
Neutral Female - Positive Male	0.64925	0.36037	1.80161	0.61931
Neutral Female - Neutral Male	0.21175	0.36037	0.58758	0.99902
Neutral Female - Control Male	2.55550	0.36037	7.09132	0.00000
Control Female - Negative Male	-5.33190	0.36037	-14.79564	0.00000
Control Female - Positive Male	-2.31627	0.36037	-6.42749	0.00000
Control Female - Neutral Male	-2.75377	0.36037	-7.64152	0.00000
Control Female - Control Male	-0.41002	0.36037	-1.13778	0.94818
Negative Male - Positive Male	3.01563	0.35140	8.58184	0.00000
Negative Male - Neutral Male	2.57813	0.35140	7.33680	0.00000
Negative Male - Control Male	4.92187	0.35140	14.00662	0.00000
Positive Male - Neutral Male	-0.43750	0.35140	-1.24503	0.91792
Positive Male - Control Male	1.90625	0.35140	5.42479	0.00000
Neutral Male - Control Male	2.34375	0.35140	6.66982	0.00000

### 2.3.2 Figure

Taking into account the results obtained in the ANOVA table, where significant values are observed for the stimulus content variable, but also for the interaction between stimulus content and gender, post-hoc tests were performed

and the contrast between variables is presented. The values by gender are presented in different panels to observe the respective differences.

```

contrastes_hom <- c("Neutral Male - Control Male",
                     "Positive Male - Control Male",
                     "Positive Male - Neutral Male",
                     "Negative Male - Control Male",
                     "Negative Male - Neutral Male",
                     "Negative Male - Positive Male")

pf_hom <- filter(pf, Gender == "Male") |>
  na.omit(pf) |>
  rename(stimulus_content = primeta_fix) |>
  rename(pri_fijacion_dur = n)

contrasts_df3_hom <- filter(contrasts_df3, contrast %in% contrastes_hom)

tbl.contrasts_df3_hom <- contrasts_df3_hom %>%
  mutate(.y. = "primeta_fix") %>%
  separate_wider_delim(contrast, " - ",
                        names = c("group1", "group2")) %>%
  select(7, 1:6) %>%
  mutate(p.signif = pval.stars(p.value)) |>
  mutate_at("group1", str_replace_all, "Negative Male",
            "Negative") |>
  mutate_at("group1", str_replace_all, "Positive Male",
            "Positive") |>
  mutate_at("group1", str_replace_all, "Neutral Male",
            "Neutral") |>
  mutate_at("group2", str_replace_all, "Positive Male",
            "Positive") |>
  mutate_at("group2", str_replace_all, "Neutral Male",
            "Neutral") |>
  mutate_at("group2", str_replace_all, "Control Male",
            "Control")

mcm3_emmeans_hom <- filter(mcm3_emmeans, Gender == "Male") |>
  select(-Gender) |>
  rename(stimulus_content = primeta_fix) |>
  rename(pri_fijacion_dur = primera_fij) |>
  rename(asymp.LCL = lower.CL) |>
  rename(asymp.UCL = upper.CL)

ggplot_male <- ggplot(pf_hom, aes(x=stimulus_content,
                                     y=pri_fijacion_dur)) +
  geom_violin(trim = FALSE,
              aes(fill = stimulus_content)) +
  geom_jitter(alpha = 0.04, width = 0.3) +
  geom_errorbar(data = mcm3_emmeans_hom,
                mapping =
                  aes(ymin = pri_fijacion_dur-SE,
                      ymax = pri_fijacion_dur+SE),
                colour = "black", width = 0.1) +
  geom_point(data = mcm3_emmeans_hom,
```

```

        shape = 21, size = 2,
        color = "black", fill = "white") +
stat_pvalue_manual(tbl.contrasts_df3_hom,
                   label = "p.signif",
                   y.position = c(25, 29, 31, 27, 27, 25)) +
labs(x = "Stimulus Content",
     y = " ",
     fill = " ") +
guides(fill = FALSE) +
theme(axis.text.x = element_text(size = 10))

contrastes_muj <- c("Negative Female - Positive Female",
                     "Negative Female - Neutral Female",
                     "Negative Female - Control Female",
                     "Positive Female - Neutral Female",
                     "Positive Female - Control Female",
                     "Neutral Female - Control Female")

pf_muj <- filter(pf, Gender == "Female") |>
  na.omit(pf) |>
  rename(stimulus_content = primeta_fix) |>
  rename(pri_fijacion_dur = n)

contrasts_df3_muj <- filter(contrasts_df3, contrast %in% contrastes_muj)

tbl.contrasts_df3_muj <- contrasts_df3_muj %>%
  mutate(.y. = "primeta_fix") %>%
  separate_wider_delim(contrast, " - ",
                        names = c("group1", "group2")) %>%
  select(7, 1:6) %>%
  mutate(p.signif = pval.stars(p.value)) |>
  mutate_at("group1", str_replace_all, "Negative Female",
            "Negative") |>
  mutate_at("group1", str_replace_all, "Positive Female",
            "Positive") |>
  mutate_at("group1", str_replace_all, "Neutral Female",
            "Neutral") |>
  mutate_at("group2", str_replace_all, "Positive Female",
            "Positive") |>
  mutate_at("group2", str_replace_all, "Neutral Female",
            "Neutral") |>
  mutate_at("group2", str_replace_all, "Control Female",
            "Control")

mcm3_emmeans_muj <- filter(mcm3_emmeans, Gender == "Female") |>
  select(-Gender) |>
  rename(stimulus_content = primeta_fix) |>
  rename(pri_fijacion_dur = primera_fij) |>
  rename(asymp.LCL = lower.CL) |>
  rename(asymp.UCL = upper.CL)

ggplot_female <- ggplot(pf_muj, aes(x=stimulus_content,

```

```

y=pri_fijacion_dur)) +
geom_violin(trim = FALSE,
            aes(fill = stimulus_content)) +
geom_jitter(alpha = 0.04, width = 0.3) +
geom_errorbar(data = mcm3_emmeans_muj,
               mapping =
                  aes(ymin = pri_fijacion_dur-SE,
                      ymax = pri_fijacion_dur+SE),
                  colour = "black", width = 0.1) +
geom_point(data = mcm3_emmeans_muj,
            shape = 21, size = 2,
            color = "black", fill = "white") +
stat_pvalue_manual(tbl.contrasts_df3_muj,
                   label = "p.signif",
                   y.position = c(25, 29, 31, 27, 27, 25)) +
labs(x = "Stimulus Content",
      y = "First Fixation Count (FFC)",
      fill = " ") +
guides(fill = FALSE) +
theme(axis.text.x = element_text(size = 10))

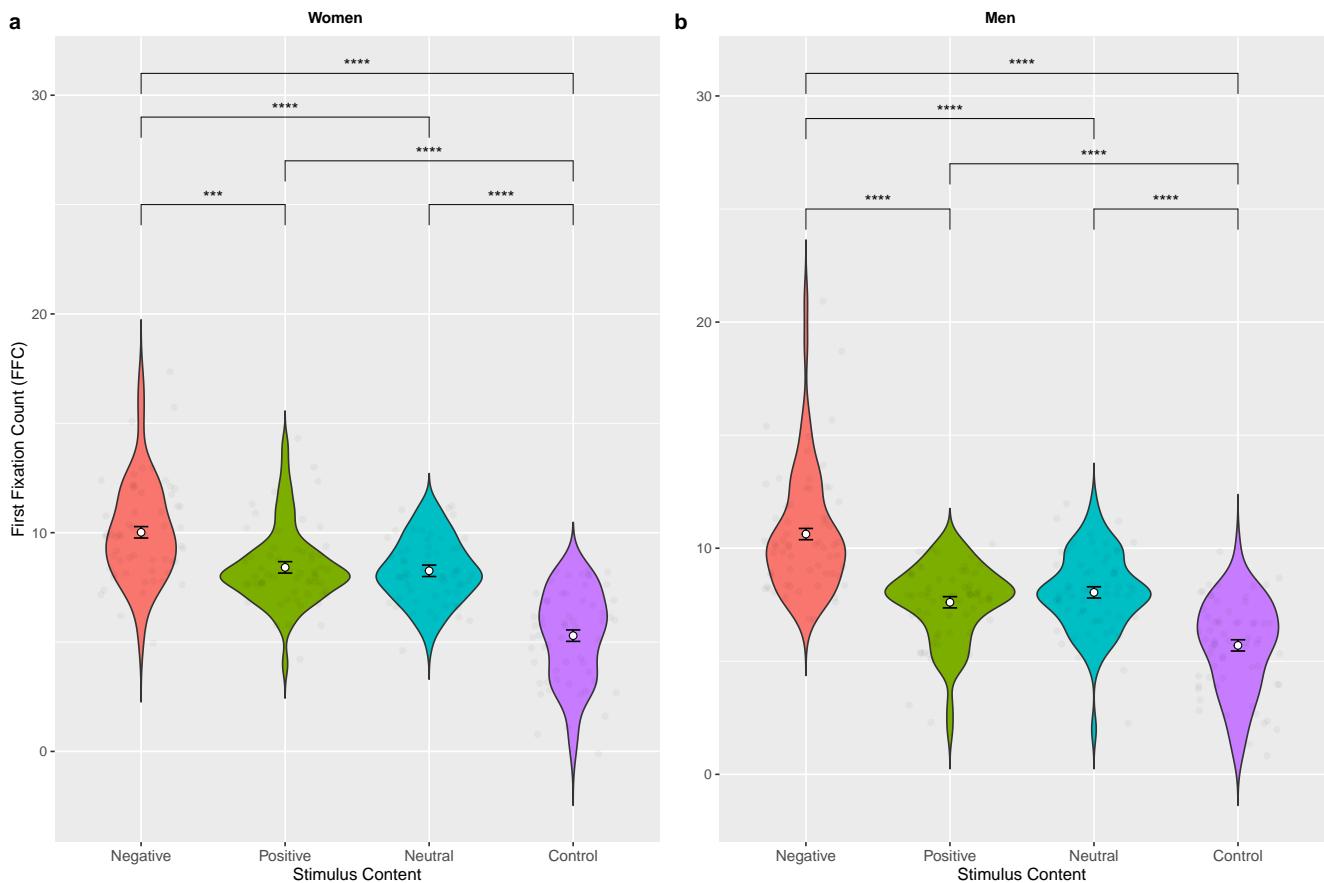
ggplot_female <- annotate_figure(ggplot_female, top = text_grob("Women",
                                                               color = "black", face = "bold", size = 10))

ggplot_male <- annotate_figure(ggplot_male, top = text_grob("Men",
                                                               color = "black", face = "bold", size = 10))

figura_ffc <- ggarrange(ggplot_female, ggplot_male,
                         nrow = 1,
                         labels = "auto")

figura_ffc

```



**Figure S3.** Dimension between the emotional content of the stimulus, images with negative, positive, neutral and control emotional content, by gender of the participants, see Table S16, where the contrasts between each dimension are observed. In all cases, significant effects are represented with lines and stars: \* $p < .05$ , \*\* $p < .01$ , \*\*\* $p < .001$ , \*\*\*\* $p < .0001$ .

### 2.3.3 Bootstrap

Considering that model 3 is a linear regression, the respective Bootstrap functions are proposed. Considering that the model did not behave normally, the distribution was estimated using Bootstrap. The bootstrap method is used to generate multiple samples of data from the original sample and, from them, obtain a sampling distribution of the statistic of interest, which allows estimating the variability and uncertainty associated with the statistic of interest, in this case the First Fixation Count (FFC).

```
set.seed(824)

term <- c("(Intercept)",
          "Stimulus content [Positive]",
          "Stimulus content [Neutral]",
          "Stimulus content [Control]",
          "Gender [Male]",
          "Stimulus content [Positive]×Gender [Male]",
          "Stimulus content [Neutral]×Gender [Male]",
          "Stimulus content [Control]×Gender [Male]")

N = 10000 #Número de Bootstrap
boots <- function(dat=pf, mod.formula = formula(n ~ primeta_fix * Gender)){
  dat.boot <- dat[sample(x = nrow(dat), size =nrow(dat), replace = T),]
  boot.lm <- lm(mod.formula, data=dat.boot)
  coef(boot.lm)
}
```

```

vector.boot <- t(replicate(N,boots()))

boots_mod3_table <- t(apply(vector.boot, MARGIN = 2,
                             quantile,
                             probs= c(0.025,0.975)))

boots_mod3_table <- as.data.frame(confint(mod3)) |>
  cbind(term) |>
  select(3,1:2) |>
  rename(lower = "2.5 %") |>
  rename(upper = "97.5 %") |>
  sapply(unname)

boots2 <- function(data= pf, index){
  data <- data [index,]
  model.boot <- lm(n ~ primeta_fix * Gender, data =data)
  coef(model.boot)
}

bootstrappel <- boot(pf,boots2, R = 10000) #Número de Bootstrap

matriz_mod3 <- as.data.frame(as.matrix(bootstrappel$t))

x <- 8 #Número para el for, cantidad de columnas

for (i in seq(1, ncol(matriz_mod3), x)) {
  grupo_columnas <- i:(i + x - 1)
  bias   <- colMeans(matriz_mod3[, grupo_columnas])
}

for (i in seq(1, ncol(matriz_mod3), x)) {
  grupo_columnas <- i:(i + x - 1)
  se <- apply(matriz_mod3[, grupo_columnas], 2, sd)
}

bootstrap_mod3 <-  as.data.frame(as.matrix(bootstrappel$t0)) |>
  cbind(term) |>
  select(2,1)|>
  mutate(rep.mean = bias)|>
  mutate(se = se) |>
  mutate(bias = bias-bootstrappel$t0) |>
  rename("observed" = V1)  |>
  sapply(unname)

columnas_a_convertir_mod3 <- c("observed", "rep.mean", "se", "bias", "lower", "upper")
unidas_mod3 <- merge(bootstrap_mod3, boots_mod3_table, by = "term") |>
  mutate(across(all_of(columnas_a_convertir_mod3), as.numeric))

unidas_mod3 <- arrange(unidas_mod3,
                        match(term, orden_deseado)) |>
  kable(digits = 4, booktabs = TRUE,
        align = c("l", "l", rep("c", 4)),

```

```

  caption = "Bootstrap estimated values of model 3",
  escape = FALSE) |>
  kable_styling(latex_options = c("HOLD_position"))

unidas_mod3

```

**Table S17.** *Bootstrap estimated values of model 3*

term	observed	rep.mean	se	bias	lower	upper
(Intercept)	10.0172	10.0146	0.3017	-0.0026	9.5044	10.5301
Stimulus content [Positive]	-1.6034	-1.5998	0.3816	0.0037	-2.3287	-0.8781
Stimulus content [Neutral]	-1.7586	-1.7582	0.3544	0.0004	-2.4839	-1.0333
Stimulus content [Control]	-4.7241	-4.7210	0.4070	0.0032	-5.4494	-3.9988
Gender [Male]	0.6078	0.6082	0.4500	0.0004	-0.1003	1.3159
Stimulus content [Control]×Gender [Male]	-0.1977	-0.1992	0.5840	-0.0015	-1.1991	0.8037
Stimulus content [Neutral]×Gender [Male]	-0.8195	-0.8188	0.5314	0.0007	-1.8209	0.1819
Stimulus content [Positive]×Gender [Male]	-1.4122	-1.4113	0.5474	0.0009	-2.4136	-0.4108

## 2.4 Total Duration of Fixation

The Total Duration of Fixation is a measure of delayed attention, which consists of the total time that the participant observes a stimulus. It should be noted that it is the cumulative time of each time the participant decides to view the image.

### 2.4.1 Fit model

For the fourth model, the total duration of fixation is predicted by the variables stimulus type and the interaction with the participant's sex. In addition, there are random intercepts for the participant. This means that each participant is expected to have his or her own effect on the response variable, rather than having a constant effect in all cases. The random effect of the stimulus was removed because the model was reported to be singular with this variable.

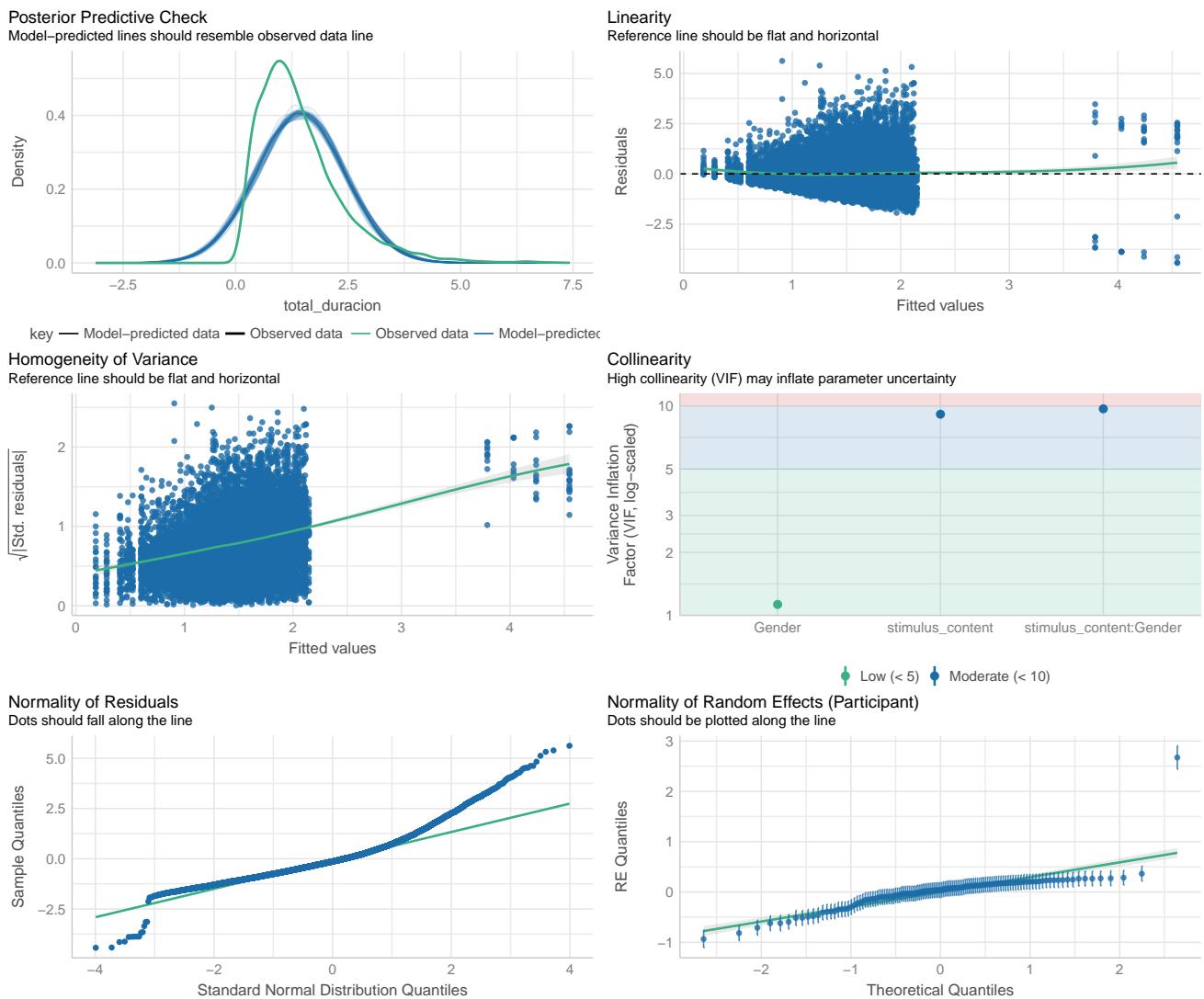
```

mod4 <- lmer(total_duracion ~ stimulus_content * Gender +
               (1 | Participant),
               data = bd)

```

**2.4.1.1 Model assumptions** The following functions ‘check\_model()’, ‘check\_distribution()’, and ‘check\_normality()’ are used to evaluate the quality of fit and distribution of residuals in a statistical model. For example, check\_model() could provide a visualization of residuals and diagnose problems such as heteroscedasticity or bias in the model. check\_distribution() could provide a visualization of the distribution of residuals and diagnose problems such as deviation from normality or outliers. check\_normality() could provide a normality test for the residuals of the model and evaluate whether normality assumptions are met.

```
check_model(mod4)
```



```
dist_checkmod4 <- check_distribution(mod4)
kable(data.frame(dist_checkmod4),
      digits = 2, booktabs = TRUE,
      caption = "Distribution of residuals model 4") %>%
  kable_styling(latex_options = c("HOLD_position"))
```

**Table S18.** Distribution of residuals model 4

Distribution	p_Residuals	p_Response
bernoulli	0.00	0.00
beta	0.00	0.00
beta-binomial	0.00	0.00
binomial	0.00	0.00
cauchy	0.50	0.00
chi	0.00	0.00
exponential	0.03	0.03
F	0.00	0.09
gamma	0.03	0.31
half-cauchy	0.00	0.00
inverse-gamma	0.00	0.09
lognormal	0.00	0.03
neg. binomial (zero-infl.)	0.00	0.00
negative binomial	0.00	0.00
normal	0.12	0.00
pareto	0.00	0.00
poisson	0.00	0.00
poisson (zero-infl.)	0.00	0.00
tweedie	0.31	0.44
uniform	0.00	0.00
weibull	0.00	0.00

```
check_normality(mod4)
```

```
## Warning: Non-normality of residuals detected (p < .001).
```

**2.4.1.2 Summary model** To obtain a summary of model 4, the ‘summary’ function was used, which provides a summary of the coefficients of model 4, along with the standard deviation, t-value, and associated p-value for each coefficient. Similarly, the ‘anova’ function returns an ANOVA table with information on the variance decomposition of model 4, sum of squares, degrees of freedom, and associated F-statistics. Finally, the ‘r2\_nakagawa’ function is used to calculate the pseudo R-squared proposed by Nakagawa & Schielzeth (2013) for mixed-effects models. The pseudo R-squared is used to evaluate the goodness of fit of a model and is interpreted similarly to an R-squared in standard linear models.

```
anova.mod4 <- anova(mod4)

anova.mod4 <- as.data.frame(anova.mod4) |>
  rownames_to_column() |>
  mutate_at("rowname", str_replace_all, ":" , " × ") |>
  mutate_at("rowname", str_replace_all, "stimulus_content",
           "Stimulus content")|>
  rename( Effect = rowname)|>
  kable(digits = 2, booktabs = TRUE,
        align = c("l", "l", rep("c", 4)),
        caption = "Effect of Stimulus Content and Participant's Gender on Total Duration of Fixations (TDF)",
        escape = FALSE)|>
  kable_styling(latex_options = c("hold_position"))
```

```
anova.mod4
```

**Table S19.** Effect of Stimulus Content and Participant's Gender on Total Duration of Fixations (TDF)

Effect	Sum Sq	Mean Sq	NumDF	DenDF	F value	Pr(>F)
Stimulus content	1012.40	337.47	3	15178.97	451.78	0.00
Gender	0.94	0.94	1	112.11	1.26	0.26
Stimulus content × Gender	7.03	2.34	3	15178.97	3.14	0.02

```
sum.mod4 <- summary(mod4)

sum.mod4_df <- as.data.frame(sum.mod4$coefficients) |>
  rownames_to_column() |>
  mutate_at("rowname", str_replace_all, ":" , " × ") |>
  mutate_at("rowname", str_replace_all,
            "stimulus_contentControl",
            "Stimulus content [Control]") |>
  mutate_at("rowname", str_replace_all,
            "stimulus_contentPositive",
            "Stimulus content [Positive]") |>
  mutate_at("rowname", str_replace_all,
            "stimulus_contentNeutral",
            "Stimulus content [Neutral]") |>
  mutate_at("rowname", str_replace_all,
            "GenderMale",
            "Gender [Male]") |>
  rename( Effect = rowname) |>
  kable(digits = 2, booktabs = TRUE,
        align = c("l", "l", rep("c", 4)),
        caption = "Total Duration of Fixations (TDF)
by stimulus content,
gender and the interaction
between stimulus content and gender",
        escape = FALSE) |>
  kable_styling(latex_options = c("HOLD_position"))

sum.mod4_df
```

**Table S20.** Total Duration of Fixations (TDF) by stimulus content, gender and the interaction between stimulus content and gender

Effect	Estimate	Std. Error	df	t value	Pr(> t )
(Intercept)	1.74	0.05	142.51	33.60	0.00
Stimulus content [Positive]	-0.24	0.03	15178.67	-8.45	0.00
Stimulus content [Neutral]	-0.45	0.03	15178.86	-15.79	0.00
Stimulus content [Control]	-0.64	0.03	15178.80	-22.23	0.00
Gender [Male]	0.14	0.07	142.69	1.94	0.05
Stimulus content [Positive] × Gender [Male]	-0.07	0.04	15178.99	-1.68	0.09
Stimulus content [Neutral] × Gender [Male]	-0.06	0.04	15179.29	-1.63	0.10
Stimulus content [Control] × Gender [Male]	-0.12	0.04	15179.19	-3.06	0.00

```
r2mod4 <- r2_nakagawa(mod4)
r2_tblmod4 <- as_tibble(r2mod4)
kable(r2_tblmod4, format = "markdown", booktabs =TRUE,
```

```


```

**Table S21.** *R model 4*

R2_conditional	R2_marginal
0.2112924	0.0724757

**2.4.1.3 Estimated marginal means** Taking into account the results obtained in the ANOVA table, where significant values are observed for the stimulus content variable, post-hoc tests are performed and the contrast between variables is presented.

```
mcm4 <- emmeans(mod4, pairwise ~ stimulus_content * Gender)

mcm4_emmeans <- tibble(data.frame(mcm4$emmeans)) |>
  rename(total_duracion = emmean) |>
  select(-df)

contrasts_df4 <- as.data.frame(mcm4$contrasts) |>
  select(-df)

kable(contrasts_df4, digits = 5,
      booktabs =TRUE,
      align = "c",
      caption = "Contrasts between variables, according to the
content of the stimulus of model 4") %>%
kable_styling(latex_options = "HOLD_position",
              font_size = 12,
              full_width = FALSE)
```

**Table S22.** Contrasts between variables, according to the content of the stimulus of model 4

contrast	estimate	SE	z.ratio	p.value
Negative Female - Positive Female	0.24067	0.02849	8.44821	0.00000
Negative Female - Neutral Female	0.45032	0.02852	15.78934	0.00000
Negative Female - Control Female	0.63567	0.02859	22.23348	0.00000
Negative Female - Negative Male	-0.13840	0.07139	-1.93862	0.52404
Negative Female - Positive Male	0.16841	0.07142	2.35792	0.26237
Negative Female - Neutral Male	0.37610	0.07143	5.26497	0.00000
Negative Female - Control Male	0.61842	0.07146	8.65392	0.00000
Positive Female - Neutral Female	0.20965	0.02853	7.34714	0.00000
Positive Female - Control Female	0.39500	0.02861	13.80867	0.00000
Positive Female - Negative Male	-0.37907	0.07140	-5.30918	0.00000
Positive Female - Positive Male	-0.07226	0.07143	-1.01156	0.97288
Positive Female - Neutral Male	0.13543	0.07144	1.89574	0.55382
Positive Female - Control Male	0.37775	0.07147	5.28563	0.00000
Neutral Female - Control Female	0.18535	0.02864	6.47251	0.00000
Neutral Female - Negative Male	-0.58872	0.07141	-8.24395	0.00000
Neutral Female - Positive Male	-0.28190	0.07144	-3.94585	0.00203
Neutral Female - Neutral Male	-0.07422	0.07145	-1.03865	0.96858
Neutral Female - Control Male	0.16810	0.07148	2.35170	0.26561
Control Female - Negative Male	-0.77408	0.07144	-10.83519	0.00000
Control Female - Positive Male	-0.46726	0.07147	-6.53769	0.00000
Control Female - Neutral Male	-0.25957	0.07148	-3.63125	0.00685
Control Female - Control Male	-0.01726	0.07151	-0.24131	1.00000
Negative Male - Positive Male	0.30682	0.02726	11.25390	0.00000
Negative Male - Neutral Male	0.51451	0.02729	18.85412	0.00000
Negative Male - Control Male	0.75682	0.02736	27.66317	0.00000
Positive Male - Neutral Male	0.20769	0.02735	7.59385	0.00000
Positive Male - Control Male	0.45000	0.02742	16.41166	0.00000
Neutral Male - Control Male	0.24231	0.02744	8.82975	0.00000

#### 2.4.2 Figure

Finally, for this model 4, a figure showing the total fixation time as a function of stimulus content and the respective differences between the variables is shown. The values by gender are presented in different panels to observe the respective differences.

```
pf_hom_mod4 <- filter(bd, Gender == "Male")

contrasts_df4_hom <- filter(contrasts_df4, contrast %in% contrastes_hom)

tbl.contrasts_df4_hom <- contrasts_df4_hom %>%
  mutate(.y. = "total_duracion") %>%
  separate_wider_delim(contrast, " - ",
                        names = c("group1", "group2")) %>%
  select(7, 1:6) %>%
  mutate(p.signif = pval.stars(p.value)) |>
  mutate_at("group1", str_replace_all, "Negative Male",
```

```

    "Negative")|>
mutate_at("group1", str_replace_all, "Positive Male",
          "Positive")|>
mutate_at("group1", str_replace_all, "Neutral Male",
          "Neutral")|>
mutate_at("group2", str_replace_all, "Positive Male",
          "Positive")|>
mutate_at("group2", str_replace_all, "Neutral Male",
          "Neutral")|>
mutate_at("group2", str_replace_all, "Control Male",
          "Control")

mcm4_emmeans_hom <- filter(mcm4_emmeans, Gender == "Male")|>
  select(-Gender)

ggplot_male_mod4 <- ggplot(pf_hom_mod4, aes(x=stimulus_content,
                                              y=total_duracion)) +
  geom_violin(trim = FALSE,
              aes(fill = stimulus_content)) +
  geom_jitter(alpha = 0.04, width = 0.3) +
  geom_errorbar(data = mcm4_emmeans_hom,
                 mapping =
                  aes(ymax = total_duracion+SE,
                      ymin = total_duracion-SE),
                 colour = "black", width = 0.1) +
  geom_point(data = mcm4_emmeans_hom,
              shape = 21, size = 2,
              color = "black", fill = "white") +
  stat_pvalue_manual(tbl.contrasts_df4_hom,
                     label = "p.signif",
                     y.position = c(10, 12, 14, 11, 13, 10)) +
  labs(x = "Stimulus Content",
       y = " ",
       fill = " ") +
  guides(fill = FALSE) +
  theme(axis.text.x = element_text(size = 10))

pf_muj_mod4 <- filter(bd, Gender == "Female")

contrasts_df4_muj <- filter(contrasts_df4, contrast %in% contrastes_muj)

tbl.contrasts_df4_muj <- contrasts_df4_muj %>%
  mutate(.y. = "total_duracion") %>%
  separate_wider_delim(contrast, " - ",
                        names = c("group1", "group2")) %>%
  select(7, 1:6) %>%
  mutate(p.signif = pval.stars(p.value))|>
  mutate_at("group1", str_replace_all, "Negative Female",
          "Negative")|>
  mutate_at("group1", str_replace_all, "Positive Female",
          "Positive")|>
  mutate_at("group1", str_replace_all, "Neutral Female",
          "Neutral")|>

```

```

  mutate_at("group2", str_replace_all, "Positive Female",
            "Positive") |>
  mutate_at("group2", str_replace_all, "Neutral Female",
            "Neutral") |>
  mutate_at("group2", str_replace_all, "Control Female",
            "Control")

mcm4_emmeans_muj <- filter(mcm4_emmeans, Gender == "Female") |>
  select(-Gender)

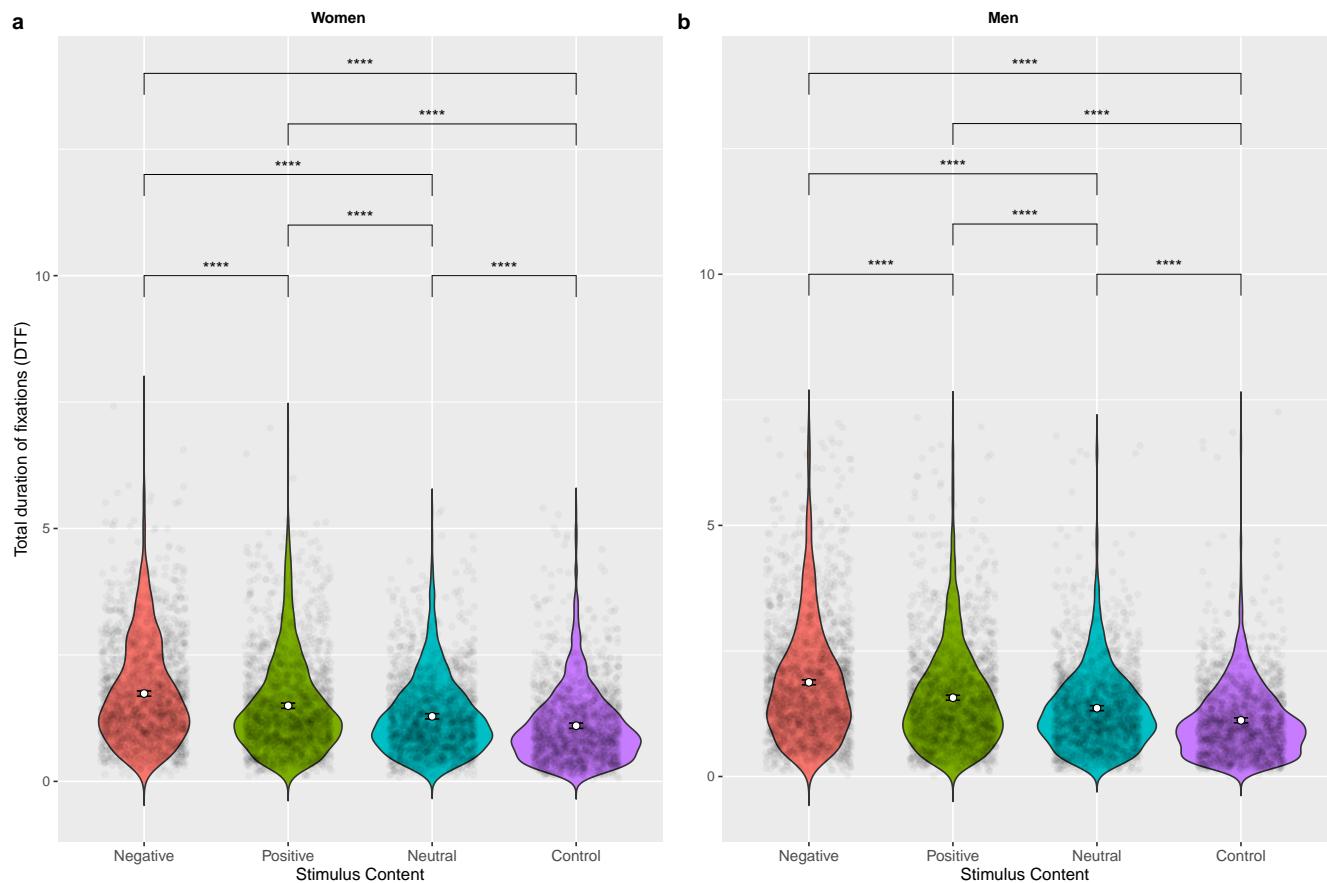
ggplot_female_mod4 <- ggplot(pf_muj_mod4, aes(x=stimulus_content,
                                                y=total_duracion)) +
  geom_violin(trim = FALSE,
               aes(fill = stimulus_content)) +
  geom_jitter(alpha = 0.04, width = 0.3) +
  geom_errorbar(data = mcm4_emmeans_muj,
                 mapping =
                   aes(ymin = total_duracion-SE,
                       ymax = total_duracion+SE),
                 colour = "black", width = 0.1) +
  geom_point(data = mcm4_emmeans_muj,
              shape = 21, size = 2,
              color = "black", fill = "white") +
  stat_pvalue_manual(tbl.contrasts_df4_muj,
                     label = "p.signif",
                     y.position = c(10, 12, 14, 11, 13, 10)) +
  labs(x = "Stimulus Content",
       y = "Total duration of fixations (DTF)",
       fill = " ") +
  guides(fill = FALSE) +
  theme(axis.text.x = element_text(size = 10))

ggplot_female_mod4 <- annotate_figure(ggplot_female_mod4, top = text_grob("Women",
                                                               color = "black", face = "bold", size = 10))

ggplot_male_mod4 <- annotate_figure(ggplot_male_mod4, top = text_grob("Men",
                                                               color = "black", face = "bold", size = 10))

figura_dtf <- ggarrange(ggplot_female_mod4, ggplot_male_mod4,
                         nrow = 1,
                         labels = "auto")
figura_dtf

```



**Figure S4.** Dimension between the emotional content of the stimulus, images with negative, positive, neutral and control emotional content, by gender of the participants, see Table S22, where the contrasts between each dimension are observed. In all cases, significant effects are represented with lines and stars: \* $p < .05$ , \*\* $p < .01$ , \*\*\* $p < .001$ , \*\*\*\* $p < .0001$ .

#### 2.4.3 Bootstrap

Considering that the model did not behave normally, the distribution was estimated using Bootstrap. The bootstrap method is used to generate multiple samples of data from the original sample and, from them, obtain a sampling distribution of the statistic of interest, which allows estimating the variability and uncertainty associated with the statistic of interest, in this case the Total duration of fixations (DTF).

```
set.seed(824)
B <- 10000

mod4_boot <- bootstrap(mod4, .f = fixef,
                        type = "residual",
                        B = B)
matriz_mod4 <- as.matrix(mod4_boot$stats)

columnas_a_convertir <- c("observed", "rep.mean", "se", "bias")

boots_mod4_table <- as.data.frame(matriz_mod4) |>
  mutate_at("term", str_replace_all, ":" , " × ") |>
  mutate_at("term", str_replace_all, "stimulus_contentControl",
            "Stimulus content [Control]")|>
  mutate_at("term", str_replace_all, "stimulus_contentPositive",
            "Stimulus content [Positive]")|>
  mutate_at("term", str_replace_all, "stimulus_contentNeutral",
```

```

"Stimulus content [Neutral])|>
mutate_at("term", str_replace_all, "GenderMale",
          "Gender [Male])|>
mutate(across(all_of(columnas_a_convertir), as.numeric))

bootstrap_mod4 <- as.data.frame(confint(mod4_boot,
                                         type = "basic")) |>
  mutate_at("term", str_replace_all, ":" , " × ") |>
  mutate_at("term", str_replace_all, "stimulus_contentControl",
            "Stimulus content [Control])|>
  mutate_at("term", str_replace_all, "stimulus_contentPositive",
            "Stimulus content [Positive])|>
  mutate_at("term", str_replace_all, "stimulus_contentNeutral",
            "Stimulus content [Neutral])|>
  mutate_at("term", str_replace_all, "GenderMale",
            "Gender [Male]")

unidas_mod4 <- merge(boots_mod4_table,
                      bootstrap_mod4,
                      by = "term")|>
  select(-estimate, -type, -level)

unidas_mod4 <- arrange(unidas_mod4,
                        match(term, orden_deseado)) |>
  kable(digits = 4, booktabs = TRUE,
        align = c("l", "l", rep("c", 4)),
        caption = "Bootstrap estimated values of model 4",
        escape = FALSE) |>
  kable_styling(latex_options = c("HOLD_position"))

unidas_mod4

```

**Table S23.** Bootstrap estimated values of model 4

term	observed	rep.mean	se	bias	lower	upper
(Intercept)	1.7368	1.7362	0.0404	-6e-04	1.6592	1.8159
Stimulus content [Positive]	-0.2407	-0.2402	0.0282	5e-04	-0.2966	-0.1873
Stimulus content [Neutral]	-0.4503	-0.4497	0.0284	6e-04	-0.5079	-0.3956
Stimulus content [Control]	-0.6357	-0.6351	0.0282	6e-04	-0.6917	-0.5818
Gender [Male]	0.1384	0.1389	0.0723	5e-04	-0.0015	0.2767
Stimulus content [Positive] × Gender [Male]	-0.0661	-0.0663	0.0392	-1e-04	-0.1423	0.0107
Stimulus content [Neutral] × Gender [Male]	-0.0642	-0.0648	0.0397	-6e-04	-0.1409	0.0134
Stimulus content [Control] × Gender [Male]	-0.1211	-0.1218	0.0390	-7e-04	-0.1975	-0.0453

## 2.5 Total number of fixations

The Total number of fixations is a measure of delayed attention, which consists of the total number of times an individual observes a stimulus, i.e., the participant can view the stimuli freely and the number of times each image is observed is counted at the end of the time.

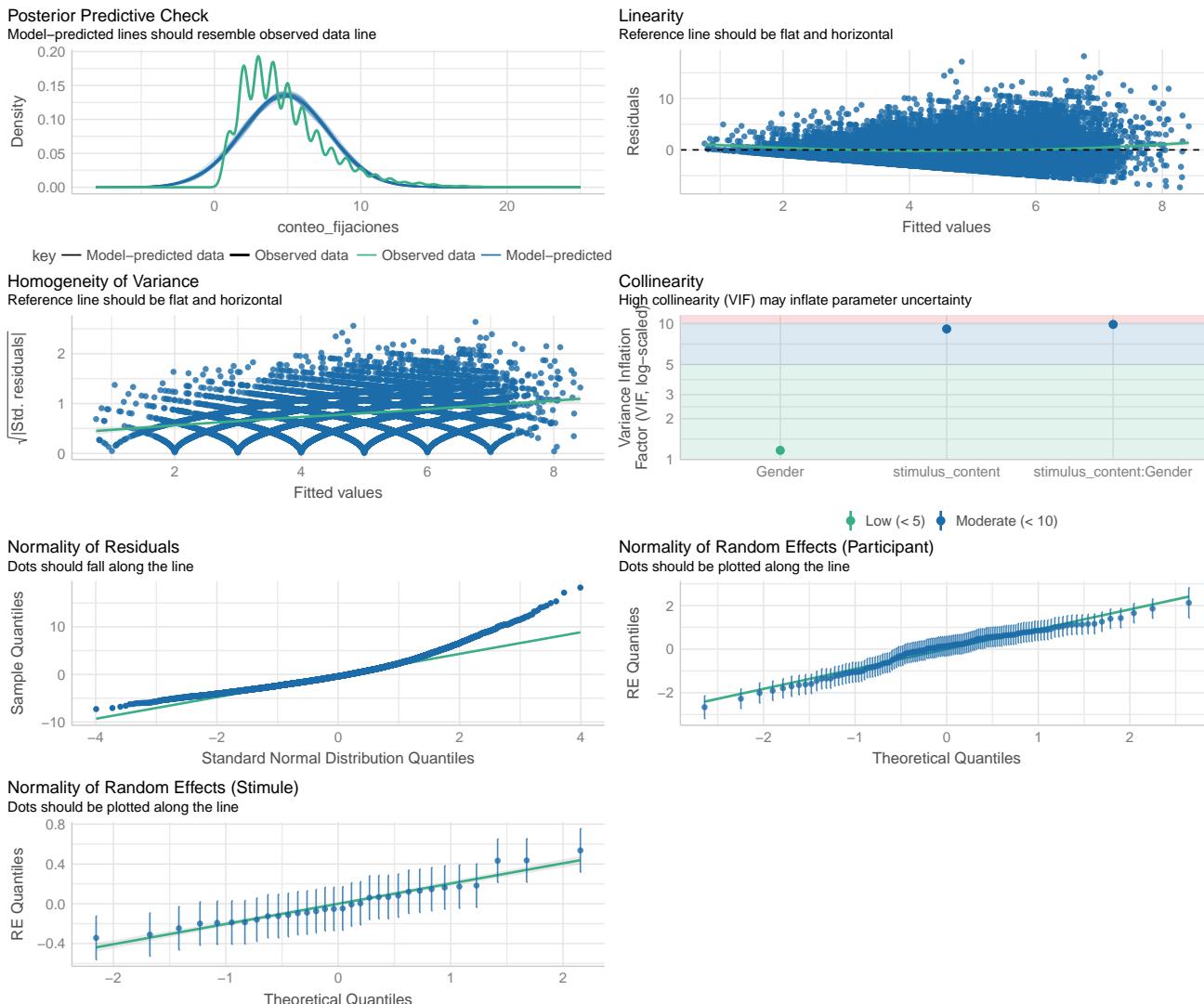
### 2.5.1 Fit model

In the fifth model, the total number of fixations is predicted by the variables stimulus type and the interaction with the participant's sex. In addition, there are random intercepts for the participant and for the stimulus. This means that each participant is expected to have his or her own effect on the response variable, rather than having a constant effect in all cases.

```
mod5 <- lmer(conteo_fijaciones ~
  stimulus_content * Gender +
  (1 | Participant) +
  (1 | Stimule),
  data = bd)
```

**2.5.1.1 Model assumptions** The following functions ‘check\_model()’, ‘check\_distribution()’, and ‘check\_normality()’ are used to evaluate the quality of fit and distribution of residuals in a statistical model. For example, check\_model() could provide a visualization of residuals and diagnose problems such as heteroscedasticity or bias in the model. check\_distribution() could provide a visualization of the distribution of residuals and diagnose problems such as deviation from normality or outliers. check\_normality() could provide a normality test for the residuals of the model and evaluate whether normality assumptions are met.

```
check_model(mod5)
```



```
dist_checkmod5 <- check_distribution(mod5)
  kable(data.frame(dist_checkmod5),
  digits = 2, booktabs = TRUE,
  caption = "Distribution of residuals model 4") %>%
  kable_styling(latex_options = c("HOLD_position"))
```

**Table S24.** Distribution of residuals model 4

Distribution	p_Residuals	p_Response
bernoulli	0.00	0.00
beta	0.00	0.00
beta-binomial	0.00	0.34
binomial	0.00	0.00
cauchy	0.59	0.00
chi	0.03	0.00
exponential	0.00	0.00
F	0.00	0.00
gamma	0.00	0.03
half-cauchy	0.00	0.00
inverse-gamma	0.00	0.00
lognormal	0.00	0.00
neg. binomial (zero-infl.)	0.00	0.16
negative binomial	0.00	0.34
normal	0.34	0.00
pareto	0.00	0.00
poisson	0.00	0.12
poisson (zero-infl.)	0.00	0.00
tweedie	0.03	0.00
uniform	0.00	0.00
weibull	0.00	0.00

```
check_normality(mod5)
```

```
## Warning: Non-normality of residuals detected (p < .001).
```

**2.5.1.2 Summary model** To obtain a summary of model 5, the ‘summary’ function was used, which provides a summary of the coefficients of model 5, along with the standard deviation, t-value, and associated p-value for each coefficient. Similarly, the ‘anova’ function returns an ANOVA table with information on the variance decomposition of model 5, sum of squares, degrees of freedom, and associated F-statistics. Finally, the ‘r2\_nakagawa’ function is used to calculate the pseudo R-squared proposed by Nakagawa & Schielzeth (2013) for mixed-effects models. The pseudo R-squared is used to evaluate the goodness of fit of a model and is interpreted similarly to an R-squared in standard linear models.

```
anova.mod5 <- anova(mod5)

anova.mod5 <- as.data.frame(anova.mod5) |>
  rownames_to_column() |>
  mutate_at("rowname", str_replace_all, ":" , " × ") |>
  mutate_at("rowname", str_replace_all, "stimulus_content",
           "Stimulus content")|>
  rename( Effect = rowname)|>
  kable(digits = 2, booktabs =TRUE,
        align = c("l", "l", rep("c", 4)),
        caption = "Effect of StimulusContent")
```

```

and Participant's Gender on
Total number of fixings (TNF)",
escape =FALSE)|>
kable_styling(latex_options = c("hold_position"))

anova.mod5

```

**Table S25.** Effect of StimulusContent and Participant's Gender on Total number of fixings (TNF)

Effect	Sum Sq	Mean Sq	NumDF	DenDF	F value	Pr(>F)
Stimulus content	9217.91	3072.64	3	15155.66	447.39	0.00
Gender	8.26	8.26	1	118.80	1.20	0.27
Stimulus content × Gender	129.31	43.10	3	15155.45	6.28	0.00

```

sum.mod5 <- summary(mod5)

sum.mod5_df <- as.data.frame(sum.mod5$coefficients)|>
rownames_to_column() |>
  mutate_at("rowname", str_replace_all, ":" , " × ") |>
  mutate_at("rowname", str_replace_all,
            "stimulus_contentControl",
            "Stimulus content [Control]")|>
  mutate_at("rowname", str_replace_all,
            "stimulus_contentPositive",
            "Stimulus content [Positive]")|>
  mutate_at("rowname", str_replace_all,
            "stimulus_contentNeutral",
            "Stimulus content [Neutral]")|>
  mutate_at("rowname", str_replace_all,
            "GenderMale",
            "Gender [Male]") |>
  rename( Effect = rowname)|>
  kable(digits = 2, booktabs = TRUE,
        align = c("l", "l", rep("c", 4)),
        caption = "Total number of fixings (TNF)
by stimylus content,gender and the
interactionbetween stimulus contentand gender",
        escape = FALSE) |>
  kable_styling(latex_options = c("HOLD_position"))

sum.mod5_df

```

**Table S26.** Total number of fixings (TNF) by stimylus content,gender and the interactionbetween stimulus contentand gender

Effect	Estimate	Std. Error	df	t value	Pr(> t )
(Intercept)	5.56	0.15	179.91	38.24	0.00
Stimulus content [Positive]	-0.45	0.09	15155.10	-5.20	0.00
Stimulus content [Neutral]	-1.12	0.09	15155.36	-12.96	0.00
Stimulus content [Control]	-1.86	0.09	15155.29	-21.50	0.00
Gender [Male]	0.46	0.19	161.98	2.41	0.02
Stimulus content [Positive] × Gender [Male]	-0.37	0.12	15155.45	-3.08	0.00
Stimulus content [Neutral] × Gender [Male]	-0.21	0.12	15155.79	-1.77	0.08
Stimulus content [Control] × Gender [Male]	-0.49	0.12	15155.77	-4.10	0.00

```
r2mod5 <- r2_nakagawa(mod5)
r2_tblmod5 <- as_tibble(r2mod5)
kable(r2_tblmod5, format = "markdown", booktabs =TRUE,
      align = "c",
      caption = "R model 5",
      escape =FALSE) %>%
      kable_styling(latex_options = c("HOLD_position"))
```

**Table S27.** *R model 5*

R2_conditional	R2_marginal
0.1881852	0.074081

**2.5.1.3 Estimated marginal means** Taking into account the results obtained in the ANOVA table, where significant values are observed for the stimulus content variable, post-hoc tests are performed and the contrast between variables is presented.

```
mcm5 <- emmeans(mod5, pairwise ~ stimulus_content * Gender)

mcm5_emmeans <- tibble(data.frame(mcm5$emmeans)) |>
  rename(conteo_fijaciones = emmean) |>
  select(-df)

contrasts_df5 <- as.data.frame(mcm5$contrasts) |>
  select(-df)

kable(contrasts_df5, digits = 5,
      booktabs =TRUE,
      align = "c",
      caption = "Contrasts between variables, according to the
      content of the stimulus of model 5") %>%
      kable_styling(latex_options = "HOLD_position",
                    font_size = 12,
                    full_width = FALSE)
```

**Table S28.** Contrasts between variables, according to the content of the stimulus of model 5

contrast	estimate	SE	z.ratio	p.value
Negative Female - Positive Female	0.44904	0.08638	5.19834	0.00001
Negative Female - Neutral Female	1.12038	0.08648	12.95529	0.00000
Negative Female - Control Female	1.86380	0.08669	21.49862	0.00000
Negative Female - Negative Male	-0.46335	0.19251	-2.40693	0.23775
Negative Female - Positive Male	0.35363	0.19261	1.83594	0.59533
Negative Female - Neutral Male	0.86872	0.19265	4.50935	0.00018
Negative Female - Control Male	1.89272	0.19274	9.82017	0.00000
Positive Female - Neutral Female	0.67134	0.08652	7.75902	0.00000
Positive Female - Control Female	1.41477	0.08674	16.31051	0.00000
Positive Female - Negative Male	-0.91239	0.19253	-4.73897	0.00006
Positive Female - Positive Male	-0.09541	0.19263	-0.49530	0.99968
Positive Female - Neutral Male	0.41968	0.19267	2.17825	0.36493
Positive Female - Control Male	1.44368	0.19276	7.48956	0.00000
Neutral Female - Control Female	0.74342	0.08684	8.56129	0.00000
Neutral Female - Negative Male	-1.58373	0.19257	-8.22404	0.00000
Neutral Female - Positive Male	-0.76675	0.19268	-3.97946	0.00177
Neutral Female - Neutral Male	-0.25166	0.19271	-1.30587	0.89700
Neutral Female - Control Male	0.77234	0.19280	4.00584	0.00159
Control Female - Negative Male	-2.32716	0.19267	-12.07841	0.00000
Control Female - Positive Male	-1.51018	0.19278	-7.83388	0.00000
Control Female - Neutral Male	-0.99508	0.19281	-5.16093	0.00001
Control Female - Control Male	0.02892	0.19290	0.14990	1.00000
Negative Male - Positive Male	0.81698	0.08267	9.88267	0.00000
Negative Male - Neutral Male	1.33208	0.08275	16.09838	0.00000
Negative Male - Control Male	2.35607	0.08296	28.40064	0.00000
Positive Male - Neutral Male	0.51510	0.08293	6.21115	0.00000
Positive Male - Control Male	1.53909	0.08314	18.51104	0.00000
Neutral Male - Control Male	1.02400	0.08321	12.30554	0.00000

### 2.5.2 Figure

Finally, for this model 5, a figure showing the Total number of fixations as a function of stimulus content and the respective differences between the variables is shown. The values by gender are presented in different panels to observe the respective differences.

```
pf_hom_mod5 <- filter(bd, Gender == "Male")

contrasts_df5_hom <- filter(contrasts_df5, contrast %in% contrastes_hom)

tbl.contrasts_df5_hom <- contrasts_df5_hom %>%
  mutate(.y. = "conteo_fijaciones") %>%
  separate_wider_delim(contrast, " - ",
                        names = c("group1", "group2")) %>%
  select(7, 1:6) %>%
  mutate(p.signif = pval.stars(p.value)) |>
  mutate_at("group1", str_replace_all, "Negative Male",
```

```

    "Negative")|>
mutate_at("group1", str_replace_all, "Positive Male",
          "Positive")|>
mutate_at("group1", str_replace_all, "Neutral Male",
          "Neutral")|>
mutate_at("group2", str_replace_all, "Positive Male",
          "Positive")|>
mutate_at("group2", str_replace_all, "Neutral Male",
          "Neutral")|>
mutate_at("group2", str_replace_all, "Control Male",
          "Control")

mcm5_emmeans_hom <- filter(mcm5_emmeans, Gender == "Male")|>
  select(-Gender)

ggplot_male_mod5 <- ggplot(pf_hom_mod5, aes(x=stimulus_content,
                                              y=conteo_fijaciones)) +
  geom_violin(trim = FALSE,
              aes(fill = stimulus_content)) +
  geom_jitter(alpha = 0.04, width = 0.3) +
  geom_errorbar(data = mcm5_emmeans_hom,
                 mapping =
                  aes(ymin = conteo_fijaciones-SE,
                      ymax = conteo_fijaciones+SE),
                 colour = "black", width = 0.1) +
  geom_point(data = mcm5_emmeans_hom,
              shape = 21, size = 2,
              color = "black", fill = "white") +
  stat_pvalue_manual(tbl.contrasts_df5_hom,
                     label = "p.signif",
                     y.position = c(29, 35, 37, 31, 33, 29)) +
  labs(x = "Stimulus Content",
       y = " ",
       fill = " ") +
  guides(fill = FALSE) +
  theme(axis.text.x = element_text(size = 10))

pf_muj_mod5 <- filter(bd, Gender == "Female")

contrasts_df5_muj <- filter(contrasts_df5, contrast %in% contrastes_muj)

tbl.contrasts_df5_muj <- contrasts_df5_muj %>%
  mutate(.y. = "conteo_fijaciones") %>%
  separate_wider_delim(contrast, " - ",
                        names = c("group1", "group2")) %>%
  select(7, 1:6) %>%
  mutate(p.signif = pval.stars(p.value))|>
  mutate_at("group1", str_replace_all, "Negative Female",
            "Negative")|>
  mutate_at("group1", str_replace_all, "Positive Female",
            "Positive")|>
  mutate_at("group1", str_replace_all, "Neutral Female",
            "Neutral")

```

```

    "Neutral")|>
  mutate_at("group2", str_replace_all, "Positive Female",
    "Positive")|>
  mutate_at("group2", str_replace_all, "Neutral Female",
    "Neutral")|>
  mutate_at("group2", str_replace_all, "Control Female",
    "Control")

mcm5_emmeans_muj <- filter(mcm5_emmeans, Gender == "Female")|>
  select(-Gender)

ggplot_female_mod5 <- ggplot(pf_muj_mod5, aes(x=stimulus_content,
  y=conteo_fijaciones)) +
  geom_violin(trim = FALSE,
    aes(fill = stimulus_content)) +
  geom_jitter(alpha = 0.04, width = 0.3) +
  geom_errorbar(data = mcm5_emmeans_muj,
    mapping =
      aes(ymin = conteo_fijaciones-SE,
          ymax = conteo_fijaciones+SE),
      colour = "black", width = 0.1) +
  geom_point(data = mcm5_emmeans_muj,
    shape = 21, size = 2,
    color = "black", fill = "white") +
  stat_pvalue_manual(tbl.contrasts_df5_muj,
    label = "p.signif",
    y.position = c(29, 35, 37, 31, 33, 29)) +
  labs(x = "Stimulus Content",
    y = "Total Number of Fixings (CTF)",
    fill = " ") +
  guides(fill = FALSE) +
  theme(axis.text.x = element_text(size = 10))

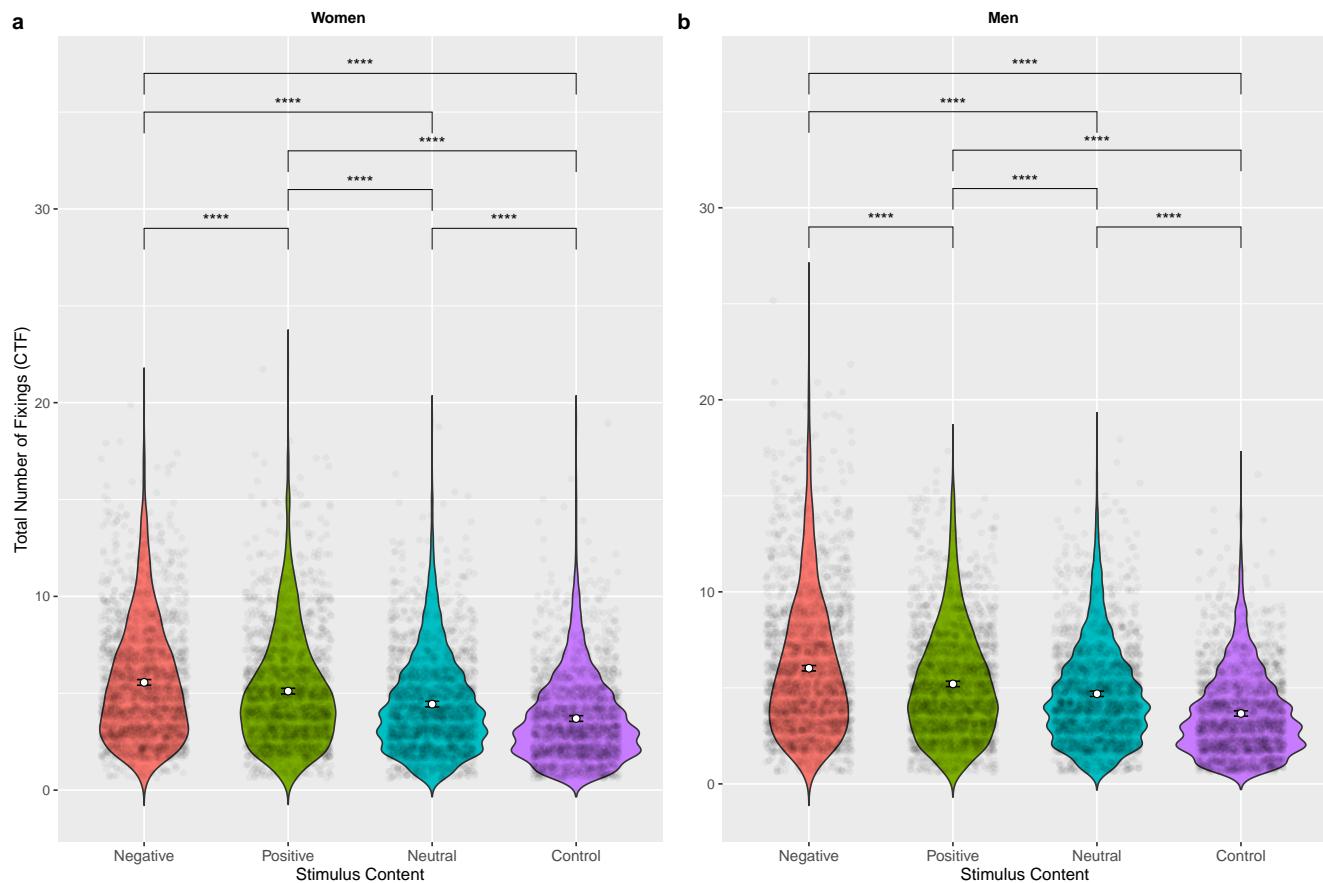
ggplot_female_mod5 <- annotate_figure(ggplot_female_mod5, top = text_grob("Women",
  color = "black", face = "bold", size = 10))

ggplot_male_mod5 <- annotate_figure(ggplot_male_mod5, top = text_grob("Men",
  color = "black", face = "bold", size = 10))

figura_ctf <- ggarrange(ggplot_female_mod5, ggplot_male_mod5,
  nrow = 1,
  labels = "auto")

figura_ctf

```



**Figure S5.** Dimension between the emotional content of the stimulus, images with negative, positive, neutral and control emotional content, by gender of the participants, see Table S28, where the contrasts between each dimension are observed. In all cases, significant effects are represented with lines and stars: \* $p < .05$ , \*\* $p < .01$ , \*\*\* $p < .001$ , \*\*\*\* $p < .0001$ .

### 2.5.3 Bootstrap

Considering that the model did not behave normally, the distribution was estimated using Bootstrap. The bootstrap method is used to generate multiple samples of data from the original sample and, from them, obtain a sampling distribution of the statistic of interest, which allows estimating the variability and uncertainty associated with the statistic of interest, in this case the Total Number of Fixings (CTF).

```
set.seed(824)
B <- 10000

mod5_boot <- bootstrap(mod5, .f = fixef,
                        type = "residual",
                        B = B)
matriz_mod5 <- as.matrix(mod5_boot$stats)

columnas_a_convertir <- c("observed", "rep.mean", "se", "bias")

boots_mod5_table <- as.data.frame(matriz_mod5) |>
  mutate_at("term", str_replace_all, ":" , " × ") |>
  mutate_at("term", str_replace_all, "stimulus_contentControl",
           "Stimulus content [Control]")|>
  mutate_at("term", str_replace_all, "stimulus_contentPositive",
           "Stimulus content [Positive]")|>
  mutate_at("term", str_replace_all, "stimulus_contentNeutral",
```

```

"Stimulus content [Neutral])|>
mutate_at("term", str_replace_all, "GenderMale",
          "Gender [Male])|>
mutate(across(all_of(columnas_a_convertir), as.numeric))

bootstrap_mod5 <- as.data.frame(confint(mod5_boot,
                                         type = "basic")) |>
  mutate_at("term", str_replace_all, ":" , " × ") |>
  mutate_at("term", str_replace_all, "stimulus_contentControl",
            "Stimulus content [Control])|>
  mutate_at("term", str_replace_all, "stimulus_contentPositive",
            "Stimulus content [Positive])|>
  mutate_at("term", str_replace_all, "stimulus_contentNeutral",
            "Stimulus content [Neutral])|>
  mutate_at("term", str_replace_all, "GenderMale",
            "Gender [Male]")

unidas_mod5 <- merge(boots_mod5_table,
                      bootstrap_mod5,
                      by = "term")|>
  select(-estimate, -type, -level)

unidas_mod5 <- arrange(unidas_mod5,
                       match(term, orden_deseado)) |>
  kable(digits = 4, booktabs = TRUE,
        align = c("l", "l", rep("c", 4)),
        caption = "Bootstrap estimated values of model 5",
        escape = FALSE) |>
  kable_styling(latex_options = c("HOLD_position"))

unidas_mod5

```

**Table S29.** Bootstrap estimated values of model 5

term	observed	rep.mean	se	bias	lower	upper
(Intercept)	5.5599	5.5578	0.1098	-0.0021	5.3448	5.7741
Stimulus content [Positive]	-0.4490	-0.4470	0.0867	0.0020	-0.6227	-0.2824
Stimulus content [Neutral]	-1.1204	-1.1193	0.0867	0.0011	-1.2912	-0.9537
Stimulus content [Control]	-1.8638	-1.8633	0.0870	0.0005	-2.0337	-1.6951
Gender [Male]	0.4634	0.4661	0.1935	0.0027	0.0823	0.8399
Stimulus content [Positive] × Gender [Male]	-0.3679	-0.3691	0.1193	-0.0011	-0.5958	-0.1323
Stimulus content [Neutral] × Gender [Male]	-0.2117	-0.2130	0.1181	-0.0013	-0.4412	0.0210
Stimulus content [Control] × Gender [Male]	-0.4923	-0.4924	0.1193	-0.0002	-0.7271	-0.2599

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