How do experiences of violence affect women's preferences for facial masculinity according to resource availability? An exploratory study using eye-tracking

Code and analyses

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Description

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

Vásquez-Amézquita, M., Castellanos-Chacón, A., Medina-Sarmiento, W., Cepeda, V., Martínez-González, M. B., & Leongómez, J. D., (in prep). *How do experiences of violence affect women's preferences for facial masculinity according to resource availability? An exploratory study using eye-tracking.*

Data available from the Open Science Framework (OSF): https://doi.org/10.XXXXX/OSF.IO/XXXXX. All analyses were planned by Milena Vásquez-Amézquita and Juan David Leongómez. This document and its underlying code were created in `R Markdown` by Juan David Leongómez using LaTeX.

Contents

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., 2023), and most figures were created or modified using `ggplot2` (Wickham, 2016). Tables were created using `knitr::kable` and `kableExtra` (Zhu, 2020).

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, 2024).

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). For a complete list of packages used to create this file, and their versions, see section 3, at the end of the document.

```r
library(car)
library(MASS)
library(ggstats)
library(tidyverse)
library(ggpubr)
library(readxl)
library(lmerTest)
library(emmeans)
library(knitr)
library(kableExtra)
library(performance)
library(GGally)
library(scales)
library(factoextra)
library(FactoMineR)
library(gtools)
library(bbmle)
library(effectsize)
```

1.2 Custom functions

1.2.1 `pval.lev`

This function takes p-values and formats them in LATEX, highlighting significant results in bold.

```r
# Define a function 'pval.lev' to format p-values based on specific thresholds.
pval.lev <- function(pvals) {
  # If the p-value is less than 0.0001, return the string '\textbf{< 0.0001}'.
  ifelse(pvals < 0.0001,
    "\\textbf{< 0.0001}",
    # If the p-value is less than 0.001, return the string '\textbf{< 0.001}'.
    ifelse(pvals < 0.001,
      "\\textbf{< 0.001}",
      # If the p-value is less than 0.05, format it with bold text and round to 4
      # decimal places.
      ifelse(pvals < 0.05,
        paste0("\\textbf{", round(pvals, 4), "}"),
        # Otherwise, round the p-value to 2 decimal places.
        round(pvals, 2)
      )
    )
  )
}
```

1.2.2 `corr.stars`

This function creates a correlation matrix, and displays significance (function `corr.stars` modified from http://myowelt.blogspot.com/2008/04/beautiful-correlation-tables-in-r.html).

```r
corr.stars <- function(x) {
  # Load the 'Hmisc' package, which is required for the 'rcorr' function.
  require(Hmisc)
  # Convert the input 'x' to a matrix in case it is not already.
  x <- as.matrix(x)
  # Compute the correlation matrix (R) and p-values (p) using the 'rcorr' function.
  R <- rcorr(x)$r # Correlation matrix
  p <- rcorr(x)$P # p-value matrix
  # Define significance levels for the stars notation.
  # *** for p < 0.001, ** for p < 0.01, * for p < 0.05, and † for p < 0.10.
  mystars <- ifelse(p < .001,
    paste0("\\textbf{", round(R, 2), "***}"),
    ifelse(p < .01,
      paste0("\\textbf{", round(R, 2), "**}"),
      ifelse(p < .05,
        paste0("\\textbf{", round(R, 2), "*}"),
        ifelse(p < .10,
          paste0(round(R, 2), "$^{\\dagger}$"),
          format(round(R, 2), nsmall = 2)
        )
      )
    )
  )
  # Build a new matrix 'Rnew' that contains the correlations and their significance stars.
  Rnew <- matrix(mystars,
    ncol = ncol(x)
  ) # Ensure the new matrix has the same number of columns as 'x'
  # Add the correlation values without stars to the diagonal (self-correlations).
  diag(Rnew) <- paste(diag(R), " ",
```

3

```
    sep = ""
  )
  # Set row names and column names of the matrix 'Rnew' to match those of the original matrix.
  rownames(Rnew) <- colnames(x)
  colnames(Rnew) <- paste(colnames(x), "", sep = "")
  # Remove the upper triangle and the diagonal of the matrix to avoid duplication.
  Rnew <- as.matrix(Rnew)
  Rnew[upper.tri(Rnew, diag = TRUE)] <- ""
  # Convert the matrix to a data frame for easier handling.
  Rnew <- as.data.frame(Rnew)
  # Remove the last column (empty column from the upper triangle) and return the result.
  Rnew <- cbind(Rnew[1:length(Rnew) - 1])
  # Return the final correlation matrix with significance stars.
  return(Rnew)
}
```

1.3   Independent stimuli evaluation

The sex typicality of all stimuli was manipulated to either enhance or reduce their sex-typical characteristics. Since all the stimuli were male faces, this involved masculinizing them to increase their typical sex characteristics and feminizing them to reduce those characteristics. Masculinized and feminized versions were independently rated for masculinity and estimated age by a panel of raters (not participants).

```
# Load the 'Evaluacion Manipulación Rostros.xlsx' Excel file into a data frame
ext_val <- read_excel("Data/Evaluacion Manipulación Rostros.xlsx")
```

1.3.1   Masculinity ratings

First, masculinity rating given to the masculinized and feminized versions of each stimuli were compared.

```
# Select relevant columns and reshape the data into long format
masc_dat <- ext_val |>
  select(
    ResponseId,
    contains("M", ignore.case = FALSE), # Select columns that contain "M" (masculinity)
    -Menstruacion
  ) |> # Exclude the 'Menstruacion' (menstruation) column
  pivot_longer(
    cols = contains("M", ignore.case = FALSE), # Reshape to long format
    names_to = "Stimulus", # Column with stimuli names
    values_to = "Masculinity"
  ) |> # Column with masculinity ratings
  # Add a column indicating sexual dimorphism based on stimulus name
  mutate(Sexual_dimorphism = ifelse(grepl("f_1", Stimulus), "Feminine", "Masculine")) |>
  # Keep only the first 3 characters of the stimulus name
  mutate(Stimulus = str_sub(Stimulus, end = 3))

# Group by stimulus and perform t-tests for masculinity ratings across
# sexual dimorphism categories
t_masc <- masc_dat |>
  group_by(Stimulus) |>
  summarise(
    t = round(t.test(Masculinity ~ Sexual_dimorphism)$statistic, 2), # Compute t values
    p = pval.lev(t.test(Masculinity ~ Sexual_dimorphism)$p.value)
  ) |> # Compute p-value
  ungroup()
```

```
# Select the first 10 rows of the data 't_masc'
t_masc[1:10, ] |>
  # Add the next 10 rows (11 to 20) as additional columns
  cbind(t_masc[11:20, ]) |>
  # Add the next 10 rows (21 to 30) as additional columns
  cbind(t_masc[21:30, ]) |>
  # Create a table using the 'kable' function
  kable(
    booktabs = TRUE, # Use 'booktabs' style for better-looking tables in LaTeX
    digits = 2, # Round numerical values to 2 decimal places
    align = "c", # Center align all columns
    linesep = "", # No lines between rows
    caption = "Difference in independent masculinity ratings given to each stimulus,
               according to its sexual dimorphism manipulation (feminized - masculinized)",
    # Caption for the table
    escape = FALSE, # Allow LaTeX commands in the table (e.g., italic or bold)
    col.names = rep(c("Stimulus", "\\textit{t}", "\\textit{p}"), times = 3) # Column names
  ) |>
  # Apply additional LaTeX styling to the table using 'kable_styling'
  kable_styling(
    latex_options = c("HOLD_position", "scale_down") # Keep table position
  ) |>
  # Add vertical lines after the 3rd and 6th columns using 'column_spec'
  column_spec(c(3, 6), border_right = TRUE) |>
  # Add a footnote with specific formatting
  footnote(
    general = "Tests are Welch's \\\\textit{t}-test. Significant results are in bold.",
    # General footnote text with LaTeX formatting
    threeparttable = TRUE, # Enable three-part table for better layout
    footnote_as_chunk = TRUE, # Render footnote as a chunk
    escape = FALSE # Allow LaTeX commands in the footnote
  )
```

Table S1. *Difference in independent masculinity ratings given to each stimulus, according to its sexual dimorphism manipulation (feminized - masculinized)*

Stimulus	t	p	Stimulus	t	p	Stimulus	t	p
A01	-6.09	< **0.0001**	A11	-6.98	< **0.0001**	A21	-7.81	< **0.0001**
A02	-9.05	< **0.0001**	A12	-7.90	< **0.0001**	A22	-10.53	< **0.0001**
A03	-8.96	< **0.0001**	A13	-10.32	< **0.0001**	A23	-6.83	< **0.0001**
A04	-8.04	< **0.0001**	A14	-7.76	< **0.0001**	A24	-6.61	< **0.0001**
A05	-9.81	< **0.0001**	A15	-10.33	< **0.0001**	A25	-8.18	< **0.0001**
A06	-7.45	< **0.0001**	A16	-10.63	< **0.0001**	A26	-8.60	< **0.0001**
A07	-7.04	< **0.0001**	A17	-7.76	< **0.0001**	A27	-6.55	< **0.0001**
A08	-9.05	< **0.0001**	A18	-10.29	< **0.0001**	A28	-7.79	< **0.0001**
A09	-12.18	< **0.0001**	A19	-8.27	< **0.0001**	A29	-11.25	< **0.0001**
A10	-6.53	< **0.0001**	A20	-9.72	< **0.0001**	A30	-11.47	< **0.0001**

Note: Tests are Welch's t-test. Significant results are in bold.

1.3.2 Age ratings

Then, estimated age of stimuli was assessed.

```
# Process age-related data: select relevant columns and reshape into long format
age_dat <- ext_val |>
  select(
```

```
    ResponseId,
    contains("E", ignore.case = FALSE)
  ) |> # Select columns related to estimated age (E)
  select(-c(2:5)) |> # Exclude columns 2 to 5 (irrelevant for this analysis)
  pivot_longer(
    cols = contains("E", ignore.case = FALSE), # Reshape to long format
    names_to = "Stimulus", # Column with stimuli names
    values_to = "Age"
  ) |> # Column with age estimates
  # Add sexual dimorphism category based on stimulus name
  mutate(Sexual_dimorphism = ifelse(grepl("f_1", Stimulus), "Feminine", "Masculine")) |>
  # Keep only the first 3 characters of the stimulus name
  mutate(Stimulus = str_sub(Stimulus, end = 3))

# Summarize age data: compute mean, standard deviation, minimum, and maximum age
sum_age_dat <- age_dat |>
  summarise(
    Mean = mean(Age, na.rm = TRUE), # Mean age
    SD = sd(Age, na.rm = TRUE), # Standard deviation of age
    Min = min(Age, na.rm = TRUE), # Minimum age
    Max = max(Age, na.rm = TRUE)
  ) # Maximum age
```

1.3.2.1 Histogram of perceived age Distribution of the estimated ages.

```
# Create a histogram of estimated age
ggplot(age_dat, aes(x = Age)) +
  geom_histogram(bins = 26, fill = "#6D9EC1", color = "black") + # Plot histogram with 26 bins
  labs(
    x = "Estimated Age", # X-axis label
    y = "Count"
  ) + # Y-axis label
  scale_x_continuous(breaks = seq(15, 40, 5)) # X-axis scale with breaks every 5 units
```
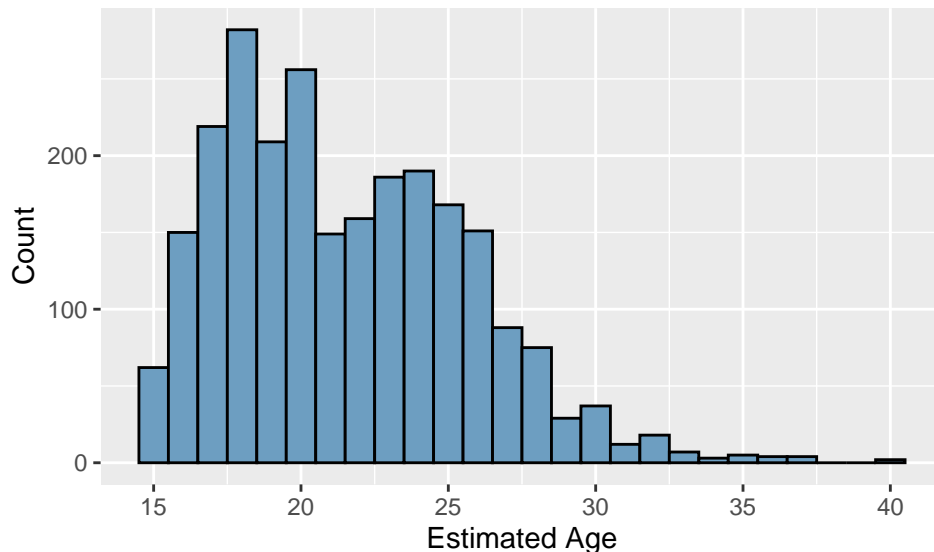

Figure S1. Histogram of estimated age of stimuli by an independent panel of raters. Age estimations were between 15 and 40 with a mean of 21.53 ± 4.11.

1.4 Load and wrangle main experiment data

1.4.1 Individual databases (by data type/source)

```r
# Load the 'CUC-UB' sheet from the 'BD-ET-CUC-UB.xlsx' dataset
dat_et <- read_excel("Data/BD-ET-CUC-UB.xlsx",
  sheet = "CUC-UB"
) |>
  # Drop unused columns
  select(-c(
    Participant, Condicion, TOI, Interval, Media_respuesta, AOI,
    AOI_Global, Respuesta, Number_of_mouse_clicks...17,
    Time_to_first_mouse_click...18, AOI_respuesta
  )) |>
  # Rename columns (to English)
  rename(
    ID = Recording,
    University = UNIVERSIDAD,
    Stimulus = Media,
    Condition = Condición,
    Relationship = Contexto,
    Sexual_dimorphism = Rostro,
    TFD = Total_duration_of_whole_fixations,
    NF = Number_of_whole_fixations,
    TFF = Time_to_first_whole_fixation,
    NMC = Number_of_mouse_clicks...21,
    TFMC = Time_to_first_mouse_click...22,
    DFF = Duration_first_fixation
  ) |>
  # Convert character columns to factors
  mutate(across(where(is.character), as.factor)) |>
  # Recode factor levels to more meaningful English labels
  mutate(
    Condition = fct_recode(Condition,
      "Low" = "BAJA",
      "High" = "ALTA"
    ),
    Relationship = fct_recode(Relationship,
      "Short term" = "CP",
      "Long term" = "LP"
    ),
    Sexual_dimorphism = fct_recode(Sexual_dimorphism,
      "Feminized" = "Feminizado",
      "Masculinized" = "Masculinizado"
    )
  ) |>
  # Modify 'Stimulus' column to include 'F' for Feminized and 'M' for Masculinized
  mutate(
    Stimulus = ifelse(Sexual_dimorphism == "Feminized",
      paste0(str_sub(str_replace(Stimulus, ".* - ", ""), 1, 2), "F"),
      ifelse(Sexual_dimorphism == "Masculinized",
        paste0(str_sub(str_replace(Stimulus, ".* - ", ""), 1, 2), "M"),
        Stimulus
      )
    ),
    # Create a new column 'Choice' to indicate whether there was a mouse click
```

```
    Choice = ifelse(NMC == 0, "No", "Yes")
  )
```

1.4.1.1 Eye-tracking data

1.4.1.2 Questionnaires   This was loaded without calculating total instrument scores (for now), to test internal consistency

```
quests <- read_excel("Data/Cuestionario Datos Sociodemográficos  (Disponibilidad) (respuestas) (1).xlsx",
  sheet = "Respuestas de formulario 1"
) |>
  # Drop unnecessary columns (such as 'Invitado', 'Servicios ayuda', and 'Correos cierre')
  select(-c(Invitado, `Servicios ayuda`, `Correos cierre`)) |>
  # Rename columns for better readability
  rename(
    Date = Fecha,
    Age = edad,
    City = Ciudad,
    Education = Escolaridad,
    Ethnicity = Etnia,
    Gender = Sexo,
    Sex = Genero,
    Sexual_orientation = OS,
    Relationship_current = "Pareja actual",
    Relationship_duration = DuracionR,
    Relationship_status = EstadoR,
    Partner_sex = SexoParejaActual,
    Partner_masculinity = Masculinidad_pareja,
    Partner_dominance = Dominancia_pareja,
    Partner_attractiveness = Atractivo_pareja,
    Number_of_children = NumHijos,
    Hormonal_contraception = "Anticonceptivos hormonales",
    Contraceptive = Cual_anticonceptivo,
    Last_mentruation = "Ultima menstruacion",
    Currently_pregnant = "Embarazo actual",
    Sexual_abuse = "Experiencia abuso sexual",
    Comments = comentarios1,
    Medical_history = "antecedentes medicos",
    SP_happiness = "AP felicidad",
    SP_financial_security = "AP seguridad economica",
    SP_money_control = "AP control dinero",
    SP_attractiveness = "AP atractivo",
    SP_self_confidence = "AP autoconfianza",
    SP_self_esteem = "AP autoestima",
    SP_health = "AP salud",
    Electricity = "SB electricidad",
    Internet_access = "SB internet",
    TV = "SB television",
    Internet_use = "Fr acceso internet",
    Hospital_access = "Acceso hospital",
    Freq_illness = "Fr enfermedades",
    Socioeconomic_level = "Estrato socioeconomico",
    Neighborhood = "Barrio de residencia",
    Perceived_neighborhood_safety = "Seguridad barrio",
    Perceived_city_safety = "Seguridad ciudad",
    Perceived_home_safety = "Seguridad hogar",
    Perceived_country_safety = "Seguridad país",
```

```r
    Freq_robery = "Fr de robos",
    Men_perceived_as_danger_to_children = "Hombres peligrosos hijos",
    Men_perceived_as_danger_to_partner = "Hombres peligrosos pareja",
    Partner_physical_violence = "VP fisica",
    Freq_partner_physical_violence = "Fr VP fisica",
    Partner_sexual_violence = "VP sexual",
    Freq_partner_sexual_violence = "Fr VP sexual",
    Partner_infidelity = "Infidelidad",
    Freq_partner_infidelity = "Fr infidelidad",
    Victim_of_violence = "Victima de alguna violencia",
    Violence_type = "Tipo violencia",
    Victim_of_gender_violence = "Victima violencia género",
    Victim_of_armed_conflict = "Victima conflicto armado",
    Control_question_1 = "Sin leer",
    Control_question_2 = "Broma"
) |>
# Recode the factor levels of several categorical variables
mutate(
    Education = factor(Education, levels = c(
      "Primaria",
      "Bachillerato",
      "Universitario",
      "Posgrado"
    )),
    Sexual_orientation = factor(Sexual_orientation,
      levels = c(
        "Exclusivamente heterosexual",
        "Principalmente heterosexual, con contactos homosexuales esporádicos",
        "Predominantemente heterosexual, aunque con contactos homosexuales más que esporádicos",
        "Bisexual",
        "Pansexual",
        "Demisexual"
      )
    ),
    Relationship_status = factor(Relationship_status,
      levels = c(
        "Soltero sin contactos sexuales en el último año",
        "Soltero con contactos sexuales en el último año",
        "Relación exclusiva o matrimonio - viven juntos",
        "Relación exclusiva - no viven juntos",
        "Relación no exclusiva - contactos sexuales con otras personas"
      )
    ),
    Internet_use = factor(Internet_use,
      levels = c("Cada día", "Cada mes", "Cada año")
    ),
    Socioeconomic_level = as.factor(Socioeconomic_level)
) |>
# Recode City variable to simplify geographical information
mutate(City = ifelse(City %in% c(
  "Bogotá D.C.", "Madrid, Cundinamarca", "Zipaquirá, Cundinamarca",
  "Zipaquirá", "Mosquera, cundinamarca", "Mosquera",
  "FUNZA, CUNDINAMARCA", "Madrid Cundinamarca", "Une- Cundinamarca"
),
"Bogota Region",
ifelse(City %in% c(
```

```r
    "Soledad", "Barranquilla", "BARRANQUILLA",
    "Soledad, Atlantico", "Costa Atlantica", "Corozal"
  ),
  "Atlantico Region",
  "Other"
  )
)) |>
# Recode several factors from Spanish to English for easier interpretation
mutate(Education = recode(Education,
  "Primaria" = "Primary school",
  "Bachillerato" = "High school",
  "Universitario" = "University",
  "Posgrado" = "Postgraduate"
)) |>
# Additional recoding of variables
mutate(Sexual_orientation = recode(Sexual_orientation,
  "Exclusivamente heterosexual" =
    "Exclusively heterosexual",
  "Principalmente heterosexual, con contactos homosexuales esporádicos" =
    "Predominantly heterosexual",
  "Predominantemente heterosexual, aunque con contactos homosexuales más que esporádicos" =
    "Predominantly heterosexual, but more than incidentally homosexual",
  "Bisexual" = "Bisexual",
  "Pansexual" = "Pansexual",
  "Demisexual" = "Demisexual"
)) |>
mutate(Relationship_status = recode(Relationship_status,
  "Soltero sin contactos sexuales en el último año" =
    "Single without sexual contacts",
  "Soltero con contactos sexuales en el último año" =
    "Single with sexual contacts",
  "Relación exclusiva o matrimonio - viven juntos" =
    "Exclusive relationship - cohabitating",
  "Relación exclusiva - no viven juntos" =
    "Exclusive relationship - not cohabitating",
  "Relación no exclusiva - contactos sexuales con otras personas" =
    "Non-exclusive relationship"
)) |>
mutate(Internet_use = recode(Internet_use,
  "Cada día" = "Daily",
  "Cada mes" = "Monthly",
  "Cada año" = "Yearly"
)) |>
# Recode several questions related to danger perceptions, replacing Spanish responses with
# numerical values.
mutate(across(
  starts_with("Men_perceived_as_danger_to_"),
  ~ recode(.,
    "Completamente en desacuerdo" = 1,
    "Ligeramente en desacuerdo" = 2,
    "Ni de acuerdo ni en desacuerdo" = 3,
    "Ligeramente deacuerdo" = 4,
    "Completamente deacuerdo" = 5
  )
)) |>
# Replace Spanish responses with corresponding English values
```

```
mutate(across(where(is.character), ~ replace(
  ., . ==
    "Si",
  "Yes"
))) |>
mutate(across(where(is.character), ~ replace(
  ., . ==
    "Sí",
  "Yes"
))) |>
mutate(across(where(is.character), ~ replace(
  ., . ==
    "No quiero responder",
  "Prefer not to answer"
))) |>
mutate(across(where(is.character), ~ replace(
  ., . ==
    "Mujer",
  "Woman"
))) |>
mutate(across(where(is.character), ~ replace(
  ., . ==
    "Hombre",
  "Man"
))) |>
mutate(across(where(is.character), ~ replace(
  ., . ==
    "Femenino",
  "Female"
))) |>
mutate(across(where(is.character), ~ replace(
  ., . ==
    "Masculino",
  "Male"
))) |>
mutate(across(where(is.character), ~ replace(
  ., . ==
    "Sin pareja actual",
  "Single"
))) |>
mutate(across(where(is.character), ~ replace(
  ., . ==
    "Sí, una vez en la adultez",
  "Once as adult"
))) |>
mutate(across(where(is.character), ~ replace(
  ., . ==
    "Sí, tanto en la infancia como en la adultez",
  "Both as child and adult"
))) |>
mutate(across(where(is.character), ~ replace(
  ., . ==
    "Sí, más de una vez en mi infancia",
  "More than once as child"
))) |>
mutate(across(where(is.character), ~ replace(
```

```
  ., . ==
    "Sí, una vez e mi infancia",
  "Once as child"
))) |>
mutate(across(where(is.character), ~ replace(
  ., . ==
    "Afrocolombiano",
  "Afrocolombian"
))) |>
mutate(across(where(is.character), ~ replace(
  ., . ==
    "Desplazado conflicto armado",
  "Undetermined"
))) |>
mutate(across(where(is.character), ~ replace(
  ., . ==
    "Ninguna",
  "Undetermined"
))) |>
mutate(across(where(is.character), ~ replace(
  ., . ==
    "Comunidad negra",
  "Afrocolombian"
))) |>
mutate(across(where(is.character), ~ replace(
  ., . ==
    "Raizal del Archipiélago de San Andrés,
     Providencia y Santa Catalina",
  "Raizal"
))) |>
mutate(across(where(is.character), ~ replace(
  ., . ==
    "Patos",
  "Indigenous"
))) |>
mutate(across(where(is.character), ~ replace(
  ., . ==
    "Indígena",
  "Indigenous"
))) |>
mutate(across(where(is.character), ~ replace(
  ., . ==
    "No estoy segura",
  "Unsure"
)))
```

1.4.1.2.1 Principal component analysis (PCA) To test whether it was possible to reduce the number of socio-ecological variables, we performed PCAs using the package FactoMineR (Lê et al., 2008), and plotted its results with function from the package factoextra (Kassambara & Mundt, 2020).

Socio-ecological factors PCA

```
# Select relevant columns for PCA from the 'quests' dataset
quests_pca_gen <- quests |>
  select(
    ID,  # Unique identifier
    Men_perceived_as_danger_to_partner,
```

```
    Men_perceived_as_danger_to_children,
    Freq_partner_physical_violence,
    Freq_partner_sexual_violence,
    Freq_partner_infidelity,
    Perceived_home_safety
) |>
# Rename columns: replace "Freq_" with "Frequency of"
rename_with(~ str_replace_all(., "Freq_", "Frequency of")) |>
# Replace underscores with spaces in column names
rename_with(~ str_replace_all(., "_", " ")) |>
# Capitalize the first letter of each column name
rename_with(~ str_to_sentence(.))

# Perform PCA on the selected variables (excluding the ID column)
pca_sef <- PCA(quests_pca_gen[, -1], graph = FALSE)

# Display summary of the PCA results
pca_sef$var$cor |>
  # Create a table using the 'kable' function
  kable(
    booktabs = TRUE, # Use 'booktabs' style for better-looking tables in LaTeX
    digits = 2, # Round numerical values to 2 decimal places
    align = "c", # Center align all columns
    linesep = "", # No lines between rows
    caption = "Correlation between variables and PCA dimensions",
    # Caption for the table
    escape = FALSE, # Allow LaTeX commands in the table (e.g., italic or bold)
  ) |>
  # Apply additional LaTeX styling to the table using 'kable_styling'
  kable_styling(
    latex_options = c("HOLD_position", "scale_down") # Keep table position
  )
```

Table S2. *Correlation between variables and PCA dimensions*

	Dim.1	Dim.2	Dim.3	Dim.4	Dim.5
Men perceived as danger to partner	0.89	-0.27	-0.03	-0.13	0.01
Men perceived as danger to children	0.89	-0.25	-0.04	-0.11	0.03
Frequency ofpartner physical violence	0.37	0.63	0.20	0.15	-0.63
Frequency ofpartner sexual violence	0.31	0.42	-0.48	0.61	0.35
Frequency ofpartner infidelity	0.19	0.59	0.54	-0.32	0.48
Perceived home safety	0.05	-0.37	0.69	0.61	0.06

Summary plot

```
# Arrange two plots side by side:
# 1. A scree plot showing the explained variance for each principal component
# 2. A plot showing the variable loadings on the principal components
ggarrange(
  fviz_eig(pca_sef, addlabels = TRUE, barfill = "#00AFBB") +
    labs(
      title = "PCA: Socio-ecological factors",  # Title for the scree plot
      subtitle = "Scree plot"  # Subtitle for the scree plot
    ),
  fviz_pca_var(pca_sef,
    col.var = "#00AFBB",  # Color the variable loadings in teal
```
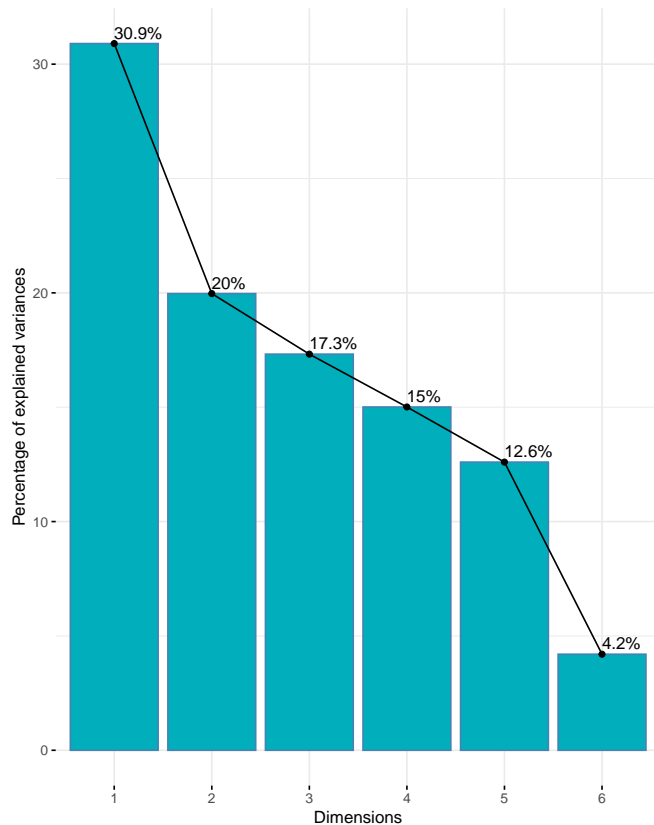
```
    repel = TRUE  # Avoid overlapping labels
  ) +
  labs(
    title = NULL,  # No title for the loading plot
    subtitle = "Loadings"  # Subtitle for the loading plot
  ),
  labels = "auto"
)
```
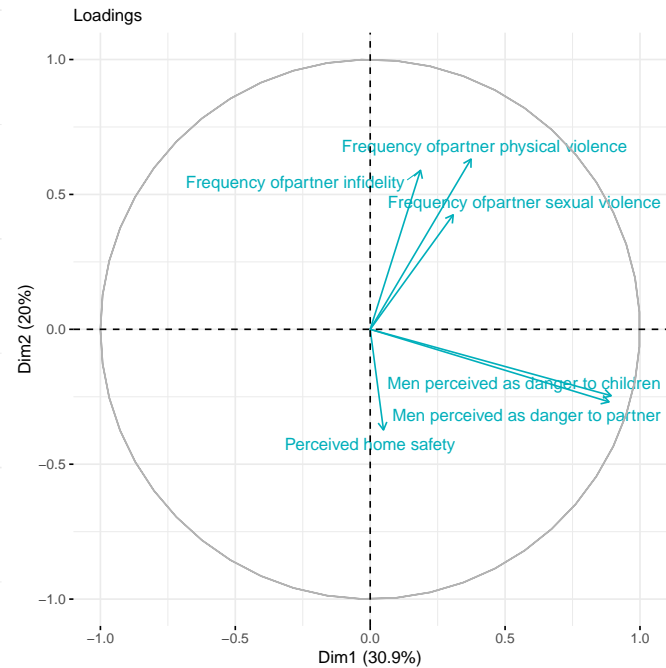

Figure S2. Summary of the PCA for all socio-ecological factors. extbf{a.} Scree plot. extbf{b.} Factor loadings.

When including all socio-ecological factors, the only variables that strongly correlate between them and with the PCA dimension (Table **??**; Fig. S2), are the two variables that evaluate participant's perception of men as dangerous to children and to their partner.

Because of this, a new PCA was performed or only these two variables, to calculate a score of Men perceived as dangerous. All remaining socio-ecological variables were kept.

Men perceived as dangerous

```
# Select relevant columns for PCA from the 'quests' dataset
quests_pca <- quests |>
  select(
    ID,
    Men_perceived_as_danger_to_partner,
    Men_perceived_as_danger_to_children
  ) |>
  # Rename columns: remove "Men_perceived_as_danger_to_"
  rename_with(~ str_remove_all(., "Men_perceived_as_danger_to_")) |>
```

```
  # Capitalize the first letter of each column name
  rename_with(~ str_to_sentence(.))


# Perform PCA on the selected variables (excluding the ID column)
pca_mpd <- PCA(quests_pca[, -1], graph = FALSE)

# Calculate score for the men perceived as dangerous dimension
mpd_scores <- data.frame(pca_mpd$ind$coord)$Dim.1

# Display summary of the PCA results
pca_mpd$var$cor |>
  # Create a table using the 'kable' function
  kable(
    booktabs = TRUE, # Use 'booktabs' style for better-looking tables in LaTeX
    digits = 2, # Round numerical values to 2 decimal places
    align = "c", # Center align all columns
    linesep = "", # No lines between rows
    caption = "Correlation between variables and PCA dimensions",
    # Caption for the table
    escape = FALSE, # Allow LaTeX commands in the table (e.g., italic or bold)
  ) |>
  # Apply additional LaTeX styling to the table using 'kable_styling'
  kable_styling(
    latex_options = c("HOLD_position", "scale_down") # Keep table position
  )
```

Table S3. *Correlation between variables and PCA dimensions*

	Dim.1	Dim.2
Partner	0.93	0.36
Children	0.93	-0.36

Summary plot

In fact, the two variables related to men perceived as dangerous, could be reduced to a single dimension, that captured over 87% of the variance.

```
# Arrange two plots side by side:
# 1. A scree plot showing the explained variance for each principal component
# 2. A plot showing the variable loadings on the principal components
ggarrange(
  fviz_eig(pca_mpd, addlabels = TRUE, barfill = "#00AFBB") +
    labs(
      title = "PCA: Men perceived as danger to...", # Title for the scree plot
      subtitle = "Scree plot"  # Subtitle for the scree plot
    ),
  fviz_pca_var(pca_mpd,
    col.var = "#00AFBB", # Color the variable loadings in teal
    repel = TRUE # Avoid overlapping labels
  ) +
    labs(
      title = NULL, # No title for the loading plot
      subtitle = "Loadings" # Subtitle for the loading plot
    ),
  labels = "auto"
```
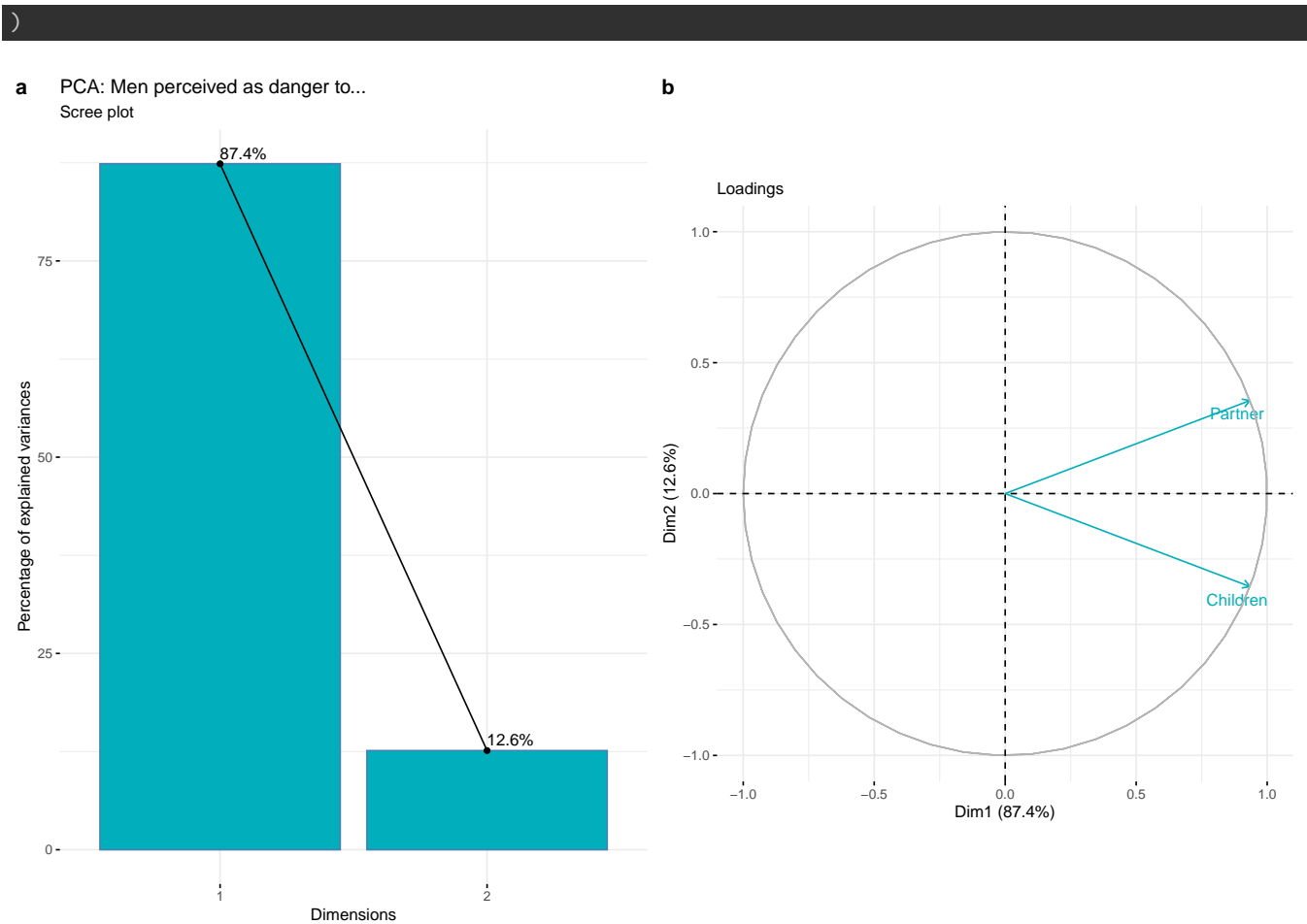
)

a PCA: Men perceived as danger to...
Scree plot

b

Figure S3. Summary of the PCA for factors related to men perceived as dangerous. extbf{a.} Scree plot. extbf{b.} Factor loadings.

1.4.1.2.2 Clean questionnaire data Less columns, with total instrument scores

```
# Clean and modify the 'quests' dataset
quests_clean <- quests |>
  # Recode values in columns that start with "Escasez alimentaria"
  mutate(across(
    starts_with("Escasez alimentaria"),
    ~ recode(.,
      "Nunca" = 0,  # Recode "Nunca" to 0
      "Rara vez/algunas veces" = 1,  # Recode "Rara vez/algunas veces" to 1
      "Casi siempre" = 2  # Recode "Casi siempre" to 2
    )
  )) |>
  # Perform row-wise operations
  rowwise() |>
  # Create new variables by summing up specific columns
  mutate(
    # Calculate Self-esteem score by summing relevant items (with reverse scoring)
    Self_esteem = sum(
      autoestima_I1, 5 - autoestima_I2, autoestima_I3, autoestima_I4,
      autoestima_I5, 5 - autoestima_I6, autoestima_I7, 5 - autoestima_I8,
      5 - autoestima_I9, autoestima_I10
    ),
```

```
    # Calculate Self-perception score by summing columns that start with "SP_"
    Self_perception = sum(across(starts_with("SP_"))),
    # Calculate Perceived safety by summing columns that end with "_safety"
    Perceived_safety = sum(across(ends_with("_safety"))),
    # Calculate Food insecurity by summing columns that start with "Escasez alimentaria"
    Food_insecurity = sum(across(starts_with("Escasez alimentaria")))
) |>
# Remove columns that start with "autoestima_"
select(!starts_with("autoestima_")) |>
# Convert character columns to factors
mutate(across(where(is.character), as.factor)) |>
# Bind the column 'Men_perceived_as_dangerous' from 'mpd_scores' (PCA scores)
bind_cols(Men_perceived_as_dangerous = mpd_scores)
```

1.4.1.3 Subjective evaluation of stimuli

```
# Load the subjective evaluation dataset, removing the last two columns (123 and 124)
eval <- read_excel("Data/Evaluación subjetiva rostros (Respuestas).xlsx") |>
  select(-c(123:124)) |>
  # Perform row-wise operations to compute new variables
  rowwise() |>
  # Calculate the sum of masculinity and attractiveness ratings for both masculinized and
  # feminized stimuli
  mutate(Masculinity_masculinized = sum(across(ends_with("M Mas"))),
         Masculinity_feminized = sum(across(ends_with("F Mas"))),
         Attractiveness_masculinized = sum(across(ends_with("M Atr"))),
         Attractiveness_feminized = sum(across(ends_with("F Atr")))) |>
  # Rename columns for clarity
  rename(Date = "Marca temporal",
         ID = "Escribe tu código de participante")
```

1.4.1.3.1 Wide format

```
# Create a long format dataset by combining attractiveness and masculinity ratings
eval_long <- left_join(
  # First, select relevant columns and pivot the attractiveness ratings to long format
  eval |>
    select(-c(123:126)) |>  # Remove unnecessary columns
    select(!ends_with(" Mas")) |>  # Exclude masculinity-related columns
    pivot_longer(cols = ends_with("Atr"),  # Pivot attractiveness ratings to long format
                 names_to = "Stimulus",
                 values_to = "Attractiveness") |>
    mutate(Stimulus = str_remove_all(Stimulus, " Atr")),  # Clean the Stimulus names
  # Next, pivot the masculinity ratings to long format
  eval |>
    select(-c(123:126)) |>  # Remove unnecessary columns
    select(!ends_with(" Atr")) |>  # Exclude attractiveness-related columns
    pivot_longer(cols = ends_with("Mas"),  # Pivot masculinity ratings to long format
                 names_to = "Stimulus",
                 values_to = "Masculinity") |>
    mutate(Stimulus = str_remove_all(Stimulus, " Mas"))  # Clean the Stimulus names
)
```

1.4.1.3.2 Long format

```r
reg <- rbind(
  read_excel("Data/3Registro Participantes Disponibilidad de Recursos-corregido.xlsx",
    sheet = "UB"
  ) |>
    mutate(University = "UB"),
  read_excel("Data/3Registro Participantes Disponibilidad de Recursos-corregido.xlsx",
    sheet = "CUC"
  ) |>
    mutate(University = "CUC")
) |>
  select(-c(
    Grupo,
    `Entrega de kit`,
    `Protocolo de bioseguridad`,
    `Requisitos previos al registro`,
    Consentimiento,
    `Código de evaluador`:`Código auxiliar que reclutó`
  )) |>
  rename(
    Date = "Fecha de registro",
    ID = "Codigo del Participante",
    Condition = "Condicion",
    Calibration = "Calibración",
    Gaze_perc = "% Gaze",
    Condition_happiness = "Q Feliz",
    Condition_physical_safety = "Q Segura físicamente",
    Condition_healthy = "Q Saludable",
    Condition_economic_security = "Q Segura económicamente",
    Body_temperature = "Temperatura",
    Ovulating = "Test de ovulación",
    Saliva_pre = "Recolección de saliva pre",
    Saliva_pre_time = "Hora...18",
    Eye_tracking = "Rastreo Ocular",
    Subjective_evaluation = "Evaluación subjetiva",
    Sociodemographic_questionnaire = "Cuestionario sociodemográfico",
    Saliva_post = "Recolección de saliva post",
    Saliva_post_time = "Hora...23",
    Notes = "Observaciones"
  ) |>
  mutate(
    Condition = fct_recode(Condition,
      "Low" = "Baja",
      "High" = "Alta"
    ),
    Calibration = fct_recode(Calibration,
      "<=0.5" = "<0.5 (menor a 0.5)",
      ">0.5" = ">0.5 (mayor a 0.5)",
      "<=0.5" = "0.5 (igual a 0.5)",
      NULL = "Selecciona"
    ),
    Ovulating = fct_recode(as.factor(Ovulating),
      "No" = "0",
      "Yes" = "1"
    )
  ) |>
```

```
mutate_all(~ str_replace_all(., "SI", "Yes")) |>
mutate_all(~ str_replace_all(., "NO", "No")) |>
mutate_all(~ str_replace_all(., "INCOMPLETO", "No")) |>
mutate_all(~ str_replace_all(., "Recuperado", "Data recovered")) |>
mutate_all(~ str_replace_all(., "RECUPERADO", "Data recovered")) |>
mutate_all(~ na_if(., "Selecciona")) |>
mutate_all(~ na_if(., "N/A")) |>
mutate(across(starts_with("Condition_"), as.numeric))
```

1.4.1.4   Resource availability

1.4.2   Full, final database

```
dat_int <- dat_et |>
  left_join(quests_clean, by = c("ID"), multiple = "all") |>
  left_join(eval_long, by = c("ID", "Stimulus"), multiple = "all") |>
  left_join(reg, by = c("ID", "University", "Condition"), multiple = "all")
```

1.4.2.1   Join data files

1.4.2.2   Filtered database   Filtered database to exclude participants who did responded the two control questions correctly, were ovulating, or did not report being exclusively heterosexual.

```
dat <- dat_int |>
  # Filter out rows where Control_question_1 and Control_question_2 are both "No",
  # Ovulating is not "Yes", and Sexual_orientation is "Exclusively heterosexual"
  filter(Control_question_1 == "No"
         & Control_question_2 == "No"
         & Ovulating != "Yes"
         & Sexual_orientation == "Exclusively heterosexual") |>
  # Remove all occurrences of the letter "F" from the Stimulus column
  # (infomation already in the column Sexual_dimorphism)
  mutate(Stimulus = str_remove_all(Stimulus, "F")) |>
  # Remove all occurrences of the letter "M" from the Stimulus column
  # (infomation already in the column Sexual_dimorphism)
  mutate(Stimulus = str_remove_all(Stimulus, "M")) |>
  # Ensure that the resulting data frame is ungrouped
  ungroup()
```

After filtering the database and removing data who did not meet these criteria, from an initial sample size of 499 women, the final database contained data from 293 exclusively heterosexual participants, who were not ovulating.

1.4.3   Final individual databases filtered to the final sample

```
reg_fin <- reg |>
  left_join(quests_clean, by = c("ID")) |>
  filter(ID %in% unique(dat$ID))
```

1.4.3.1   Resource availability (filtered)

```
quests_fin <- quests_clean |>
  filter(ID %in% unique(dat$ID))
```

1.4.3.2   Questionnaires (filtered)

2   Descriptives

2.1   Number and age of participants in each condition

```
dat |>
  group_by(ID) |>
  summarise(Age = first(Age),
            Condition = first(Condition)) |>
  ungroup() |>
  group_by(Condition) |>
  summarise(n = n_distinct(ID),
            Mean = mean(Age, na.rm = TRUE),
            SD = sd(Age, na.rm = TRUE),
            Min = min(Age, na.rm = TRUE),
            Max = max(Age, na.rm = TRUE)) |>
  kable(
    booktabs = TRUE, # Use 'booktabs' style for better-looking tables in LaTeX
    digits = 2, # Round numerical values to 2 decimal places
    align = "c", # Center align all columns
    linesep = "", # No lines between rows
    caption = "Number and age of participants in each condition",
    # Caption for the table
    escape = FALSE, # Allow LaTeX commands in the table (e.g., italic or bold)
    col.names = c("Condition",
                  "\\textit{n}",
                  "Mean",
                  "SD",
                  "Min.",
                  "Max.")
  ) |>
  # Apply additional LaTeX styling to the table using 'kable_styling'
  kable_styling(
    latex_options = c("HOLD_position", "scale_down") # Keep table position
  )
```

Table S4. *Number and age of participants in each condition*

Condition	n	Mean	SD	Min.	Max.
High	165	21.41	2.25	18	27
Low	128	21.50	2.25	18	25

3   Session info (for reproducibility)

```
library(pander)
pander(sessionInfo(), locale = FALSE)
```

R version 4.4.1 (2024-06-14)

Platform: x86_64-pc-linux-gnu

attached base packages: *stats4*, *stats*, *graphics*, *grDevices*, *utils*, *datasets*, *methods* and *base*

other attached packages: *pander(v.0.6.5)*, *effectsize(v.0.8.9)*, *bbmle(v.1.0.25.1)*, *gtools(v.3.9.5)*, *FactoMineR(v.2.11)*, *factoextra(v.1.0.7)*, *scales(v.1.3.0)*, *GGally(v.2.2.1)*, *performance(v.0.12.2)*, *kableExtra(v.1.4.0)*, *emmeans(v.1.10.3)*, *lmerTest(v.3.1-3)*, *lme4(v.1.1-35.5)*, *Matrix(v.1.7-0)*, *readxl(v.1.4.3)*, *ggpubr(v.0.6.0)*, *lubridate(v.1.9.3)*, *forcats(v.1.0.0)*, *stringr(v.1.5.1)*, *dplyr(v.1.1.4)*, *purrr(v.1.0.2)*, *readr(v.2.1.5)*, *tidyr(v.1.3.1)*,

tibble(v.3.2.1), *ggplot2(v.3.5.1)*, *tidyverse(v.2.0.0)*, *ggstats(v.0.6.0)*, *MASS(v.7.3-61)*, *car(v.3.1-2)*, *carData(v.3.0-5)* and *knitr(v.1.48)*

loaded via a namespace (and not attached): *rlang(v.1.1.4)*, *magrittr(v.2.0.3)*, *compiler(v.4.4.1)*, *systemfonts(v.1.1.0)*, *vctrs(v.0.6.5)*, *pkgconfig(v.2.0.3)*, *fastmap(v.1.2.0)*, *backports(v.1.5.0)*, *labeling(v.0.4.3)*, *utf8(v.1.2.4)*, *rmarkdown(v.2.28)*, *tzdb(v.0.4.0)*, *nloptr(v.2.1.1)*, *xfun(v.0.47)*, *flashClust(v.1.01-2)*, *highr(v.0.11)*, *broom(v.1.0.6)*, *cluster(v.2.1.6)*, *R6(v.2.5.1)*, *stringi(v.1.8.4)*, *RColorBrewer(v.1.1-3)*, *boot(v.1.3-30)*, *cellranger(v.1.1.0)*, *numDeriv(v.2016.8-1.1)*, *estimability(v.1.5.1)*, *Rcpp(v.1.0.13)*, *bookdown(v.0.40)*, *parameters(v.0.22.1)*, *splines(v.4.4.1)*, *timechange(v.0.3.0)*, *tidyselect(v.1.2.1)*, *rstudioapi(v.0.16.0)*, *abind(v.1.4-5)*, *yaml(v.2.3.10)*, *lattice(v.0.22-5)*, *plyr(v.1.8.9)*, *withr(v.3.0.1)*, *bayestestR(v.0.14.0)*, *coda(v.0.19-4.1)*, *evaluate(v.0.24.0)*, *xml2(v.1.3.6)*, *pillar(v.1.9.0)*, *DT(v.0.33)*, *insight(v.0.20.2)*, *generics(v.0.1.3)*, *hms(v.1.1.3)*, *munsell(v.0.5.1)*, *minqa(v.1.2.7)*, *xtable(v.1.8-4)*, *leaps(v.3.2)*, *glue(v.1.7.0)*, *scatterplot3d(v.0.3-44)*, *tools(v.4.4.1)*, *ggsignif(v.0.6.4)*, *mvtnorm(v.1.2-5)*, *cowplot(v.1.1.3)*, *grid(v.4.4.1)*, *bdsmatrix(v.1.3-7)*, *datawizard(v.0.12.2)*, *colorspace(v.2.1-1)*, *nlme(v.3.1-165)*, *cli(v.3.6.3)*, *fansi(v.1.0.6)*, *viridisLite(v.0.4.2)*, *svglite(v.2.1.3)*, *gtable(v.0.3.5)*, *rstatix(v.0.7.2)*, *digest(v.0.6.37)*, *ggrepel(v.0.9.5)*, *htmlwidgets(v.1.6.4)*, *farver(v.2.1.2)*, *htmltools(v.0.5.8.1)*, *lifecycle(v.1.0.4)* and *multcompView(v.0.1-10)*

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