Funciones evolutivas del habla dirigida a bebés: Impacto en la atención, las preferencias auditivas y el desarrollo lingüístico y musical temprano

Estimación de poder con base en simulaciones

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Description

Data simulation and power analysis approach:

This technical appendix reports a Monte Carlo simulation study conducted to estimate the statistical power to detect main and interaction effects in a planned $2\times2\times2$ within-subjects design. The outcome variable is total fixation time, modeled as a function of three binary acoustic predictors: pitchvariability (f_0 SD), pitch mean (f_0 mean), and perceptual distance (D_f). Realistic effect sizes and noise were incorporated to reflect expected experimental conditions. Simulated datasets were analyzed using linear mixed-effects models with random intercepts for participants. Results demonstrate that with approximately 160 participants, the study would achieve>80% power to detect all main effects. Interaction effects are weaker and would require larger samples to detect reliably. These findings support the proposed sample size and analytic strategy in the accompanying grant application.

Reproducibility:

This document contains all code, and step by step explanations for all analyses, figures and tables (including supplementary figures and tables) for the simulation-based power analysis for *Funciones* evolutivas del habla dirigida a bebés: Impacto en la atención, las preferencias auditivas y el desarrollo lingüístico y musical temprano

Data are available on the Open Science Framework (OSF): https://doi.org/10.XXXXXX. The power analysis strategy was designed by Juan David Leongómez, and the main analyses/models were designed by Christopher D. Watkins and Juan David Leongómez. This document and all its underlying code were created in R Markdown by Juan David Leongómez using R and LATEX.

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1 Preliminaries

1.1 Load Packages

This file was created using knitr (Xie, 2014, 2025), and analyses were performed using tidyverse packages for data manipulation and plotting (Wickham et al., 2019), including dplyr (Wickham et al., 2023), stringr (Wickham, 2023), and ggplot2 (Wickham, 2016). Power simulations were run using purr and furrr (Vaughan & Dancho, 2022) for functional and parallel programming, and models were fit using lmerTest (Kuznetsova et al., 2017), an extension of lme4 that provides p-values for mixed-effects models. Effect size estimates were calculated using effectsize (Ben-Shachar et al., 2020), and visualizations include enhanced plots using ggdist (Kay, 2024, 2025) for raincloud plots and tidyquant (Dancho & Vaughan, 2025) for custom color palettes. All packages can be installed from the Comprehensive R Archive Network (CRAN). For a complete list of package versions used in this analysis, see the Session Info section at the end of the document.

```
library(tidyverse)
                     # Data manipulation and plotting
library(ggdist)
                     # For raincloud plots
library(tidyquant)
library(effectsize)
library(lmerTest)
library(furrr)
                     # Parallel processing with purrr
library(scales)
library(stringr)
                     # String handling
library(ggpubr)
library(truncnorm)
                     # Truncated normal distribution
library(TOSTER)
```

2 Study 1

2.1 Simulation Strategy

This simulation models **total fixation time** (in milliseconds) as a function of three binary within-subject factors that are experimentally manipulated:

- f_0 SD: Pitch variability (Low vs High)
- f_0 mean: Mean pitch (Low vs High)
- D_f : Formant dispersion (Low vs High)

Each of 1000 participants views stimuli representing all 8 combinations of these factors. Fixation time is sampled from a normal distribution, with the following logic:

- Main effects:
- f_0 SD: Strongest effect. Adds 100 ms when High.
- f_0 mean: Adds 75 ms when High.

- D_f : Adds 50 ms when High.
- Interactions:
- $f_0 SD \times f_0 mean$: Adds 100 ms when both High.
- $f_0 SD \times D_f$: Adds 100 ms when both High.
- $f_0 mean \times D_f$: Adds 50 ms when both High.
- 3-way interaction: Adds 120 ms when all three are High.

A normal distribution with SD = 1000 ms is used to generate noisy trial-level data. Values are clamped between 0 and 5000 ms.

2.2 Simulate the Data

```
set.seed(42)
stimulus_conditions <- expand_grid(
 f0_sd = c("Low", "High"),
 f0_mean = c("Low", "High"),
          = c("Low", "High")
 Df
participant_ids <- str_c("P", str_pad(1:1000, width = 4, pad = "0"))
design <- expand_grid(</pre>
  ID = participant_ids,
 stimulus_conditions
simulated_data <- design |>
 mutate(
   f0_sd_val = if_else(f0_sd == "Low", 0, 1),
   f0 mean val = if else(f0 mean == "Low", 0, 1),
              = if_else(Df == "Low", 0, 1),
   Df val
   base_mean = 2500 + 100 * f0_sd_val,
   effect_mean = 75 * f0_mean_val,
    effect_df = 50 * Df_val,
    interaction_effect = 100 * f0_sd_val * f0_mean_val +
      100 * f0_sd_val * Df_val +
     50 * f0_mean_val * Df_val +
     120 * f0_sd_val * f0_mean_val * Df_val,
   mu = base_mean + effect_mean + effect_df + interaction_effect,
   fixation_time = round(rnorm(n(), mean = mu, sd = 1000)),
    fixation_time = pmin(pmax(fixation_time, 0), 5000)
  select(ID, f0_sd, f0_mean, Df, fixation_time)
```

${\bf 2.2.1} \quad {\bf Fit~the~Linear~Mixed\text{-}Effects~Model}$

We fit a linear mixed model with participant as a random effect, and test all main effects and interactions.

The equation for the model is:

```
fixation_time<sub>i</sub> ~ N(\mu, \sigma^2)

\mu = \alpha_{j[i]} + \beta_1(\text{f0\_sd}_{\text{Low}}) + \beta_2(\text{f0\_mean}_{\text{Low}}) + \beta_3(\text{Df}_{\text{Low}}) + \beta_4(\text{f0\_mean}_{\text{Low}} \times \text{f0\_sd}_{\text{Low}}) + \beta_5(\text{Df}_{\text{Low}} \times \text{f0\_sd}_{\text{Low}}) + \alpha_j \sim N(\mu_{\alpha_j}, \sigma_{\alpha_j}^2), for ID j = 1, . . . ,J
```

```
mod <- lmer(fixation_time ~ f0_sd * f0_mean * Df + (1 | ID), data = simulated_data)</pre>
anova(mod)
## Type III Analysis of Variance Table with Satterthwaite's method
                              Mean Sq NumDF DenDF F value
##
                     Sum Sq
                                                            Pr(>F)
## f0_sd
                   123939509 123939509 1 6993 126.3168 < 2.2e-16 ***
## f0_mean
                   55029861 55029861 1 6993 56.0854 7.791e-14 ***
                                      1 6993 49.8560 1.814e-12 ***
## Df
                   48917697
                             48917697
                6209270
                                      1 6993
## f0_sd:f0_mean
                              6209270
                                                   6.3284 0.011904 *
## f0_sd:Df
                                      1 6993
                                                   3.4585 0.062968 .
                    3393438
                              3393438
## f0_mean:Df
                    9645563
                              9645563
                                         1 6993
                                                   9.8306 0.001723 **
## f0_sd:f0_mean:Df
                      60836
                                60836
                                         1 6993
                                                  0.0620 0.803365
## ---
## Signif. codes: 0 '*** 0.001 '** 0.01 '* 0.05 '.' 0.1 ' ' 1
```

2.2.2 Estimate Partial Eta-Squared for Fixed Effects

We estimate partial omega squared (ω_p^2) to quantify the effect size of each fixed term in the model.

```
pop_effect <- omega_squared(mod, partial = TRUE)</pre>
pop_effect
## # Effect Size for ANOVA (Type III)
##
## Parameter
               | Omega2 (partial) |
                                               95% CI
## -----
## f0_sd
                                  0.02 | [0.01, 1.00]
                             7.81e-03 | [0.00, 1.00]
## f0_mean
                              6.94e-03 | [0.00, 1.00]
## f0_sd:f0_mean |
                              7.61e-04 | [0.00, 1.00]
## f0_sd:Df
                              3.51e-04 | [0.00, 1.00]
## f0_mean:Df
                              1.26e-03 | [0.00, 1.00]
                                  0.00 | [0.00, 1.00]
## f0_sd:f0_mean:Df |
##
```

2.2.3 Visualizing Effects: Raincloud Plot

- One-sided CIs: upper bound fixed at [1.00].

Below is a raincloud plot showing fixation time distributions for each condition. The plot allows visual inspection of differences by f_0 SD, split by f_0 mean and D_f .

```
# Prepare data with clean factor levels
plot_data <- simulated_data |>
    mutate(
      f0_mean = factor(f0_mean, levels = c("Low", "High")),
      Df = factor(Df, levels = c("Low", "High")),
      f0_sd = factor(f0_sd, levels = c("Low", "High"))
)
# Labels for facets
```

```
label_f0_mean <- c("Low" = "'Low '*italic(f)[0]*' mean'",
label Df <- c("Low" = "'Low" * italic(D)[f]",
              "High" = "'High '*italic(D)[f]")
ggplot(plot_data, aes(x = f0_sd, y = fixation_time, fill = f0_sd)) +
  stat_halfeye(
    adjust = 0.5,
   justification = -0.3,
    .width = 0,
   point_colour = NA,
   alpha = 0.6
  # Raw points
  geom_jitter(
    aes(color = f0_sd),
   width = 0.1,
   alpha = 0.05,
   size = 0.7
  stat_summary(
   fun = mean,
   geom = "point",
   size = 2,
    position = position_nudge(x = 0.2)
  stat_summary(
   fun.data = mean_se,
   geom = "errorbar",
   width = 0.1,
    position = position_nudge(x = 0.2)
  facet_grid(
   Df ~ f0_mean,
   labeller = labeller(
      f0_mean = as_labeller(label_f0_mean, default = label_parsed),
      Df = as_labeller(label_Df, default = label_parsed)
  labs(
   x = expression(italic(f)[0]*" SD"),
   fill = expression(italic(f)[0]*" SD"),
    color = expression(italic(f)[0]*" SD")
  scale_colour_tq() +
  scale_fill_tq() +
  theme_tq(base_size = 14)
```



Figure S1. Distribution of fixation times as a function of f_0 SD (x-axis), split by f_0 mean (columns) and D_f (rows). Each panel includes both the density distribution, individual data points (jittered dots), and condition means with error bars. Fixation times increase with higher f_0 SD, and effects are modulated by the other acoustic features.

2.3 Power Estimation via Monte Carlo Simulation

We estimate statistical power for detecting each effect by simulating 1 000 random samples from the simulated population at varying sample sizes. Specifically, from the simulated population ($N = 1\,000$), we draw 1 000 random samples of size n = 10, another 1 000 samples of size n = 20, and so on, continuing in this way until we draw 1 000 samples of size n = 200. For each of the 20 000 samples, we fit the same linear mixed model, examine the resulting distribution of p-values, and estimate the probability of detecting a statistically significant effect for each model term.

```
# Define alpha level
alpha_lev = 0.05

# Function to run multiple power simulations for each n
run_power_sim <- function(dat, n_sample, n_sim, alpha = alpha_lev) {
    # Run `n_sim` simulations for each sample size
    map_dfr(seq_len(n_sim), \(i) {
        # Sample participants
        ids <- dat |> distinct(ID) |> slice_sample(n = n_sample) |> pull(ID)
        sampled_data <- dat |> filter(ID %in% ids)

# Fit model
    mod <- lmer(fixation_time ~ f0_sd * f0_mean * Df + (1 | ID), data = sampled_data)</pre>
```

```
anova_res <- anova(mod)</pre>
    term_names <- rownames(anova_res)</pre>
    map_dfr(term_names, \((term) {
      tibble(
        sim = i,
        n_sample = n_sample,
        p_value = anova_res[term, "Pr(>F)"],
        signif = ifelse(p_value < alpha, "Significant", "Non-significant")</pre>
    filter(!is.na(p_value))
sample_sizes \leftarrow seq(10, 200, by = 10)
term_order <- c(
  "f0_sd",
  "f0_mean",
  "Df",
  "f0_sd:f0_mean",
  "f0 sd:Df",
  "f0_mean:Df",
  "f0_sd:f0_mean:Df"
plan(multisession) # Parallel if available
power_results <- map_dfr(</pre>
  sample_sizes,
  run_power_sim(simulated_data, n_sample = .x, n_sim = 1000),
  .id = "sample_step"
  mutate(term = factor(term, levels = term_order))
```

2.3.1 Power summary

This aggregates the simulation results to compute average power for each term and sample size.

```
power_summ <- power_results |>
  group_by(term, n_sample) |>
  summarise(
  power = mean(p_value < alpha_lev, na.rm = TRUE),
    .groups = "drop"
)</pre>
```

2.3.2 Power curve

This plot shows the power curves for all main effects and interactions, highlighting the sample sizes where power exceeds 80%.

```
term labels <- c(
  "f0_mean"
                       = "italic(f)[0]*' mean'",
                       = "italic(D)[f]",
                     = "italic(f)[0]*' SD × '*italic(f)[0]*' mean'",
                      = "italic(f)[0]*' SD \times '*italic(D)[f]",
                       = "italic(f)[0]*' mean × '*italic(D)[f]",
  "f0_sd:f0_mean:Df" = "italic(f)[0]*' SD \times '*italic(f)[0]*' mean \times '*italic(D)[f]"
main_power_summ <- power_summ |>
  filter(!str_detect(term, ":"))
int_power_summ <- power_summ |>
  filter(str_detect(term, ":"))
sample_power_08 <- main_power_summ |>
  filter(power > 0.8) |>
  group_by(term) |>
  filter(power == min(power, na.rm = TRUE))
final_sample_size_st1 <- max(sample_power_08$n_sample)</pre>
# Power at final n
sample_fin <- main_power_summ |>
  filter(n_sample == final_sample_size_st1) |>
  arrange(desc(power))
ggarrange(
  ggplot(main_power_summ, aes(x = n_sample, y = power)) +
    geom_line(linewidth = 0.5) +
    geom_point(aes(color = power > 0.8), size = 2) + # Color by condition
    geom_hline(yintercept = 0.8, linetype = "dashed", color = "red") +
    scale_colour_tq(
      labels = c("FALSE" = " <= 80\%", "TRUE" = " > 80\%"),
      name = "Power threshold"
    scale_y_continuous(labels = scales::percent_format(accuracy = 1)) +
      title = "Power Curves for Main Effects",
      x = "Number of Participants",
    theme_tq() +
    facet_wrap(~term, labeller = as_labeller(term_labels, label_parsed)),
  ggplot(int_power_summ, aes(x = n_sample, y = power)) +
    geom_line(linewidth = 0.5) +
    geom_point(aes(color = power > 0.8), size = 2) + # Color by condition
    geom_hline(yintercept = 0.8, linetype = "dashed", color = "red") +
    scale_colour_tq(
      labels = c("FALSE" = " <= 80\%", "TRUE" = "> 80\%"),
```

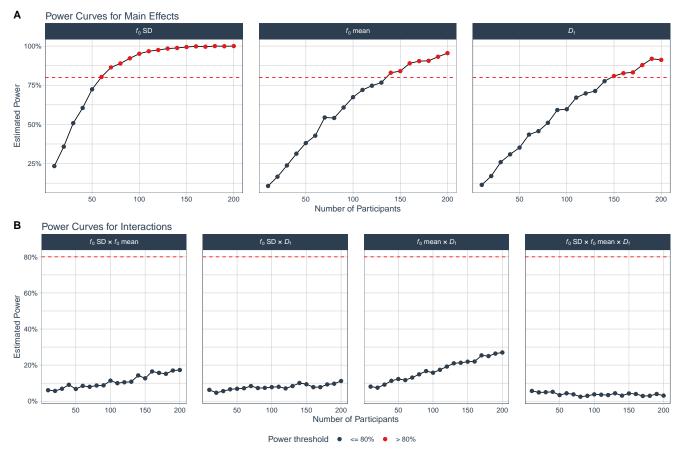


Figure S2. Power curves for detecting main effects and interactions. Panels show statistical power as a function of sample size for each fixed effect (A) and interaction (B). Dots indicate simulation-based power estimates at each sample size, with red dashed lines marking the 80% power threshold. Most main effects achieve high power with sample sizes under 160, whereas interaction terms remain underpowered across this range, reflecting smaller true effects.

2.3.3 Estimating a sample size

In the simulated population, the effects of the interactions are extremely weak and would require a very large sample size to be reliably detected. In contrast, the main effects of f_0 SD, f_0 mean, and D_f are detectable with a more reasonable sample size. If the true population effects are as simulated ($\omega_p^2 = 0.018, 0.008, 0.007$, respectively), a

statistical power of 0.8 would be reached with a sample size of n = 60 for f_0 SD, n = 140 for f_0 mean, and n = 150 for D_f .

Based on simulations:

- Power exceeds 80% for the main effects at n=150
- Corresponding partial omega squared values were: 0.018, 0.008, 0.007

Therefore, n = 150 participants would reliably detect all main effects. Interaction effects require larger samples due to weaker true effects.

2.4 Power Distribution at Final Sample

Below we visualize the distribution of p-values at the final sample size for all effects, illustrating expected Type I/II error profiles.

```
# Filter for final n
final_power <- power_summ |>
  filter(n_sample == final_sample_size_st1)
# Get full p-value data at that n
main_power_results <- power_results |>
  filter(!str_detect(term, ":")) |>
  group_by(term) |>
  filter(n_sample == final_sample_size_st1) |>
  left_join(final_power, by = c("term", "n_sample"))
int_power_results <- power_results |>
  filter(str_detect(term, ":")) |>
  group_by(term) |>
  filter(n_sample == final_sample_size_st1) |>
  left_join(final_power, by = c("term", "n_sample"))
# Plot distributions
ggarrange(
  ggplot(main_power_results, aes(x = p_value, fill = signif)) +
    geom_histogram(
      bins = 100,
      breaks = seq(0, 1, 0.01),
      alpha = 0.8,
      colour = NA
    geom_text(
      data = main_power_results |> distinct(term, power),
        x = Inf, y = Inf,
        label = paste0("Power = ", round(power, 2))
      vjust = 1.5, hjust = 1.1,
      inherit.aes = FALSE
    labs(
      fill = "Significance",
      title = "Distribution of p values for Interactions"
    scale_fill_tq(name = "Significance") +
    scale_x_continuous(breaks = scales::pretty_breaks(n = 10)) +
    facet_wrap(~term, labeller = as_labeller(term_labels, label_parsed)) +
```

```
theme_tq() +
  guides(
   fill = guide_legend(override.aes = list(colour = NA), reverse = TRUE),
   colour = "none"
ggplot(int_power_results, aes(x = p_value, fill = signif)) +
  geom_histogram(
   bins = 100,
   breaks = seq(0, 1, 0.01),
   alpha = 0.8,
   colour = NA
  geom_text(
   data = int_power_results |> distinct(term, power),
   aes(
     x = Inf, y = Inf,
     label = paste0("Power = ", round(power, 2))
   vjust = 1.5, hjust = 1.1,
   inherit.aes = FALSE
  labs(
   fill = "Significance",
 scale_fill_tq(name = "Significance") +
  scale_x_continuous(breaks = scales::pretty_breaks(n = 10)) +
  facet_wrap(~term, labeller = as_labeller(term_labels, label_parsed),
            nrow = 1) +
  theme_tq() +
  guides(
   fill = guide_legend(override.aes = list(colour = NA), reverse = TRUE),
   colour = "none"
labels = "AUTO",
common.legend = TRUE,
legend = "bottom",
nrow = 2
```



Figure S3. Distribution of p-values across simulations at n = 150. This figure shows the p-value distribution for each effect, based on 1000 simulation runs using the final recommended sample size. Main effects show a strong skew toward low p-values, consistent with high power. Interactions yield more uniform distributions, indicating limited sensitivity to detect those effects at this sample size.

2.5 Notes

- This simulation estimates power for detecting the main effect of f_0 SD only.
- You can modify the function to test other terms (e.g., interactions) by indexing a different row in the anova() output.
- For precision in planning, repeat this with multiple n_sample values.

3 Study 2

This section reports a power analysis for Study 2, which investigates the relationship between two continuous variables using Pearson's correlation. We evaluate two complementary statistical goals:

- 1. **Detecting a correlation** of at least $\rho = 0.30$ (directional, one-sided test).
- 2. **Testing for equivalence**, to determine whether an observed correlation is statistically indistinguishable from zero, within a predefined margin of ± 0.25 .

We used the TOSTER::power_z_cor() function to compute power analytically across a range of sample sizes (Caldwell, 2022; Lakens, 2017).

```
# Parameters
eq_bounds <- 0.15
rho_pop <- 0.30</pre>
```

```
alpha <- 0.05
n_sim <- 100000
# Panel A: Power curves
sample_sizes \leftarrow seq(10, 600, by = 10)
power_detect <- map_dbl(sample_sizes, ~</pre>
                           power_z_cor(
                             alternative = "greater",
                             alpha = alpha,
                             rho = rho_pop,
                             power = NULL
                           )$power
power_equiv <- map_dbl(sample_sizes, ~</pre>
                          power_z_cor(
                            alternative = "equivalence",
                            alpha = alpha,
                            null = eq_bounds,
                            rho = 0,
                            power = NULL
                          )$power
power_df <- tibble(</pre>
 n = sample_sizes,
  Detection = power_detect,
  Equivalence = power_equiv
  pivot_longer(-n, names_to = "Test", values_to = "Power")
subtitle_text <- substitute(</pre>
  expression("Effect size for detection: " * rho == r * ", Equivalence bounds: ±" * eq),
  list(r = rho_pop, eq = eq_bounds)
final_sample_size_st2 <- power_df |>
  filter(Test == "Equivalence", Power >= 0.9) |>
  summarise(min_n = min(n)) |>
  pull(min_n)
p_sample_size_st2 <- power_df |>
  filter(Test == "Detection", Power >= 0.9) |>
  summarise(min_n = min(n)) |>
  pull(min_n)
# Power curves
ggplot(power_df, aes(x = n, y = Power, color = Test)) +
  geom_line(linewidth = 0.5) +
  geom_point(size = 1) +
  geom_hline(yintercept = 0.8, linetype = "dashed") +
  geom_hline(yintercept = 0.9, linetype = "dashed") +
  geom_vline(xintercept = final_sample_size_st2, colour = "#E31A1C", linetype = "dotted") +
```

```
annotate("text", y = 0.5, x = final_sample_size_st2,
         label = bquote(italic(n) == .(final_sample_size_st2)),
         hjust = 0.5, vjust = 1.3, angle = 90,
         color = "#E31A1C", size = 2.5) +
geom_vline(xintercept = p_sample_size_st2, colour = "#2c3e50", linetype = "dotted") +
annotate("text", y = 0.5, x = p_sample_size_st2,
         label = bquote(italic(n) == .(p_sample_size_st2)),
         hjust = 0.5, vjust = 1.3, angle = 90,
         color = "#2c3e50", size = 2.5) +
scale_y_continuous(labels = scales::percent_format(accuracy = 1)) +
labs(
  title = "Power Curves for Correlation Detection and Equivalence Testing",
 subtitle = eval(subtitle_text),
 y = "Statistical Power",
 color = "Test Type"
scale_colour_tq() +
theme_tq()
```

Power Curves for Correlation Detection and Equivalence Testing

Effect size for detection: ρ = 0.3, Equivalence bounds: ±0.15

100%

75%

50%

25%

0%

Sample Size (n)

Figure S4. Power curves for detecting a positive correlation (gray line) and for concluding statistical equivalence to zero (red line) across different sample sizes. Dashed horizontal lines represent 80% and 90% power thresholds. Vertical dotted lines represents the sample size where power reaches $1 - \beta = 0.9$.

Test Type → Detection → Equivalence

In general, with a sample of 477 participants, correlations of $\rho \geq 0.23$ will likely produce conclusive evidence of a positive effect **not** equivalent to zero; correlations of $\rho \leq 0.07$ will lead to conclusive evidence of equivalence to zero. Correlations between $\rho = 0.08$ and 0.22 will typically result in inconclusive outcomes (possibly statistically significant, but not distinguishable from equivalence).

```
# Panel B: Simulated outcomes under $\rho$ = 0
set.seed(123)
```

```
z_sim_0 <- rnorm(n_sim, mean = atanh(0), sd = 1 / sqrt(final_sample_size_st2 - 3))
r_sim_0 <- tanh(z_sim_0)
ci_low_0 <- tanh(z_sim_0 - qnorm(1 - alpha) * (1 / sqrt(final_sample_size_st2 - 3)))</pre>
ci_high_0 <- tanh(z_sim_0 + qnorm(1 - alpha) * (1 / sqrt(final_sample_size_st2 - 3)))</pre>
equiv_0 <- ci_low_0 > -eq_bounds & ci_high_0 < eq_bounds
df_sim_0 <- tibble(r_obs = r_sim_0, equiv = equiv_0)</pre>
# Panel C: Simulated positive detections under $\rho$ = 0.3
# Simulate observed correlations for true $\rho$ = 0.3
z_sim_3 <- rnorm(n_sim, mean = atanh(0.3), sd = 1 / sqrt(final_sample_size_st2 - 3))</pre>
r_sim_3 <- tanh(z_sim_3)
se_z <- 1 / sqrt(final_sample_size_st2 - 3)</pre>
ci_low_3 \leftarrow tanh(z_sim_3 - qnorm(1 - alpha) * se_z)
ci_high_3 \leftarrow tanh(z_sim_3 + qnorm(1 - alpha) * se_z)
test_outcome <- case_when(</pre>
  ci_low_3 > eq_bounds ~ "Positive effect",
  ci_low_3 < 0 & ci_high_3 > 0 ~ "Not significant",
  TRUE ~ "Inconclusive"
df_sim_3 <- tibble(</pre>
 r_{obs} = r_{sim_3}
  outcome = factor(test_outcome,
                    levels = c("Positive effect", "Inconclusive", "Not significant"))
ggarrange(
  # Panel A: Simulated equivalence under $\rho$ = 0
  ggplot(df_sim_0, aes(x = r_obs, fill = equiv)) +
    geom_rect(aes(xmin = -eq_bounds, xmax = eq_bounds, ymin = 0, ymax = Inf),
              fill = "gray90", alpha = 0.4) +
    geom_histogram(binwidth = 0.01, center = 0, alpha = 0.8, color = "gray30") +
    geom_vline(xintercept = c(-eq_bounds, eq_bounds), linetype = "dashed", color = "gray40") +
    geom_vline(xintercept = 0, linetype = "dashed", color = "black") +
    scale_x_continuous(breaks = scales::pretty_breaks(n = 10), limits = c(-0.3, 0.3)) +
    scale_fill_manual(
      values = c("TRUE" = "#D55E00", "FALSE" = "gray70"),
      labels = c("Inconclusive", "Equivalence concluded"),
      name = NULL
    labs(
      title = "Simulated Equivalence Test Outcomes ($\rho$ = 0)",
    theme_tq(),
  # Panel B: Simulated non-equivalence under $\rho$ = 0.3
  ggplot(df_sim_3, aes(x = r_obs, fill = outcome)) +
    geom_rect(aes(xmin = -eq_bounds, xmax = eq_bounds, ymin = 0, ymax = Inf),
```

```
fill = "gray90", alpha = 0.4) +
  geom_histogram(binwidth = 0.01, center = 0, alpha = 0.85, color = "gray30") +
  geom_vline(xintercept = c(-eq_bounds, eq_bounds), linetype = "dashed", color = "gray40") +
  scale_x_continuous(breaks = scales::pretty_breaks(n = 10), limits = c(-0.15, 0.45)) +
  scale fill manual(
    values = c("Positive effect" = "forestgreen",
               "Inconclusive" = "gray70",
               "Not significant" = "red"),
    name = NULL
  labs(
    title = "Simulated Test Outcomes Under $\rho$ = 0.3",
    subtitle = "Shaded bars show CIs fully within ±0.15 (90% CI)",
  theme_tq(),
labels = "AUTO",
nrow = 1,
common.legend = FALSE
```

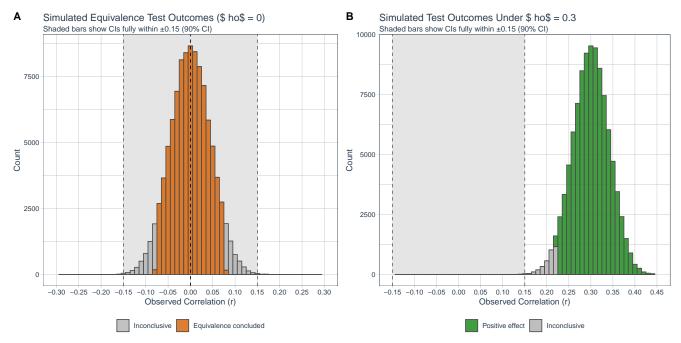


Figure S5. Power analysis for detecting or rejecting a correlation of ho = 0.30. (A) Simulated observed correlations assuming the true population value is ho = 0 (i.e., the null hypothesis is true). Orange bars indicate cases where the 90% confidence interval (CI) falls entirely within the equivalence bounds (± 0.15), allowing equivalence to be concluded. Gray bars are inconclusive. (B) Simulated observed correlations assuming the true population correlation is ho = 0.3. Green bars indicate clear positive effects (lower bound of the 90% CI > 0.15), red bars show nonsignificant results (CI overlaps 0), and gray bars represent inconclusive outcomes (CI lies entirely above 0 but also within the equivalence bounds).

4 Session info (for reproducibility)

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

R version 4.5.1 (2025-06-13)

Platform: x86_64-pc-linux-gnu

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

other attached packages: pander(v.0.6.6), TOSTER(v.0.8.4), truncnorm(v.1.0-9), ggpubr(v.0.6.0), scales(v.1.4.0), furrr(v.0.3.1), future(v.1.58.0), lmerTest(v.3.1-3), lme4(v.1.1-37), Matrix(v.1.7-3), effectsize(v.1.0.0), PerformanceAnalytics(v.2.0.8), quantmod(v.0.4.28), TTR(v.0.24.4), xts(v.0.14.1), zoo(v.1.8-14), tidyquant(v.1.0.11), ggdist(v.3.3.3), lubridate(v.1.9.4), forcats(v.1.0.0), stringr(v.1.5.1), dplyr(v.1.1.4), purrr(v.1.0.4), readr(v.2.1.5), tidyr(v.1.3.1), tibble(v.3.2.1), ggplot2(v.3.5.2), tidyverse(v.2.0.0) and knitr(v.1.50)

loaded via a namespace (and not attached): Rdpack(v.2.6.4), gridExtra(v.2.3), sandwich(v.3.1-1), rlang(v.1.1.6), magrittr(v.2.0.3), multcomp(v.1.4-28), compiler(v.4.5.1), vctrs(v.0.6.5), quadprog(v.1.5-8), pkgconfig(v.2.0.3), fastmap(v.1.2.0), backports(v.1.5.0), labeling(v.0.4.3), rmarkdown(v.2.29), tzdb(v.0.5.0), nloptr(v.2.2.1), xfun(v.0.52), broom(v.1.0.8), parallel(v.4.5.1), R6(v.2.6.1), stringi(v.1.8.7), RColorBrewer(v.1.1-3), parallelly(v.1.45.0), car(v.3.1-3), boot(v.1.3-31), numDeriv(v.2016.8-1.1), estimability(v.1.5.1), Rcpp(v.1.0.14), bookdown(v.0.43), parameters(v.0.24.2), splines(v.4.5.1), timechange(v.0.3.0), tidyselect(v.1.2.1), rstudioapi(v.0.17.1), abind(v.1.4-8), yaml(v.2.3.10), codetools(v.0.2-20), curl(v.6.2.2), listenv(v.0.9.1), lattice(v.0.22-7), withr(v.3.0.2), bayestestR(v.0.15.2), coda(v.0.19-4.1), evaluate(v.1.0.4), survival(v.3.8-3), pillar(v.1.10.2), carData(v.3.0-5), reformulas(v.0.4.0), insight(v.1.1.0), distributional(v.0.5.0), generics(v.0.1.3), hms(v.1.1.3), minqa(v.1.2.8), globals(v.0.18.0), xtable(v.1.8-4), glue(v.1.8.0), emmeans(v.1.11.0), tools(v.4.5.1), ggsignif(v.0.6.4), mvtnorm(v.1.3-3), cowplot(v.1.1.3), grid(v.4.5.1), rbibutils(v.2.3), RobStatTM(v.1.0.11), datawizard(v.1.0.2), nlme(v.3.1-168), Formula(v.1.2-5), cli(v.3.6.5), gtable(v.0.3.6), rstatix(v.0.7.2), digest(v.0.6.37), TH.data(v.1.1-3), farver(v.2.1.2), htmltools(v.0.5.8.1), lifecycle(v.1.0.4) and MASS(v.7.3-65)

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