

PROST P600 Analysis (JS)

Joanna Morris

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Setup and load files

Set parameters

Used when comparing two conditions measured in the same participants (e.g., repeated measures, paired t-test, within-subject contrasts in LMMs).

Formula:

$$d_z = \frac{\bar{X}_{\text{diff}}}{s_{\text{diff}}}$$

Or, using the t value and sample size:

$$d_z = \frac{t}{\sqrt{n}}$$

Where:

- \bar{X}_{diff} is the mean of the difference scores
- s_{diff} is the standard deviation of the difference scores
- n is the number of participants

This version assumes the standard deviation of the difference scores already accounts for the within-subject correlation.

Load and format data files

```
p600 <- read_csv('prost_mea_500800_202508.csv')
subjlist <- read_csv('prost_subjlist_20250812.csv')
subjlist <- as.list(subjlist$x)

centroparietal_channels <- c('C3', 'Cz', 'C4', 'CP3', 'CPZ', 'CP4', 'P3', 'PZ', 'P4')
posterior_channels <- c('PZ', 'P4', 'P8', 'TP8', 'CP4', 'TP7', 'P7', 'P3', 'CP3', 'CPZ')
frontal_channels <- c('FZ', 'F4', 'F8', 'FT8', 'FC4', 'FT7', 'F7', 'F3', 'FC3', 'FCZ')

p600_labels <- p600 |> filter(ERPset %in% subjlist) |>
  filter(chlabel %in% posterior_channels) |>
  mutate(SubjID = str_extract(ERPset, "\\d{3}")) |>
  mutate(Referentiality = case_when(grepl("Bound variable", binlabel) ~ "Bound variable",
                                     grepl("Referential", binlabel) ~ "Referential")) |>
  mutate(Gender_Status = case_when(grepl("NonGendered", binlabel) ~ "NonGendered",
                                    grepl("Gendered", binlabel) ~ "Gendered")) |>
  mutate(Pronoun = case_when(grepl("Gender-congruent", binlabel) ~ "Congruent",
                              grepl("Gender-incongruent", binlabel) ~ "Incongruent",
                              grepl("Gender-neutral", binlabel) ~ "Neutral",
                              grepl("Masculine", binlabel) ~ "Masculine",
                              grepl("Feminine", binlabel) ~ "Feminine")) |>
  mutate(Group = case_when(grepl("S4", ERPset) ~ "NonBinary",
                             grepl("S3", ERPset) ~ "NonBinary",
                             grepl("S2", ERPset) ~ "Binary"))

p600_gdr <- p600_labels |> filter(Gender_Status == "Gendered") |>
  select(-Gender_Status) |>
  mutate(Referentiality = factor(Referentiality, levels= c("Referential", "Bound variable"))) |>
  mutate(Pronoun = factor(Pronoun, levels = c("Congruent",
                                              "Incongruent",
                                              "Neutral")))

p600_ngd <- p600_labels |> filter(Gender_Status == "NonGendered") |>
  select(-Gender_Status) |>
  mutate(Referentiality = factor(Referentiality, levels= c("Referential", "Bound variable"))) |>
```

```
mutate(Pronoun = factor(Pronoun, levels = c("Masculine",
                                             "Feminine",
                                             "Neutral")))
```

Test of ANOVA Model with Electrode nested within subject

This model includes Referentiality and Pronoun as fixed effects and their interaction (Referentiality * Pronoun). It estimates the main effect of Referentiality, the main effect of Pronoun and the Referentiality \times Pronoun interaction. It specifies random intercepts and random slopes for both Referentiality and Pronoun by subject (1 + Referentiality + Pronoun | SubjID), thereby accounting for individual differences in baseline (intercept) as well as individual variability in how Referentiality and Pronoun affect the outcome. It adds random intercepts by electrode (chlabel) nested within subject (1 | SubjID:chlabel) which captures the idea that each electrode may behave differently for each subject (i.e., nested variability across electrode sites within subjects).

To determine whether including random intercepts for electrode site nested within subject improved model fit, we compared a full model including this term to a simplified model without it. R code to test the nested electrode random effect across all four models, comparing:

- A full model with the nested electrode term: (1 + Referentiality + TrialType | SubjID) + (1 | SubjID:chlabel)
- A simpler model without it: (1 + Referentiality + TrialType | SubjID)

```
library(afex)
library(lme4)

# Create a function to compare nested vs non-nested models
compare_models <- function(data, label) {
  message("Running model comparisons for: ", label)

  # Full model: includes nested electrode intercept
  model_full <- mixed(
    value ~ Referentiality * Pronoun +
      (1 + Referentiality + Pronoun | SubjID) +
      (1 | SubjID:chlabel),
    data = data,
    method = "KR",
    return = "merMod"
  )

  # Simpler model: no nested electrode term
  model_simple <- mixed(
    value ~ Referentiality * Pronoun +
      (1 + Referentiality + Pronoun | SubjID),
    data = data,
    method = "KR",
    return = "merMod"
  )

  # Likelihood ratio test between full and simplified models
  comp <- anova(model_simple, model_full)
  print(comp)

  # Return model comparison object for inspection
  return(comp)
}

# Run comparisons for all datasets
comp_gdr <- compare_models(p600_gdr, "Gendered")

|| Data: data
|| Models:
|| model_simple: value ~ Referentiality * Pronoun + (1 + Referentiality + Pronoun | SubjID)
|| model_full: value ~ Referentiality * Pronoun + (1 + Referentiality + Pronoun | SubjID) + (1 | SubjID:chlabel)
||      npar   AIC    BIC logLik deviance  Chisq Df Pr(>Chisq)
|| model_simple  17 24052 24166 -12009    24018
|| model_full    18 24009 24130 -11987    23973 44.668  1 2.335e-11 ***
|| ---
|| Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
comp_ngd <- compare_models(p600_ngd, "NonGendered")

|| Data: data
|| Models:
|| model_simple: value ~ Referentiality * Pronoun + (1 + Referentiality + Pronoun | SubjID)
|| model_full: value ~ Referentiality * Pronoun + (1 + Referentiality + Pronoun | SubjID) + (1 | SubjID:chlabel)
||      npar   AIC    BIC logLik deviance  Chisq Df Pr(>Chisq)
|| model_simple  17 24143 24258 -12055    24109
|| model_full    18 24124 24245 -12044    24088 20.949  1 4.716e-06 ***
|| ---
|| Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

ANOVA Model I Gendered

```
#Fit ANOVA model
anova_elec_nested_1 <- mixed(
  value ~ Referentiality * Pronoun +
    (1 + Referentiality + Pronoun | SubjID) +
    (1 | SubjID:chlabel),
  data = p600_gdr,
  method = "KR")
anova_elec_nested_1

|| Mixed Model Anova Table (Type 3 tests, KR-method)
||
|| Model: value ~ Referentiality * Pronoun + (1 + Referentiality + Pronoun |
|| Model: SubjID) + (1 | SubjID:chlabel)
|| Data: p600_gdr
||
||          Effect          df          F p.value
|| 1          Referentiality    1, 37.98      0.40   .531
|| 2             Pronoun        2, 36      3.68 *   .035
|| 3 Referentiality:Pronoun    2, 5584.00 138.17 *** <.001
|| ---
|| Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '+' 0.1 ' ' 1

# m1 <- anova_elec_nested_1$full_model # Extract the lmer model
# ranova(m1) # Run random effects comparison
# drop1(m1)

# Extract effect sizes from your ANOVA model
eta_squared(anova_elec_nested_1, partial = TRUE)

|| # Effect Size for ANOVA (Type III)
||
|| Parameter | Eta2 (partial) | 95% CI
|| -----|-----|-----|
|| Referentiality | 0.01 | [0.00, 1.00]
|| Pronoun | 0.17 | [0.01, 1.00]
|| Referentiality:Pronoun | 0.05 | [0.04, 1.00]
||
|| - One-sided CIs: upper bound fixed at [1.00].

# Compute Marginal(fixed effects only) and Conditional(fixed + random effects) R²
r2(anova_elec_nested_1)

|| # R2 for Mixed Models
||
|| Conditional R2: 0.281
|| Marginal R2: 0.045
```

Simple Effects Analyses

```
tt.ref.contrasts_gdr <- c("Referential Congruent - Referential Incongruent",
  "Referential Congruent - Referential Neutral",
  "Bound variable Congruent - Bound variable Incongruent",
  "Bound variable Congruent - Bound variable Neutral")
emmeans_obj_1 <- emmeans(anova_elec_nested_1, pairwise ~ Referentiality * Pronoun,
  adjust = "none", pbkrtest.limit = 6480)
tt.ref.means_1 <- as_tibble(emmeans_obj_1$emmeans)
tt.ref.contrasts_df_1 <- as_tibble(subset(emmeans_obj_1$contrasts, contrast %in% tt.ref.contrasts_gdr))

tt.ref.contrasts_df_1 <- tt.ref.contrasts_df_1 |>
  mutate(p.value.adjusted = p.adjust(p.value, method = "bonferroni"))

# Number of subjects
n <- 38
tt.ref.contrasts_df_with_dz_1 <- tt.ref.contrasts_df_1 |>
  rowwise() |>
  mutate(result = list(get_dz_CI(t.ratio, df, n))) |>
  unnest_wider(result)

# Means and Contrasts
tt.ref.means_1

|| # A tibble: 6 x 7
||   Referentiality Pronoun    emmean    SE    df lower.CL upper.CL
||   <fct>          <fct>    <dbl> <dbl> <dbl>   <dbl>   <dbl>
|| 1 Referential    Congruent    0.973 0.156  41.5    0.658    1.29
|| 2 Bound variable Congruent    0.261 0.163  41.1   -0.0683   0.591
|| 3 Referential    Incongruent    0.569 0.198  39.7    0.168    0.969
|| 4 Bound variable Incongruent    1.75 0.191  39.9    1.36    2.14
|| 5 Referential    Neutral    0.789 0.118  39.6    0.551    1.03
|| 6 Bound variable Neutral    0.556 0.136  38.9    0.280    0.832
```

```
tt.ref.contrasts_df_with_dz_1
```

```

|| # A tibble: 4 x 10
|| contrast estimate SE df t.ratio p.value p.value.adjusted dz CI_lower CI_upper
|| <chr> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>
|| 1 Referential Congruent - Referential Incongruent 0.404 0.212 43.8 1.91 6.26e-2 0.250 0.310 -0.0161 0.633
|| 2 Referential Congruent - Referential Neutral 0.184 0.157 46.8 1.17 2.48e-1 0.994 0.190 -0.132 0.509
|| 3 Bound variable Congruent - Bound variable Incongruent -1.49 0.212 43.8 -7.03 1.04e-8 0.0000000418 -1.14 -1.53 -0.739
|| 4 Bound variable Congruent - Bound variable Neutral -0.294 0.157 46.8 -1.87 6.72e-2 0.269 -0.304 -0.626 0.0214

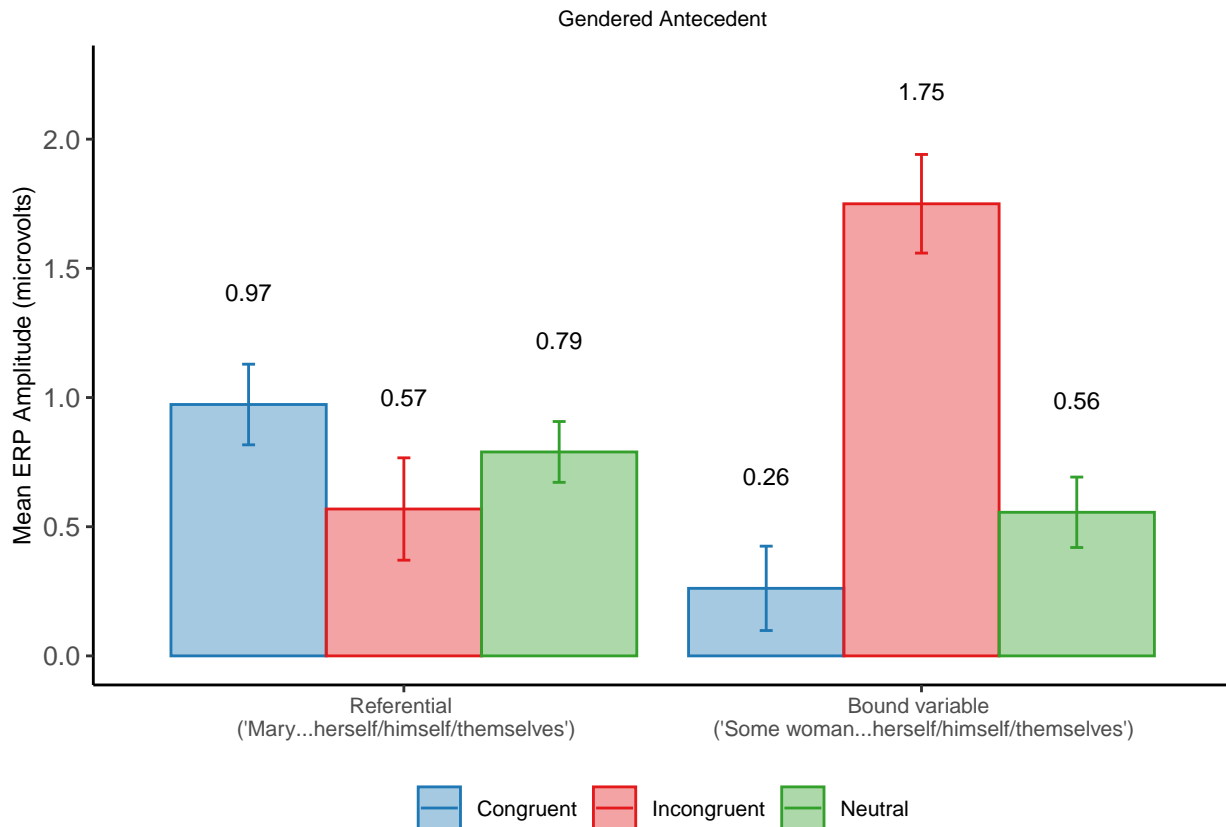
```

Interaction Plot

```

p1 <- tt.ref.means_1 |>
  ggplot(aes(x = Referentiality, y = emmean, fill = Pronoun, colour = Pronoun)) +
  geom_col(alpha = .4, position = position_dodge(.9)) +
  geom_text(aes(label = round(emmean, digits = 2), vjust = -6),
    colour = "black", size = 3, position = position_dodge(.9)) +
  coord_cartesian(ylim = c(0, 2.25)) +
  geom_errorbar(aes(ymin = emmean - SE, ymax = emmean + SE),
    width = .075,
    position = position_dodge(.9)) +
  ylab("Mean ERP Amplitude (microvolts)") +
  scale_color_custom() +
  scale_fill_custom() +
  labs(title = "Gendered Antecedent") +
  theme(plot.title = element_text(size = 8, hjust = .5),
    legend.title = element_blank(),
    legend.text = element_text(size = 8),
    axis.title.x = element_blank(),
    axis.text.x = element_text(size = 8)) +
  scale_x_discrete(labels=c("Referential" = "Referential \n ('Mary...herself/himself/themselves')",
    "Bound variable" = "Bound variable \n ('Some woman...herself/himself/themselves')"))
p1

```



ANOVA Model II Singular NonGendered (NonReferential—Someone... himself/herself; Referential—The runner... himself/herself)

```
#Fit ANOVA model
anova_elec_nested_2 <- mixed(
  value ~ Referentiality * Pronoun +
    (1 + Referentiality + Pronoun | SubjID) +
    (1 | SubjID:chlabel),
  data = p600_ngd,
  method = "KR")
anova_elec_nested_2

|| Mixed Model Anova Table (Type 3 tests, KR-method)
||
|| Model: value ~ Referentiality * Pronoun + (1 + Referentiality + Pronoun |
|| Model: SubjID) + (1 | SubjID:chlabel)
|| Data: p600_ngd
||
||      Effect      df      F p.value
|| 1      Referentiality 1, 37.32      2.15      .151
|| 2      Pronoun 2, 36.33      1.10      .344
|| 3 Referentiality:Pronoun 2, 5584 24.99 *** <.001
|| ---
|| Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

m2 <- anova_elec_nested_2$full_model # Extract the lmer model
ranova(m2) # Run random effects comparison

|| ANOVA-like table for random-effects: Single term deletions
||
|| Model:
|| value ~ Referentiality + Pronoun + (1 + Referentiality + Pronoun | SubjID) + (1 | SubjID:chlabel) + Referentiality:Pronoun
||
||      npar logLik  AIC    LRT Df Pr(>Chisq)
|| <none>      18 -12056 24148
|| Referentiality in (1 + Referentiality + Pronoun | SubjID) 14 -12164 24355 215.01 4 < 2.2e-16 ***
|| Pronoun in (1 + Referentiality + Pronoun | SubjID) 11 -12250 24522 387.58 7 < 2.2e-16 ***
|| (1 | SubjID:chlabel) 17 -12066 24167 20.90 1 4.832e-06 ***
|| ---
|| Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

drop1(m2)

|| Single term deletions using Satterthwaite's method:
||
|| Model:
|| value ~ Referentiality * Pronoun + (1 + Referentiality + Pronoun | SubjID) + (1 | SubjID:chlabel)
||
||      Sum Sq Mean Sq NumDF DenDF F value Pr(>F)
|| Referentiality:Pronoun 143.13 71.564 2 5584.1 24.99 1.567e-11 ***
|| ---
|| Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# Extract effect sizes from your ANOVA model
eta_squared(anova_elec_nested_2, partial = TRUE)

|| # Effect Size for ANOVA (Type III)
||
|| Parameter | Eta2 (partial) | 95% CI
|| -----|-----|-----
|| Referentiality | 0.05 | [0.00, 1.00]
|| Pronoun | 0.06 | [0.00, 1.00]
|| Referentiality:Pronoun | 8.87e-03 | [0.01, 1.00]
||
|| - One-sided CIs: upper bound fixed at [1.00].

# Compute Marginal(fixed effects only) and Conditional(fixed + random effects) R²
r2(anova_elec_nested_2)

|| # R2 for Mixed Models
||
|| Conditional R2: 0.213
|| Marginal R2: 0.012
```

Simple Effects Analyses

```
tt.ref.contrasts_ngd <- c("Referential Masculine - Referential Feminine",
  "Referential Masculine - Referential Neutral",
  "Bound variable Masculine - Bound variable Feminine",
  "Bound variable Masculine - Bound variable Neutral")
emmeans_obj_2 <- emmeans(anova_elec_nested_2, pairwise ~ Referentiality * Pronoun,
  adjust = "none", pbkrtest.limit = 6480)
tt.ref.means_2 <- as_tibble(emmeans_obj_2$emmeans)
tt.ref.contrasts_df_2 <- as_tibble(subset(emmeans_obj_2$contrasts, contrast %in% tt.ref.contrasts_ngd))
```

```
tt.ref.contrasts_df_2 <- tt.ref.contrasts_df_2 |>
  mutate(p.value.adjusted = p.adjust(p.value, method = "bonferroni"))

# Number of subjects
n <- 38
tt.ref.contrasts_df_with_dz_2 <- tt.ref.contrasts_df_2 |>
  rowwise() |>
  mutate(result = list(get_dz_CI(t.ratio, df, n))) |>
  unnest_wider(result)

# Means and Contrasts
tt.ref.means_2
```

```
## # A tibble: 6 x 7
##   Referentiality Pronoun   emmean   SE    df lower.CL upper.CL
##   <fct>          <fct>   <dbl> <dbl> <dbl>   <dbl>   <dbl>
## 1 Referential   Masculine 0.530 0.132 43.4   0.263   0.797
## 2 Bound variable Masculine 0.372 0.166 40.9   0.0358  0.708
## 3 Referential   Feminine 0.260 0.135 43.1  -0.0125  0.533
## 4 Bound variable Feminine 0.938 0.203 39.5   0.527   1.35
## 5 Referential   Neutral 0.649 0.117 47.5   0.413   0.885
## 6 Bound variable Neutral 0.732 0.122 37.9   0.485   0.979
tt.ref.contrasts_df_with_dz_2
```

```
## # A tibble: 4 x 10
##   contrast                                     estimate   SE    df t.ratio p.value p.value.adjusted    dz CI_lower CI_upper
##   <chr>                                     <dbl> <dbl> <dbl>   <dbl>   <dbl>         <dbl>   <dbl>   <dbl>   <dbl>
## 1 Referential Masculine - Referential Feminine      0.270 0.176 47.9    1.53  0.132         0.530  0.248 -0.0747  0.569
## 2 Referential Masculine - Referential Neutral     -0.119 0.175 51.2   -0.680  0.499         1      -0.110 -0.428  0.209
## 3 Bound variable Masculine - Bound variable Feminine -0.567 0.176 47.9   -3.21  0.00235      0.00939 -0.521 -0.853 -0.184
## 4 Bound variable Masculine - Bound variable Neutral -0.360 0.167 43.1   -2.15  0.0368      0.147  -0.350 -0.674 -0.0213
```

Interaction Plot

```
p2 <- tt.ref.means_2 |>
  ggplot(aes(x = Referentiality, y = emmean, fill = Pronoun, colour = Pronoun)) +
  geom_col(alpha = .4, position = position_dodge(.9)) +
  geom_text(aes(label = round(emmean, digits = 2), vjust = -6),
    colour = "black", size = 3, position = position_dodge(.9)) +
  coord_cartesian(ylim = c(0, 2.25)) +
  geom_errorbar(aes(ymin = emmean - SE, ymax = emmean + SE),
    width = .075,
    position = position_dodge(.9)) +
  ylab("Mean ERP Amplitude (microvolts)") +
  scale_color_custom() +
  scale_fill_custom() +
  labs(title = "Non-Gendered Antecedent") +
  theme(plot.title = element_text(size = 8, hjust = .5),
    legend.title = element_blank(),
    legend.text = element_text(size = 8),
    axis.title.x = element_blank(),
    axis.text.x = element_text(size = 8)) +
  scale_x_discrete(labels = c("Referential" = "Referential \n ('The runner...himself/herself/themselves')",
    "Bound variable" = "Bound variable \n ('Someone...himself/herself/themselves')"))

p2
```

