

PROST Nref Analysis (JS)

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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

```
nref <- read_csv('prost_mea_300500_202207.csv')
subjlist <- read_csv('prost_subjlist_20250720.csv')
subjlist <- as.list(subjlist$x)

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

nref <- nref |> filter(ERPset %in% subjlist) |>
  filter(chlabel %in% frontal_channels) |>
  mutate(SubjID = str_extract(ERPset, "\\d{3}")) |>
  mutate(Referentiality = case_when(grepl("NonReferential", binlabel) ~ "NonReferential",
                                     grepl("Referential", binlabel) ~ "Referential")) |>
  mutate(Gender_Status = case_when(grepl("NonGendered", binlabel) ~ "NonGendered",
                                    grepl("Gendered", binlabel) ~ "Gendered")) |>
  mutate(TrialType = case_when(grepl("Critical", binlabel) ~ "Experimental",
                                  grepl("Baseline", binlabel) ~ "Control")) |>
  mutate(Group = case_when(grepl("prost4", ERPset) ~ "NonBinary",
                              grepl("prost3", ERPset) ~ "NonBinary",
                              grepl("prost2", ERPset) ~ "Binary")) |>
  mutate(Number = case_when(grepl("himself_herself", binlabel) ~ "Singular",
                              grepl("themselves", binlabel) ~ "Plural")) |>
  mutate(Pronoun = case_when((Number == "Singular" & TrialType == "Experimental") ~ "Singular Pronoun Gender Incongruent",
                              (Number == "Singular" & TrialType == "Control") ~ "Singular Pronoun Gender Congruent",
                              (Number == "Plural" & TrialType == "Experimental") ~ "Plural Pronoun Singular Antecedent",
                              (Number == "Plural" & TrialType == "Control") ~ "Plural Pronoun Plural Antecedent"))

nref_gdr <- nref |> filter(Gender_Status == "Gendered") |>
  select(-Gender_Status) |>
  mutate(Referentiality = factor(Referentiality, levels= c("Referential", "NonReferential"))) |>
  mutate(Pronoun = factor(Pronoun, levels = c("Singular Pronoun Gender Congruent",
                                              "Singular Pronoun Gender Incongruent",
                                              "Plural Pronoun Singular Antecedent",
                                              "Plural Pronoun Plural Antecedent")) |>
```

```

filter(!(Pronoun == "Plural Pronoun Plural Antecedent"))

nref_ngd <- nref |> filter(Gender_Status == "NonGendered") |>
  select(-Gender_Status) |>
  mutate(Referentiality = factor(Referentiality, levels= c("Referential", "NonReferential"))) |>
  mutate(Pronoun = factor(Pronoun, levels = c("Singular Pronoun Gender Congruent",
                                              "Singular Pronoun Gender Incongruent",
                                              "Plural Pronoun Singular Antecedent",
                                              "Plural Pronoun Plural Antecedent"))) |>
  filter(!(Pronoun == "Plural Pronoun Plural Antecedent"))

```

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 × 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(nref_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 17968 18075 -8966.9   17934
|| model_full    18 17967 18081 -8965.5   17931 2.8039 1 0.09404 .
|| ---
|| Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
comp_ngd <- compare_models(nref_ngd, "Non-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 17249 17356 -8607.4   17215
|| model_full     18 17233 17347 -8598.7   17197 17.378 1 3.064e-05 ***
|| ---
|| 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),
  data = nref_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)
|| Data: nref_gdr
||
||           Effect      df      F p.value
|| 1      Referentiality    1, 37    0.46  .500
|| 2      Pronoun          2, 36    2.51 +  .095
|| 3 Referentiality:Pronoun 2, 3950 44.18 *** <.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 | 0.12 | [0.00, 1.00]
|| Referentiality:Pronoun | 0.02 | [0.01, 1.00]
||
|| - One-sided CIs: upper bound fixed at [1.00].

```

```

# Compute Marginal(fixed effects only) and Conditional(fixed + random effects) R^2
r2(anova_elec_nested_1)

```

```

|| # R2 for Mixed Models
||
|| Conditional R2: 0.293
|| Marginal R2: 0.022

```

Simple Effects Analyses

```

tt.ref.contrasts <- c("Referential Singular Pronoun Gender Congruent - Referential Singular Pronoun Gender Incongruent",
  "Referential Singular Pronoun Gender Congruent - Referential Plural Pronoun Singular Antecedent",
  "NonReferential Singular Pronoun Gender Congruent - NonReferential Singular Pronoun Gender Incongruent",
  "NonReferential Singular Pronoun Gender Congruent - NonReferential Plural Pronoun Singular Antecedent")
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))

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 Singular Pronoun Gender Congruent 0.861 0.234 40.0 0.387 1.33
|| 2 NonReferential Singular Pronoun Gender Congruent 0.524 0.221 40.4 0.0788 0.970
|| 3 Referential Singular Pronoun Gender Incongruent -0.255 0.225 40.2 -0.710 0.199
|| 4 NonReferential Singular Pronoun Gender Incongruent 0.727 0.185 41.9 0.353 1.10
|| 5 Referential Plural Pronoun Singular Antecedent 0.632 0.250 39.6 0.127 1.14
|| 6 NonReferential Plural Pronoun Singular Antecedent 0.368 0.212 40.7 -0.0594 0.796
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 Singular Pronoun Gender Congruent -- 1.12 0.226 48.0 4.94 9.91e-6 0.0000396 0.801 0.442 1.15
|| 2 Referential Singular Pronoun Gender Congruent -- 0.228 0.257 45.1 0.890 3.78e-1 1 0.144 -0.176 0.463
|| 3 NonReferential Singular Pronoun Gender Congruen- -0.203 0.226 48.0 -0.898 3.74e-1 1 -0.146 -0.464 0.174
|| 4 NonReferential Singular Pronoun Gender Congruen- 0.156 0.257 45.1 0.610 5.45e-1 1 0.0989 -0.220 0.417

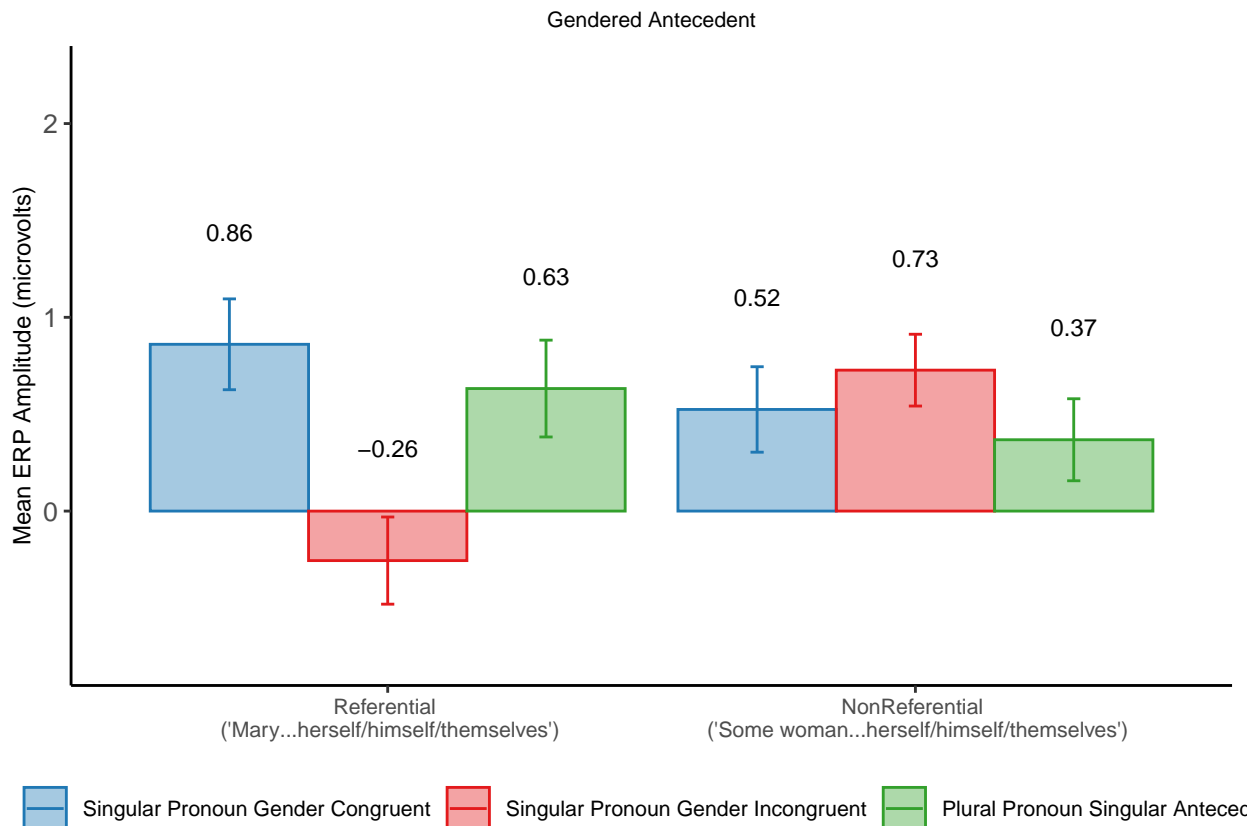
```

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(-.75, 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')",
    "NonReferential" = "NonReferential \n ('Some woman...herself/himself/themselves')"))

```



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 = nref_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: nref_ngd
||
||      Effect      df      F p.value
|| 1      Referentiality  1, 37      0.00      .961
|| 2      Pronoun      2, 36      0.24      .786
|| 3 Referentiality:Pronoun 2, 3646 20.04 *** <.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 -8608.5 17253
|| Referentiality in (1 + Referentiality + Pronoun | SubjID) 14 -8691.1 17410 165.22 4 < 2.2e-16 ***
|| Pronoun in (1 + Referentiality + Pronoun | SubjID) 11 -8805.4 17633 393.83 7 < 2.2e-16 ***
|| (1 | SubjID:chlabel) 17 -8617.2 17268 17.32 1 3.163e-05 ***
|| ---
|| 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 138.5 69.249 2 3646 20.038 2.213e-09 ***
|| ---
|| 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 | 6.71e-05 | [0.00, 1.00]
|| Pronoun | 0.01 | [0.00, 1.00]
|| Referentiality:Pronoun | 0.01 | [0.01, 1.00]
||
|| - One-sided CIs: upper bound fixed at [1.00].

# Compute Marginal(fixed effects only) and Conditional(fixed + random effects) R^2
r2(anova_elec_nested_2)

|| # R2 for Mixed Models
||
|| Conditional R2: 0.353
|| Marginal R2: 0.007
```

Simple Effects Analyses

```
tt.ref.contrasts <- c("Referential Singular Pronoun Gender Congruent - Referential Singular Pronoun Gender Incongruent",
  "Referential Singular Pronoun Gender Congruent - Referential Plural Pronoun Singular Antecedent",
  "NonReferential Singular Pronoun Gender Congruent - NonReferential Singular Pronoun Gender Incongruent",
  "NonReferential Singular Pronoun Gender Congruent - NonReferential Plural Pronoun Singular Antecedent")
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))
```

```
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   Singular Pronoun Gender Congruent  0.770 0.184 41.0  0.398    1.14
|| 2 NonReferential Singular Pronoun Gender Congruent  0.285 0.222 39.7 -0.164    0.734
|| 3 Referential   Singular Pronoun Gender Incongruent  0.403 0.214 39.9 -0.0289   0.835
|| 4 NonReferential Singular Pronoun Gender Incongruent  0.799 0.234 39.4  0.326    1.27
|| 5 Referential   Plural Pronoun Singular Antecedent  0.408 0.236 39.3 -0.0690   0.884
|| 6 NonReferential Plural Pronoun Singular Antecedent  0.520 0.258 38.9 -0.00238   1.04
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 Singular Pronoun Gender Congruent - 0.367 0.246 44.1  1.49  0.143    0.570 0.242 -0.0810  0.563
|| 2 Referential Singular Pronoun Gender Congruent - 0.362 0.216 46.5  1.67  0.101    0.404 0.272 -0.0526  0.593
|| 3 NonReferential Singular Pronoun Gender Congruent - -0.514 0.246 44.1 -2.09 0.0422    0.169 -0.339 -0.663 -0.0119
|| 4 NonReferential Singular Pronoun Gender Congruent - -0.235 0.216 46.5 -1.08 0.284      1 -0.176 -0.495  0.145
```

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')",
    "NonReferential" = "NonReferential \n ('Someone...himself/herself/themselves')"))
```

p2

