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:

- $\bar{X}_{\text{diff}}$ 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_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', 'CP4',  'P3',  'CP3', 'CPZ')
frontal_channels <- c('FZ', 'F4', 'F8', 'FT8', 'FC4', 'FT7', 'F7', 'F3',  'FC3', 'FCZ')

nref_labels <- nref |>  filter(ERPset %in% subjlist) |>  filter(ERPset %in% subjlist) |>
  filter(chlabel %in% frontal_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"))


nref_gdr <- nref_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")))

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

```r
    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 × 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)

```r
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 23881 23994 -11924    23847
|| model_full     18 23868 23987 -11916    23832 15.543  1  8.065e-05 ***
|| ---
|| Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
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 23220 23332 -11593    23186
|| model_full     18 23182 23300 -11573    23146 40.305  1  2.172e-10 ***
|| ---
|| 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   = 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) + (1 | SubjID:chlabel)
|| Data: nref_gdr
||              Effect        df         F p.value
|| 1       Referentiality 1, 37.97      1.17    .286
|| 2             Pronoun    2, 36      2.32    .113
|| 3 Referentiality:Pronoun   2, 5014 43.18 ***   <.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     |           0.03 | [0.00, 1.00]
|| Pronoun            |           0.11 | [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) R²
r2(anova_elec_nested_1)
```

```
|| # R2 for Mixed Models
||
|| Conditional R2: 0.253
||    Marginal R2: 0.018
```

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      0.861 0.229  40.5    0.397     1.32
|| 2 Bound variable Congruent      0.524 0.217  40.9    0.0865    0.962
|| 3 Referential    Incongruent   -0.255 0.223  40.7   -0.705     0.194
|| 4 Bound variable Incongruent    0.727 0.177  43.1    0.370     1.08
|| 5 Referential    Neutral        0.398 0.197  38.5   -0.00117   0.798
|| 6 Bound variable Neutral        0.281 0.140  40.1   -0.00192   0.564
```

```
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   1.12 0.226  47.9    4.94  9.86e-6        0.0000394  0.802    0.442     1.15
|| 2 Referential Congruent - Referential Neutral       0.462 0.214  45.8    2.16  3.60e-2        0.144      0.351    0.0228    0.675
|| 3 Bound variable Congruent - Bound variable Incong~ -0.203 0.226  47.9   -0.898 3.73e-1        1         -0.146   -0.464    0.174
|| 4 Bound variable Congruent - Bound variable Neutral  0.244 0.214  45.8    1.14  2.61e-1        1          0.185   -0.137    0.504
```

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')",
                                  "Bound variable" = "Bound variable \n ('Some woman...herself/himself/themselves')"))
p1
```
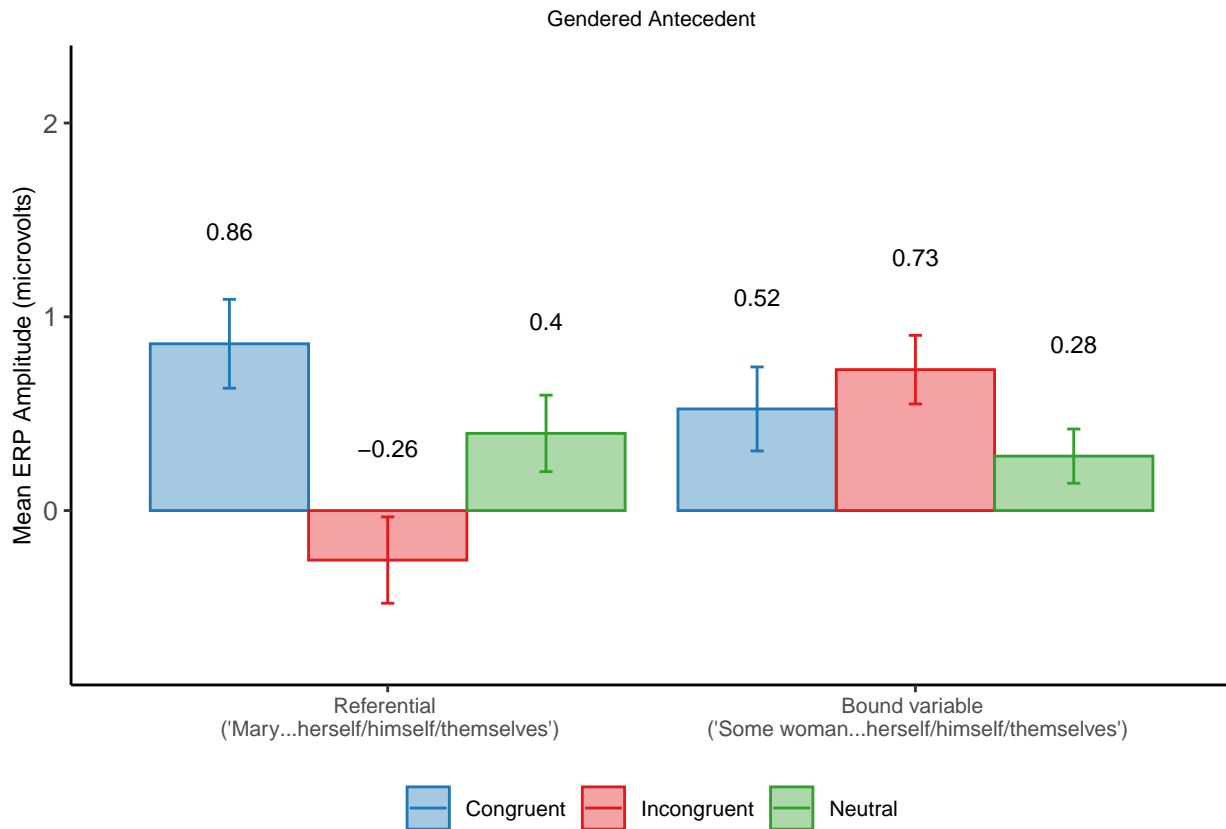
ANOVA Model II Singular NonGendered (NonReferential—Someone. . . himself/herself; Referential—The runner. . . himself/herself)

```r
#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, 37.25      0.38    .540
|| 2              Pronoun 2, 36.32      0.19    .826
|| 3 Referentiality:Pronoun  2, 5014 19.98 ***   <.001
|| ---
|| Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '+' 0.1 ' ' 1
```

```r
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 -11583 23202
|| Referentiality in (1 + Referentiality + Pronoun | SubjID)   14 -11725 23477 283.66  4  < 2.2e-16 ***
|| Pronoun in (1 + Referentiality + Pronoun | SubjID)         11 -11827 23676 488.80  7  < 2.2e-16 ***
|| (1 | SubjID:chlabel)                                       17 -11603 23240  40.23  1  2.253e-10 ***
|| ---
|| Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
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   146  72.999     2  5014  19.984 2.268e-09 ***
|| ---
|| Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# 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       |          0.01 | [0.00, 1.00]
|| Pronoun              |          0.01 | [0.00, 1.00]
|| Referentiality:Pronoun |       7.91e-03 | [0.00, 1.00]
||
|| - One-sided CIs: upper bound fixed at [1.00].
```

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

```
|| # R2 for Mixed Models
||
||   Conditional R2: 0.321
||      Marginal R2: 0.007
```

Simple Effects Analyses

```r
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))
```

```r
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   0.770 0.174  42.1   0.419     1.12
|| 2 Bound variable Masculine   0.285 0.240  39.6  -0.201     0.771
|| 3 Referential    Feminine    0.403 0.218  40.2  -0.0381    0.844
|| 4 Bound variable Feminine    0.799 0.240  39.6   0.314     1.28
|| 5 Referential    Neutral     0.606 0.239  40.1   0.123     1.09
|| 6 Bound variable Neutral     0.351 0.192  37.5  -0.0376    0.739
```

```r
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    0.367 0.247  44.5   1.49  0.143             0.574  0.242  -0.0816   0.562
|| 2 Referential Masculine - Referential Neutral     0.164 0.236  47.4   0.695 0.491             1      0.113  -0.207    0.431
|| 3 Bound variable Masculine - Bound variable Femin~ -0.514 0.247  44.5  -2.09  0.0426            0.171 -0.339  -0.662   -0.0111
|| 4 Bound variable Masculine - Bound variable Neutr~ -0.0658 0.228  41.5 -0.288 0.774             1     -0.0468 -0.365   0.272
```

Interaction Plot

```r
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(-.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 = "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
```

Non−Gendered Antecedent

Mean ERP Amplitude (microvolts)

Referential
('The runner...himself/herself/themselves')

Bound variable
('Someone...himself/herself/themselves')

Masculine   Feminine   Neutral