

Psychonomics 2023 ANOVA ALL SHAPES

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Let's import our data

```
library(readr)
subjectProfiles <- read_csv("M21_subjectProfiles_hampshire_2.csv")

## Rows: 45 Columns: 3
## -- Column specification -----
## Delimiter: ","
## chr (3): Sensitivity, ReadingProfile, SubjID
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
n400 <- read_csv("m21_vsl_300500_150050.csv")

## Rows: 32805 Columns: 6
## -- Column specification -----
## Delimiter: ","
## chr (3): chlabel, binlabel, SubjID
## dbl (3): value, chindex, bini
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

Next lets join the subject reading profile data and erp data into a single dataframes

```
library(dplyr)

##
## Attaching package: 'dplyr'
##
## The following objects are masked from 'package:stats':
##
##   filter, lag
##
## The following objects are masked from 'package:base':
##
##   intersect, setdiff, setequal, union

library(tidyr)
n400_subj <- left_join(n400, subjectProfiles, by = "SubjID")
```

Now let's divide this data frame into four separate ones—for responses to 1st, 2nd, 3rd and all shapes

```
library(tidyr)
n400_subj <- separate_wider_delim(n400_subj,
                                  binlabel,
```

```

delim = "_",
names = c("TrialType", "file"),
too_few = "align_start")
n400_first <- filter(n400_subj, file == 1)
n400_second <- filter(n400_subj, file == 2)
n400_third <- filter(n400_subj, file == 3)
n400_all <- filter(n400_subj, is.na(n400_subj$file))
n400_all$file <- NULL

```

Now for the `n400_all` dataframe which is what we will be analysing, we need to extract just the bins and channels that we intend to analyse.

```

channels <- c(3, 2, 25, 7, 20, 21, 12, 11, 16)
n400_subset <- n400_all |> filter(chindex %in% channels)
n400_subset_a <- separate_wider_position(n400_subset,
                                        cols = chlabel,
                                        widths = c(anteriority = 1, laterality = 1),
                                        cols_remove = FALSE) # separate by dividing into two columns

n400_subset_b <- mutate(n400_subset_a,
                        Laterality = case_when((laterality == "z"|laterality == "Z") ~ "Midline",
                                                laterality == "3" ~ "Left",
                                                laterality == "4" ~ "Right"),
                        Anteriority = case_when(anteriority == "F" ~ "Frontal",
                                                anteriority == "C" ~ "Central",
                                                anteriority == "P" ~ "Parietal"),
                        .keep = "unused")

n400_subset_oldnew <- n400_subset_b |> filter(TrialType == "New" | TrialType == "Old")

```

Now we can run our anova. First let's check to make sure we have no empty cells

```

(responses_table <- table(n400_subset_oldnew$ReadingProfile,
                          n400_subset_oldnew$Anteriority,
                          n400_subset_oldnew$Laterality))

```

```

## , , = Left
##
##
##           Central Frontal Parietal
## ORTHOGRAPHIC      38      38      38
## SEMANTIC          52      52      52
##
## , , = Midline
##
##
##           Central Frontal Parietal
## ORTHOGRAPHIC      38      38      38
## SEMANTIC          52      52      52
##
## , , = Right
##
##
##           Central Frontal Parietal
## ORTHOGRAPHIC      38      38      38

```

```
## SEMANTIC          52          52          52
```

Then we run the anova

```
library(ez)
ezANOVA(n400_subset_oldnew,
        dv = value,
        wid = SubjID,
        within = .(TrialType, Anterority, Laterality),
        between = ReadingProfile,
        type = 3)
```

```
## Warning: Converting "SubjID" to factor for ANOVA.
## Warning: Converting "TrialType" to factor for ANOVA.
## Warning: Converting "Anterority" to factor for ANOVA.
## Warning: Converting "Laterality" to factor for ANOVA.
## Warning: Converting "ReadingProfile" to factor for ANOVA.
## Warning: Data is unbalanced (unequal N per group). Make sure you specified a
## well-considered value for the type argument to ezANOVA().

## $ANOVA
##
##           Effect DFn DFd          F
## 2           ReadingProfile      1  43   3.61972545
## 3           TrialType          1  43  22.79408110
## 5           Anterority        2  86 142.16267404
## 7           Laterality        2  86   7.35754130
## 4 ReadingProfile:TrialType      1  43   2.70693870
## 6 ReadingProfile:Anterority     2  86   0.06987984
## 8 ReadingProfile:Laterality     2  86   0.02357012
## 9           TrialType:Anterority 2  86   1.11573285
## 11          TrialType:Laterality 2  86   1.40719742
## 13          Anterority:Laterality 4 172   4.79901840
## 10 ReadingProfile:TrialType:Anterority 2  86   0.88159675
## 12 ReadingProfile:TrialType:Laterality 2  86   3.63947025
## 14 ReadingProfile:Anterority:Laterality 4 172   0.47203023
## 15          TrialType:Anterority:Laterality 4 172   5.47117162
## 16 ReadingProfile:TrialType:Anterority:Laterality 4 172   0.81539921
##
##           p p<.05          ges
## 2  6.380873e-02    4.944306e-02
## 3  2.112275e-05    * 8.730103e-02
## 5  5.424322e-28    * 2.676525e-01
## 7  1.122973e-03    * 3.863945e-03
## 4  1.072042e-01    1.123163e-02
## 6  9.325588e-01    1.796149e-04
## 8  9.767118e-01    1.242613e-05
## 9  3.323710e-01    8.362583e-04
## 11 2.504084e-01    3.949317e-04
## 13 1.076662e-03    * 1.342742e-03
## 10 4.178298e-01    6.608858e-04
## 12 3.039054e-02    * 1.020782e-03
## 14 7.562189e-01    1.322319e-04
## 15 3.600657e-04    * 1.532720e-03
## 16 5.169316e-01    2.287281e-04
```

```
##
## $`Mauchly's Test for Sphericity`
##
##           Effect          W          p p<.05
## 5           Anteriority 0.4897225 3.082837e-07 *
## 6      ReadingProfile:Anteriority 0.4897225 3.082837e-07 *
## 7           Laterality 0.9809798 6.681308e-01
## 8      ReadingProfile:Laterality 0.9809798 6.681308e-01
## 9           TrialType:Anteriority 0.5925132 1.685228e-05 *
## 10      ReadingProfile:TrialType:Anteriority 0.5925132 1.685228e-05 *
## 11           TrialType:Laterality 0.8498691 3.283922e-02 *
## 12      ReadingProfile:TrialType:Laterality 0.8498691 3.283922e-02 *
## 13           Anteriority:Laterality 0.4729829 2.989510e-04 *
## 14      ReadingProfile:Anteriority:Laterality 0.4729829 2.989510e-04 *
## 15           TrialType:Anteriority:Laterality 0.2323901 1.156823e-09 *
## 16 ReadingProfile:TrialType:Anteriority:Laterality 0.2323901 1.156823e-09 *
##
## $`Sphericity Corrections`
##
##           Effect          GGe          p[GG]
## 5           Anteriority 0.6621300 2.272524e-19
## 6      ReadingProfile:Anteriority 0.6621300 8.583570e-01
## 7           Laterality 0.9813348 1.215634e-03
## 8      ReadingProfile:Laterality 0.9813348 9.752875e-01
## 9           TrialType:Anteriority 0.7104862 3.168724e-01
## 10      ReadingProfile:TrialType:Anteriority 0.7104862 3.867756e-01
## 11           TrialType:Laterality 0.8694662 2.506938e-01
## 12      ReadingProfile:TrialType:Laterality 0.8694662 3.684591e-02
## 13           Anteriority:Laterality 0.7779044 2.942203e-03
## 14      ReadingProfile:Anteriority:Laterality 0.7779044 7.092038e-01
## 15           TrialType:Anteriority:Laterality 0.5750576 3.798250e-03
## 16 ReadingProfile:TrialType:Anteriority:Laterality 0.5750576 4.603493e-01
##
## p[GG]<.05      HFe      p[HF] p[HF]<.05
## 5      * 0.6750622 1.061735e-19 *
## 6      0.6750622 8.624738e-01
## 7      * 1.0278138 1.122973e-03 *
## 8      1.0278138 9.767118e-01
## 9      0.7278043 3.181004e-01
## 10     0.7278043 3.890219e-01
## 11     0.9029460 2.507185e-01
## 12     * 0.9029460 3.506940e-02 *
## 13     * 0.8455543 2.163108e-03 *
## 14     0.8455543 7.249127e-01
## 15     * 0.6094023 3.132128e-03 *
## 16     0.6094023 4.663254e-01
```

We have a significant ReadingProfile x Trial Type by Laterality Interaction. Let's examine the means for the conditions.

```
library(knitr)
library(plotrix)
kable(means_table <- n400_subset_oldnew |>
  group_by(Laterality, ReadingProfile, TrialType ) |>
  summarise(Mean = mean(value),
            SE = std.error(value),
            SD = sd(value),
            Max = max(value),
```

```
Min = min(value)), digits = 2)
```

`summarise()` has grouped output by 'Laterality', 'ReadingProfile'. You can
override using the `.groups` argument.

Laterality	ReadingProfile	TrialType	Mean	SE	SD	Max	Min
Left	ORTHOGRAPHIC	New	3.29	0.57	4.30	13.79	-4.31
Left	ORTHOGRAPHIC	Old	1.11	0.49	3.74	8.65	-6.67
Left	SEMANTIC	New	1.52	0.34	2.96	7.93	-5.61
Left	SEMANTIC	Old	0.11	0.35	3.05	7.15	-7.48
Midline	ORTHOGRAPHIC	New	3.55	0.61	4.58	14.31	-5.41
Midline	ORTHOGRAPHIC	Old	0.65	0.50	3.75	7.82	-7.41
Midline	SEMANTIC	New	1.29	0.39	3.41	9.97	-7.77
Midline	SEMANTIC	Old	0.07	0.37	3.29	8.40	-7.50
Right	ORTHOGRAPHIC	New	3.80	0.56	4.21	13.24	-4.62
Right	ORTHOGRAPHIC	Old	1.25	0.50	3.80	10.16	-6.79
Right	SEMANTIC	New	1.70	0.33	2.96	8.68	-4.57
Right	SEMANTIC	Old	0.61	0.37	3.24	7.44	-6.66

Now, let's run some post-hoc tests

```
library(pander)
pander(t.test(value ~ TrialType
  , filter(n400_subset_oldnew, ReadingProfile == "SEMANTIC" & Laterality == "Left" )
  , paired=TRUE))
```

Table 2: Paired t-test: value by TrialType

Test statistic	df	P value	Alternative hypothesis	mean difference
5.353	77	8.652e-07 * * *	two.sided	1.41

```
library(pander)
pander(t.test(value ~ TrialType
  , filter(n400_subset_oldnew, ReadingProfile == "SEMANTIC" & Laterality == "Right" )
  , paired=TRUE))
```

Table 3: Paired t-test: value by TrialType

Test statistic	df	P value	Alternative hypothesis	mean difference
3.941	77	0.0001774 * * *	two.sided	1.087

```
library(pander)
pander(t.test(value ~ TrialType
  , filter(n400_subset_oldnew, ReadingProfile == "ORTHOGRAPHIC" & Laterality == "Left" )
  , paired=TRUE))
```

Table 4: Paired t-test: value by TrialType

Test statistic	df	P value	Alternative hypothesis	mean difference
4.748	56	1.466e-05 * * *	two.sided	2.176

```
library(pander)
pander(t.test(value ~ TrialType
  , filter(n400_subset_oldnew, ReadingProfile == "ORTHOGRAPHIC" & Laterality == "Right" )
  , paired=TRUE))
```

Table 5: Paired t-test: value by TrialType

Test statistic	df	P value	Alternative hypothesis	mean difference
5.451	56	1.166e-06 * * *	two.sided	2.546

Let's plot the means

```
library(ggplot2)
library(ggsci)
n400_right <- filter(n400_subset_oldnew, Laterality == "Right") |>
  group_by(ReadingProfile, TrialType) |>
  summarise(mean = mean(value), se = std.error(value)) |>
  mutate(lwr = mean - (1.96*se), upr = mean + (1.96*se))
```

`summarise()` has grouped output by 'ReadingProfile'. You can override using
the `.groups` argument.

```
n400_left <- filter(n400_subset_oldnew, Laterality == "Left") |>
  group_by(ReadingProfile, TrialType) |>
  summarise(mean = mean(value), se = std.error(value)) |>
  mutate(lwr = mean - (1.96*se), upr = mean + (1.96*se))
```

`summarise()` has grouped output by 'ReadingProfile'. You can override using
the `.groups` argument.

```
plot1 <- ggplot(n400_left, aes(x = ReadingProfile,
  y = mean,
  ymin = lwr,
  ymax = upr,
  fill = TrialType,
  group = TrialType)) +
  geom_bar(position=position_dodge(), stat="identity", colour = "black") +
  geom_errorbar(width = .2, position = position_dodge(.9)) +
  scale_fill_npg() + ylab("Voltage in microvolts") +
  ggtitle("Reading Profile by Trial Type Interaction: Left") + theme_classic()

plot2 <- ggplot(n400_right, aes(x = ReadingProfile,
  y = mean,
  ymin = lwr,
  ymax = upr,
  fill = TrialType,
  group = TrialType)) +
  geom_bar(position=position_dodge(), stat="identity", colour = "black") +
```

```
geom_errorbar(width = .2, position = position_dodge(.9)) +  
scale_fill_npg() + ylab("Voltage in microvolts") +  
ggtitle("Reading Profile by Trial Type Interaction: Right") + theme_classic()  
  
library(gridExtra)  
  
##  
## Attaching package: 'gridExtra'  
##  
## The following object is masked from 'package:dplyr':  
##  
##      combine  
grid.arrange(plot1, plot2, ncol=1)
```

