Psychonomics 2023: First Shape: Old vs New

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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_first |> 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$TrialType,
                          n400_subset_oldnew$ReadingProfile,
                          n400_subset_oldnew$Anteriority,
                          n400_subset_oldnew$Laterality))
```

```
## , ,  = Central,  = Left
##
##
##       ORTHOGRAPHIC SEMANTIC
##   New           19       26
##   Old           19       26
##
## , ,  = Frontal,  = Left
##
##
##       ORTHOGRAPHIC SEMANTIC
##   New           19       26
##   Old           19       26
##
## , ,  = Parietal,  = Left
##
##
##       ORTHOGRAPHIC SEMANTIC
```

```
##   New            19       26
##   Old            19       26
##
## , ,  = Central,  = Midline
##
##
##       ORTHOGRAPHIC SEMANTIC
##   New            19       26
##   Old            19       26
##
## , ,  = Frontal,  = Midline
##
##
##       ORTHOGRAPHIC SEMANTIC
##   New            19       26
##   Old            19       26
##
## , ,  = Parietal,  = Midline
##
##
##       ORTHOGRAPHIC SEMANTIC
##   New            19       26
##   Old            19       26
##
## , ,  = Central,  = Right
##
##
##       ORTHOGRAPHIC SEMANTIC
##   New            19       26
##   Old            19       26
##
## , ,  = Frontal,  = Right
##
##
##       ORTHOGRAPHIC SEMANTIC
##   New            19       26
##   Old            19       26
##
## , ,  = Parietal,  = Right
##
##
##       ORTHOGRAPHIC SEMANTIC
##   New            19       26
##   Old            19       26
```

Then we run the anova

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

```
## Warning: Converting "SubjID" to factor for ANOVA.

## Warning: Converting "TrialType" to factor for ANOVA.

## Warning: Converting "Anteriority" 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   0.05891418
## 3                                            TrialType   1  43  60.89551915
## 5                                          Anteriority   2  86 135.81472410
## 7                                           Laterality   2  86   9.16489770
## 4                             ReadingProfile:TrialType   1  43   4.65773619
## 6                           ReadingProfile:Anteriority   2  86   2.01295868
## 8                            ReadingProfile:Laterality   2  86   1.06997553
## 9                                TrialType:Anteriority   2  86  12.51121490
## 11                                TrialType:Laterality   2  86   7.15412666
## 13                              Anteriority:Laterality   4 172   5.49693132
## 10               ReadingProfile:TrialType:Anteriority   2  86   1.04972728
## 12                ReadingProfile:TrialType:Laterality   2  86   4.30011427
## 14             ReadingProfile:Anteriority:Laterality   4 172   1.07943633
## 15                  TrialType:Anteriority:Laterality   4 172   8.81177195
## 16 ReadingProfile:TrialType:Anteriority:Laterality   4 172   1.22633911
##                  p p<.05          ges
## 2  8.093745e-01       0.0006904835
## 3  9.012590e-10     * 0.2327703469
## 5  2.431099e-27     * 0.2459878724
## 7  2.465325e-04     * 0.0064466714
## 4  3.654161e-02     * 0.0226792630
## 6  1.398391e-01       0.0048120318
## 8  3.475384e-01       0.0007569405
## 9  1.701266e-05     * 0.0261678981
## 11 1.336462e-03     * 0.0035295829
## 13 3.452857e-04     * 0.0017500712
## 10 3.544745e-01       0.0022494882
## 12 1.659852e-02     * 0.0021245096
## 14 3.682906e-01       0.0003441467
## 15 1.703319e-06     * 0.0041554498
## 16 3.014658e-01       0.0005803924
##
## $`Mauchly's Test for Sphericity`
##                                                 Effect         W            p p<.05
## 5                                          Anteriority 0.5779930 1.000862e-05     *
## 6                            ReadingProfile:Anteriority 0.5779930 1.000862e-05     *
## 7                                           Laterality 0.9595767 4.204103e-01
## 8                            ReadingProfile:Laterality 0.9595767 4.204103e-01
## 9                                TrialType:Anteriority 0.3766500 1.243650e-09     *
## 10               ReadingProfile:TrialType:Anteriority 0.3766500 1.243650e-09     *
## 11                                TrialType:Laterality 0.9699653 5.270849e-01
## 12                ReadingProfile:TrialType:Laterality 0.9699653 5.270849e-01
```

```
## 13                           Anteriority:Laterality 0.7287464 1.582517e-01
## 14             ReadingProfile:Anteriority:Laterality 0.7287464 1.582517e-01
## 15                  TrialType:Anteriority:Laterality 0.4588994 1.820760e-04     *
## 16 ReadingProfile:TrialType:Anteriority:Laterality 0.4588994 1.820760e-04     *
##
## $`Sphericity Corrections`
##                                            Effect       GGe        p[GG]
## 5                                      Anteriority 0.7032314 5.831103e-20
## 6                        ReadingProfile:Anteriority 0.7032314 1.549360e-01
## 7                                       Laterality 0.9611472 3.064955e-04
## 8                         ReadingProfile:Laterality 0.9611472 3.456157e-01
## 9                             TrialType:Anteriority 0.6160101 3.813264e-04
## 10              ReadingProfile:TrialType:Anteriority 0.6160101 3.257718e-01
## 11                             TrialType:Laterality 0.9708411 1.505983e-03
## 12              ReadingProfile:TrialType:Laterality 0.9708411 1.757296e-02
## 13                           Anteriority:Laterality 0.8724533 6.994195e-04
## 14             ReadingProfile:Anteriority:Laterality 0.8724533 3.648215e-01
## 15                  TrialType:Anteriority:Laterality 0.7396429 2.605336e-05
## 16 ReadingProfile:TrialType:Anteriority:Laterality 0.7396429 3.028385e-01
##    p[GG]<.05       HFe        p[HF] p[HF]<.05
## 5          * 0.7198758 2.245697e-20         *
## 6            0.7198758 1.541355e-01
## 7          * 1.0051798 2.465325e-04         *
## 8            1.0051798 3.475384e-01
## 9          * 0.6249870 3.544153e-04         *
## 10           0.6249870 3.267302e-01
## 11         * 1.0160428 1.336462e-03         *
## 12         * 1.0160428 1.659852e-02         *
## 13         * 0.9589412 4.331654e-04         *
## 14           0.9589412 3.672883e-01
## 15         * 0.8002783 1.376995e-05         *
## 16           0.8002783 3.028816e-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	2.60	0.67	5.05	13.89	-9.05
Left	ORTHOGRAPHIC	Old	-2.16	0.70	5.26	10.61	-12.53
Left	SEMANTIC	New	1.58	0.35	3.10	9.90	-6.23
Left	SEMANTIC	Old	-1.72	0.48	4.26	6.19	-11.90
Midline	ORTHOGRAPHIC	New	2.99	0.74	5.62	14.75	-9.48

Laterality	ReadingProfile	TrialType	Mean	SE	SD	Max	Min
Midline	ORTHOGRAPHIC	Old	-3.53	0.72	5.44	7.28	-15.35
Midline	SEMANTIC	New	1.47	0.37	3.30	10.68	-5.61
Midline	SEMANTIC	Old	-1.84	0.52	4.59	8.48	-11.06
Right	ORTHOGRAPHIC	New	3.27	0.63	4.74	11.68	-7.77
Right	ORTHOGRAPHIC	Old	-1.80	0.75	5.63	14.16	-11.78
Right	SEMANTIC	New	1.65	0.31	2.75	7.87	-4.93
Right	SEMANTIC	Old	-1.00	0.51	4.51	9.11	-10.06

Now, let's run some post-hoc tests

```
library(pander)

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

Table 2: Paired t-test: `value` by `TrialType`

Test statistic	df	P value	Alternative hypothesis	mean difference
11.3	233	6.671e-24 * * *	two.sided	3.089

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

Table 3: Paired t-test: `value` by `TrialType`

Test statistic	df	P value	Alternative hypothesis	mean difference
13.01	170	2.753e-27 * * *	two.sided	5.451

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

Table 4: Paired t-test: `value` by `TrialType`

Test statistic	df	P value	Alternative hypothesis	mean difference
6.993	77	8.566e-10 * * *	two.sided	3.307

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

Table 5: Paired t-test: `value` by `TrialType`

Test statistic	df	P value	Alternative hypothesis	mean difference
5.706	77	2.051e-07 * * *	two.sided	2.65

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

Table 6: Paired t-test: `value` by `TrialType`

Test statistic	df	P value	Alternative hypothesis	mean difference
7.148	56	1.969e-09 * * *	two.sided	4.765

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

Table 7: Paired t-test: `value` by `TrialType`

Test statistic	df	P value	Alternative hypothesis	mean difference
6.869	56	5.698e-09 * * *	two.sided	5.071

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))
```

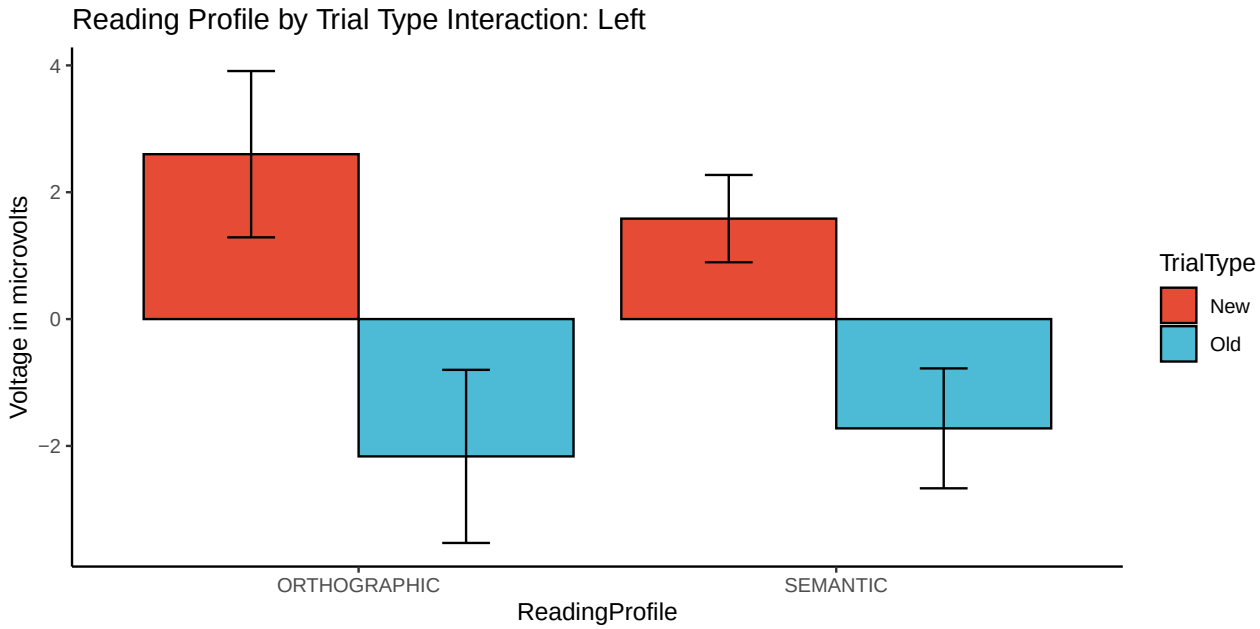
```
## `summarise()` has grouped output by 'ReadingProfile'. You can override using
## the `.groups` argument.
```

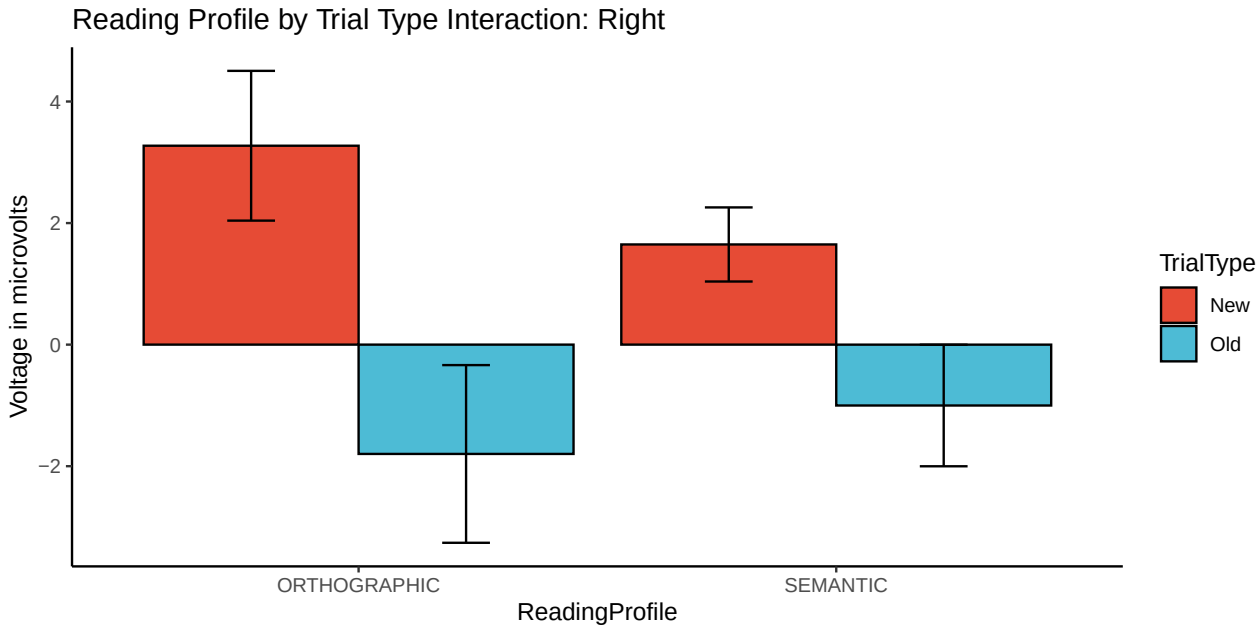
```
plot1<- ggplot(n400_left, aes(x = ReadingProfile,
                          y = mean,
                          ymin = lwr,
                          ymax = upr,
                          fill = TrialType,
                          group = TrialType)) +
  geom_bar(position=position_dodge(), stat="identity", 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)
```





Plot Just the Reading Profile by Trial Type Interaction

```
library(ggplot2)
library(ggsci)
n400_right <- n400_subset_oldnew |>
  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.
```

```
(plot3<- 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())
```