SPC Exp1

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**This contains the analysis script of the first experiment in the Sensory pre conditioning series**

#### DATA PREPARATION

* Unnecessary columns are removed from the main dataframe
* The Reaction Time columns are saved again such that the values from Phase 1 (Saved as SSResp.rt) and values from Phase 2 and 3 (saved as REsponse.rt) are combined into one column named RT\_Trials. So a dummy variable is created to identify rows with Phase 1 RT and Phase2&3 RT to later combine together as RT\_Trials.
* Similar process is done for Accuracy
* Error Rate column is created

### DESCRIPTIVES

Exp1data <- Exp1data%>%drop\_na(RT\_Trials)  
  
pander(summary(Exp1data$Age),style = 'rmarkdown', caption = "Age")

Age

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. |
| 18 | 20 | 22 | 24.54 | 29 | 35 |

pander(summary(Exp1data$RT\_Trials), style = 'rmarkdown',caption = 'Mean RT')

Mean RT

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. |
| 1 | 406.8 | 479.3 | 526.7 | 577.4 | 20026 |

pander(table(Exp1data$ACC\_trials),style = 'rmarkdown',caption = "Accuracy")

Accuracy

|  |  |
| --- | --- |
| 0 | 1 |
| 1641 | 29315 |

pander(round(table(Exp1data$ACC\_trials)/nrow(Exp1data)\*100, digits = 3), style = 'rmarkdown', caption = "Percentage of errors")

Percentage of errors

|  |  |
| --- | --- |
| 0 | 1 |
| 5.301 | 94.7 |

#### OUTLIERS AND EXCLUSIONS

#incorrect trials RT are not used  
  
Exp1data$RT\_Trials[Exp1data$ACC\_trials==0] <- NA  
  
#creating function to remove the outliers and farouts  
computeTukeys <- function(x){  
 P25 <- quantile(x$RT\_Trials, .25, na.rm = TRUE, type = 6) #type = 6 -> used in SPSS  
 P75 <- quantile(x$RT\_Trials, .75, na.rm = TRUE, type = 6)  
 x$Outlier <- P75 + 1.5\*(P75 - P25)  
 x$Farouts <- P75 + 3.0\*(P75 - P25)  
 return(x)  
}  
  
  
#identifying the outliers and farouts at individual level  
Exp1data <- ddply(Exp1data, .(PROLIFIC\_PID), computeTukeys)  
  
#creating new column with RT trials after removing outliers/farouts  
Exp1data$RT\_ifo <- Exp1data$RT\_Trials #ifo refers to individual farouts  
Exp1data$RT\_io <- Exp1data$RT\_Trials #io refers to individual outliers  
  
  
#RTs above outliers and farouts and very fast RTs below 200ms  
Exp1data <- Exp1data %>%   
 mutate(RT\_ifo = ifelse((RT\_ifo > Farouts)|(RT\_ifo < 200),NA,RT\_ifo),  
 RT\_io = ifelse((RT\_io > Outlier)|(RT\_io < 200),NA, RT\_io))  
  
  
#printing the summary table for RTs columns in rmarkdown style after exluding outliers and farouts  
pander(summary(Exp1data$RT\_ifo), style = 'rmarkdown', caption = "Summary of RT after removing Farouts")

Summary of RT after removing Farouts

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA’s |
| 200 | 413.3 | 480 | 508.7 | 570.1 | 1639 | 2467 |

pander(summary(Exp1data$RT\_io), style = 'rmarkdown', caption = "Summary of RT after removing Outliers")

Summary of RT after removing Outliers

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. | NA’s |
| 200 | 409.2 | 472 | 494 | 556.1 | 1187 | 3476 |

# Manipulation Checks

## 1. Phase 1

First checking whether participants picked up on the association between **S1-S2** by looking at the contingency effect in Phase 1.

The word pairs were:

High(S1) + fair(S2) even(S1) + warm(S2)

T.test result shows that there is a significant difference between valid and invalid trials . The mean difference is *~32.7 ms* This also replicates at the Error Rate level with a significant difference between valid and invalid trials .

Both the results show that the performance is better in valid than in invalid trials indicating that the participants picked up on the association between S1-s2 and used the predictive property of S1

#aggregating the RT and ER in Phase 1  
Exp1\_phase1 <- Exp1data %>%   
 group\_by(PROLIFIC\_PID,Validity) %>%   
 filter(Phase == 1) %>%   
 summarise(ER= mean(ER,na.rm=TRUE),  
 RT = mean(RT\_io, na.rm = TRUE))  
  
# Paired T test in RTs between Valid and invalid Pairs  
pander((t.test(data = Exp1\_phase1, RT~Validity,paired = TRUE)), style = 'rmarkdown', caption = "t test showing differences between valid and invalid trials-excluding outliers")

t test showing differences between valid and invalid trials-excluding outliers (continued below)

|  |  |  |  |
| --- | --- | --- | --- |
| Test statistic | df | P value | Alternative hypothesis |
| 6.156 | 70 | 4.142e-08 \* \* \* | two.sided |

|  |
| --- |
| mean of the differences |
| 32.81 |

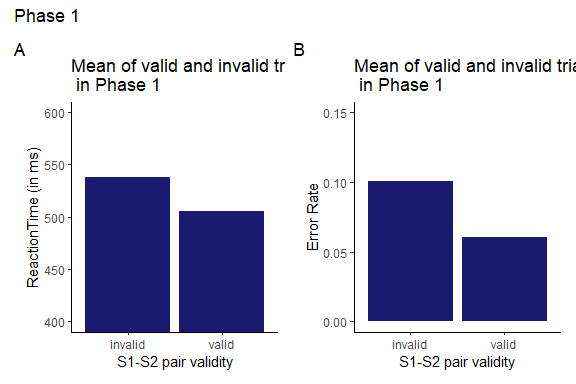
valmain <- ggplot(Exp1\_phase1, aes(x=Validity, y=RT))+  
 geom\_bar(stat = "summary", fun = "mean", fill = "midnightblue")+  
 coord\_cartesian(ylim = c(400,600))+  
 theme\_classic()+  
 xlab("S1-S2 pair validity")+  
 ylab("ReactionTime (in ms)")+  
 ggtitle("Mean of valid and invalid trials \n in Phase 1")+  
 theme(text = element\_text(size = 20))  
  
  
# for error rate  
pander((t.test(data = Exp1\_phase1, ER~Validity,paired = TRUE)), style = 'rmarkdown', caption = "t test showing differences between valid and invalid trials-error rate")

t test showing differences between valid and invalid trials-error rate (continued below)

|  |  |  |  |
| --- | --- | --- | --- |
| Test statistic | df | P value | Alternative hypothesis |
| 3.388 | 70 | 0.001158 \* \* | two.sided |

|  |
| --- |
| mean of the differences |
| 0.03995 |

valmainer <- ggplot(Exp1\_phase1, aes(x=Validity, y=ER))+  
 geom\_bar(stat = "summary", fun = "mean", fill = "midnightblue")+  
 coord\_cartesian(ylim = c(0,0.15))+  
 theme\_classic()+  
 xlab("S1-S2 pair validity")+  
 ylab("Error Rate")+  
 ggtitle("Mean of valid and invalid trials \n in Phase 1")+  
 theme(text = element\_text(size = 20))  
  
  
Phase1Fig <- (valmain + valmainer) +  
 plot\_annotation(tag\_levels = "A", title = "Phase 1")+  
 plot\_layout(guides = "collect") & theme\_classic()  
  
Phase1Fig



## 2. Phase 2: S2-R contingency check

Paired t test shows that there is a contingency effect for **S2-R** while comparing valid and invalid trials which is significant with a mean difference of ~39 ms

Similarly while looking at errors as well there is a significant difference

This shows that the participants successfully bound the contingent response with the S2 in Phase 2.

# aggregate file with RT and ER for phase 2  
  
Exp1\_phase2 <- Exp1data %>%   
 group\_by(PROLIFIC\_PID,Validity) %>%   
 filter(Phase == 2) %>%   
 summarise(ER= mean(ER,na.rm=TRUE),  
 RT = mean(RT\_io, na.rm = TRUE))  
#paired ttest  
pander((t.test(data = Exp1\_phase2, RT~Validity,paired = TRUE)), style = 'rmarkdown', caption = "t test showing differences between valid and invalid trials-excluding outliers")

t test showing differences between valid and invalid trials-excluding outliers (continued below)

|  |  |  |  |
| --- | --- | --- | --- |
| Test statistic | df | P value | Alternative hypothesis |
| 10.6 | 70 | 3.372e-16 \* \* \* | two.sided |

|  |
| --- |
| mean of the differences |
| 39.63 |

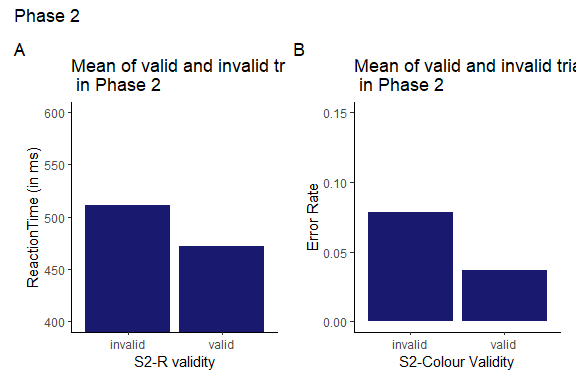
valmain2 <- ggplot(Exp1\_phase2, aes(x=Validity, y=RT))+  
 geom\_bar(stat = "summary", fun = "mean", fill = "midnightblue")+  
 coord\_cartesian(ylim = c(400,600))+  
 theme\_classic()+  
 xlab("S2-R validity")+  
 ylab("ReactionTime (in ms)")+  
 ggtitle("Mean of valid and invalid trials \n in Phase 2")+  
 theme(text = element\_text(size = 20))  
  
  
## for Error RAte  
pander((t.test(data = Exp1\_phase2, ER~Validity,paired = TRUE)), style = 'rmarkdown', caption = "t test showing differences between valid and invalid trials-error rate")

t test showing differences between valid and invalid trials-error rate (continued below)

|  |  |  |  |
| --- | --- | --- | --- |
| Test statistic | df | P value | Alternative hypothesis |
| 4.509 | 70 | 2.554e-05 \* \* \* | two.sided |

|  |
| --- |
| mean of the differences |
| 0.04173 |

valmain2er <- ggplot(Exp1\_phase2, aes(x=Validity, y=ER))+  
 geom\_bar(stat = "summary", fun = "mean", fill = "midnightblue")+  
 coord\_cartesian(ylim = c(0,0.15))+  
 theme\_classic()+  
 xlab("S2-Colour Validity")+  
 ylab("Error Rate")+  
 ggtitle("Mean of valid and invalid trials \n in Phase 2")+  
 theme(text = element\_text(size = 20))  
  
  
Phase2Fig <- (valmain2+valmain2er)+  
 plot\_annotation(tag\_levels = "A", title = "Phase 2")+  
 plot\_layout(guides = "collect")&theme\_classic()  
  
Phase2Fig



## Phase 3.1 : Checking for sustainance of S2-R Contingency effect

While only looking at the S2 trials, a t.test was conducted to compare the performance in the valid and invalid trials to check for a possible contingency effect that might have carried forward into Phase 3, where S1 was also present.

The t.test revealed that there is a significant difference between valid and invalid trials for S2 and that the contingency effect remains significant for RT and for ER.

Exp1\_phase3.1 <- Exp1data %>%   
 group\_by(PROLIFIC\_PID,Validity,Condition) %>%   
 filter(Phase == 3.1) %>%   
 summarise(ER= mean(ER,na.rm=TRUE),  
 RT = mean(RT\_io, na.rm = TRUE)) %>%   
 rename(StimulusType = Condition)  
   
pander((t.test(data = Exp1\_phase3.1, RT~Validity,subset = (StimulusType == "S2-R Transfer"),paired = TRUE, alternative = "greater")), style = 'rmarkdown', caption = "t test showing differences between valid and invalid trials for S2-excluding outliers")

t test showing differences between valid and invalid trials for S2-excluding outliers (continued below)

|  |  |  |  |
| --- | --- | --- | --- |
| Test statistic | df | P value | Alternative hypothesis |
| 6.773 | 70 | 1.615e-09 \* \* \* | greater |

|  |
| --- |
| mean of the differences |
| 34.34 |

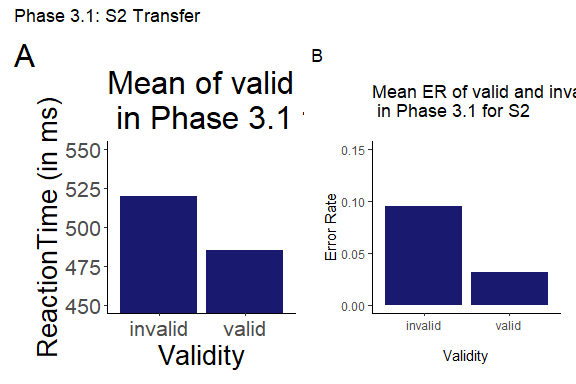
valmain3 <- ggplot(subset(Exp1\_phase3.1,StimulusType == "S2-R Transfer"),   
 aes(x=Validity, y=RT))+  
 geom\_bar(stat = "summary", fun = "mean", fill = "midnightblue")+  
 coord\_cartesian(ylim = c(450,550))+  
 theme\_classic()+  
 ylab("ReactionTime (in ms)")+  
 ggtitle("Mean of valid and invalid trials \n in Phase 3.1 for S2")+  
 theme(text = element\_text(size = 20))  
  
  
## Error Rate  
pander((t.test(data = Exp1\_phase3.1, ER~Validity,subset = (StimulusType == "S2-R Transfer"),paired = TRUE, alternative = "greater")), style = 'rmarkdown', caption = "t test showing differences between valid and invalid trials(ER) for S2-Error Rate")

t test showing differences between valid and invalid trials(ER) for S2-Error Rate (continued below)

|  |  |  |  |
| --- | --- | --- | --- |
| Test statistic | df | P value | Alternative hypothesis |
| 4.134 | 70 | 4.874e-05 \* \* \* | greater |

|  |
| --- |
| mean of the differences |
| 0.06382 |

valmain3er <- ggplot(subset(Exp1\_phase3.1, StimulusType == "S2-R Transfer"), aes(x=Validity, y=ER))+  
 geom\_bar(stat = "summary", fun = "mean", fill = "midnightblue")+  
 coord\_cartesian(ylim = c(0,0.15))+  
 theme\_classic()+  
 ylab("Error Rate")+  
 ggtitle("Mean ER of valid and invalid trials \n in Phase 3.1 for S2")+  
 theme(text = element\_text(size = 20))  
  
Phase31\_s2 <- (valmain3+valmain3er)+  
 plot\_annotation(tag\_levels = "A", title = "Phase 3.1: S2 Transfer")+  
 plot\_layout(guides = "collect") + theme\_classic()  
  
Phase31\_s2



# Transfer ANALYSES

## 1. Comparing contingency effects between stimulus types in Phase 3.1

### Reaction Time

ANOVA is conducted in the aggregated data with Phase 3.1 with the factors of validity and the Stimulus Type. The results show that there is a significant main effect of Validity and there is also a main effect of StimulusType which shows that transfer to S1 was not present as S2 remained the only condition where contingency effect existed.

This is also seen in the significant interaction between validity and stimulus type

## Reaction Time  
anova31RT <- ezANOVA(data = Exp1\_phase3.1,  
 dv = RT,  
 wid = PROLIFIC\_PID,  
 within = .(Validity,StimulusType),  
 detailed = TRUE)   
pander(anova\_out(anova31RT), style = "rmarkdown", caption = "ANOVA (RT): for Phase 3.1 across stimulus type")

$--- ANOVA RESULTS ------------------------------------ Effect MSE df1 df2 F p petasq getasq 1 (Intercept) 18352.6771 1 70 3835.36 0.000 0.98 0.98 2 Validity 715.5864 1 70 22.68 0.000 0.24 0.01 3 StimulusType 927.8947 1 70 6.34 0.014 0.08 0.00 4 Validity:StimulusType 654.1714 1 70 40.09 0.000 0.36 0.02

$--- SPHERICITY TESTS ------------------------------------ [1] “N/A”

$--- FORMATTED RESULTS ------------------------------------ Effect Text 1 (Intercept) F(1, 70) = 3835.36, p < .001, np2 = .98 2 Validity F(1, 70) = 22.68, p < .001, np2 = .24 3 StimulusType F(1, 70) = 6.34, p = .014, np2 = .08 4 Validity:StimulusType F(1, 70) = 40.09, p < .001, np2 = .36

$NOTE: [1] “Reporting unadjusted p-values.”

* **— ANOVA RESULTS ————————————**:

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| * Effect | * MSE | * df1 | * df2 | * F | * p | * petasq | * getasq |
| * (Intercept) | * 18353 | * 1 | * 70 | * 3835.36 | * 0.000 | * 0.98 | * 0.98 |
| * Validity | * 715.6 | * 1 | * 70 | * 22.68 | * 0.000 | * 0.24 | * 0.01 |
| * StimulusType | * 927.9 | * 1 | * 70 | * 6.34 | * 0.014 | * 0.08 | * 0.00 |
| * Validity:StimulusType | * 654.2 | * 1 | * 70 | * 40.09 | * 0.000 | * 0.36 | * 0.02 |

* **— SPHERICITY TESTS ————————————**: N/A
* **— FORMATTED RESULTS ————————————**:

|  |  |
| --- | --- |
| * Effect | * Text |
| * (Intercept) | * F(1, 70) = 3835.36, p < .001, np2 = .98 |
| * Validity | * F(1, 70) = 22.68, p < .001, np2 = .24 |
| * StimulusType | * F(1, 70) = 6.34, p = .014, np2 = .08 |
| * Validity:StimulusType | * F(1, 70) = 40.09, p < .001, np2 = .36 |

* **NOTE:**: Reporting unadjusted p-values.

mean3\_1 <- summarySEwithin(Exp1\_phase3.1, measurevar= "RT", withinvars=c("Validity","StimulusType"), idvar="PROLIFIC\_PID", na.rm=FALSE, conf.interval=.95)  
  
inter3.1 <- ggplot(mean3\_1, aes(x=StimulusType, y=RT,fill = Validity))+  
 geom\_bar(stat = "identity",position = position\_dodge())+  
 geom\_errorbar(aes(ymin = RT - ci, ymax = RT + ci),width = .1, size = 1,position = position\_dodge(.9))+  
 scale\_fill\_manual(values = c("midnightblue","skyblue"))+  
 coord\_cartesian(ylim = c(400,550))+  
 ggtitle("Valid and Invalid trials mean \n per Stimulus Type in Phase 3.1")+  
 theme\_classic()+  
 ylab("ReactionTime (in ms)")+  
 xlab("StimulusType")+  
 theme(text = element\_text(size = 20))

### Error Rate

In the case of Error rate, there is still the main effect of validity, but no main effect of stimulus type . There is also a significant interaction between validity and stimulus type, .

More insight on the CL effect per stimulus type using paired t test is listed below.

## Error Rate  
anova31ER <- ezANOVA(data = Exp1\_phase3.1,  
 dv = ER,  
 wid = PROLIFIC\_PID,  
 within = .(Validity,StimulusType),  
 detailed = TRUE)   
pander(anova\_out(anova31ER), style = "rmarkdown", caption = "ANOVA(ER) for Phase 3.1 transfer")

$--- ANOVA RESULTS ------------------------------------ Effect MSE df1 df2 F p petasq getasq 1 (Intercept) 0.011350387 1 70 81.60 0.000 0.54 0.33 2 Validity 0.005679581 1 70 20.01 0.000 0.22 0.06 3 StimulusType 0.005058574 1 70 2.06 0.156 0.03 0.01 4 Validity:StimulusType 0.005165560 1 70 7.79 0.007 0.10 0.02

$--- SPHERICITY TESTS ------------------------------------ [1] “N/A”

$--- FORMATTED RESULTS ------------------------------------ Effect Text 1 (Intercept) F(1, 70) = 81.60, p < .001, np2 = .54 2 Validity F(1, 70) = 20.01, p < .001, np2 = .22 3 StimulusType F(1, 70) = 2.06, p = .156, np2 = .03 4 Validity:StimulusType F(1, 70) = 7.79, p = .007, np2 = .10

$NOTE: [1] “Reporting unadjusted p-values.”

* **— ANOVA RESULTS ————————————**:

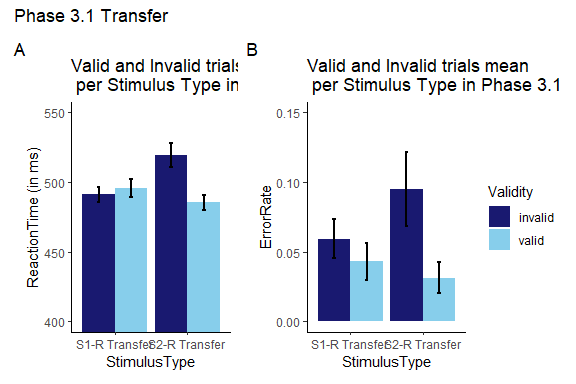
|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| * Effect | * MSE | * df1 | * df2 | * F | * p | * petasq | * getasq |
| * (Intercept) | * 0.01135 | * 1 | * 70 | * 81.60 | * 0.000 | * 0.54 | * 0.33 |
| * Validity | * 0.00568 | * 1 | * 70 | * 20.01 | * 0.000 | * 0.22 | * 0.06 |
| * StimulusType | * 0.005059 | * 1 | * 70 | * 2.06 | * 0.156 | * 0.03 | * 0.01 |
| * Validity:StimulusType | * 0.005166 | * 1 | * 70 | * 7.79 | * 0.007 | * 0.10 | * 0.02 |

* **— SPHERICITY TESTS ————————————**: N/A
* **— FORMATTED RESULTS ————————————**:

|  |  |
| --- | --- |
| * Effect | * Text |
| * (Intercept) | * F(1, 70) = 81.60, p < .001, np2 = .54 |
| * Validity | * F(1, 70) = 20.01, p < .001, np2 = .22 |
| * StimulusType | * F(1, 70) = 2.06, p = .156, np2 = .03 |
| * Validity:StimulusType | * F(1, 70) = 7.79, p = .007, np2 = .10 |

* **NOTE:**: Reporting unadjusted p-values.

mean3\_1er <- summarySEwithin(Exp1\_phase3.1, measurevar="ER", withinvars=c("Validity","StimulusType"),  
 idvar="PROLIFIC\_PID", na.rm=FALSE, conf.interval=.95)  
  
inter3.1er <- ggplot(mean3\_1er, aes(x=StimulusType, y=ER,fill = Validity))+  
 geom\_bar(stat = "identity",position = position\_dodge())+  
 geom\_errorbar(aes(ymin = ER - ci, ymax = ER + ci),width = .1, size = 1,position = position\_dodge(.9))+  
 scale\_fill\_manual(values = c("midnightblue","skyblue"))+  
 coord\_cartesian(ylim = c(0,0.15))+  
 ggtitle("Valid and Invalid trials mean \n per Stimulus Type in Phase 3.1")+  
 theme\_classic()+  
 ylab("ErrorRate")+  
 xlab("StimulusType")+  
 theme(text = element\_text(size = 20))  
  
Phase31\_transfer <- (inter3.1+inter3.1er)+  
 plot\_annotation(tag\_levels = "A", title = "Phase 3.1 Transfer")+  
 plot\_layout(guides = "collect") & theme\_classic()  
Phase31\_transfer

 #### Differences per Stimulus Type

1. For S1 the CLeffect in RT is not significant but in the ER it is significant .

Signs of this could also be spotted in the plot where in ER the trend towards a CL effect for S1 is visible. However it is likely that this is a chance finding and more in depth analysis needs to be done

1. For S2 it is highly significant in both RT and ER as seen in Manipulation Check, point 3.

pander(t.test(data = Exp1\_phase3.1, RT~Validity,subset = (StimulusType == "S1-R Transfer"), paired = TRUE, alternative = "greater"), style = 'rmarkdown', caption = "t test showing differences between valid and invalid trials for S1 in Phase 3.1-excluding outliers")

t test showing differences between valid and invalid trials for S1 in Phase 3.1-excluding outliers (continued below)

|  |  |  |  |
| --- | --- | --- | --- |
| Test statistic | df | P value | Alternative hypothesis |
| -1.143 | 70 | 0.8715 | greater |

|  |
| --- |
| mean of the differences |
| -4.102 |

## ER  
pander(t.test(data = Exp1\_phase3.1, ER~Validity,subset = (StimulusType == "S1-R Transfer"), paired = TRUE, alternative = "greater"), style = 'rmarkdown', caption = "t test (ER) showing differences between valid and invalid trials for S1 in Phase 3.1-excluding outliers")

t test (ER) showing differences between valid and invalid trials for S1 in Phase 3.1-excluding outliers (continued below)

|  |  |  |  |
| --- | --- | --- | --- |
| Test statistic | df | P value | Alternative hypothesis |
| 1.976 | 70 | 0.02604 \* | greater |

|  |
| --- |
| mean of the differences |
| 0.0162 |

## 2. Comparing contingency learning effects in Phase 3.2

The transfer effect is tested again in this Phase 3.2 where there is no contingency for S2 and all the stimuli have 50% contingency.

### Reaction Time

Similar to Phase 3.1, the main effect of validity and interaction between Validity and StimulusType are significant but not the main effect of StimulusType, . This is now not signfiicant, contrary to what was found in Phase 3.1

Exp1\_phase3.2 <- Exp1data %>%   
 group\_by(PROLIFIC\_PID,Validity,Condition) %>%   
 filter(Phase == 3.2) %>%   
 summarise(ER = mean(ER, na.rm = TRUE),  
 RT = mean(RT\_io, na.rm = TRUE)) %>%   
 rename(StimulusType = Condition)  
  
##ANOVA  
anova3.2RT <- ezANOVA(data = Exp1\_phase3.2,  
 dv = RT,  
 wid = PROLIFIC\_PID,  
 within = .(Validity,StimulusType),  
 detailed = TRUE)  
pander(anova\_out(anova3.2RT), style = "rmarkdown", caption = "ANOVA:RT for 3.2 transfer")

$--- ANOVA RESULTS ------------------------------------ Effect MSE df1 df2 F p petasq getasq 1 (Intercept) 16569.8745 1 70 4169.53 0.000 0.98 0.98 2 Validity 332.9347 1 70 13.11 0.001 0.16 0.00 3 StimulusType 287.8861 1 70 1.64 0.205 0.02 0.00 4 Validity:StimulusType 485.7169 1 70 9.24 0.003 0.12 0.00

$--- SPHERICITY TESTS ------------------------------------ [1] “N/A”

$--- FORMATTED RESULTS ------------------------------------ Effect Text 1 (Intercept) F(1, 70) = 4169.53, p < .001, np2 = .98 2 Validity F(1, 70) = 13.11, p = .001, np2 = .16 3 StimulusType F(1, 70) = 1.64, p = .205, np2 = .02 4 Validity:StimulusType F(1, 70) = 9.24, p = .003, np2 = .12

$NOTE: [1] “Reporting unadjusted p-values.”

* **— ANOVA RESULTS ————————————**:

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| * Effect | * MSE | * df1 | * df2 | * F | * p | * petasq | * getasq |
| * (Intercept) | * 16570 | * 1 | * 70 | * 4169.53 | * 0.000 | * 0.98 | * 0.98 |
| * Validity | * 332.9 | * 1 | * 70 | * 13.11 | * 0.001 | * 0.16 | * 0.00 |
| * StimulusType | * 287.9 | * 1 | * 70 | * 1.64 | * 0.205 | * 0.02 | * 0.00 |
| * Validity:StimulusType | * 485.7 | * 1 | * 70 | * 9.24 | * 0.003 | * 0.12 | * 0.00 |

* **— SPHERICITY TESTS ————————————**: N/A
* **— FORMATTED RESULTS ————————————**:

|  |  |
| --- | --- |
| * Effect | * Text |
| * (Intercept) | * F(1, 70) = 4169.53, p < .001, np2 = .98 |
| * Validity | * F(1, 70) = 13.11, p = .001, np2 = .16 |
| * StimulusType | * F(1, 70) = 1.64, p = .205, np2 = .02 |
| * Validity:StimulusType | * F(1, 70) = 9.24, p = .003, np2 = .12 |

* **NOTE:**: Reporting unadjusted p-values.

mean3.2 <- summarySEwithin(Exp1\_phase3.2, measurevar= "RT", withinvars=c("Validity","StimulusType"),idvar="PROLIFIC\_PID", na.rm=FALSE, conf.interval=.95)  
  
inter3.2 <- ggplot(mean3.2, aes(x=StimulusType, y=RT,fill = Validity))+  
 geom\_bar(stat = "identity",position = position\_dodge())+  
 geom\_errorbar(aes(ymin = RT - ci, ymax = RT + ci),width = .1, size = 1,position = position\_dodge(.9))+  
 scale\_fill\_manual(values = c("midnightblue","skyblue"))+  
 coord\_cartesian(ylim = c(400,550))+  
 ggtitle("Valid and Invalid trials mean \n per Stimulus Type in Phase 3.2")+  
 theme\_classic()+  
 ylab("ReactionTime (in ms)")+  
 xlab("StimulusType")+  
 theme(text = element\_text(size = 20))

### Error Rate

THe validity effect has weakened and not significant anymore and the interaction is just missed significance and weakened compared to 3.1 and .

However, this lack of interaction is not very meaningful as from the graph it can be seen that the direction of CL effect is reversed for S1, hence the lack of interaction cannot be attributed to transfer of associations

# Error Rate  
anova32ER <- ezANOVA(data = Exp1\_phase3.2,  
 dv = ER,  
 wid = PROLIFIC\_PID,  
 within = .(Validity,StimulusType),  
 detailed = TRUE)   
pander(anova\_out(anova32ER), style = "rmarkdown", caption = "ANOVA:ER for 3.2 transfer")

$--- ANOVA RESULTS ------------------------------------ Effect MSE df1 df2 F p petasq getasq 1 (Intercept) 0.005551531 1 70 128.49 0.000 0.65 0.47 2 Validity 0.002109770 1 70 2.02 0.160 0.03 0.01 3 StimulusType 0.001269171 1 70 0.69 0.408 0.01 0.00 4 Validity:StimulusType 0.002433266 1 70 3.86 0.053 0.05 0.01

$--- SPHERICITY TESTS ------------------------------------ [1] “N/A”

$--- FORMATTED RESULTS ------------------------------------ Effect Text 1 (Intercept) F(1, 70) = 128.49, p < .001, np2 = .65 2 Validity F(1, 70) = 2.02, p = .160, np2 = .03 3 StimulusType F(1, 70) = 0.69, p = .408, np2 = .01 4 Validity:StimulusType F(1, 70) = 3.86, p = .053, np2 = .05

$NOTE: [1] “Reporting unadjusted p-values.”

* **— ANOVA RESULTS ————————————**:

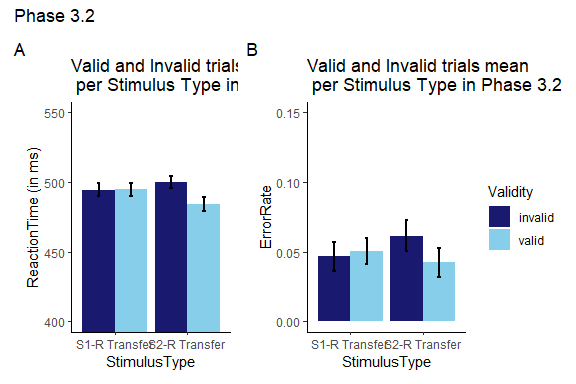
|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| * Effect | * MSE | * df1 | * df2 | * F | * p | * petasq | * getasq |
| * (Intercept) | * 0.005552 | * 1 | * 70 | * 128.49 | * 0.000 | * 0.65 | * 0.47 |
| * Validity | * 0.00211 | * 1 | * 70 | * 2.02 | * 0.160 | * 0.03 | * 0.01 |
| * StimulusType | * 0.001269 | * 1 | * 70 | * 0.69 | * 0.408 | * 0.01 | * 0.00 |
| * Validity:StimulusType | * 0.002433 | * 1 | * 70 | * 3.86 | * 0.053 | * 0.05 | * 0.01 |

* **— SPHERICITY TESTS ————————————**: N/A
* **— FORMATTED RESULTS ————————————**:

|  |  |
| --- | --- |
| * Effect | * Text |
| * (Intercept) | * F(1, 70) = 128.49, p < .001, np2 = .65 |
| * Validity | * F(1, 70) = 2.02, p = .160, np2 = .03 |
| * StimulusType | * F(1, 70) = 0.69, p = .408, np2 = .01 |
| * Validity:StimulusType | * F(1, 70) = 3.86, p = .053, np2 = .05 |

* **NOTE:**: Reporting unadjusted p-values.

mean3.2er <- summarySEwithin(Exp1\_phase3.2, measurevar="ER", withinvars=c("Validity","StimulusType"), idvar="PROLIFIC\_PID", na.rm=FALSE, conf.interval=.95)  
  
  
inter3.2er <- ggplot(mean3.2er, aes(x=StimulusType, y=ER,fill = Validity))+  
 geom\_bar(stat = "identity",position = position\_dodge())+  
 geom\_errorbar(aes(ymin = ER - ci, ymax = ER + ci),width = .1, size = 1,position = position\_dodge(.9))+  
 scale\_fill\_manual(values = c("midnightblue","skyblue"))+  
 coord\_cartesian(ylim = c(0,0.15))+  
 ggtitle("Valid and Invalid trials mean \n per Stimulus Type in Phase 3.2")+  
 theme\_classic()+  
 ylab("ErrorRate")+  
 xlab("StimulusType")+  
 theme(text = element\_text(size = 20))  
  
  
Phase32\_transfer <- (inter3.2+inter3.2er)+  
 plot\_annotation(tag\_levels = "A", title = "Phase 3.2")+  
 plot\_layout(guides = "collect") & theme\_classic()  
  
Phase32\_transfer



#### Differences within stimulus type

The paired t tests results for each stimulus type will reveal the strength of the contingency effect

1. For S1, there is no significant difference in RT as well as ER
2. For S2, both RT and ER show significant differences

## for S1  
  
pander(t.test(data = Exp1\_phase3.2, RT~Validity,subset = (StimulusType == "S1-R Transfer"), paired = TRUE, alternative = "greater"), style = 'rmarkdown', caption = "t test, RT showing differences between valid and invalid trials for S1 in Phase 3.2-excluding outliers")

t test, RT showing differences between valid and invalid trials for S1 in Phase 3.2-excluding outliers (continued below)

|  |  |  |  |
| --- | --- | --- | --- |
| Test statistic | df | P value | Alternative hypothesis |
| -0.03364 | 70 | 0.5134 | greater |

|  |
| --- |
| mean of the differences |
| -0.1114 |

pander(t.test(data = Exp1\_phase3.2, ER~Validity,subset = (StimulusType == "S1-R Transfer"), paired = TRUE, alternative = "greater"), style = 'rmarkdown', caption = "t test, ER showing differences between valid and invalid trials for S1 in Phase 3.2")

t test, ER showing differences between valid and invalid trials for S1 in Phase 3.2 (continued below)

|  |  |  |  |
| --- | --- | --- | --- |
| Test statistic | df | P value | Alternative hypothesis |
| -0.4973 | 70 | 0.6897 | greater |

|  |
| --- |
| mean of the differences |
| -0.003756 |

## For S2  
pander(t.test(data = Exp1\_phase3.2, RT~Validity,subset = (StimulusType == "S2-R Transfer"), paired = TRUE, alternative = "greater"), style = 'rmarkdown', caption = "t test, RT showing differences between valid and invalid trials for S1 in Phase 3.2-excluding outliers")

t test, RT showing differences between valid and invalid trials for S1 in Phase 3.2-excluding outliers (continued below)

|  |  |  |  |
| --- | --- | --- | --- |
| Test statistic | df | P value | Alternative hypothesis |
| 4.542 | 70 | 1.129e-05 \* \* \* | greater |

|  |
| --- |
| mean of the differences |
| 15.79 |

pander(t.test(data = Exp1\_phase3.2, ER~Validity,subset = (StimulusType == "S2-R Transfer"), paired = TRUE, alternative = "greater"), style = 'rmarkdown', caption = "t test, ER showing differences between valid and invalid trials for S1 in Phase 3.2")

t test, ER showing differences between valid and invalid trials for S1 in Phase 3.2 (continued below)

|  |  |  |  |
| --- | --- | --- | --- |
| Test statistic | df | P value | Alternative hypothesis |
| 2.285 | 70 | 0.01266 \* | greater |

|  |
| --- |
| mean of the differences |
| 0.01925 |

Considering the above aggregated data there does not seem to be transfer between S2 and S1 other than the trend shown in ER in Phase 3.1

### Thoughts

1. It is possible that the contingency relation between S1-S2 became extinct with time, as participants might have unlearnt. As shown by [(Schmidt,Crump & Besner,2007)](https://linkinghub.elsevier.com/retrieve/pii/S1053810009002025) the contingencies can rapidly go extinct and in this case the relation with S2 could have been overwritten with R
2. Possible memory load which was also mentioned in the Schmidt et al., (2007) that there might be more memory resources that makes the encoding/retrieval of the contingency weaker

# Transfer with Awareness Analyses

There were questions at the end of the experiment that tested participants level of awareness of the S-S Associations and the S2-R and S1-R contingencies

The questions were as follows:

1. Do you think “high” was always followed by a particular word? Type “y” for yes, “n” for no, and “k” in case you do not know.
2. What do you think the word is? Type in your answer in the textbox
3. Do you think “even” was always followed by a particular word? Type “y” for yes, “n” for no, and “k” in case you do not know.
4. What do you think the word was? Type your answer
5. Do you think “warm” mostly appeared in a particular colour?. If yes, then type “y”, “n” for no and if you don’t know type “k”.
6. Which colour almost always occurred with “warm”? Type the response key you pressed for that particular colour
7. Do you think “fair” mostly appeared in a particular colour?. If yes, then type “y”, if no then type “n” and if you don’t know type “k”.
8. Which colour almost always occurred with “fair”? Type the response key you pressed for that particular colour
9. Do you think “high” mostly appeared in a particular colour?. If yes, then type “y”, if no then type “n” and if you don’t know type “k”.
10. Which colour almost always occurred with “high”? Type the response key you pressed for that particular colour
11. Do you think “even” mostly appeared in a particular colour?. If yes, then type “y”, if no then type “n” and if you don’t know type “k”.
12. Which colour almost always occurred with “even”? Type the response key you pressed for that particular colour

The Awareness analysis resulted in two more conditions depending on the performance on particular questions. The variables were called as:

1. Awareness : where participants who responded either one of the y/n questions accurately
   * S-S aware: for questions related to Phase 1 (Q1, Q3)
   * S2-R aware: for questions related to Phase 2 (Q5, Q7)
   * S1-R aware: for questions related to Phase 3 (Q9, Q11)
2. Awareness\_detailed: where participants who responded either to one of textbox typed answers accurately.
   * S-S aware: for questions related to Phase 1 (Q2, Q4)
   * S2-R aware: for questions related to Phase 2 (Q6, Q8)
   * S1-R aware: for questions related to Phase 3 (Q10, Q12)

These values were then merged to the aggregate files from Phase 3.1 and Phase 3.2 to check for transfer effects

Exp1Aware <- read\_csv(here("Data","Exp1AwarenessRecoded.csv"))

## Rows: 852 Columns: 13

## -- Column specification --------------------------------------------------------  
## Delimiter: ","  
## chr (7): PROLIFIC\_PID, Answer.text, AwareResponse, recoded, awarenext.keys, ...  
## dbl (6): awarenext.rt, Awareness.thisRepN, Awareness.thisTrialN, Awareness.t...

##   
## 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.

Exp1Aware <- Exp1Aware %>%   
 mutate(AwareAccuracy = ifelse(recoded == AwareAnswer, 1, 0))  
  
Exp1Aware <- Exp1Aware %>%   
 mutate(QuesType = ifelse((Awareness.thisIndex == 0 | Awareness.thisIndex == 2),"S-S Association",  
 ifelse((Awareness.thisIndex == 1 | Awareness.thisIndex == 3),"S-S Association\_typed",  
 ifelse((Awareness.thisIndex == 4 | Awareness.thisIndex == 6), "S2-R",  
 ifelse((Awareness.thisIndex == 5 | Awareness.thisIndex == 7), "S2-R\_typed",  
 ifelse((Awareness.thisIndex == 8 | Awareness.thisIndex == 10),"S1-R",  
 ifelse((Awareness.thisIndex == 9 | Awareness.thisIndex == 11),"S1-R\_typed",NA)))))))  
  
Exp1Aware %>% count(QuesType)

## # A tibble: 6 x 2  
## QuesType n  
## <chr> <int>  
## 1 S-S Association 142  
## 2 S-S Association\_typed 142  
## 3 S1-R 142  
## 4 S1-R\_typed 142  
## 5 S2-R 142  
## 6 S2-R\_typed 142

AwareSummary <-Exp1Aware %>%   
 group\_by(PROLIFIC\_PID,QuesType) %>%   
 summarise(TotalAcc = sum(AwareAccuracy, na.rm = TRUE))

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

AwareSummary <- AwareSummary %>%   
 mutate(Awareness\_detailed = ifelse(QuesType == "S-S Association\_typed" & TotalAcc > 0, "S-S Aware",  
 ifelse(QuesType == "S2-R\_typed" & TotalAcc > 0, "S2-R Aware",  
 ifelse(QuesType == "S1-R\_typed" & TotalAcc > 0, "S1-R Aware",NA))),  
 Awareness = ifelse(QuesType == "S-S Association" & TotalAcc > 0, "S-S Aware",  
 ifelse(QuesType == "S2-R" & TotalAcc > 0, "S2-R Aware",  
 ifelse(QuesType == "S1-R" & TotalAcc > 0, "S1-R Aware",NA))))  
  
AwareSummary %>% group\_by(Awareness) %>% tally() %>% kable()

|  |  |
| --- | --- |
| Awareness | n |
| S-S Aware | 32 |
| S1-R Aware | 35 |
| S2-R Aware | 51 |
| NA | 308 |

Aware <- AwareSummary %>% distinct(PROLIFIC\_PID, Awareness, Awareness\_detailed)  
  
wide <- Aware %>% pivot\_wider(id\_cols = PROLIFIC\_PID,  
 names\_from = c(Awareness,Awareness\_detailed),  
 values\_from = c(Awareness,Awareness\_detailed))  
  
wide <- wide %>%   
 select(`Awareness\_detailed\_NA\_S-S Aware`,`Awareness\_detailed\_NA\_S1-R Aware`,`Awareness\_detailed\_NA\_S2-R Aware`,`Awareness\_S-S Aware\_NA`,`Awareness\_S2-R Aware\_NA`,`Awareness\_S1-R Aware\_NA`) %>%   
 rename(Awareness\_d\_S2 = "Awareness\_detailed\_NA\_S2-R Aware",  
 Awareness\_d\_S1 = "Awareness\_detailed\_NA\_S1-R Aware",  
 Awareness\_d\_SS = "Awareness\_detailed\_NA\_S-S Aware",  
 Awareness\_S1 = "Awareness\_S1-R Aware\_NA",  
 Awareness\_S2 = "Awareness\_S2-R Aware\_NA",  
 Awareness\_SS = "Awareness\_S-S Aware\_NA")

## Adding missing grouping variables: `PROLIFIC\_PID`

wide <- wide %>%   
 mutate(BothAwareSS = ifelse((Awareness\_SS == "S-S Aware" | Awareness\_d\_SS == "S-S Aware"), "Aware","Unaware"),  
 BothAwareS1 = ifelse((Awareness\_S1 == "S1-R Aware" | Awareness\_d\_S1 == "S1-R Aware"),"Aware","Unaware"),  
 BothAwareS2 = ifelse((Awareness\_S2 == "S2-R Aware" | Awareness\_d\_S2 == "S2-R Aware"),"Aware","Unaware"))  
  
wide <- wide %>%   
 mutate(BothAwareSS = replace(BothAwareSS,is.na(BothAwareSS),"Unaware"),  
 BothAwareS1 = replace(BothAwareS1,is.na(BothAwareS1),"Unaware"),  
 BothAwareS2 = replace(BothAwareS2,is.na(BothAwareS2),"Unaware"))  
  
  
Exp1\_phase3.1\_A <- merge(Exp1\_phase3.1,wide, by = "PROLIFIC\_PID")  
Exp1\_phase3.2\_A <- merge(Exp1\_phase3.2,wide, by = "PROLIFIC\_PID")  
  
# splitting by awareness for 3.1  
# Exp1\_phase3.1\_SS <- Exp1\_phase3.1\_A %>%   
# filter(Awareness == "S-S Aware")  
#   
# Exp1\_phase3.1\_S2 <- Exp1\_phase3.1\_A %>%   
# filter(Awareness == "S2-R Aware")  
#   
# Exp1\_phase3.1\_S1 <- Exp1\_phase3.1\_A %>%   
# filter(Awareness == "S1-R Aware")  
  
  
  
#   
# #splitting by awareness for 3.2  
# Exp1\_phase3.2\_SS <- Exp1\_phase3.2\_A %>%   
# filter(Awareness == "S-S Aware")  
#   
# Exp1\_phase3.2\_S2 <- Exp1\_phase3.2\_A %>%   
# filter(Awareness == "S2-R Aware")  
#   
# Exp1\_phase3.2\_S1 <- Exp1\_phase3.2\_A %>%   
# filter(Awareness == "S1-R Aware")

## Awareness results: ANOVA

## Phase 3.1

### RT

anova31RT\_A\_SS <- ezANOVA(data = Exp1\_phase3.1\_A,  
 dv = RT,  
 wid = PROLIFIC\_PID,  
 within = .(Validity,StimulusType),  
 between = .(BothAwareSS),  
 detailed = TRUE)   
pander(anova\_out(anova31RT\_A\_SS), style = "rmarkdown", caption = "ANOVA (RT): for Phase 3.1 across stimulus type based on SS AWareness")  
  
anova31RT\_A\_S1 <- ezANOVA(data = Exp1\_phase3.1\_A,  
 dv = RT,  
 wid = PROLIFIC\_PID,  
 within = .(Validity,StimulusType),  
 between = .(BothAwareS1),  
 detailed = TRUE)   
pander(anova\_out(anova31RT\_A\_S1), style = "rmarkdown", caption = "ANOVA (RT): for Phase 3.1 across stimulus type based on S1 AWareness")  
  
anova31RT\_A\_S2 <- ezANOVA(data = Exp1\_phase3.1\_A,  
 dv = RT,  
 wid = PROLIFIC\_PID,  
 within = .(Validity,StimulusType),  
 between = .(BothAwareS2),  
 detailed = TRUE)   
pander(anova\_out(anova31RT\_A\_S2), style = "rmarkdown", caption = "ANOVA (RT): for Phase 3.1 across stimulus type")  
  
  
ggplot(Exp1\_phase3.1\_A, aes(x=StimulusType, y=RT,fill = Validity))+  
 geom\_bar(stat = "summary", fun = "mean",position = position\_dodge())+  
 #geom\_errorbar(aes(ymin = RT - ci, ymax = RT + ci),width = .1, size = 1,position = position\_dodge(.9))+  
 scale\_fill\_manual(values = c("midnightblue","skyblue"))+  
 coord\_cartesian(ylim = c(400,550))+  
 ggtitle("Valid and Invalid trials mean \n per Stimulus Type in Phase 3.1")+  
 theme\_classic()+  
 ylab("ReactionTime (in ms)")+  
 xlab("StimulusType")+  
 facet\_grid(.~BothAwareSS)+  
 labs(subtitle = "Awareness of S-S Association")+  
 theme(text = element\_text(size = 20), axis.text.x = element\_text(angle = 45))

### ER

Also no effect of awareness in the S-R Transfer

anova31ER\_A\_SS <- ezANOVA(data = Exp1\_phase3.1\_A,  
 dv = ER,  
 wid = PROLIFIC\_PID,  
 within = .(Validity,StimulusType),  
 between = .(BothAwareSS),  
 detailed = TRUE)   
pander(anova\_out(anova31RT\_A\_SS), style = "rmarkdown", caption = "ANOVA (ER): for Phase 3.1 across stimulus type")  
  
anova31ER\_A\_S1 <- ezANOVA(data = Exp1\_phase3.1\_A,  
 dv = ER,  
 wid = PROLIFIC\_PID,  
 within = .(Validity,StimulusType),  
 between = .(BothAwareS1),  
 detailed = TRUE)   
pander(anova\_out(anova31ER\_A\_S1), style = "rmarkdown", caption = "ANOVA (ER): for Phase 3.1 across stimulus type")  
  
anova31ER\_A\_S2 <- ezANOVA(data = Exp1\_phase3.1\_A,  
 dv = ER,  
 wid = PROLIFIC\_PID,  
 within = .(Validity,StimulusType),  
 between = .(BothAwareS2),  
 detailed = TRUE)   
pander(anova\_out(anova31ER\_A\_S2), style = "rmarkdown", caption = "ANOVA (ER): for Phase 3.1 across stimulus type")  
  
  
ggplot(Exp1\_phase3.1\_A, aes(x=StimulusType, y=ER,fill = Validity))+  
 geom\_bar(stat = "summary", fun = "mean",position = position\_dodge())+  
 #geom\_errorbar(aes(ymin = RT - ci, ymax = RT + ci),width = .1, size = 1,position = position\_dodge(.9))+  
 scale\_fill\_manual(values = c("midnightblue","skyblue"))+  
 coord\_cartesian(ylim = c(0,0.15))+  
 ggtitle("Valid and Invalid trials mean \n per Stimulus Type in Phase 3.1")+  
 theme\_classic()+  
 ylab("Error Rate")+  
 xlab("StimulusType")+  
 facet\_grid(.~BothAwareSS)+  
 labs(subtitle = "awareness of SS association")+  
 theme(text = element\_text(size = 20), axis.text.x = element\_text(angle = 15))

## Phase 3.2

### RT

1. Awareness: No significant 3-way interaction
2. Awareness\_detailed: There is no significant 3-way interaction but the F value is a bit larger than the previous results with

anova32RT\_A\_SS <- ezANOVA(data = Exp1\_phase3.2\_A,  
 dv = RT,  
 wid = PROLIFIC\_PID,  
 within = .(Validity,StimulusType),  
 between = .(BothAwareSS),  
 detailed = TRUE)   
pander(anova\_out(anova32RT\_A\_SS), style = "rmarkdown", caption = "ANOVA (RT): for Phase 3.1 across stimulus type")  
  
anova32RT\_A\_S1 <- ezANOVA(data = Exp1\_phase3.2\_A,  
 dv = RT,  
 wid = PROLIFIC\_PID,  
 within = .(Validity,StimulusType),  
 between = .(BothAwareS1),  
 detailed = TRUE)   
pander(anova\_out(anova32RT\_A\_S1), style = "rmarkdown", caption = "ANOVA (RT): for Phase 3.1 across stimulus type")  
  
anova32RT\_A\_S2 <- ezANOVA(data = Exp1\_phase3.2\_A,  
 dv = RT,  
 wid = PROLIFIC\_PID,  
 within = .(Validity,StimulusType),  
 between = .(BothAwareS2),  
 detailed = TRUE)   
pander(anova\_out(anova32RT\_A\_S2), style = "rmarkdown", caption = "ANOVA (RT): for Phase 3.1 across stimulus type")

ggplot(Exp1\_phase3.2\_A, aes(x=StimulusType, y=RT,fill = Validity))+  
 geom\_bar(stat = "summary", fun = "mean",position = position\_dodge())+  
 #geom\_errorbar(aes(ymin = RT - ci, ymax = RT + ci),width = .1, size = 1,position = position\_dodge(.9))+  
 scale\_fill\_manual(values = c("midnightblue","skyblue"))+  
 coord\_cartesian(ylim = c(450,550))+  
 ggtitle("Valid and Invalid trials mean \n per Stimulus Type in Phase 3.2")+  
 theme\_classic()+  
 ylab("ReactionTime (in ms)")+  
 xlab("StimulusType")+  
 facet\_grid(.~BothAwareSS)+  
 labs(subtitle = "awareness of SS association")+  
 theme(text = element\_text(size = 20), axis.text.x = element\_text(angle = 15))

### ER

No 3-way interaction

anova32ER\_A\_SS <- ezANOVA(data = Exp1\_phase3.2\_A,  
 dv = ER,  
 wid = PROLIFIC\_PID,  
 within = .(Validity,StimulusType),  
 between = .(BothAwareSS),  
 detailed = TRUE)   
pander(anova\_out(anova32ER\_A\_SS), style = "rmarkdown", caption = "ANOVA (RT): for Phase 3.1 across stimulus type")  
  
anova32ER\_A\_S1 <- ezANOVA(data = Exp1\_phase3.2\_A,  
 dv = ER,  
 wid = PROLIFIC\_PID,  
 within = .(Validity,StimulusType),  
 between = .(BothAwareS1),  
 detailed = TRUE)   
pander(anova\_out(anova32ER\_A\_S1), style = "rmarkdown", caption = "ANOVA (RT): for Phase 3.1 across stimulus type")  
  
anova32ER\_A\_S2 <- ezANOVA(data = Exp1\_phase3.2\_A,  
 dv = ER,  
 wid = PROLIFIC\_PID,  
 within = .(Validity,StimulusType),  
 between = .(BothAwareS2),  
 detailed = TRUE)   
pander(anova\_out(anova32ER\_A\_S2), style = "rmarkdown", caption = "ANOVA (RT): for Phase 3.1 across stimulus type")  
  
ggplot(Exp1\_phase3.2\_A, aes(x=StimulusType, y=ER,fill = Validity))+  
 geom\_bar(stat = "summary", fun = "mean",position = position\_dodge())+  
 #geom\_errorbar(aes(ymin = RT - ci, ymax = RT + ci),width = .1, size = 1,position = position\_dodge(.9))+  
 scale\_fill\_manual(values = c("midnightblue","skyblue"))+  
 coord\_cartesian(ylim = c(0,0.15))+  
 ggtitle("Valid and Invalid trials mean \n per Stimulus Type in Phase 3.2")+  
 theme\_classic()+  
 ylab("Error Rate")+  
 xlab("StimulusType")+  
 facet\_grid(.~BothAwareSS)+  
 labs(subtitle = "awareness of SS association")+  
 theme(text = element\_text(size = 20), axis.text.x = element\_text(angle = 15))