

Supplementary Material 1: R analysis of accuracy and saccadic reaction times

Correct Responses

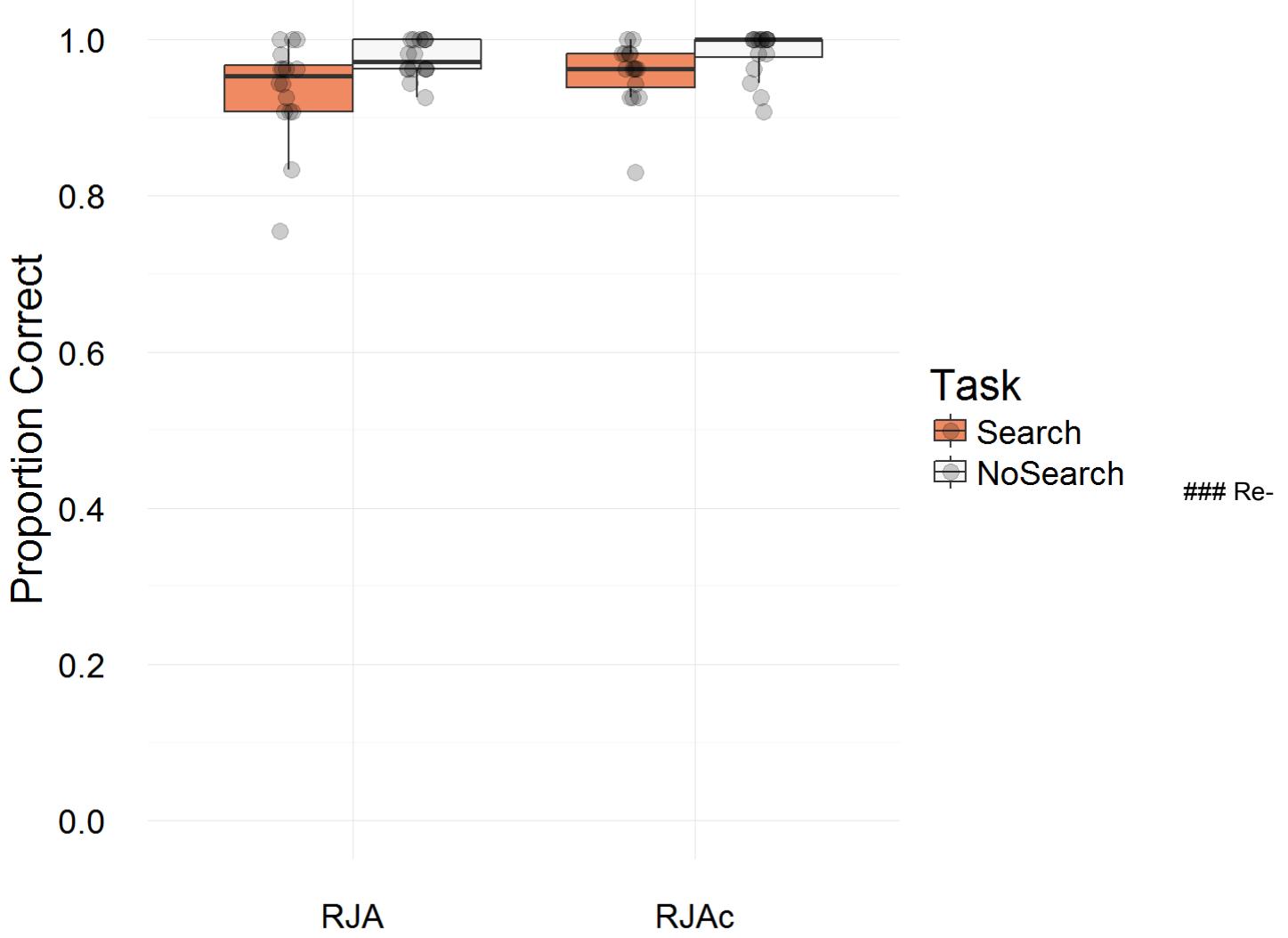
ANOVA

ANOVA analysis of the proportion of correct trials shows significantly more errors in the Search task compared to the NoSearch task (even after excluding trials that involved a Search Error)

```
ScreenedData <- RespondData[which(RespondData$RecalibrationError==0 & RespondData$SearchError==0),]  
BySubjectsData <- aggregate(x = ScreenedData$CorrectResponse, list(SubNum = ScreenedData$SubNum, Condition = ScreenedData$Condition, Task = ScreenedData$Task), FUN=mean)  
ezANOVA(BySubjectsData, dv = x, wid = SubNum, within = .(Condition, Task), between = NULL, type = 3)
```

```
## $ANOVA  
##          Effect DFn DFD      F      p p<.05      ges  
## 2      Condition   1   15  2.9896129 0.104319875    0.02515127  
## 3          Task    1   15 11.8130546 0.003668318    * 0.13839232  
## 4 Condition:Task   1   15  0.5933351 0.453094059    0.00821435
```

```
ggplot(BySubjectsData, aes(factor(Condition), y=x, fill=Task))+  
  geom_boxplot(outlier.colour=NA)+  
  scale_fill_brewer(palette="RdBu") +  
  theme_minimal(base_size = 18, base_family = "")+  
  scale_x_discrete("")+  
  geom_point(position=position_jitterdodge(dodge.width=0.75, jitter.width=0.3), alpha=0.2, size=3)+  
  scale_y_continuous("Proportion Correct",limits=c(0,1), breaks=seq(0, 1, 0.2))
```



analysis: mixed random effects logistic regression We re-analysed the accuracy data taking a mixed random effects approach, which treats each trial as a binary (Correct/Incorrect) data point and includes subject and item as random factors. Consistent with the ANOVA, we found a main effect of task (Search vs NoSearch).

```
summary(glmer(CorrectResponse ~ ConditionC * TaskC + (1|SubNum) + (1|TrialID), ScreenedData, family=binomial))
```

```

## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: binomial ( logit )
## Formula:
## CorrectResponse ~ ConditionC * TaskC + (1 | SubNum) + (1 | TrialID)
## Data: ScreenedData
##
##      AIC      BIC  logLik deviance df.resid
## 1056.0 1092.8 -522.0   1044.0     3439
##
## Scaled residuals:
##    Min     1Q Median     3Q    Max
## -9.8833  0.1213  0.1580  0.2123  0.5877
##
## Random effects:
## Groups   Name        Variance Std.Dev.
## TrialID (Intercept) 0.3259   0.5709
## SubNum   (Intercept) 0.4375   0.6614
## Number of obs: 3445, groups: TrialID, 216; SubNum, 16
##
## Fixed effects:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  3.7005    0.2274 16.275 < 2e-16 ***
## ConditionC -0.3678    0.2196 -1.674  0.0941 .
## TaskC       -0.9872    0.2029 -4.866 1.14e-06 ***
## ConditionC:TaskC -0.1535    0.4051 -0.379  0.7047
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##          (Intr) CndtnC TaskC
## ConditionC -0.086
## TaskC       -0.204  0.035
## CndtnC:TskC  0.012 -0.367 -0.147

```

Saccadic reaction time

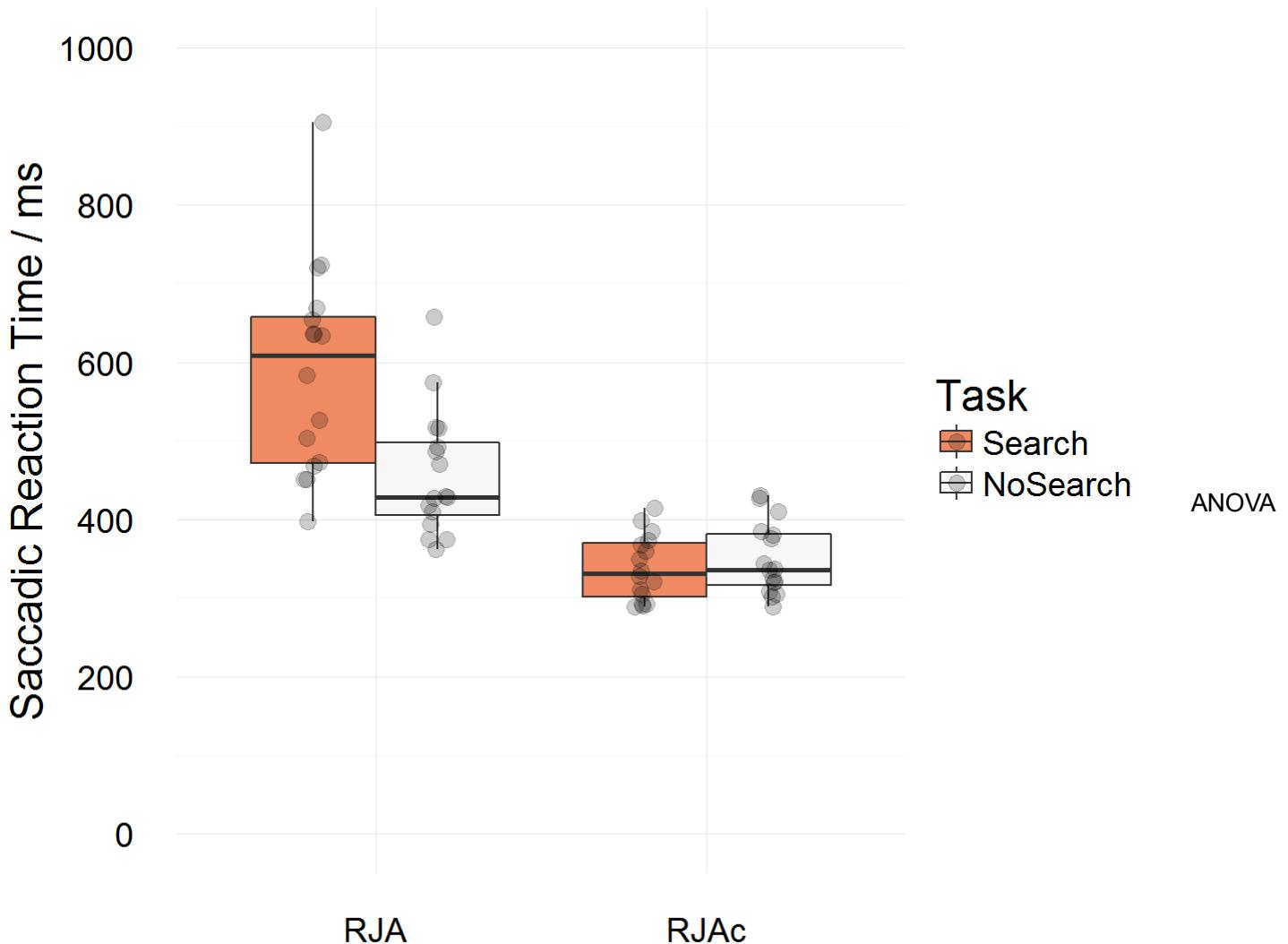
ANOVA

Reaction times were analysed for correct trials only. We also trimmed trials with reaction times less than 150ms as these are likely to be anticipations.

```

ScreenedData <- RespondData[which(RespondData$CorrectResponse==1 & RespondData$FirstSaccadeSRT>150),]
BySubjectsData <- aggregate(x = ScreenedData$FirstSaccadeSRT, list(SubNum = ScreenedData$SubNum, Condition = ScreenedData$Condition, Task = ScreenedData$Task), FUN=mean)
ggplot(BySubjectsData, aes(factor(Condition), y=x, fill=Task))+
  geom_boxplot(outlier.colour=NA)+
  scale_fill_brewer(palette="RdBu") +
  theme_minimal(base_size = 18, base_family = "")+
  scale_x_discrete("")+
  geom_point(position=position_jitterdodge(dodge.width=0.75, jitter.width=0.3), alpha=0.2, size=3)+ 
  scale_y_continuous("Saccadic Reaction Time / ms",limits=c(0,1000), breaks=seq(0, 1000, 200))

```



shows effects of Condition (RJa vs RJAc) and Task (Search vs NoSearch). Crucially, as predicted, there was also a significant interaction between Condition and Task

```
ezANOVA(BySubjectsData, dv = x, wid = SubNum, within = .(Condition, Task), between = NULL, type = 3)
```

```
## $ANOVA
##          Effect DFn DFd      F      p p<.05     ges
## 2      Condition   1   15 86.33668 1.301783e-07    * 0.5526201
## 3          Task   1   15 10.76380 5.053748e-03    * 0.1205873
## 4 Condition:Task   1   15 47.71347 4.997711e-06    * 0.1622947
```

T-tests show this interaction arises because the effect of Search task is significant for the RJA condition but not for the RJAc condition.

```
t.test(x ~ Task, BySubjectsData[(BySubjectsData$Condition=="RJA"),], paired=TRUE)
```

```

## 
## Paired t-test
## 
## data: x by Task
## t = 4.9146, df = 15, p-value = 0.0001869
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## 74.3403 188.2055
## sample estimates:
## mean of the differences
## 131.2729

```

```
t.test(x ~ Task, BySubjectsData[(BySubjectsData$Condition=="RJAc"),], paired=TRUE)
```

```

## 
## Paired t-test
## 
## data: x by Task
## t = -0.8729, df = 15, p-value = 0.3965
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -38.94428 16.31482
## sample estimates:
## mean of the differences
## -11.31473

```

Re-analysis: ANOVA on median reaction times

Importantly, the predicted interaction remains if we take the median rather than the mean reaction time (although the main effect of Task is no longer significant)

```

BySubjectsData <- aggregate(x = ScreenedData$FirstSaccadeSRT, list(SubNum = ScreenedData$SubNum, Condition = ScreenedData$Condition, Task = ScreenedData$Task), FUN=median)
ezANOVA(BySubjectsData, dv = x, wid = SubNum, within = .(Condition, Task), between = NULL, type = 3)

```

```

## $ANOVA
##          Effect DFn DFd      F      p p<.05      ges
## 2      Condition    1   15 46.8958524 5.524461e-06     * 0.380765270
## 3          Task    1   15  0.1049131 7.504838e-01     0.001171857
## 4 Condition:Task    1   15  5.5919794 3.194891e-02     * 0.032843195

```

Re-analysis: mixed random effects

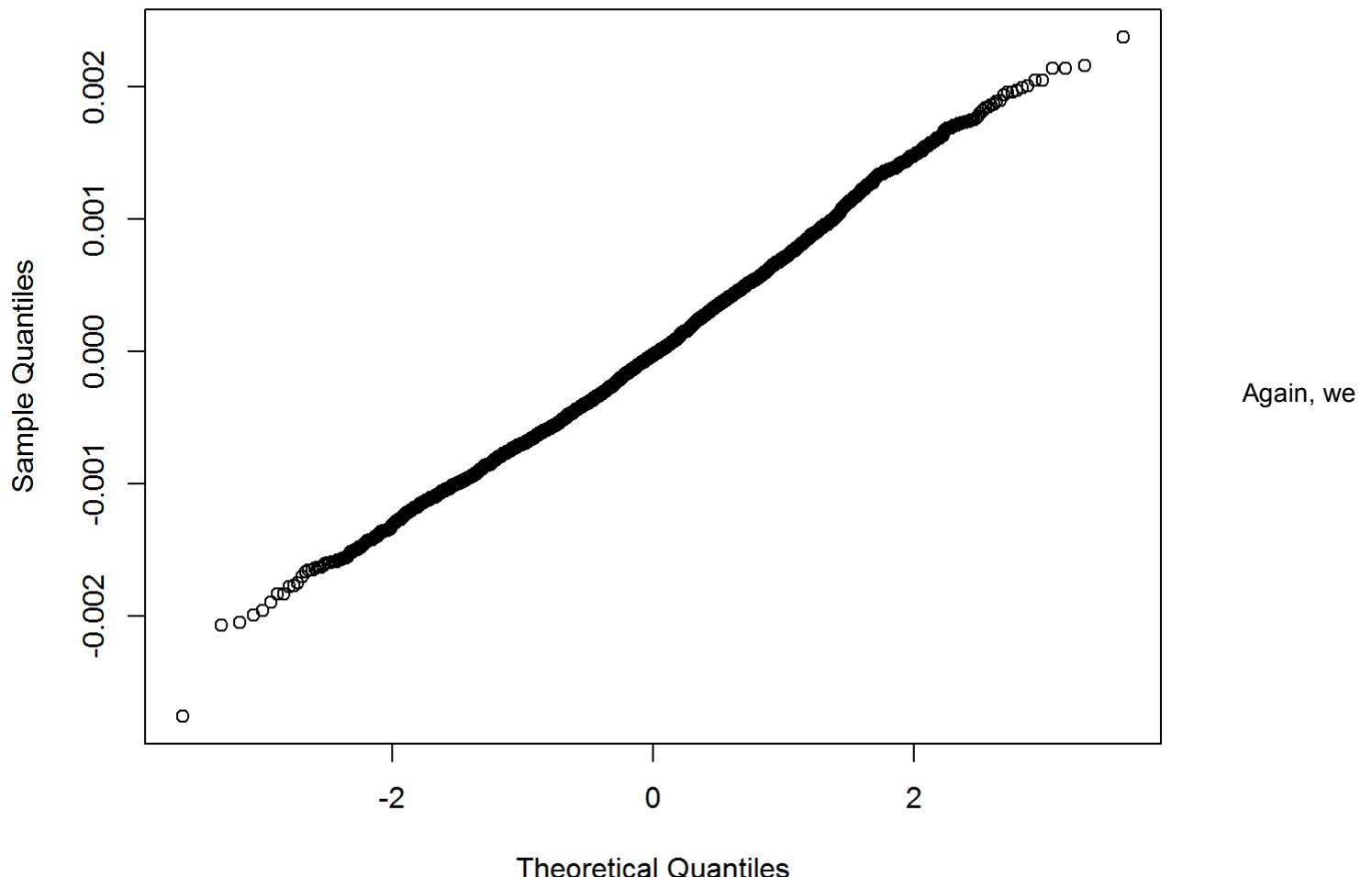
We also re-analysed the data taking a mixed random effects approach. To ensure that the residuals were normally distributed, we applied an inverse transformation on reaction times. The success of this transformation is demonstrated by the near-linear quantile-quantile plot.

```

ScreenedData$invSRT <- -1/ScreenedData$FirstSaccadeSRT
M1 <- lmer(invSRT ~ ConditionC * TaskC + (1|SubNum) + (1|TrialID), ScreenedData)
qqnorm(residuals(M1))

```

Normal Q-Q Plot



Again, we

find the predicted interaction between Task and Condition

```
summary(M1)
```

```

## Linear mixed model fit by REML t-tests use Satterthwaite approximations
## to degrees of freedom [lmerMod]
## Formula: invSRT ~ ConditionC * TaskC + (1 | SubNum) + (1 | TrialID)
## Data: ScreenedData
##
## REML criterion at convergence: -37766.2
##
## Scaled residuals:
##    Min     1Q Median     3Q    Max
## -3.8629 -0.7060 -0.0422  0.6509  3.3265
##
## Random effects:
## Groups   Name        Variance Std.Dev.
## TrialID (Intercept) 2.735e-08 0.0001654
## SubNum   (Intercept) 7.355e-08 0.0002712
## Residual           5.100e-07 0.0007141
## Number of obs: 3263, groups: TrialID, 216; SubNum, 16
##
## Fixed effects:
##             Estimate Std. Error      df t value Pr(>|t|)    
## (Intercept) -2.730e-03 6.986e-05 1.600e+01 -39.080 < 2e-16 ***
## ConditionC  7.645e-04 3.368e-05 2.130e+02  22.702 < 2e-16 ***
## TaskC       3.930e-05 2.505e-05 3.176e+03   1.569    0.117  
## ConditionC:TaskC 3.241e-04 5.010e-05 3.176e+03   6.471 1.13e-10 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##          (Intr) CndtnC TaskC
## ConditionC  0.001
## TaskC       0.006  0.002
## CndtnC:TskC 0.000  0.024  0.008

```

Finally, we performed the mixed random effects analysis with a fully-saturated random effects structure (cf. Barr, 2013). In this case, we have random slopes and interactions for each subject as well as random intercepts. Again, we find the predicted Task by Condition interaction.

```
summary(lmer(invSRT ~ ConditionC * TaskC + (1+ConditionC*TaskC|SubNum) + (1|TrialID), ScreenedData))
```

```

## Linear mixed model fit by REML t-tests use Satterthwaite approximations
## to degrees of freedom [lmerMod]
## Formula:
## invSRT ~ ConditionC * TaskC + (1 + ConditionC * TaskC | SubNum) +
##      (1 | TrialID)
## Data: ScreenedData
##
## REML criterion at convergence: -37976.5
##
## Scaled residuals:
##    Min     1Q Median     3Q    Max
## -3.3915 -0.6782 -0.0584  0.6111  3.6658
##
## Random effects:
## Groups   Name        Variance Std.Dev. Corr
## TrialID (Intercept) 2.493e-08 0.0001579
## SubNum   (Intercept) 7.403e-08 0.0002721
##          ConditionC 5.826e-08 0.0002414  0.28
##          TaskC       1.133e-07 0.0003366  0.02  0.15
##          ConditionC:TaskC 8.895e-08 0.0002982  0.19  0.53 -0.21
## Residual           4.661e-07 0.0006827
## Number of obs: 3263, groups: TrialID, 216; SubNum, 16
##
## Fixed effects:
##             Estimate Std. Error      df t value Pr(>|t|)    
## (Intercept) -2.730e-03 6.990e-05 1.570e+01 -39.053 < 2e-16 ***
## ConditionC  7.632e-04 6.840e-05 1.780e+01  11.158 1.83e-09 ***
## TaskC       4.364e-05 8.751e-05 1.493e+01   0.499  0.62528  
## ConditionC:TaskC 3.180e-04 8.866e-05 1.513e+01   3.586  0.00267 ** 
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##          (Intr) CndtnC TaskC
## ConditionC  0.243
## TaskC       0.024  0.132
## CndtnC:TskC 0.153  0.399 -0.166

```

References

Barr, D. J. (2013). Random effects structure for testing interactions in linear mixed-effects models. *Frontiers in Psychology*, 4, 328.