exp1\_results

In total, 0 participant where excluded due to low accuracy (> 70%). Resulting in a loss of 0 percent of the data.

Furthermore, 4 trials were lost due to deviating (2.5 SD) response times and none response(s). Representing a loss of 1.78 percent of the data.

Lastly, 102 trials were removed due to a wrong response on the inducer trial. Representing a loss of 45.33 percent of the data.

A total of 106 trials were lost. Representing a loss of 47.11 percent of the data.

# Diagnostic

## Table

t is large; approximation invoked.

Table XX *Test statistics for the experimental conditions*

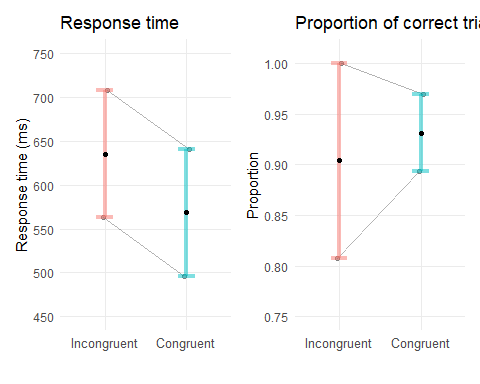
|  | Incongruent | |  | Congruent | |  |  | Bayes | | |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | *M* | *SD* |  | *M* | *SD* | *M*~diff~ |  | *M*~est~ | BF~10~ | HDI |  | *d* |
| RT | 635.0 | 102.00 |  | 569.00 | 102.00 | 66.8\* |  | 60.10 | 5.99 | [-1.57, 95.4] |  | 0.37 |
| PCT | 0.9 | 0.14 |  | 0.93 | 0.05 | -0.03 |  | -0.01 | 0.58 | [-0.15, 0.12] |  | 0.15 |

*Note.* P’s are Bonferroni corrected for 2 tests. The tests have 1 degrees of freedom. \* *p* < .05 \*\* *p* < .01 *M* = Mean, *SD* = standard deviation, *M*diff = Differences of the means, HDI = highest density interval, *d* = Effect size.

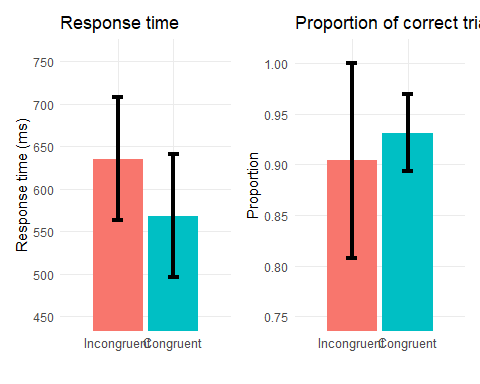
**remove extra zeros**

## Figures

### Linerange



### Bar plot



# Exploratory

## LISAS

### Table

Table XXX *Linear integrated speed-accuracy score (LISAS) test statistic*

|  |  |  |  | Bayesian | | |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Incongruent | Congruent | *M*~diff~ |  | *M*~est~ | BF~10~ | HDI |  | *d* |
| 666 | 604 | 61.3 |  | 36.9 | 1.01 | [-69, 143] |  | 0.41 |

*Note.* In/congruent are response time corrected using the linear integrated speed-accuracy score (LISAS). The test have 1 degrees of freedom. *M*diff = Difference between means, *M*est = Bayesian sampling mean, BF10 = Bayesian factor, HDI = highest density interval, *d* = Effect size.

**remove extra zeros**

### Table: Combined

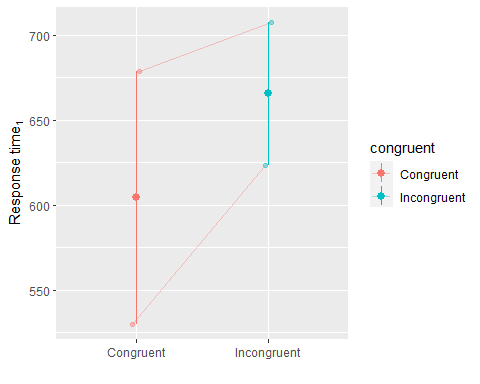
Table YYYY *Test statistic of response time (RT), proportion of correct trials (PCT) and linear integrated speed-accuracy score (LISAS)*

|  | Incongruent | |  | Congruent | |  |  | Bayes | | |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | *M* | *SD* |  | *M* | *SD* | *M*~diff~ |  | *M*~est~ | BF~10~ | HDI |  | *d* |
| RT | 635.0 | 102 |  | 569.00 | 102 | 66.8\* |  | 60.10 | 5.99 | [-1.57, 95.4] |  | 0.37 |
| PCT | 0.9 | 0.14 |  | 0.93 | 0.05 | -0.03 |  | -0.01 | 0.58 | [-0.15, 0.12] |  | 0.15 |
| LISAS^1^ | 666.0 |  |  | 604.00 |  | 61.3 |  | 36.90 | 1.01 | [-69, 143] |  | 0.41 |

*Note*. The test have 1 degrees of freedom. In/congruent are response time corrected using the linear integrated speed-accuracy score (LISAS). The test have 1 degrees of freedom. 1 LISAS yields a single integrated score of response time that is corrected based on the proportion of error, see Vandierendonck 2017. *M* = Mean, *SD* = standard deviation, *M*diff = Difference between means, *M*est = Bayesian sampling mean, BF10 = Bayesian factor, HDI = highest density interval, *d* = Effect size.

### Figure

Figure XX *The instruction-based congruency effect with the linear integrated speed-accuracy score (LISAS)*



*Note*. \*Response time corrected score. 1 Response time are corrected using the linear integrated speed-accuracy score (LISAS), see Vandierendonck 2017.

## BIS

Balanced integration score (BIS)

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

### Table: Combined

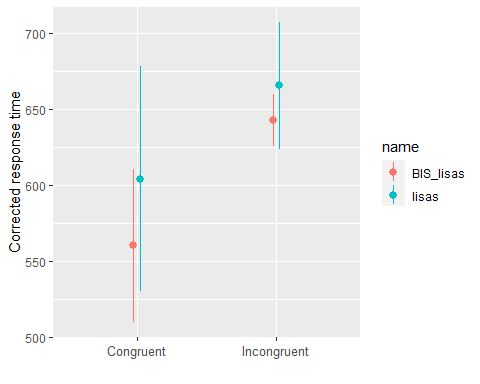
t is large; approximation invoked.

|  | Incongruent | |  | Congruent | |  |  |  |  | Bayesian | | |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| name | *M* | *SD* |  | *M* | *SD* |  | *M*~diff~ | *p* |  | B~est~ | BF~10~ | HDI |  | *d* |
| rt | 635.00 | 102.00 |  | 569.00 | 102.00 |  | 66.80 | .002 |  | 57.00 | 5.99 | [1.14, 93.8] |  | 0.37 |
| pe | 0.10 | 0.14 |  | 0.07 | 0.05 |  | 0.03 | .718 |  | 0.01 | 0.58 | [-0.12, 0.15] |  | 0.15 |
| lisas | 666.00 | 59.40 |  | 604.00 | 105.00 |  | 61.30 | .31 |  | 36.00 | 1.01 | [-78.6, 159] |  | 0.41 |
| BIS\_lisas | 643.00 | 24.20 |  | 560.00 | 71.30 |  | 82.50 | .244 |  | 54.40 | 1.17 | [-78.4, 209] |  | 0.89 |
| BIS | -0.28 | 0.15 |  | 0.24 | 0.45 |  | -0.52 | .244 |  | -0.32 | 1.17 | [-1.16, 0.46] |  | 0.89 |

### Figure

#### Summarized:

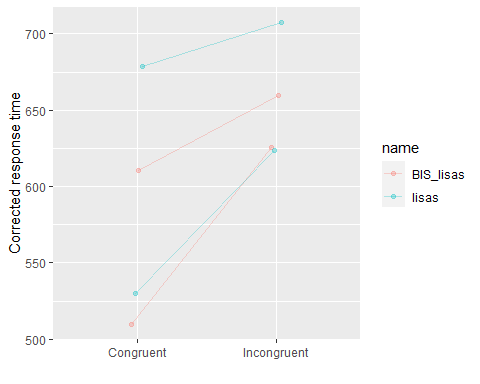
##### Linerange - RT



*Note*. Balanced integration score (BIS) is inversed (i.e., -1\*BIS) to correspond with the linear integration speed-accuracy score (LISAS).

#### Combined

Combined BIS + LISAS



*Note*. The balanced integration score (BIS) is inversed to scale with the scaled linear integration speed-accuracy score (LISAS).

## Inducer:

### Corr: Encoding <-> Inducer RT

#### Table

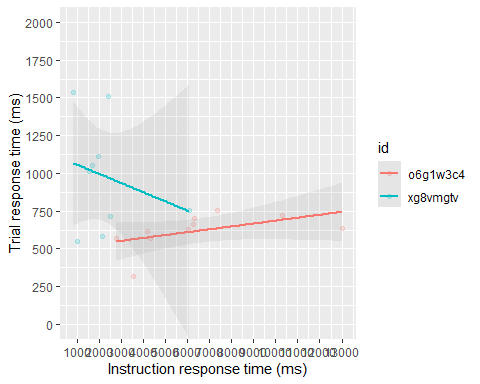
Grand correlation, encoding time (ms) and response time (ms) for the inducer task

# A tibble: 1 × 6  
 cor encoding encoding\_sd d trial trial\_sd  
 <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>  
1 -0.397 4290. 3254. 1.20 850. NA

#### Figure

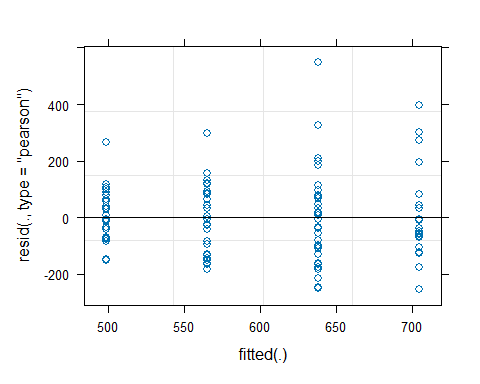


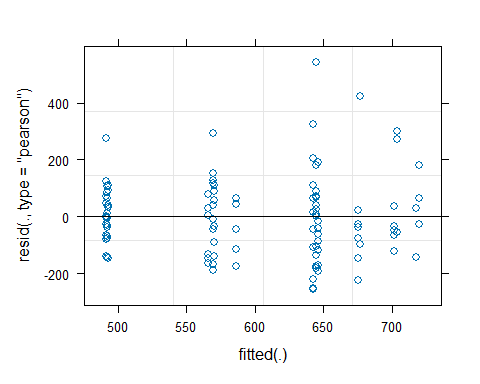
#### Figure: ind



## ANCOVA: Inducer RT \* Congruency

Individual correlation, encoding time (ms) and response time (ms)





refitting model(s) with ML (instead of REML)

[1] NA 0.7752776

Linear mixed model fit by REML ['lmerMod']  
Formula: rt ~ congruent \* trial + (1 | id)  
 Data: filter(an\_d, trial\_info == "Diagnostic trial")  
  
REML criterion at convergence: 1367.6  
  
Scaled residuals:   
 Min 1Q Median 3Q Max   
-1.7991 -0.6439 -0.0529 0.4716 3.8293   
  
Random effects:  
 Groups Name Variance Std.Dev.  
 id (Intercept) 12880 113.5   
 Residual 20044 141.6   
Number of obs: 108, groups: id, 2  
  
Fixed effects:  
 Estimate Std. Error t value  
(Intercept) 681.63777 102.58594 6.645  
congruentTRUE -109.61979 69.72599 -1.572  
trial -0.05469 0.07063 -0.774  
congruentTRUE:trial 0.05019 0.07497 0.669  
  
Correlation of Fixed Effects:  
 (Intr) cnTRUE trial   
congrntTRUE -0.383   
trial -0.589 0.560   
cngrntTRUE: 0.346 -0.918 -0.600

Loading required package: Rcpp

Loading 'brms' package (version 2.19.0). Useful instructions  
can be found by typing help('brms'). A more detailed introduction  
to the package is available through vignette('brms\_overview').

Attaching package: 'brms'

The following object is masked \_by\_ '.GlobalEnv':  
  
 loss

The following object is masked from 'package:lme4':  
  
 ngrps

The following object is masked from 'package:stats':  
  
 ar

This is cmdstanr version 0.6.0

- CmdStanR documentation and vignettes: mc-stan.org/cmdstanr

- CmdStan path: C:/Users/steff/Documents/.cmdstan/cmdstan-2.32.2

- CmdStan version: 2.32.2

A newer version of CmdStan is available. See ?install\_cmdstan() to install it.  
To disable this check set option or environment variable CMDSTANR\_NO\_VER\_CHECK=TRUE.

This is bayesplot version 1.10.0

- Online documentation and vignettes at mc-stan.org/bayesplot

- bayesplot theme set to bayesplot::theme\_default()

\* Does \_not\_ affect other ggplot2 plots

\* See ?bayesplot\_theme\_set for details on theme setting

Attaching package: 'bayesplot'

The following object is masked from 'package:brms':  
  
 rhat

Start sampling

Chain 1 Informational Message: The current Metropolis proposal is about to be rejected because of the following issue:

Chain 1 Exception: normal\_id\_glm\_lpdf: Scale vector is inf, but must be positive finite! (in 'C:/Users/steff/AppData/Local/Temp/RtmpamINC5/model-48587aca265a.stan', line 54, column 4 to column 55)

Chain 1 If this warning occurs sporadically, such as for highly constrained variable types like covariance matrices, then the sampler is fine,

Chain 1 but if this warning occurs often then your model may be either severely ill-conditioned or misspecified.

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Chain 2 If this warning occurs sporadically, such as for highly constrained variable types like covariance matrices, then the sampler is fine,

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Chain 3 If this warning occurs sporadically, such as for highly constrained variable types like covariance matrices, then the sampler is fine,

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Chain 3

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Warning: 54 of 12000 (0.0%) transitions ended with a divergence.  
See https://mc-stan.org/misc/warnings for details.

Start sampling

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Chain 6 Exception: normal\_id\_glm\_lpdf: Scale vector is inf, but must be positive finite! (in 'C:/Users/steff/AppData/Local/Temp/RtmpamINC5/model-48585334831.stan', line 54, column 4 to column 55)

Chain 6 If this warning occurs sporadically, such as for highly constrained variable types like covariance matrices, then the sampler is fine,

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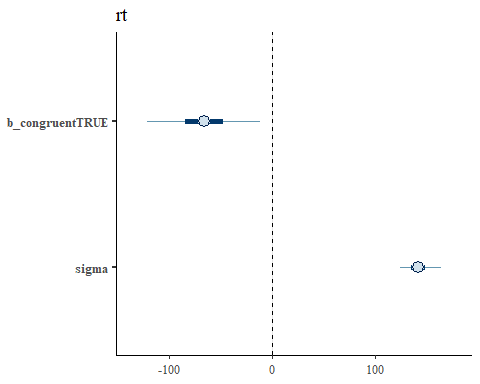
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Warning: 34 of 12000 (0.0%) transitions ended with a divergence.  
See https://mc-stan.org/misc/warnings for details.

[1] "max: 1.00278639220423"  
[1] "mean: 1.0019751946911"  
[1] "median: 1.0021474603697"



[1] "max: 1.00331861295796"  
[1] "mean: 1.00163186440365"  
[1] "median: 1.00167125553783"

