The IAT as an analogical learning task: Experiment 2

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Contents

Note that R treats the two conditions alphabetically (i.e., Insects, Flowers), so that all effects sizes are retured as negative despite being in line with the hypotheses. All are inverted when reported in the manuscript to make the reported results congruent with the wording of the hypothesis.

```
## Dependencies
library(tidyverse)
library(psych)
library(effsize)
library(lsr)  # for eta sq
library(MBESS)  # for ci.pvaf(), 95% CI on eta2
library(BayesFactor)

## Data acquisition
data_df <-
  read.csv("/Users/Ian/Dropbox/Work/Manuscripts/Hussey & De Houwer - the IAT as an analogical learning 
  mutate(SCIAT_block_order = as.factor(SCIAT_block_order))
```

Descriptive statistics

Gender counts

```
data_df %>% dplyr::count(gender)
```

```
## # A tibble: 2 × 2
##   gender     n
##   <fctr> <int>
## 1      f    75
## 2      m    25
```

Descriptives for all participants

```
data_df %>%
  select(age,
```

```r
         flowers_ratings,
         insects_ratings,
         SCIAT1_accuracy,
         SCIAT1_mean_RT,
         SCIAT2_accuracy,
         SCIAT2_mean_RT,
         IAT_accuracy,
         IAT_mean_RT) %>%
  psych::describe(fast = TRUE,  # subset of descriptive stats
                  ranges = FALSE,
                  trim = 0)
```

```
##                 vars   n   mean     sd    se
## age                1 100  21.55   3.29  0.33
## flowers_ratings    2 100   5.80   0.72  0.07
## insects_ratings    3 100   2.16   1.03  0.10
## SCIAT1_accuracy    4 100  94.59   3.63  0.36
## SCIAT1_mean_RT     5 100 642.26 108.23 10.82
## SCIAT2_accuracy    6 100  92.91   4.69  0.47
## SCIAT2_mean_RT     7 100 621.90  79.32  7.93
## IAT_accuracy       8 100  93.51   4.86  0.49
## IAT_mean_RT        9 100 668.91  98.13  9.81
```

Descriptives by experimental condition

```r
data_df %>%
  select(gender,
         age,
         ratings_pre,
         ratings_post,
         ratings_change_scores,
         SCIAT1_D1,
         SCIAT2_D1,
         SCIAT_D1_change_scores,
         IAT_D1) %>%
  psych::describeBy(data_df$condition,
                    fast = TRUE,  # subset of descriptive stats
                    ranges = FALSE,
                    trim = 0)
```

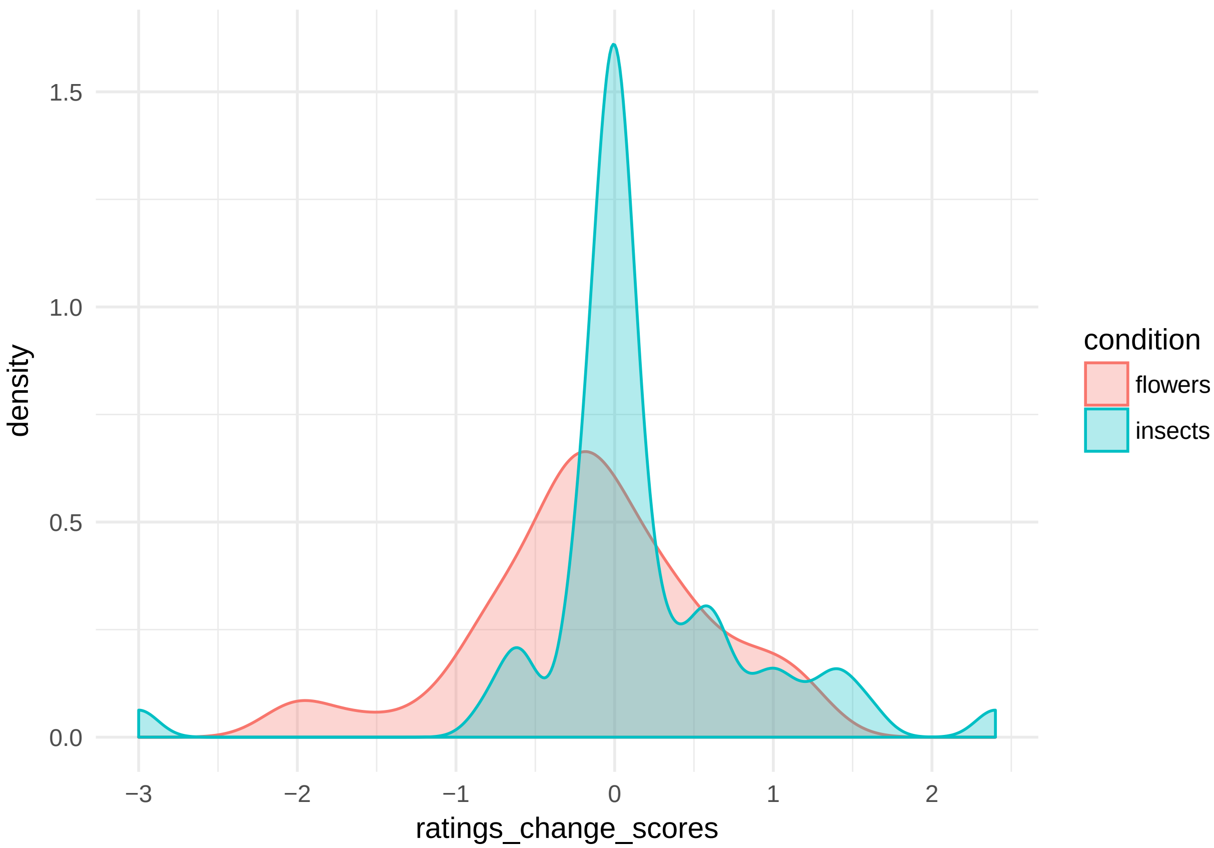
```
## $flowers
##                        vars  n  mean   sd   se
## gender*                   1 48   NaN   NA   NA
## age                       2 48 20.98 1.93 0.28
## ratings_pre               3 48  3.85 0.59 0.09
## ratings_post              4 48  3.70 0.68 0.10
## ratings_change_scores     5 48 -0.15 0.72 0.10
## SCIAT1_D1                 6 48 -0.02 0.32 0.05
## SCIAT2_D1                 7 48 -0.13 0.26 0.04
## SCIAT_D1_change_scores    8 48 -0.10 0.35 0.05
## IAT_D1                    9 48 -0.32 0.32 0.05
##
## $insects
##                        vars  n  mean   sd   se
## gender*                   1 52   NaN   NA   NA
## age                       2 52 22.08 4.12 0.57
```

```
## ratings_pre                 3 52  3.95 0.60 0.08
## ratings_post                4 52  4.11 0.61 0.08
## ratings_change_scores       5 52  0.15 0.74 0.10
## SCIAT1_D1                   6 52 -0.13 0.26 0.04
## SCIAT2_D1                   7 52 -0.02 0.23 0.03
## SCIAT_D1_change_scores      8 52  0.11 0.33 0.05
## IAT_D1                      9 52 -0.03 0.38 0.05
##
## attr(,"call")
## by.data.frame(data = x, INDICES = group, FUN = describe, type = type,
##     fast = TRUE, ranges = FALSE, trim = 0)
```

Distribution plots

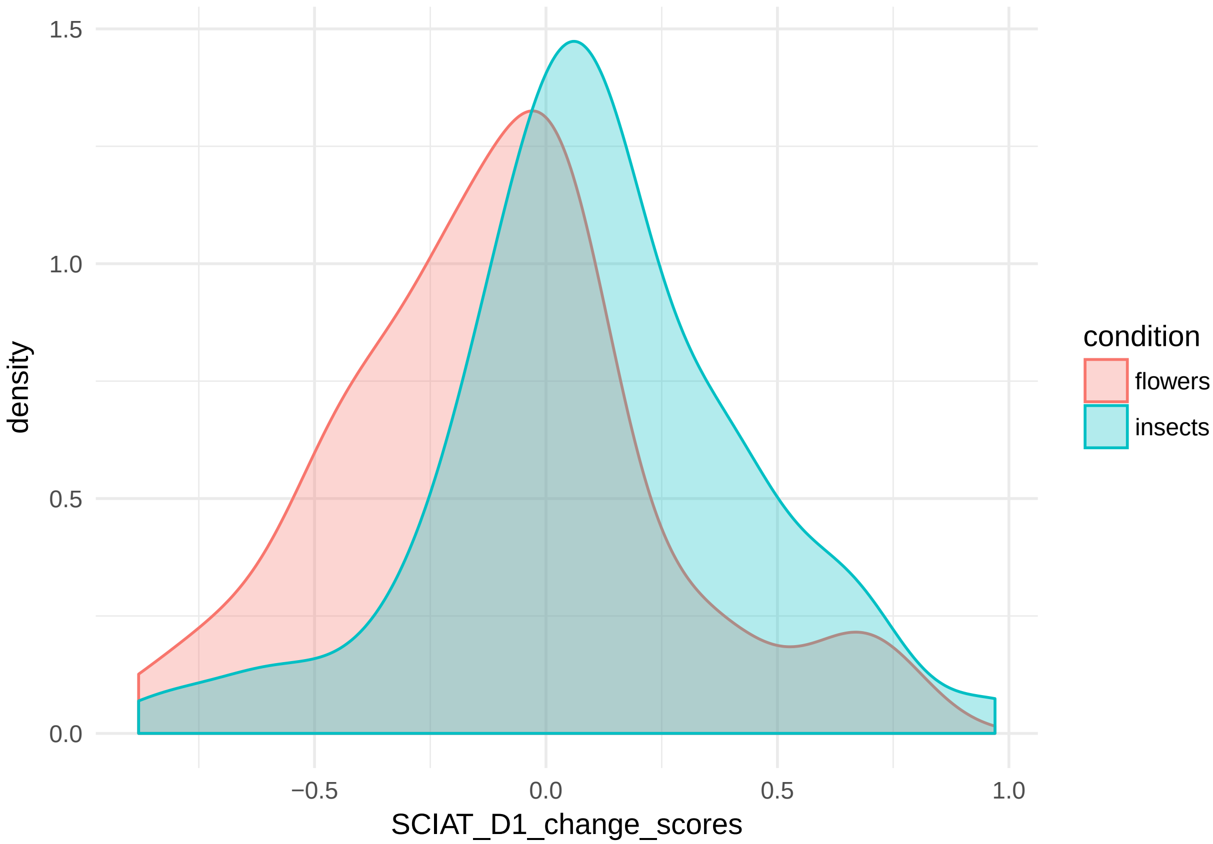
Ratings change scores

```r
ggplot(data = data_df, aes(x = ratings_change_scores, colour = condition, fill = condition)) +
  geom_density(alpha = 0.3) +
  theme_minimal()
```



SCIAT change scores

```r
ggplot(data = data_df, aes(x = SCIAT_D1_change_scores, colour = condition, fill = condition)) +
  geom_density(alpha = 0.3) +
  theme_minimal()
```



Manipulation checks

Differences in ratings of valenced images

Frequentist

T test

```
attach(data_df)

t.test(flowers_ratings,
       insects_ratings,
       paired = TRUE,
       alternative = "greater")
```

```
##
##  Paired t-test
##
## data:  flowers_ratings and insects_ratings
## t = 26.913, df = 99, p-value < 2.2e-16
## alternative hypothesis: true difference in means is greater than 0
## 95 percent confidence interval:
##  3.412808      Inf
## sample estimates:
## mean of the differences
##                  3.6372
```

```r
cohen.d(flowers_ratings,
        insects_ratings)
```

```
##
## Cohen's d
##
## d estimate: 4.084668 (large)
## 95 percent confidence interval:
##      inf      sup
## 3.590638 4.578697
```

Bayes factors

```r
ttestBF(x = data_df$flowers_ratings,
        y = data_df$insects_ratings,
        rscale = "medium",  # i.e., r = .707
        nullInterval = c(-Inf,0)) # directional hypothesis
```

```
## t is large; approximation invoked.
## t is large; approximation invoked.
## t is large; approximation invoked.
## t is large; approximation invoked.
```

```
## Bayes factor analysis
## --------------
## [1] Alt., r=0.707 -Inf<d<0    : 0.0006724181 ±NA%
## [2] Alt., r=0.707 !(-Inf<d<0) : 2.107218e+69 ±NA%
##
## Against denominator:
##   Null, mu1-mu2 = 0
## ---
## Bayes factor type: BFindepSample, JZS
```

Differences in (training) IAT effects betwen conditions

Frequentist

T test

```r
t.test(IAT_D1 ~ condition,
       alternative = "less")
```

```
##
##  Welch Two Sample t-test
##
## data:  IAT_D1 by condition
## t = -4.1104, df = 97.529, p-value = 4.119e-05
## alternative hypothesis: true difference in means is less than 0
## 95 percent confidence interval:
##        -Inf -0.1716731
## sample estimates:
## mean in group flowers mean in group insects
##           -0.32208333           -0.03403846
```

```r
cohen.d(IAT_D1 ~ condition)
```

```
##
## Cohen's d
##
## d estimate: -0.8177824 (large)
## 95 percent confidence interval:
##        inf        sup
## -1.2357635 -0.3998013
```

Bayes factors

```
ttestBF(formula = IAT_D1 ~ condition,
        rscale = "medium",  # i.e., r = .707
        nullInterval = c(-Inf,0), # directional hypothesis
        data = data_df)
```

```
## Bayes factor analysis
## --------------
## [1] Alt., r=0.707 -Inf<d<0    : 484.1207  ±0%
## [2] Alt., r=0.707 !(-Inf<d<0) : 0.0446024 ±0.01%
##
## Against denominator:
##   Null, mu1-mu2 = 0
## ---
## Bayes factor type: BFindepSample, JZS
```

Hypothesis tests

Differences in ratings change scores between conditions

Frequentist

T test

```
# t test
t.test(ratings_change_scores ~ condition,
       data = data_df, alternative = "less")
```

```
##
##  Welch Two Sample t-test
##
## data:  ratings_change_scores by condition
## t = -2.0763, df = 97.695, p-value = 0.02025
## alternative hypothesis: true difference in means is less than 0
## 95 percent confidence interval:
##        -Inf -0.0608346
## sample estimates:
## mean in group flowers mean in group insects
##            -0.1500000             0.1538462
```

```
# effect size
cohen.d(ratings_change_scores ~ condition,
        data = data_df)
```

```
##
## Cohen's d
##
## d estimate: -0.4151755 (small)
## 95 percent confidence interval:
##          inf          sup
## -0.820799479 -0.009551444
```

Alternative strategy: ANCOVA with pre as covariate

```
model1 <- lm(ratings_post ~ ratings_pre + condition,
             data = data_df)

ratings_ANCOVA <-
  etaSquared(model1,
             type = 3,
             anova = TRUE) %>% # output full anova results, not just eta2
  as.data.frame()

ratings_ANCOVA
```

```
##                 eta.sq eta.sq.part        SS df       MS         F
## ratings_pre 0.08534276  0.09419114  3.846398  1 3.846398 10.086610
## condition   0.07762137  0.08640554  3.498395  1 3.498395  9.174024
## Residuals   0.82071648          NA 36.989692 97 0.381337        NA
##                       p
## ratings_pre 0.002002777
## condition   0.003145624
## Residuals            NA
```

```
# 90% CI on eta2
## (nb 90% not 95%, see Wuensch, 2009; Steiger. 2004)
# from http://daniellakens.blogspot.be/2014/06/calculating-confidence-intervals-for.html
# 1. extract individual stats
ancova_F        <-  ratings_ANCOVA$F[2]         # where 2 specifies the main effect row
ancova_df_1     <-  ratings_ANCOVA$df[2]        # where 2 specifies the main effect row
ancova_df_2     <-  ratings_ANCOVA$df[3]        # where 3 specifies the residuals row
ancova_p        <-  ratings_ANCOVA$p[2]         # where 2 specifies the main effect row
ancova_eta2     <-  ratings_ANCOVA$eta.sq[2]    # where 2 specifies the main effect row

n_df <- data_df %>% dplyr::summarize(n_variable = n())
n_integer <- n_df$n_variable

# 2. Use to calculate 90% CIs
ci.pvaf(F.value = ancova_F,
        df.1 = ancova_df_1,
        df.2 = ancova_df_2,
        N = n_integer,
        conf.level=.90)
```

```
## $Lower.Limit.Proportion.of.Variance.Accounted.for
## [1] 0.01758685
##
## $Probability.Less.Lower.Limit
## [1] 0.05
##
```

```
## $Upper.Limit.Proportion.of.Variance.Accounted.for
## [1] 0.1812139
##
## $Probability.Greater.Upper.Limit
## [1] 0.05
##
## $Actual.Coverage
## [1] 0.9
```

Bayes factors

```
ttestBF(formula = ratings_change_scores ~ condition,
        rscale = "medium",  # i.e., r = .707
        nullInterval = c(-Inf,0), # directional hypothesis
        data = data_df)
```

```
## Bayes factor analysis
## --------------
## [1] Alt., r=0.707 -Inf<d<0    : 2.721385  ±0%
## [2] Alt., r=0.707 !(-Inf<d<0) : 0.0737461 ±0%
##
## Against denominator:
##   Null, mu1-mu2 = 0
## ---
## Bayes factor type: BFindepSample, JZS
```

Differences in SCIAT change scores between conditions

Frequentist

T test

```
t.test(SCIAT_D1_change_scores ~ condition,
       alternative = "less")
```

```
##
##  Welch Two Sample t-test
##
## data:  SCIAT_D1_change_scores by condition
## t = -3.0676, df = 96.766, p-value = 0.001399
## alternative hypothesis: true difference in means is less than 0
## 95 percent confidence interval:
##        -Inf -0.0959201
## sample estimates:
## mean in group flowers mean in group insects
##            -0.1039583             0.1051923
```

```
cohen.d(SCIAT_D1_change_scores ~ condition)
```

```
##
## Cohen's d
##
## d estimate: -0.6148113 (medium)
## 95 percent confidence interval:
##        inf        sup
```

```
## -1.0255991 -0.2040235
```

Alternative strategy: ANCOVA with pre as covariate

```
model1 <- lm(SCIAT2_D1 ~ SCIAT1_D1 + condition,
             data = data_df)

ratings_ANCOVA <-
  etaSquared(model1,
             type = 3,
             anova = TRUE) %>% # output full anova results, not just eta2
  as.data.frame()

ratings_ANCOVA
```

```
##               eta.sq eta.sq.part        SS df         MS        F
## SCIAT1_D1 0.03986319  0.04169002 0.2495762  1 0.24957622 4.219858
## condition 0.05840117  0.05991592 0.3656392  1 0.36563916 6.182260
## Residuals 0.91631752          NA 5.7368981 97 0.05914328       NA
##                    p
## SCIAT1_D1 0.04264335
## condition 0.01461260
## Residuals         NA
```

```
# 90% CI on eta2
## (nb 90% not 95%, see Wuensch, 2009; Steiger. 2004)
# from http://daniellakens.blogspot.be/2014/06/calculating-confidence-intervals-for.html
# 1. extract individual stats
ancova_F       <-  ratings_ANCOVA$F[2]        # where 2 specifies the main effect row
ancova_df_1    <-  ratings_ANCOVA$df[2]       # where 2 specifies the main effect row
ancova_df_2    <-  ratings_ANCOVA$df[3]       # where 3 specifies the residuals row
ancova_p       <-  ratings_ANCOVA$p[2]        # where 2 specifies the main effect row
ancova_eta2    <-  ratings_ANCOVA$eta.sq[2]   # where 2 specifies the main effect row

n_df <- data_df %>% dplyr::summarize(n_variable = n())
n_integer <- n_df$n_variable

# 2. Use to calculate 90% CIs
ci.pvaf(F.value = ancova_F,
        df.1 = ancova_df_1,
        df.2 = ancova_df_2,
        N = n_integer,
        conf.level=.90)
```

```
## $Lower.Limit.Proportion.of.Variance.Accounted.for
## [1] 0.00641116
##
## $Probability.Less.Lower.Limit
## [1] 0.05
##
## $Upper.Limit.Proportion.of.Variance.Accounted.for
## [1] 0.1469769
##
## $Probability.Greater.Upper.Limit
## [1] 0.05
##
```

```
## $Actual.Coverage
## [1] 0.9
```

Bayes factors

```
ttestBF(formula = SCIAT_D1_change_scores ~ condition,
        rscale = "medium",  # i.e., r = .707
        nullInterval = c(-Inf,0), # directional hypothesis
        data = data_df)
```

```
## Bayes factor analysis
## --------------
## [1] Alt., r=0.707 -Inf<d<0    : 24.87347   ±0%
## [2] Alt., r=0.707 !(-Inf<d<0) : 0.05534284 ±0.12%
##
## Against denominator:
##   Null, mu1-mu2 = 0
## ---
## Bayes factor type: BFindepSample, JZS
```

Post hoc exploratory tests

Added at the request of our peer reviewers.

Is the effect influenced by IAT (or SCIAT) block order?

Ratings

Explore interaction effect between condition and block order.

Frequentist

```
model2 <-
  lm(ratings_change_scores ~ condition * IAT_block_order,
     contrasts = list(condition = "contr.sum", IAT_block_order = "contr.sum"),  # effect coding for fac
     data = data_df)

etaSquared(model2,
           type = 3,
           anova = TRUE)
```

```
##                                eta.sq  eta.sq.part           SS df
## condition                4.225284e-02 4.230391e-02  2.315185219  1
## IAT_block_order          6.554937e-05 6.852289e-05  0.003591686  1
## condition:IAT_block_order 1.360352e-03 1.420139e-03  0.074538568  1
## Residuals                9.565399e-01           NA 52.412266667 96
##                                   MS           F          p
## condition                2.315185219 4.240568004 0.04217664
## IAT_block_order          0.003591686 0.006578648 0.93552423
## condition:IAT_block_order 0.074538568 0.136527248 0.71257189
## Residuals                0.545961111          NA         NA
```

Bayes factors

```
anovaBF(ratings_change_scores ~ condition * IAT_block_order,
        data = data_df,
        rscaleFixed = "medium",
        multicore = TRUE)

## Note: Progress bars and callbacks are suppressed when running multicore.

## Bayes factor analysis
## --------------
## [1] condition                                               : 1.397565   ±0%
## [2] IAT_block_order                                         : 0.2118788  ±0.03%
## [3] condition + IAT_block_order                             : 0.2885863  ±2.25%
## [4] condition + IAT_block_order + condition:IAT_block_order : 0.08589121 ±2.35%
##
## Against denominator:
##   Intercept only
## ---
## Bayes factor type: BFlinearModel, JZS
```

SCIAT

Explore interaction effect between condition and block order.

Frequentist

```
model3 <-
  lm(SCIAT_D1_change_scores ~ condition * IAT_block_order,
     contrasts = list(condition = "contr.sum", IAT_block_order = "contr.sum"),  # effect coding for fac
     data = data_df)

etaSquared(model3,
           type = 3,
           anova = TRUE)

##                                eta.sq  eta.sq.part         SS df         MS
## condition                 0.089091136 0.0905440299  1.1076786  1 1.1076786
## IAT_block_order           0.000210197 0.0002348379  0.0026134  1 0.0026134
## condition:IAT_block_order 0.017231926 0.0188926981  0.2142462  1 0.2142462
## Residuals                 0.894862591           NA 11.1259125 96 0.1158949
##                                    F           p
## condition                 9.55761154 0.002606512
## IAT_block_order           0.02254973 0.880948948
## condition:IAT_block_order 1.84862452 0.177128394
## Residuals                         NA          NA
```

Bayes factors

```
anovaBF(SCIAT_D1_change_scores ~ condition * IAT_block_order,
        data = data_df,
        rscaleFixed = "medium",
        multicore = TRUE)

## Note: Progress bars and callbacks are suppressed when running multicore.
```

```
## Bayes factor analysis
## --------------
## [1] condition                                                : 12.46441  ±0%
## [2] IAT_block_order                                          : 0.2129371 ±0.03%
## [3] condition + IAT_block_order                              : 2.59201   ±2.13%
## [4] condition + IAT_block_order + condition:IAT_block_order : 1.766106  ±9.83%
##
## Against denominator:
##   Intercept only
## ---
## Bayes factor type: BFlinearModel, JZS
```