The IAT as an analogical learning task: Experiment 1 $_{Ian\ Hussey}$

Contents

Descriptive statistics

| Distribution plots | 2 |
|--|---|
| Manipulation checks | 3 |
| Differences in ratings of valenced stimuli | 3 |
| Differences in (training) IAT effects betwee conditions | 4 |
| Hypothesis tests | 5 |
| Differences in ratings changes between conditions | 5 |
| Post hoc exploratory tests | 7 |
| Note that R treats the two conditions alphabetically (i.e., Insects, Flowers), so that all effects sizes are retu as negative despite being in line with the hypotheses. All are inverted when reported in the manuscrip make the reported results congruent with the wording of the hypothesis. | |
| ## Dependencies | |
| library(tidyverse) | |
| library(psych) | |

1

```
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

Descriptive statistics

```
Gender counts
```

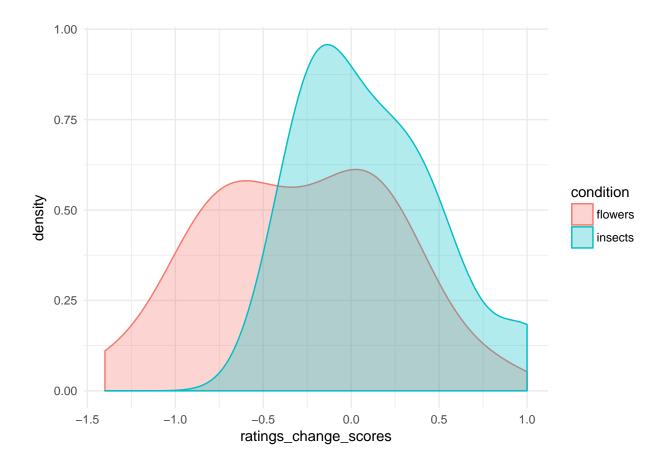
```
data_df %>% count(gender)
## # A tibble: 2 × 2
    gender
##
               n
## <fctr> <int>
## 1
         f
               37
## 2
               15
Descriptives for all participants
data_df %>%
  select(age,
         IAT_accuracy,
         IAT_mean_RT) %>%
  psych::describe(fast = TRUE, # subset of descriptive stats
```

```
ranges = FALSE,
                  trim = 0
##
                vars n
                          mean
                                  sd
                                         se
                   1 52 22.06 3.46 0.48
## age
## IAT_accuracy
                   2 52 92.80 4.62 0.64
                   3 52 659.23 92.52 12.83
## IAT mean RT
Descriptives by experimental condition
data_df %>%
  select(gender,
         age,
         ratings_pre,
         ratings_post,
         ratings_change_scores,
         D1) %>%
  psych::describeBy(data_df$condition,
                    fast = TRUE, # subset of descriptive stats
                    ranges = FALSE,
                    trim = 0)
## $flowers
##
                         vars n mean
## gender*
                            1 26
                                  \mathtt{NaN}
                                        NA
                                               NΑ
## age
                            2 26 22.00 2.56 0.50
                            3 26 2.85 0.52 0.10
## ratings_pre
## ratings_post
                            4 26 2.55 0.63 0.12
## ratings_change_scores
                            5 26 -0.29 0.53 0.10
## D1
                            6 26 -0.33 0.41 0.08
##
## $insects
##
                         vars n mean
                                          sd
## gender*
                            1 26
                                   {\tt NaN}
                                          NΑ
                                               NA
## age
                            2 26 22.12 4.22 0.83
## ratings_pre
                            3 26 2.92 0.42 0.08
## ratings_post
                            4 26 3.04 0.52 0.10
## ratings_change_scores
                            5 26 0.12 0.40 0.08
## D1
                            6 26 -0.08 0.38 0.07
##
## attr(,"call")
## by.data.frame(data = x, INDICES = group, FUN = describe, type = type,
       fast = TRUE, ranges = FALSE, trim = 0)
```

Distribution plots

```
Ratings change scores
```

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



Manipulation checks

Differences in ratings of valenced stimuli

Frequentist

```
T test
t.test(formula = valenced_stimuli_ratings ~ condition,
       data = data_df, alternative = "greater")
##
##
   Welch Two Sample t-test
##
## data: valenced_stimuli_ratings by condition
## t = 14.523, df = 50, p-value < 2.2e-16
\#\# alternative hypothesis: true difference in means is greater than 0
## 95 percent confidence interval:
## 2.034584
## sample estimates:
## mean in group flowers mean in group insects
                4.261538
                                      1.961538
cohen.d(formula = valenced_stimuli_ratings ~ condition,
        data = data df)
```

```
##
## Cohen's d
##
## d estimate: 4.027894 (large)
## 95 percent confidence interval:
       inf
                sup
## 3.026171 5.029617
Bayes factors
ttestBF(formula = valenced_stimuli_ratings ~ condition,
       nullInterval = c(-Inf,0),
       rscale = "medium", # i.e., r = .707 # directional hypothesis
       data = data_df)
## t is large; approximation invoked.
## t is large; approximation invoked.
## Bayes factor analysis
## -----
                                : 0.002744922 ±NA%
## [1] Alt., r=0.707 -Inf<d<0
## [2] Alt., r=0.707 !(-Inf<d<0) : 3.829152e+16 ±NA%
## Against denominator:
## Null, mu1-mu2 = 0
## ---
## Bayes factor type: BFindepSample, JZS
```

Differences in (training) IAT effects between conditions

Frequentist

```
T test
t.test(formula = D1 ~ condition,
       data = data df,
       alternative = "less")
##
## Welch Two Sample t-test
##
## data: D1 by condition
## t = -2.2382, df = 49.817, p-value = 0.01486
## alternative hypothesis: true difference in means is less than 0
## 95 percent confidence interval:
           -Inf -0.06134149
## sample estimates:
## mean in group flowers mean in group insects
             -0.32615385
                                   -0.08192308
cohen.d(formula = D1 ~ condition,
        data = data df)
##
## Cohen's d
```

```
##
## d estimate: -0.6207546 (medium)
## 95 percent confidence interval:
##
           inf
## -1.20291635 -0.03859292
Bayes factors
ttestBF(formula = D1 ~ condition,
        data = data df,
       rscale = "medium", # i.e., r = .707
       nullInterval = c(-Inf,0)) # directional hypothesis
## Bayes factor analysis
## [1] Alt., r=0.707 -Inf<d<0
                                 : 4.08138
                                              ±0%
## [2] Alt., r=0.707 !(-Inf<d<0) : 0.09713165 ±0.01%
## Against denominator:
   Null, mu1-mu2 = 0
## ---
## Bayes factor type: BFindepSample, JZS
```

Hypothesis tests

Differences in ratings changes 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 = -3.1351, df = 46.262, p-value = 0.001491
## alternative hypothesis: true difference in means is less than 0
## 95 percent confidence interval:
          -Inf -0.1894193
##
## sample estimates:
## mean in group flowers mean in group insects
              -0.2923077
                                     0.1153846
# effect size
cohen.d(ratings_change_scores ~ condition,
        data = data_df)
##
## Cohen's d
##
```

```
## d estimate: -0.869507 (large)
## 95 percent confidence interval:
         inf
                    sup
## -1.4648774 -0.2741366
Alternative strategy: ANCOVA with pre as covariate
model1 <- lm(ratings_post ~ ratings_pre + condition,</pre>
            data = data df)
ratings_ANCOVA <-
 etaSquared(model1,
            anova = TRUE) %>% # output full anova results, not just eta2
 as.data.frame()
ratings_ANCOVA
##
                 eta.sq eta.sq.part
                                           SS df
                                                        MS
0.1197851
                          0.1859310 2.352488 1 2.3524878 11.19145
## condition
## Residuals
              0.5244601
                                 NA 10.299992 49 0.2102039
##
## ratings_pre 1.524150e-06
## condition 1.583157e-03
## Residuals
# 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$F[2]</pre>
                                               # where 2 specifies the main effect row
ancova_df_1
               <- ratings_ANCOVA$df[2]</pre>
                                               # where 2 specifies the main effect row
ancova_df_2
               <- ratings_ANCOVA$df[3]</pre>
                                               # where 3 specifies the residuals row
ancova_p
               <- ratings_ANCOVA$p[2]</pre>
                                               # where 2 specifies the main effect row
               <- ratings_ANCOVA$eta.sq[2]</pre>
                                               # where 2 specifies the main effect row
ancova_eta2
n_df <- data_df %>% dplyr::summarize(n_variable = n())
n_integer <- n_df$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] 0.04656081
##
## $Probability.Less.Lower.Limit
## [1] 0.05
## $Upper.Limit.Proportion.of.Variance.Accounted.for
## [1] 0.330375
##
```

```
## $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
                                 : 25.98621
                                               ±0%
## [2] Alt., r=0.707 !(-Inf<d<0) : 0.07743824 ±0.13%
## 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 block order?

check factors are indeed set to factors

Explore interaction effect between condition and block order.

Frequentist

etaSquared(model2,

```
sapply(data_df, class)
##
                participant
                                                gender
                                                                             age
##
                  "integer"
                                              "factor"
                                                                       "integer"
##
               IAT_accuracy
                                          block_order
##
                  "numeric"
                                              "factor"
                                                                       "numeric"
                                                                     ratings_pre
##
                  condition
                                          IAT_mean_RT
##
                   "factor"
                                             "integer"
                                                                       "numeric"
##
               ratings_post valenced_stimuli_ratings
                                                          ratings_change_scores
##
                   "numeric"
                                             "numeric"
                                                                       "numeric"
model2 <-
  lm(ratings_change_scores ~ condition * block_order,
     contrasts = list(condition = "contr.sum", block_order = "contr.sum"), # effect coding for factor
     data = data df)
```

```
type = 3,
          anova = TRUE)
##
                              eta.sq eta.sq.part
                       1.642786e-01 0.1642978300 2.160769e+00 1
## block_order
## condition
                        5.848295e-05 0.0000699839 7.692308e-04 1
## condition:block_order 5.848295e-05 0.0000699839 7.692308e-04 1
## Residuals
                        8.356044e-01
                                             NA 1.099077e+01 48
                                 MS
                                              F
## condition
                      2.1607692308 9.436730123 0.003498669
## block_order 0.0007692308 0.003359462 0.954020420
## condition:block_order 0.0007692308 0.003359462 0.954020420
## Residuals
                        0.2289743590
                                             NA
Bayes factors
anovaBF(formula = ratings_change_scores ~ condition * block_order,
       data = data_df,
       rscaleFixed = "medium",
       multicore = TRUE)
## Note: Progress bars and callbacks are suppressed when running multicore.
## Bayes factor analysis
## -----
## [1] block_order
                                                     : 0.278549 ±0.02%
## [2] condition
                                                     : 13.03182 ±0%
## [3] block_order + condition
                                                     : 3.652007 ±0.81%
## [4] block_order + condition + block_order:condition : 1.251991 ±2.95%
## Against denominator:
## Intercept only
## ---
## Bayes factor type: BFlinearModel, JZS
```