

Analysis of learning via the IAT using race stimuli

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Hypotheses

H1: Completing an IAT serves to train attitudes as well as test them. Participants who complete a race IAT will demonstrate more negative implicit evaluations of the outgroup (black people) on the SCIAT than participants who completed a control (flowers-insects) IAT.

H2: Completing an IAT serves to train attitudes as well as test them. Participants who complete a race IAT will demonstrate more negative self-reported evaluations of the outgroup (black people) on the ratings than participants who completed a control (flowers-insects) IAT.

`# dependencies`

`library(tidyverse)`

`## Loading tidyverse: ggplot2`

`## Loading tidyverse: tibble`

`## Loading tidyverse: tidyr`

`## Loading tidyverse: readr`

`## Loading tidyverse: purrr`

`## Loading tidyverse: dplyr`

`## Conflicts with tidy packages -----`

`## filter(): dplyr, stats`

`## lag(): dplyr, stats`

`library(psych)`

`##`

`## Attaching package: 'psych'`

`## The following objects are masked from 'package:ggplot2':`

`##`

`## %+%, alpha`

```

library(afex)

## Loading required package: lme4
## Loading required package: Matrix
##
## Attaching package: 'Matrix'
## The following object is masked from 'package:tidyr':
##
##     expand
## Loading required package: reshape2
##
## Attaching package: 'reshape2'
## The following object is masked from 'package:tidyr':
##
##     smiths
## Loading required package: lsmeans
## Loading required package: estimability
## *****
## Welcome to afex. Important changes in the current version:
## - Functions for ANOVAs have been renamed to: aov_car(), aov_ez(), and aov_4().
## - ANOVA functions return an object of class 'afex_aov' as default, see: ?aov_car
## - 'afex_aov' objects can be passed to lsmeans for contrasts and follow-up tests.
## - Reset previous (faster) behavior via: afex_options(return_aov='nice')
## - Many more arguments can now be set globally via options, see: afex_options()
## *****

library(effsize)
library(weights) # for rd(), a round() alternative

## Loading required package: Hmisc
## Loading required package: lattice
## Loading required package: survival
## Loading required package: Formula
##
## Attaching package: 'Hmisc'
## The following object is masked from 'package:psych':
##
##     describe
## The following objects are masked from 'package:dplyr':
##
##     combine, src, summarize
## The following objects are masked from 'package:base':
##
##     format.pval, round.POSIXt, trunc.POSIXt, units
## Loading required package: gdata
## gdata: read.xls support for 'XLS' (Excel 97-2004) files ENABLED.

```

```
##
## gdata: read.xls support for 'XLSX' (Excel 2007+) files ENABLED.
##
## Attaching package: 'gdata'
## The following object is masked from 'package:Hmisc':
##
##      combine
## The following objects are masked from 'package:dplyr':
##
##      combine, first, last
## The following object is masked from 'package:purrr':
##
##      keep
## The following object is masked from 'package:stats':
##
##      nobs
## The following object is masked from 'package:utils':
##
##      object.size
## The following object is masked from 'package:base':
##
##      startsWith
## Loading required package: mice
## Loading required package: Rcpp
## mice 2.25 2015-11-09
##
## Attaching package: 'mice'
## The following object is masked from 'package:tidyr':
##
##      complete
library(plotrix) # for std.error
##
## Attaching package: 'plotrix'
## The following object is masked from 'package:psych':
##
##      rescale
```

Descriptive statistics

All participants

Descriptive data for sample.

```

setwd(params$location_of_data)

data_df <-
  read.csv("processed data/wide all tasks data.csv") %>%
  mutate(gender = as.factor(gender))

colnames(data_df)

## [1] "participant"
## [2] "condition"
## [3] "IAT_condition"
## [4] "block_order"
## [5] "task_order"
## [6] "gender"
## [7] "age"
## [8] "mean_rating"
## [9] "IAT_D1"
## [10] "IAT_mean_RT"
## [11] "IAT_perc_acc"
## [12] "IAT_exclude_based_on_fast_trials"
## [13] "SCIAT_D1"
## [14] "SCIAT_mean_RT"
## [15] "SCIAT_perc_acc"
## [16] "SCIAT_exclude_based_on_fast_trials"
## [17] "modern_racism_scale_total"

data_df %>% dplyr::count(gender)

## # A tibble: 6 × 2
##   gender      n
##   <fctr> <int>
## 1      24      1
## 2      33      1
## 3 female    48
## 4 feminine   1
## 5      male  101
## 6 nonbinary   1

data_df %>%
  dplyr::select(age) %>%
  psych::describe(fast = TRUE, # subset of descriptive stats
                  ranges = FALSE,
                  trim = 0) %>%
  dplyr::select(-vars, -se)

##      n mean  sd
## age 153 31.93 11.03

```

Sample descriptive statistics

```

passers_df <-
  data_df %>%
  filter(IAT_exclude_based_on_fast_trials == FALSE & SCIAT_exclude_based_on_fast_trials == FALSE)

passers_df %>% dplyr::count(IAT_condition)

```

```
## # A tibble: 2 × 2
##       IAT_condition      n
##       <fctr> <int>
## 1 Flowers-Insects IAT    75
## 2           Race IAT    71

passers_df %>%
  dplyr::select(IAT_mean_RT,
                IAT_perc_acc,
                SCIAT_mean_RT,
                SCIAT_perc_acc) %>%
  psych::describe(fast = TRUE, # subset of descriptive stats
                  ranges = FALSE,
                  trim = 0) %>%
  dplyr::select(-vars, -se)

##           n      mean      sd
## IAT_mean_RT  146 828.19 187.70
## IAT_perc_acc  146   0.93   0.07
## SCIAT_mean_RT 146 692.54 136.30
## SCIAT_perc_acc 146   0.93   0.05
```

H1: Differences in IAT effects between contrast pair conditions

Outlier removal

```
# get data
setwd(params$location_of_data)

# exclude participants who had more than 10% of trials in less than 300ms, and make variables factors
SCIAT_data <-
  read.csv("processed data/long SCIAT data.csv") %>%
  mutate(participant = as.factor(participant),
         block = as.factor(ifelse(block == "compatible", "black-positive",
                                   ifelse(block == "incompatible", "black-negative", NA))),
         IAT_condition = as.factor(IAT_condition)) %>%
  filter(IAT_exclude_based_on_fast_trials == FALSE & SCIAT_exclude_based_on_fast_trials == FALSE)

# exclude outliers
SCIAT_data_outliers_removed <-
  SCIAT_data %>%
  schoRsch::outlier(dv = "rt", # exclude individual RTs that are greater than 2.5 SD from the mean
                   todo="elim",
                   upper.z = 2.5,
                   lower.z = -2.5)

## [1] "Function outlier() has screened 20440 trial(s) in total. Of these were 113 trial(s) identified as outliers"
```

Descriptive statistics

```
SCIAT_summary_data <-
  SCIAT_data_outliers_removed %>%
  group_by(IAT_condition, block) %>%
```

```

dplyr::summarize(mean_rt = round(mean(rt), 0),
                  sd_rt = round(sd(rt), 0),
                  se_rt = round(std.error(rt), 2))

SCIAT_summary_data

## Source: local data frame [4 x 5]
## Groups: IAT_condition [?]
##
##           IAT_condition      block mean_rt sd_rt se_rt
##           <fctr>          <fctr>   <dbl> <dbl> <dbl>
## 1 Flowers-Insects IAT black-negative    671   260   3.59
## 2 Flowers-Insects IAT black-positive    664   265   3.67
## 3 Race IAT black-negative    677   260   3.70
## 4 Race IAT black-positive    688   283   4.02

```

Plots

```

# apa theme for all plots
apatheme <-
  theme_bw() +
  theme(panel.grid.major = element_blank(),
        panel.grid.minor = element_blank(),
        panel.background = element_blank(),
        panel.border = element_blank(),
        #text = element_text(family='Arial'), # doesn't play nice with knitr
        legend.title = element_blank(),
        legend.position = c(.9,.9),
        axis.line.x = element_line(color='black'),
        axis.line.y = element_line(color='black'))

# add a combined condition*IAT block variable for plotting
SCIAT_data_outliers_removed <-
  SCIAT_data_outliers_removed %>%
  mutate(exp_factor = paste(IAT_condition, block, sep = "_"))

```

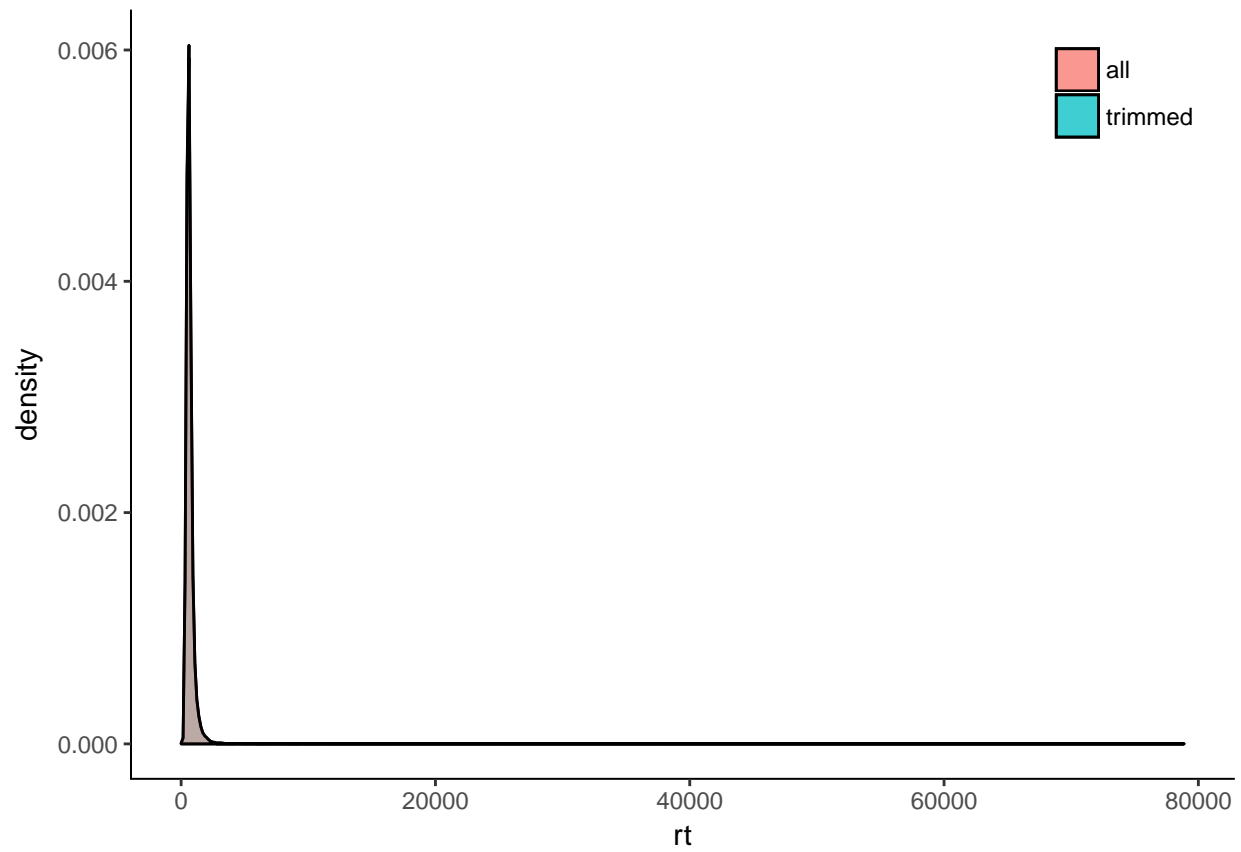
Outlier removal

Distribution of RTs before and after trimming outliers.

```

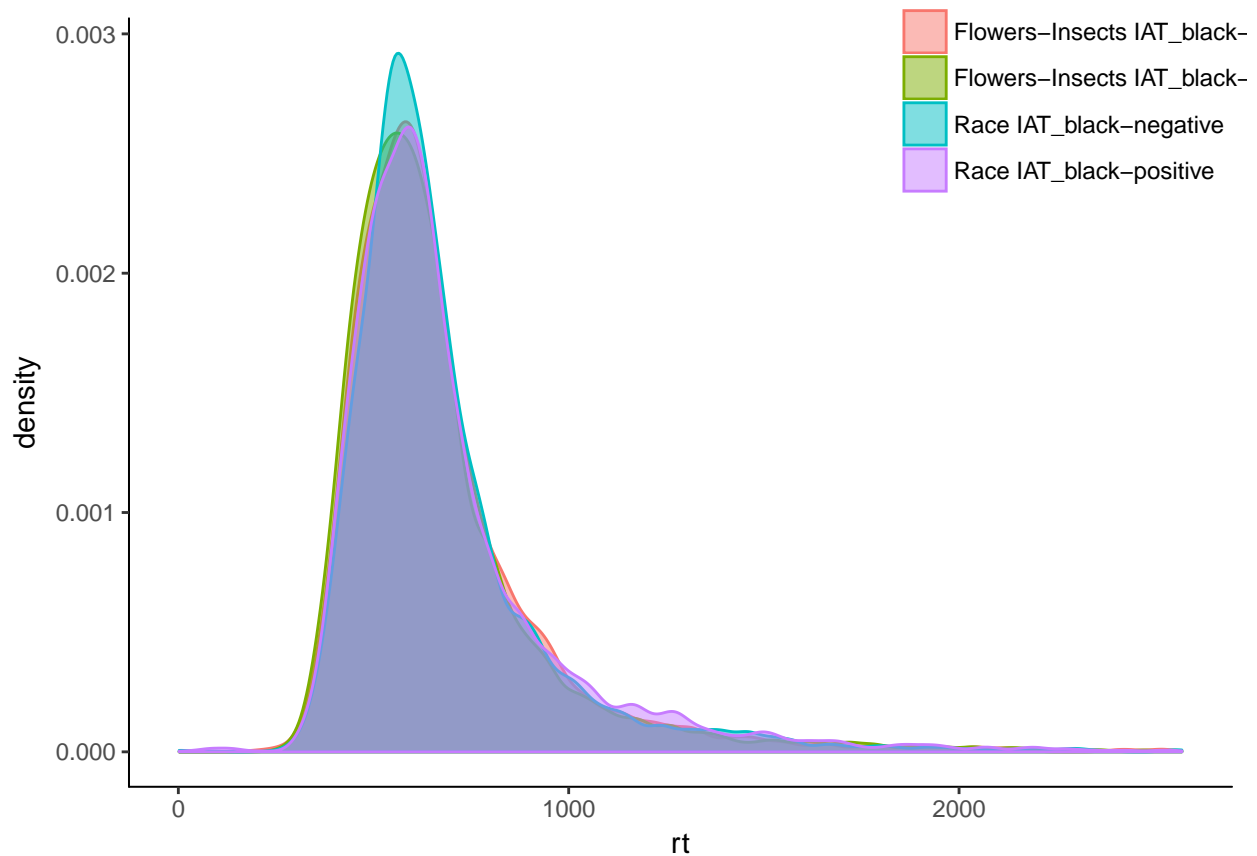
ggplot(data = SCIAT_data_outliers_removed, aes(rt, fill = "trimmed")) +
  geom_density(alpha=0.50) +
  geom_density(data = SCIAT_data,
              aes(rt, fill = "all"),
              alpha=0.50) +
  apatheme

```



Density plot split by factor

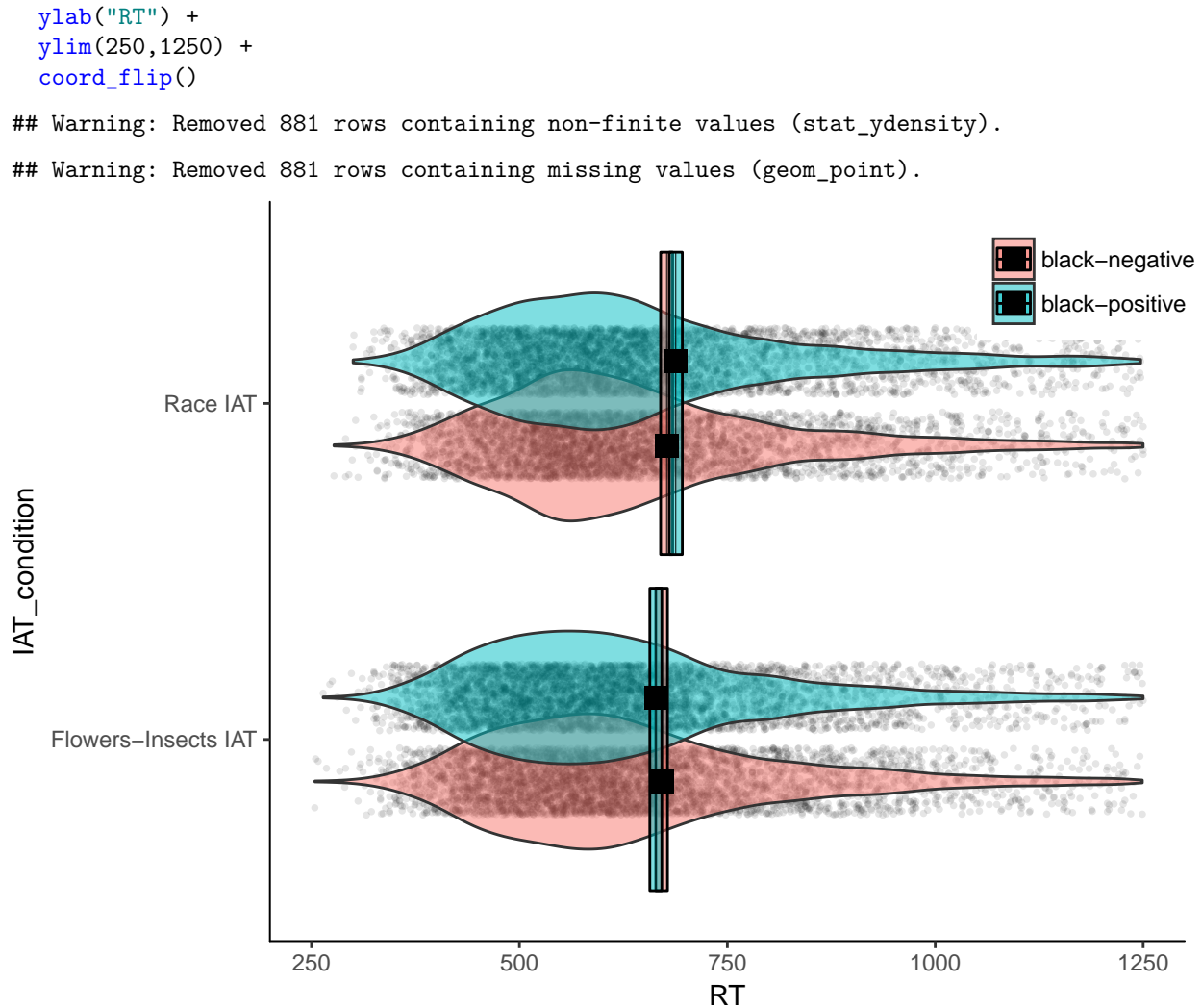
```
ggplot(SCIAT_data_outliers_removed,  
  aes(rt, colour = exp_factor, fill = exp_factor)) +  
  geom_density(alpha=0.50) +  
  apatheme
```



Distribution and inference plot

Black squares are means, horizontal lines are 95% CIs, coloured shapes are distributions. I've chosen to omit presenting jittered raw data as it looks overplotted. NB scale was limited to 250 to 1250ms to make it more informative, although (non-outlier) values extend beyond the visible plot (and are included in the analysis).

```
ggplot(data = SCIAT_summary_data,
  aes(x = IAT_condition, y = mean_rt, fill = block)) +
  geom_point(data = SCIAT_data_outliers_removed,
    aes(x = IAT_condition, y = rt, fill = block),
    size = 1,
    shape = 16,
    alpha = 0.1,
    position = position_jitterdodge(dodge.width = .5)) +
  geom_violin(data = SCIAT_data_outliers_removed,
    aes(x = IAT_condition, y = rt, fill = block),
    alpha = 0.5,
    position = position_dodge(width = .5)) +
  geom_crossbar(aes(ymin = mean_rt + (-1.96*se_rt),
    ymax = mean_rt + (1.96*se_rt)),
    alpha = 0.5,
    fatten = 0) +
  geom_point(size = 4,
    shape = 15,
    position = position_dodge(width = .5)) +
  apatheme +
```

Preregistered hypothesis test

Frequentist mixed linear effects model with participant as a random effect. Entering participant as a random effect acknowledges the non-independence of the multiple data points for each participants. Specifically, allowing for a random intercept allows for differences in general responding speed between participants, therefore controlling for age, IQ, etc., as the *D1* score does. Using a LMM here therefore serves a dual purpose of controlling for within-subject variation (traditionally served by *D1* scoring) and between subject analysis, while making use of all data points rather than collapsing the IAT's 80 RTs into just one score.

Two important considerations:

1. Production of *p* values (over LRs, etc.) is contentious, but cite the following as recent evidence for the use of Kenward Roger method estimation: <http://link.springer.com/article/10.3758%2Fs13428-016-0809-y>
2. No effect sizes are produced due to contention over how to use the random factor error. See <http://stats.stackexchange.com/questions/95054/how-to-get-an-overall-p-value-and-effect-size-for-a-categorical-factor-in-a-mi>

The model is `rt ~ block * IAT_condition + modern_racism_scale_total + (1 | participant)`. That is, RT is predicted by the interaction between SCIAM block and training IAT condition, after controlling for differences in racism, and while allowing for participants to have a random intercept (i.e., variable mean RT).

Our preregistered *a priori* hypothesis, that SCIAT effects would differ between conditions, relates to the interaction effect and not the main effects. We therefore employ type 3 sum of squares and examine only the results of the interaction.

```
# Check that variables that should be factors are indeed factors
sapply(SCIAT_data_outliers_removed, class)

##              participant              block
##              "factor"              "factor"
##              trial_n                rt
##              "integer"            "integer"
##              accuracy              IAT_condition
##              "integer"            "factor"
##              block_order          task_order
##              "factor"            "factor"
##              gender                age
##              "factor"            "integer"
##      modern_racism_scale_total  IAT_exclude_based_on_fast_trials
##              "integer"            "logical"
##  SCIAT_exclude_based_on_fast_trials
##              "logical"            "numeric"
##              zscores              exp_factor
##              "numeric"            "character"

# LME analysis
model_1 <- afex::mixed(rt ~ block * IAT_condition + modern_racism_scale_total + (1 | participant),
  contrasts = TRUE,
  data = SCIAT_data_outliers_removed,
  type = 3,
  method = "KR",
  progress = TRUE,
  return = "mixed")

## Fitting 5 (g)lmer() models:
## [.....]
## Obtaining 4 p-values:
## [....]

print(model_1)

##              Effect              df F.scaling      F p.value
## 1              block 1, 20179.20      1.00  0.38      .54
## 2              IAT_condition      1, 143.00      1.00  0.80      .37
## 3 modern_racism_scale_total      1, 143.02      1.00  0.25      .62
## 4      block:IAT_condition 1, 20179.20      1.00  6.31 *      .01
```

H2: Differences in self-reported ratings between contrast pair conditions

Descriptive statistics

```
# get data
setwd(params$location_of_data)

# exclude participants who had more than 10% of trials in less than 300ms, and make variables factors
```

```

ratings_data <-
  read.csv("processed data/long ratings data.csv") %>%
  mutate(participant = as.factor(participant),
         IAT_condition = as.factor(IAT_condition)) %>%
  filter(IAT_exclude_based_on_fast_trials == FALSE & SCIAT_exclude_based_on_fast_trials == FALSE)

ratings_summary_data <-
  ratings_data %>%
  group_by(IAT_condition) %>%
  dplyr::summarize(mean_rating = round(mean(rating), 2),
                  sd_rating = round(sd(rating), 2),
                  se_rating = round(std.error(rating), 2))

ratings_summary_data
## # A tibble: 2 × 4
##       IAT_condition mean_rating sd_rating se_rating
##       <fctr>         <dbl>      <dbl>    <dbl>
## 1 Flowers-Insects IAT      4.26      1.03     0.05
## 2 Race IAT          4.21      1.14     0.06

```

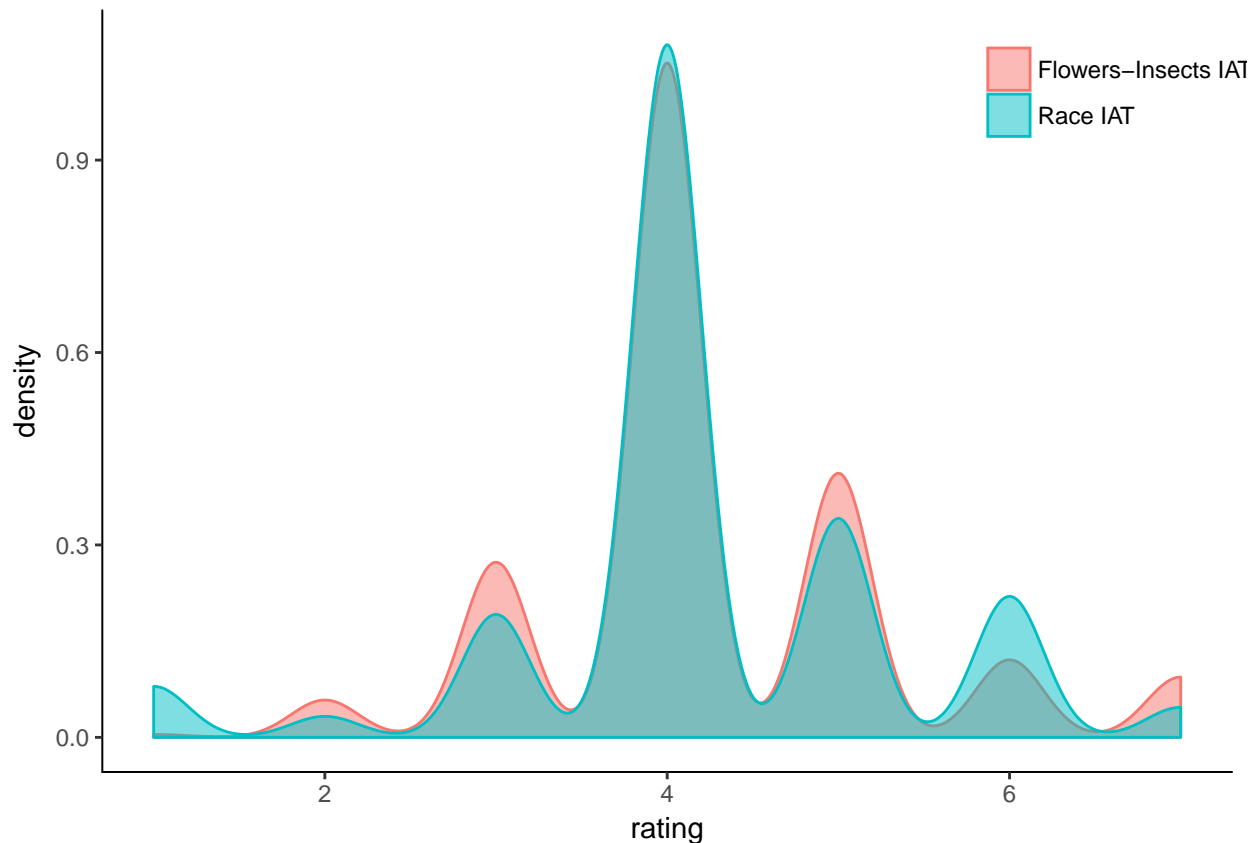
Plots

Density plot split by factor

```

ggplot(ratings_data,
       aes(rating, colour = IAT_condition, fill = IAT_condition)) +
  geom_density(alpha=0.50) +
  apatheme

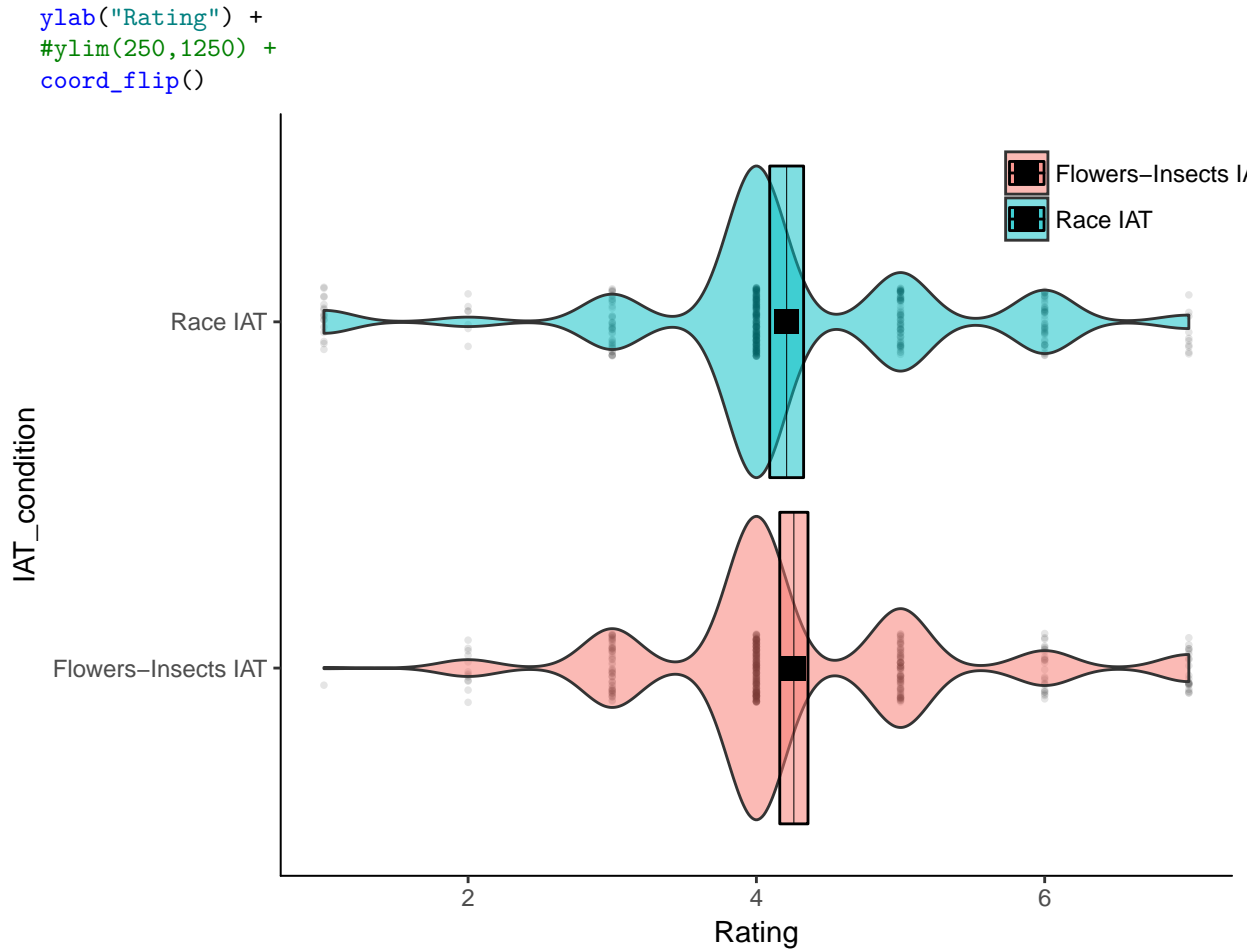
```



Distribution and inference plot

Black squares are means, horizontal lines are 95% CIs, coloured shapes are distributions. I've chosen to omit presenting jittered raw data as it looks overplotted. NB scale was limited to 250 to 1250ms to make it more informative, although (non-outlier) values extend beyond the visible plot (and are included in the analysis).

```
ggplot(data = ratings_summary_data,
  aes(x = IAT_condition, y = mean_rating, fill = IAT_condition)) +
  geom_point(data = ratings_data,
    aes(x = IAT_condition, y = rating, fill = IAT_condition),
    size = 1,
    shape = 16,
    alpha = 0.1,
    position = position_jitterdodge(dodge.width = .5)) +
  geom_violin(data = ratings_data,
    aes(x = IAT_condition, y = rating, fill = IAT_condition),
    alpha = 0.5,
    position = position_dodge(width = .5)) +
  geom_crossbar(aes(ymin = mean_rating - (1.96*se_rating),
    ymax = mean_rating + (1.96*se_rating)),
    alpha = 0.5,
    fatten = 0) +
  geom_point(size = 4,
    shape = 15,
    position = position_dodge(width = .5)) +
  apatheme +
```



Preregistered hypothesis test

Frequentist mixed linear effects model with participant as a random effect. Entering participant as a random effect acknowledges the non-independence of the multiple data points for each participants. Specifically, allowing for a random intercept allows for differences in general responding speed between participants, therefore controlling for age, IQ, etc., as the *D1* score does. Using a LMM here therefore serves a dual purpose of controlling for within-subject variation (traditionally served by *D1* scoring) and between subject analysis, while making use of all data points rather than collapsing the IAT's 80 RTs into just one score.

Two important considerations:

1. Production of *p* values (over LRs, etc.) is contentious, but cite the following as recent evidence for the use of Kenward Roger method estimation: <http://link.springer.com/article/10.3758%2Fs13428-016-0809-y>
2. No effect sizes are produced due to contention over how to use the random factor error. See <http://stats.stackexchange.com/questions/95054/how-to-get-an-overall-p-value-and-effect-size-for-a-categorical-factor-in-a-mi>

The model is `rating ~ IAT_condition + (1 | participant)`. That is, rating is predicted by training IAT condition, after controlling for racism and while allowing participants to have a random intercept (i.e., acknowledging the non-independence of participants ratings of the images).

Our preregistered *a priori* hypothesis, that ratings would differ between conditions, relates to the main effect for IAT_condition. We therefore examine only the results of this main effect.

```

# Check that variables that should be factors are indeed factors
sapply(ratings_data, class)

##           participant           trial_n
##           "factor"           "integer"
##           rating           IAT_condition
##           "integer"           "factor"
##           block_order           task_order
##           "factor"           "factor"
##           gender           age
##           "factor"           "integer"
##           modern_racism_scale_total   IAT_exclude_based_on_fast_trials
##           "integer"           "logical"
##           SCIAT_exclude_based_on_fast_trials
##           "logical"

# LME analysis
model_1 <- afex::mixed(rating ~ IAT_condition + modern_racism_scale_total + (1 | participant),
                      contrasts = TRUE,
                      data = ratings_data,
                      type = 3,
                      method = "KR",
                      progress = TRUE,
                      return = "mixed")

## Fitting 3 (g)lmer() models:
## [...]
## Obtaining 2 p-values:
## [...]

print(model_1)

##           Effect      df F.scaling      F p.value
## 1           IAT_condition 1, 143      1.00    0.46    .50
## 2 modern_racism_scale_total 1, 143      1.00 35.29 *** <.0001

```