Still suspicious: The suspicious coincidence effect revisited

Supplementary Information

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Contents

This document was created from an R markdown file. The manuscript itself was also produced from an R markdown file, and all analyses presented in the paper can be reproduced from that document (https://github.com/mllewis/XTMEM/blob/master/paper/xtmem.Rmd). The SI can be viewed interactively online at https://mlewis.shinyapps.io/xtmem_SI/.

View experiments

To directly view an experiment, select an experiment from the dropdown menu, and click the "View Experiment" button. The experiment will open in a new window.

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Effect size calculation

The classical Cohen's d measure was originally developed for between-subject designs and, as such, researchers have adapted the measure to within-subject designs in a variety of ways (http://jakewestfall.org/blog/index.php/category/effect-size/). We calculate our effect sizes using the "classic" Cohen's d formula, which takes the mean difference between conditions divided by the pooled standard deviation. Note that because this

method does not take into account the fact that the means are within-subject, these are conservative estimates of effect size (since within-subject designs have more power). We use the `mes` function from the `compute.es` package (AC Del Re, 2013) to calculate our effect sizes

Here is an example calculation of the effect size for Exp. 1. We first get the means and variances across participants of the proportion basic selections for the 1 subordinate and 3 subordinate conditions.

```
# this data has been pre-processed with analysis/munge_anonymize_data.R script
all_d <- read_csv("data/anonymized_data/all_data_munged_A.csv") %>%
           mutate(condition = fct_recode(condition,
                                         "1 sub." = "one",
                                         "3 basic"= "three_basic",
                                         "3 sub." = "three_subordinate",
                                         "3 super." = "three_superordinate",
                                         "3 basic" = "3bas",
                                         "3 super." = "3sup",
                                         "3 sub." = "3sub"),
                  condition = fct_relevel(condition, "1 sub.", "3 sub.",
                                         "3 basic", "3 super."))

## key to experiment factors
exp_key <- read_csv("data/experiment_key.csv") %>%
              mutate(order = gsub("\"", "", order),
                     exp = as.integer(exp)
) %>%
              select(-preregistered)
```

```
es_1_calc <- all_d %>%
      left_join(exp_key %>% select(exp, exp_recoded)) %>%
      filter(exp_recoded == 1) %>% # we only want exp 1
      filter(condition == "1 sub." | condition == "3 sub.") %>% #  conds relevant for d
      gather(variable, value, c(prop_sub, prop_bas, prop_sup)) %>%
      filter(variable == "prop_bas") %>% # we only care about this DV for calculating d
      group_by(condition, subids) %>%
      summarize(value = mean(value)) %>% # get the mean for each subjects across trials
      group_by(condition) %>%
      summarize(mean_prop_bas = mean(value),
                var_prop_bas = var(value)) # get the mean for each condition acros subjects


kable(es_1_calc, digits = 2, col.names = c("Condition", "Mean", "Var"))
```

Condition	Mean	Var
1 sub.	0.64	0.15
3 sub.	0.18	0.09

We then calculate Cohen's d as follows:

$$\begin{aligned} d &= \frac{M_1 - M_2}{\sigma_{pooled}} \\ &= \frac{M_{1sub} - M_{3sub}}{\sqrt{(\frac{var_{1sub} + var_{3sub}}{2})}} \\ &= \frac{.64 - .18}{\sqrt{(\frac{.15 + .09}{2})}} \\ &\approx 1.32 \end{aligned}$$

For Exp. 1, we calculate Cohen's $d = 1.32$.

Results for all conditions and measures

In the Main Text, we report the proportion basic level selections for two training conditions, one-subordinate and three-subordinate. Here we report the data for all four conditions and all three dependent measures (proportion basic level, subordinate level, and superordinate level selections).

```
all_plot_data <- all_d %>%
  gather(variable, value, c(prop_sub, prop_bas, prop_sup)) %>%
  group_by(exp, condition, variable) %>%
  mutate(value = as.numeric(value)) %>%
  multi_boot_standard(col = "value")  %>%
  ungroup() %>%
  mutate(variable = as.factor(variable),
         variable = fct_recode(variable, "basic" = "prop_bas",
                                         "subordinate"= "prop_sub",
                                         "superordinate" = "prop_sup")) %>%
  left_join(exp_key %>% select(exp, exp_recoded))
```

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Timing = presentation timing (sequential or simultaneous); Order = relative ordering of 1 and 3 subordinate trials; Blocking = trials blocked by category or pseudo-random; Label = same or different label in 1 and 3 trials; Ranges are 95% confidence intervals.

By category analyses

In the Main Text, we report our analyses collapsed across all three stimulus categories (animals, vehicles and vegetables). Here we present the effect sizes for each experiment separately for the different stimulus categories. While there is some variability in effect size by category (the effect is generally larger for animals), this variability is small relative to the effect of condition order.

```
# remap condition values and select relevant conditions
all_d_clean <- all_d %>%
      mutate(condition = as.factor(condition)) %>%
      filter(condition == "1 sub." | condition == "3 sub.") %>%
      select(exp, everything())

all_ms_subj_cat <- all_d_clean %>%
  left_join(exp_key %>% select(exp, exp_recoded)) %>%
```

```
  select(-exp) %>%
  gather(variable, value, c(prop_sub, prop_bas, prop_sup))  %>%
  group_by(condition, category, variable, exp_recoded, subids) %>%
  mutate(value = as.numeric(value)) %>%
  summarize(value = mean(value)) %>%
filter(variable == 'prop_bas') %>%
  spread(condition, value) %>%
  ungroup()  %>%
  select(-variable)

LF_means_cat <- all_ms_subj_cat %>%
  group_by(exp_recoded, category) %>%
  summarize(m_one = mean(`1 sub.`),
            sd_one = sd(`1 sub.`),
            m_3sub = mean(`3 sub.`),
            sd_3sub = sd(`3 sub.`),
            n = n())

LF_effect_sizes_cat <- LF_means_cat %>%
  ungroup() %>%
  do(data.frame(d = mes(.$m_one, .$m_3sub, .$sd_one,
                        .$sd_3sub, .$n, .$n, verbose = F)$d,
                d_var = mes(.$m_one, .$sd_3sub, .$sd_one,
                            .$sd_3sub, .$n, .$n, verbose = F)$var.d)) %>%
  mutate(high = d + (1.96*d_var),
         low = d - (1.96*d_var),
         es_type = "nonpaired",
         exp_recoded = LF_means_cat$exp_recoded,
         category = LF_means_cat$category)
```

Shiny applications not supported in static R Markdown documents

Timing = presentation timing (sequential or simultaneous); Order = relative ordering of 1 and 3 subordinate trials; Blocking = trials blocked by category or pseudo-random; Label = same or different label in 1 and 3 trials; Ranges are bootstrapped 95% confidence intervals.

Repeat participants excluded

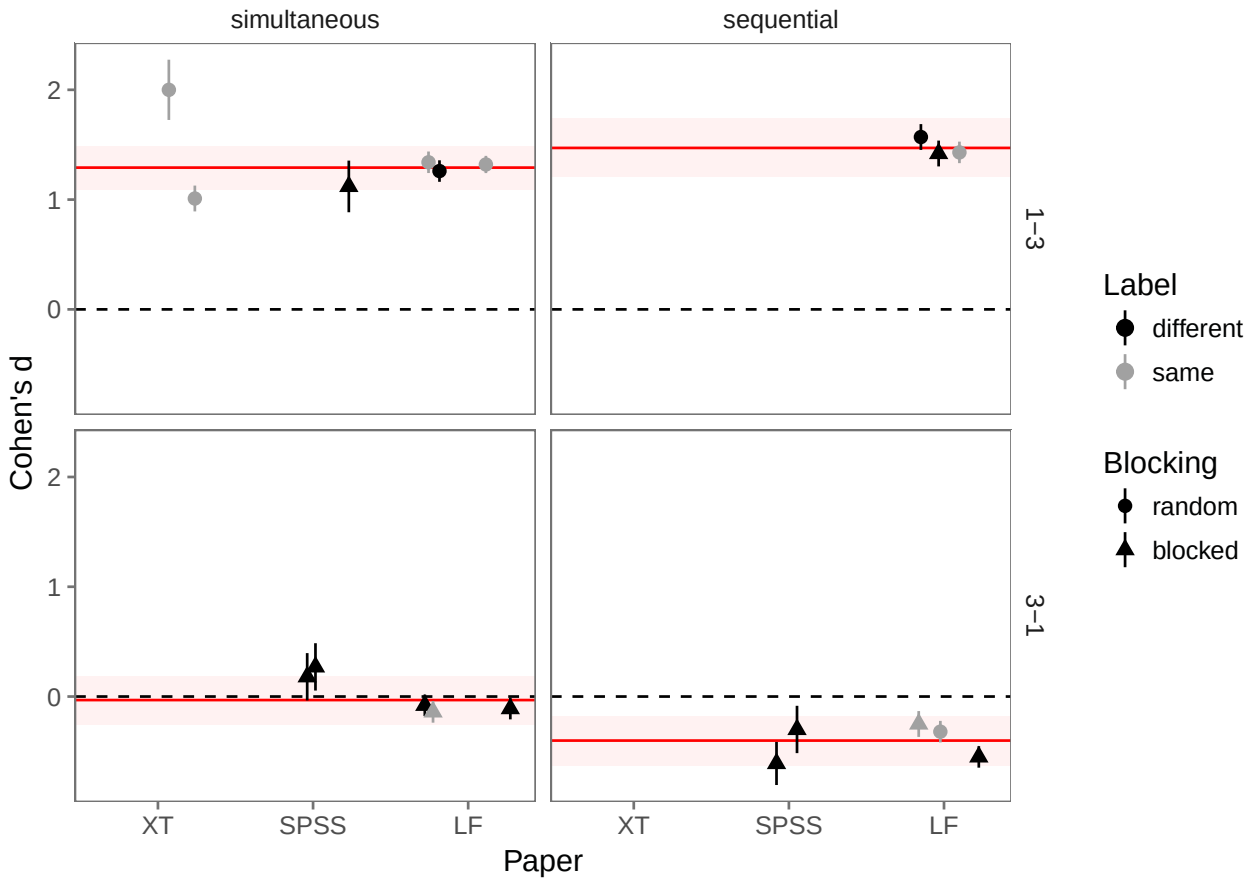
```
all_d_filtered <- read_csv("data/anonymized_data/no_dups_data_munged_A.csv")  %>%
    mutate(condition = as.factor(condition),
             condition = fct_recode(condition,
                                    three_basic = "3bas",
                                    three_subordinate = "3sub",
                                    three_superordinate = "3sup")) %>%
      filter(condition == "one" | condition == "three_subordinate") %>%
      select(exp, everything())
# this file has been pre-processed with analysis/munge_anonymize_data_no_dups.R script

n_unique <- all_d_filtered %>%
  distinct(exp, subids) %>%
  summarize(n = n())
```

```r
n_total <- all_d %>%
  distinct(exp, subids) %>%
  summarize(n = n())

percent_duplicates <- round((n_total-n_unique)/n_total, 2) * 100
```

13% of all participants (N = 600) completed more than one experiment. The data reported in the Main Text include all participants. Below we plot the effect sizes with participants excluded who had already participated in a prior experiment (effect size estimates from XT and SPSS are also included for reference). The overall pattern looks the same as with all participants.

```r
all_ms_subj <- all_d_filtered %>%
  left_join(exp_key %>% select(exp, exp_recoded)) %>%
  select(-exp) %>%
  gather(variable, value, c(prop_sub, prop_bas, prop_sup)) %>%
  group_by(condition,variable, exp_recoded, subids) %>%
  mutate(value = as.numeric(value)) %>%
  summarize(value = mean(value)) %>%
  filter(condition == "one" | condition == "three_subordinate",
         variable == 'prop_bas') %>%
  spread(condition, value)

  # means across participants (condition means)
LF_means_wide <- all_ms_subj %>%
  group_by(exp_recoded) %>%
  summarize(m_one = mean(one),
            sd_one = sd(one),
            m_3sub = mean(three_subordinate),
            sd_3sub = sd(three_subordinate),
            n = n())

LF_effect_sizes <- LF_means_wide %>%
  do(data.frame(d = compute.es::mes(.$m_one, .$m_3sub, .$sd_one,
                      .$sd_3sub, .$n, .$n, verbose = F)$d,
                d_var = compute.es::mes(.$m_one, .$sd_3sub, .$sd_one,
                     .$sd_3sub, .$n, .$n, verbose = F)$var.d)) %>%
  mutate(high = d + (1.96*d_var),
         low = d - (1.96*d_var),
         es_type = "nonpaired",
         exp_recoded = LF_means_wide$exp_recoded) %>%
  left_join(LF_means_wide %>% select(exp_recoded, n)) %>%
  select(exp_recoded, n, everything())

literature_effect_sizes <- read_csv("data/literature_ES.csv")
# see ../../analysis/get_literature_ES.R

all_es <- literature_effect_sizes %>%
            bind_rows(LF_effect_sizes) %>%
            left_join(exp_key) %>%
            mutate(source = ifelse(str_detect(exp_recoded, "XT"), "XT2007a",
                                   ifelse(str_detect(exp_recoded, "SPSS"), "SPSS2011", "LF")),
                   source = fct_relevel(source, "XT2007a","SPSS2011","LF"),
                   source = as.numeric(source),
                   timing = fct_relevel(timing,"simultaneous", "sequential"))
```

```r
seq13 <- rma(d, d_var, dat = filter(all_es, timing == "sequential", order == "1-3"))
seq31 <- rma(d, d_var, dat = filter(all_es, timing == "sequential", order == "3-1"))
sim13 <- rma(d, d_var, dat = filter(all_es, timing == "simultaneous", order == "1-3"))
sim31 <- rma(d, d_var, dat = filter(all_es, timing == "simultaneous", order == "3-1"))

ma_es <- data.frame(order = c("1-3", "3-1", "1-3", "3-1"),
           timing = c("sequential", "sequential", "simultaneous", "simultaneous"),
           d = c(seq13$b[[1]], seq31$b[[1]], sim13$b[[1]], sim31$b[[1]]),
           d_low = c(seq13$ci.lb[[1]], seq31$ci.lb[[1]], sim13$ci.lb[[1]], sim31$ci.lb[[1]]),
           d_high = c(seq13$ci.ub[[1]], seq31$ci.ub[[1]], sim13$ci.ub[[1]], sim31$ci.ub[[1]]))

ggplot(all_es) +
  geom_rect(aes(xmin = -Inf, xmax = Inf, ymin = d_low, ymax = d_high),
            fill = "red", alpha = 0.05, inherit.aes = FALSE, data = ma_es) +
  geom_hline(aes(yintercept = d), data = ma_es, color = "red") +
  scale_color_manual(values = c("black", "grey63")) +
  geom_pointrange(aes(x = jitter(source, 1.4),  y = d, ymax = high,
                      ymin = low, color = one_3sub_label, shape = fct_rev(blocking)),
                  size = .5) +
  geom_hline(yintercept = 0, linetype = 2, color = "black") +
  facet_grid(order ~ timing) +
  scale_x_continuous(breaks = c(1:3), limits = c(.6, 3.3),
                     labels = c("XT","SPSS","LF")) +
  ylab("Cohen's d") +
  xlab("Paper") +
  guides(color = guide_legend("Label"),
         shape = guide_legend("Blocking"))  +
  ggthemes::theme_few()
```



Below is the meta-analytical model presented in the Main Text for the sample with repeat-participants excluded. The pattern is the same as for the full sample.

```
mod <- metafor::rma(d ~ timing + order + one_3sub_label + blocking, d_var, dat = all_es)

mod_df <- data.frame(fixed_effect = c("Intercept",
                                      "Simultaneous vs. sequential timing",
                                      "1-3 vs. 3-1 trial order",
                                      "Different vs. same label",
                                      "Blocked vs. pseudo-random trial structure"),
                     beta_string = paste0(round(mod$beta, 2),
                                          " [", round(mod$ci.lb, 2), ", "
                                        , round(mod$ci.ub,2) , "]"),
                     zval = mod$zval,
                     pval_string = round(mod$pval, 2)) %>%
          mutate(pval_string = ifelse(pval_string == 0, "<.0001", pval_string))

# MA model table

kable(mod_df, caption = "Meta-analytic model with manipulations as fixed effects.",
      align = c('l', 'r', 'r', 'r'), digits = 2,
      col.names = c("Fixed effect", "beta", "z-value", "p-value")) %>%
      kable_styling(font_size = 12)
```

Table 2: Meta-analytic model with manipulations as fixed effects.

Fixed effect	beta	z-value	p-value
Intercept	1.42 [1.1, 1.73]	8.76	<.0001
Simultaneous vs. sequential timing	-0.11 [-0.34, 0.12]	-0.95	0.34
1-3 vs. 3-1 trial order	-1.56 [-1.89, -1.23]	-9.31	<.0001
Different vs. same label	-0.03 [-0.3, 0.24]	-0.23	0.82
Blocked vs. pseudo-random trial structure	0 [-0.38, 0.37]	-0.02	0.99

Demographics

Below we report the demographic characteristics (education, language, gender, and age) of our full sample (N = 600).

```
raw_d <- read_csv("data/anonymized_data/all_raw_A.csv")

raw_d_munged <- raw_d %>%
  left_join(exp_key %>% select(exp, exp_recoded, timing)) %>%
  mutate(exp_recoded = fct_relevel(exp_recoded, "10", after = 11),
         exp_recoded = fct_relevel(exp_recoded, "11", after = 11),
         exp_recoded = fct_relevel(exp_recoded, "12", after = 11)) %>%
  select(-exp) %>%
  ungroup()
```

Education

```
raw_d_munged %>%
  mutate(education = as.factor(education),
         education = fct_recode(education,
                          "No Response" = "-1",
                          "Some High School" = "0",
                          "Graduated High School" = "1",
                          "Some College"= "2",
                          "Graduated College" = "3",
                          "Hold a higher degree" = "4")) %>%
  group_by(education) %>%
  summarise(n = n()) %>%
  mutate(prop = round(n / sum(n),2)) %>%
  kable()
```

education	n	prop
No Response	2	0.00
Some High School	6	0.01
Graduated High School	83	0.14
Some College	207	0.34
Graduated College	256	0.43
Hold a higher degree	46	0.08

First language

```
raw_d_munged %>%
  mutate(language = tolower(language),
         language = ifelse(substr(language,0,1) == "e", # all e lanuages are english
                           "English", "Other")) %>%
  group_by(language) %>%
    summarise(n = n()) %>%
  mutate(prop = round(n / sum(n),2)) %>%
  kable()
```

language	n	prop
English	589	0.98
Other	10	0.02
NA	1	0.00

Gender

```
raw_d_munged %>%
  group_by(gender) %>%
  summarise(n = n()) %>%
  mutate(prop = round(n / sum(n),2)) %>%
  kable()
```

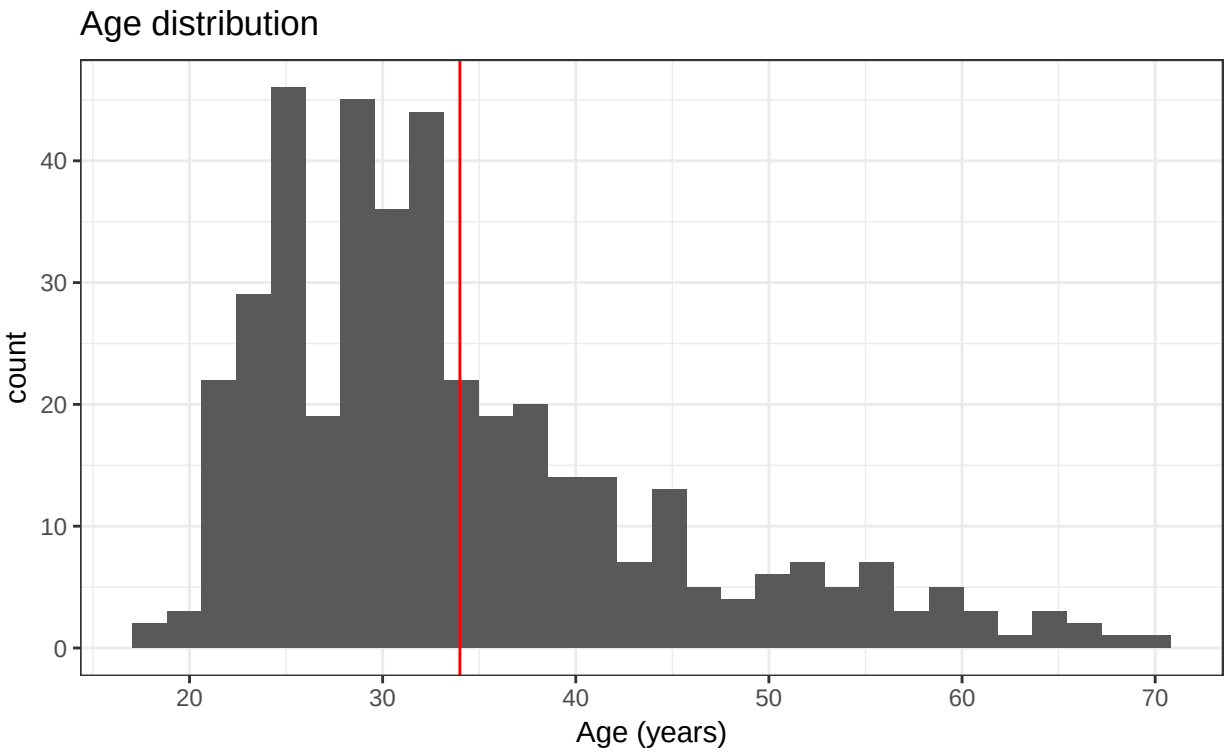
gender	n	prop
Female	179	0.30
Male	225	0.38
Other	1	0.00
NA	195	0.32

Age

```
mean_age <- round(mean(as.numeric(as.character(raw_d_munged$age)), na.rm = T),2)
```

Histogram of participant age. The red line indicates the mean ($M = 34$).

```
raw_d_munged %>%
  mutate(age = ) %>%
  ggplot(aes(x = age)) +
  geom_histogram() +
  geom_vline(aes(xintercept = mean_age),
                 color = "red") +
  xlab("Age (years)") +
  theme_bw() +
  ggtitle("Age distribution")
```



Task feedback

These questions were presented to participants after the main task. Their completion was optional.

Enjoyment

```
raw_d_munged %>%
  mutate(enjoyment = as.factor(enjoyment),
         enjoyment = fct_recode(enjoyment,
                        "No Response" = "-1",
                        "Worse than the Average HIT" = "0",
                        "An Average HIT" = "1",
                        "Better than average HIT" = "2")) %>%
  rename(`Did you enjoy the hit?` = "enjoyment") %>%
  group_by(`Did you enjoy the hit?`) %>%
  summarise(n = n()) %>%
  mutate(prop = round(n / sum(n),2)) %>%
  kable()
```

Did you enjoy the hit?	n	prop
No Response	1	0.00
Worse than the Average HIT	7	0.01
An Average HIT	210	0.35
Better than average HIT	382	0.64

Understanding

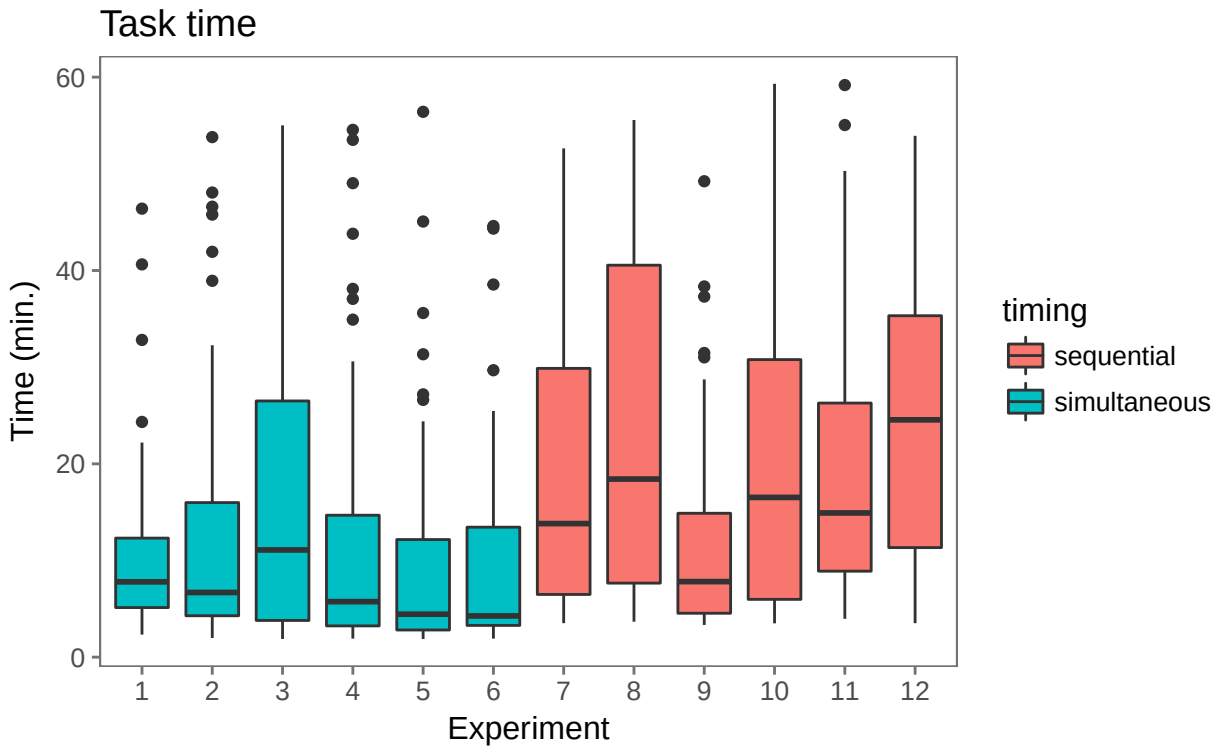
```
raw_d_munged %>%
  mutate(asess = as.factor(asses)) %>%
  rename(`Did you read instructions?` = "asses") %>%
  group_by(`Did you read instructions?`) %>%
  summarise(n = n()) %>%
  mutate(prop = round(n / sum(n),2)) %>%
  kable()
```

Did you read instructions?	n	prop
Confused	15	0.02
No	11	0.02
Yes	372	0.62
NA	202	0.34

Task time

Task times were variable across experiments, but overall shorter for simultaneous timing experiments (green) compared to sequential (pink).

```
# dplyr doesn't play well with dates
raw_d_mungedT <- raw_d_munged

raw_d_mungedT$SubmitTime = gsub("T|Z","",raw_d_mungedT$SubmitTime)
raw_d_mungedT$AcceptTime = gsub("T|Z","",raw_d_mungedT$AcceptTime)
raw_d_mungedT$SubmitTime = strptime(raw_d_munged$SubmitTime, "%F%T")
raw_d_mungedT$AcceptTime = strptime(raw_d_mungedT$AcceptTime, "%F%T")
raw_d_mungedT$total_time = as.numeric(raw_d_mungedT$SubmitTime) -
  as.numeric(raw_d_mungedT$AcceptTime)

ggplot(raw_d_mungedT,
       aes(x = exp_recoded, y = total_time/60, fill = timing)) +
    ylab("Time (min.)") +
    xlab("Experiment") +
    ggtitle("Task time")+
    geom_boxplot() +
    ggthemes::theme_few()
```



References

AC Del Re (2013). compute.es: Compute Effect Sizes. R package version 0.2-2. URL http://cran.r-project.org/web/packages/compute.es.