Task Switching Replication

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Read in and Check Raw Data

```
#Import current data
task_switching_raw <- read.csv(paste0(workingdir,
                                      "/Data/task-switching-replication-recoded-2.csv"))
head(task_switching_raw)
```

```
##   participant session condition  trialType  posture blockNum trialNum switchTrialType
## 1           1       1         1 experiment standing        1        1          buffer
## 2           1       1         1 experiment standing        1        2        noswitch
## 3           1       1         1 experiment standing        1        3          switch
## 4           1       1         1 experiment standing        1        4        noswitch
## 5           1       1         1 experiment standing        1        5        noswitch
## 6           1       1         1 experiment standing        1        6        noswitch
##   congruentTrialType cueType shapeType shapeColor response correctResponse correct reactionTime
## 1        incongruent   solid    square       blue    right            left      no    0.9088130
## 2        incongruent   solid    square       blue     left            left     yes    0.5947349
## 3        incongruent  dashed    square       blue    right           right     yes    0.7084870
## 4        incongruent  dashed    square       blue    right           right     yes    0.5995200
## 5          congruent  dashed    square     yellow    right           right     yes    0.4399409
## 6          congruent  dashed    square     yellow    right           right     yes    0.3847258
##                  date    utcTime
## 1 2021-11-10 10:22:00 1636561737
## 2 2021-11-10 10:22:00 1636561744
## 3 2021-11-10 10:22:00 1636561746
## 4 2021-11-10 10:22:00 1636561748
## 5 2021-11-10 10:22:00 1636561750
## 6 2021-11-10 10:22:00 1636561752
```

```
#does every person have 392 trials?
ntrials_sub <- task_switching_raw %>%
  group_by(participant) %>%
  summarize(ntrials = n()) %>%
  pull(ntrials)

all(ntrials_sub == 392)
```

```
## [1] TRUE
```

```
#does every block start with a buffer and have 49 trials?
task_switching_raw <- task_switching_raw %>%
  mutate(condblock = paste0(posture, blockNum))
```

```
blocktrials <- task_switching_raw %>%
  group_by(participant, condblock) %>%
  summarize(ntrials = n(), firsttrial = first(switchTrialType))
```

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

```
all(blocktrials$ntrials == 49)
```

```
## [1] TRUE
```

```
all(blocktrials$firsttrial == "buffer")
```

```
## [1] TRUE
```

Clean Data

```
#Drop buffer trials
task_switching_raw2 <- task_switching_raw %>%
  filter(switchTrialType != "buffer")

#Recode Correct to 1 and Incorrect to 0
task_switching_raw2$correct_bin <- recode(task_switching_raw2$correct,
                                          "no"  = 0,
                                          "yes" = 1)

#Calc overall acc by participant
ts_overall_acc <- task_switching_raw2 %>%
  group_by(participant)  %>%
  summarize(Accuracy    = mean(correct_bin))

#find participants with less than 80% accuracy
#2, 8, 15, 44, 49, 51
#First exclusion criteria
low_acc_subs <- ts_overall_acc %>% filter(Accuracy < 0.80) %>%
  pull(participant)


task_switching_raw3 <- task_switching_raw2 %>%
  filter(!(participant %in% low_acc_subs))

#Calc mean Acc by participant and conditions (posture, con, switch)
#Narrow format
ts_acc_mean <- task_switching_raw3 %>%
  group_by(participant,
           posture,
           congruentTrialType,
           switchTrialType) %>%
  summarize(Accuracy    = mean(correct_bin))
```

```
## `summarise()` has grouped output by 'participant', 'posture', 'congruentTrialType'. You can
## override using the `.groups` argument.
```

```
#Convert data to wide format (for statview/SPSS/etc)
ts_acc_mean_wide <- ts_acc_mean %>%
  pivot_wider(names_from = c(posture,
```

```
                            congruentTrialType,
                            switchTrialType),
              values_from =   Accuracy)

write.csv(ts_acc_mean_wide, file = "output/new_recoded_for_statview.csv", row.names = F)

ts_acc_mean <- data.frame(ts_acc_mean)
ts_acc_mean$posture <- as.factor(ts_acc_mean$posture)
ts_acc_mean$participant <- as.factor(ts_acc_mean$participant)
ts_acc_mean$congruentTrialType <- as.factor(ts_acc_mean$congruentTrialType)
ts_acc_mean$switchTrialType <- as.factor(ts_acc_mean$switchTrialType)
str(ts_acc_mean)
```

```
## 'data.frame':    408 obs. of  5 variables:
##  $ participant       : Factor w/ 51 levels "1","3","4","5",..: 1 1 1 1 1 1 1 1 2 2 ...
##  $ posture           : Factor w/ 2 levels "sitting","standing": 1 1 1 1 2 2 2 2 1 1 ...
##  $ congruentTrialType: Factor w/ 2 levels "congruent","incongruent": 1 1 2 2 1 1 2 2 1 1 ...
##  $ switchTrialType   : Factor w/ 2 levels "noswitch","switch": 1 2 1 2 1 2 1 2 1 2 ...
##  $ Accuracy          : num  0.96 0.978 0.957 0.88 0.981 ...
```

```
#Total N = 51 (6 dropped for total acc < 80%)
length(unique(ts_acc_mean$participant))
```

```
## [1] 51
```

Summarize Demographics

```
demo_raw <- read.csv(paste0(workingdir, "/Data/Task Switching_February 24, 2022_13.05.csv"),
                     skip = 1) %>%
  slice(-1) %>%
  select(-c(Response.Type,IP.Address, Recipient.Last.Name:Distribution.Channel))
colnames(demo_raw)[10:15] <- c("Gender.Pick", "Gender.Text","Age","Race.Pick","Race.Text","Eng.First")

dim(demo_raw)
```

```
## [1] 59 15
```

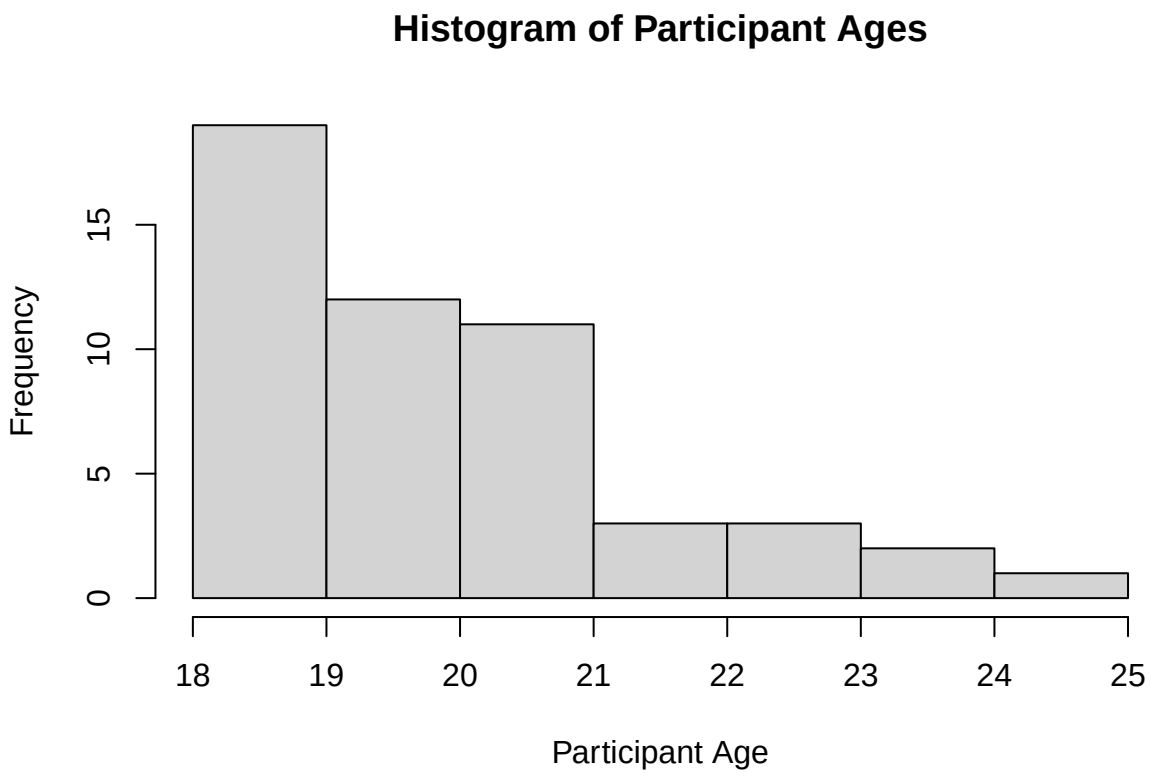
```
#59 records
#first two are test data
# need to match up the 6 dropped participants from behavioral data
demo_df <- demo_raw %>%
  filter(!(X %in% c("test", low_acc_subs)))
dim(demo_df)
```

```
## [1] 51 15
```

```
demo_df <- demo_df %>%
  mutate(Gender.New = ifelse(Gender.Pick %in% c("Man","Woman"), Gender.Pick, Gender.Text),
         Eng.First = toupper(Eng.First))

#gender breakdown
gender_table <- demo_df %>%
  group_by(Gender.New) %>%
  summarize(n = n())
gender_table
```

```
## # A tibble: 3 x 2
##   Gender.New      n
##   <chr>       <int>
## 1 Man            23
## 2 non binaary     1
## 3 Woman          27
```

```
#age breakdown
hist(as.numeric(demo_df$Age),
     main = "Histogram of Participant Ages",
     xlab = "Participant Age")
```




```
age_table <- demo_df %>%
  group_by(Age) %>%
  summarize(n = n())
age_table
```

```
## # A tibble: 8 x 2
##   Age       n
##   <chr> <int>
## 1 18        9
## 2 19       10
## 3 20       12
## 4 21       11
## 5 22        3
## 6 23        3
## 7 24        2
```

```
## 8 25        1
```

```
#age mean and sd
mean_age <- mean(as.numeric(demo_df$Age))
sd_age <- sd(as.numeric(demo_df$Age))

kable(matrix(c(mean_age, sd_age), nrow = 1), col.names = c("Mean of Age", "SD of Age"))
```

Mean of Age	SD of Age
20.21569	1.73567

```
#race breakdown
race_table <- demo_df %>%
  group_by(Race.Pick) %>%
  summarize(n = n()) %>%
  arrange(desc(n))
race_table
```

```
## # A tibble: 6 x 2
##   Race.Pick                              n
##   <chr>                              <int>
## 1 White /European American              22
## 2 Black / African American              11
## 3 Hispanic/Latino/Latina/Latinx         11
## 4 Asian /South Pacific Islander          3
## 5 Central Asian /Indian /Pakistani       3
## 6 Native American / American Indian      1
```

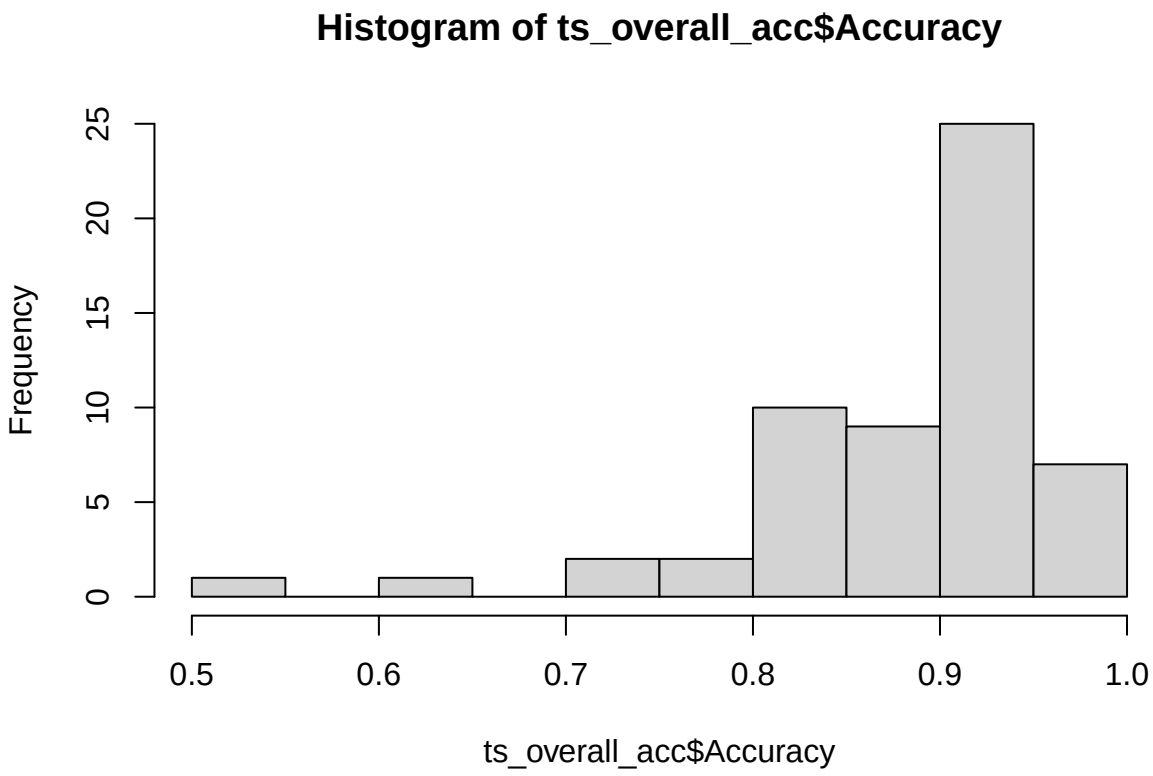
```
#language breakdown
lang_table <- demo_df %>%
  group_by(Eng.First) %>%
  summarize(n=n())
lang_table
```

```
## # A tibble: 2 x 2
##   Eng.First     n
##   <chr>     <int>
## 1 NO            8
## 2 YES          43
```

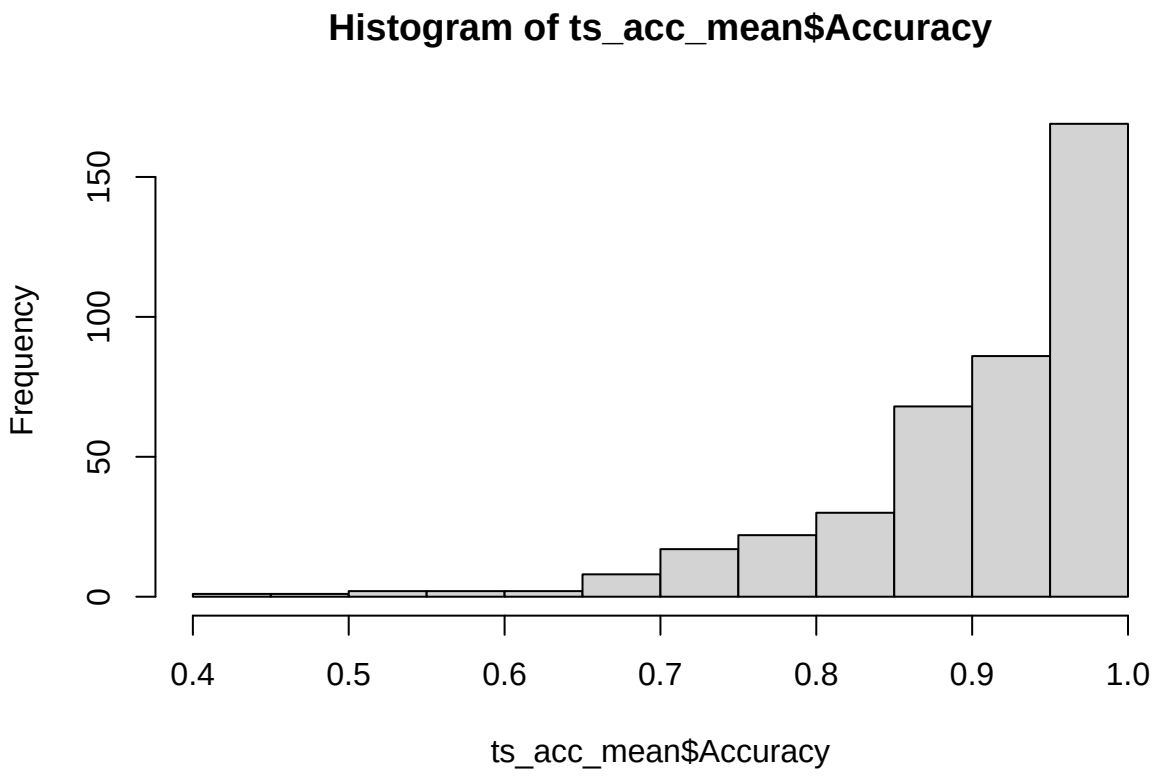
Plots and Analyses

Accuracy

```
#Accuracy by participant, before drops
hist(ts_overall_acc$Accuracy)
```




```
#Accuracy for all cells
hist(ts_acc_mean$Accuracy)
```




```
exp1_anova <- ezANOVA(ts_acc_mean,
                      dv = Accuracy,
                      wid = participant,
                      within = .(posture, congruentTrialType, switchTrialType),
                      type = 3,
                      detailed = TRUE,
                      return_aov = T
)

exp1_anova2 <- aov_ez(data = ts_acc_mean,
                      dv = "Accuracy",
                      id = "participant",
                      within = c("posture", "congruentTrialType", "switchTrialType"),
                      type = 3,
                      anova_table = list(es = "pes")
)

exp1_stats <- ezStats(ts_acc_mean,
                      dv = Accuracy,
                      wid = participant,
                      within = .(posture, congruentTrialType, switchTrialType),
                      type = 3
)
write.csv(exp1_stats[ ,-7], file = "output/Task_Switching_Descriptives_ACC.csv", row.names = F)

#data.frame(exp1_anova$ANOVA)
```

```
output_acc <- aovEffectSize(exp1_anova, effectSize = "pes")
output_acc <- data.frame(output_acc$ANOVA) %>%
  mutate(MSE = c(NA, exp1_anova2$anova_table$MSE), .before = F)
write.csv(output_acc, "output/Task_switching_ANOVA_acc.csv")
output_acc
```

```
##                                       Effect DFn DFd          SSn         SSd         MSE
## 1                                  (Intercept)   1  50 3.331616e+02 0.84392719          NA
## 2                                      posture   1  50 9.386943e-03 0.44204149 0.008840830
## 3                          congruentTrialType   1  50 8.577579e-01 0.43034136 0.008606827
## 4                             switchTrialType   1  50 2.633377e-01 0.14305407 0.002861081
## 5                  posture:congruentTrialType   1  50 1.038526e-04 0.20920092 0.004184018
## 6                     posture:switchTrialType   1  50 1.767731e-03 0.12000107 0.002400021
## 7          congruentTrialType:switchTrialType   1  50 8.851220e-02 0.07573624 0.001514725
## 8 posture:congruentTrialType:switchTrialType   1  50 2.360230e-03 0.09401427 0.001880285
##               F            p p..05         pes
## 1 1.973876e+04 1.301952e-66     * 0.9974733137
## 2 1.061772e+00 3.077703e-01       0.0207938669
## 3 9.966017e+01 1.702444e-13     * 0.6659097700
## 4 9.204131e+01 6.367282e-13     * 0.6479897331
## 5 2.482125e-02 8.754478e-01       0.0004961787
## 6 7.365482e-01 3.948644e-01       0.0145171124
## 7 5.843451e+01 5.925302e-10     * 0.5388921804
## 8 1.255251e+00 2.679047e-01       0.0244901935
```

```
#Calculate confidence interval: PES for posture x switch/condition interaction
#using ANOVA results            (partial eta-squared)
interaction_effect_CI <-
  get.ci.partial.eta.squared(exp1_anova$ANOVA$F[6],
                             exp1_anova$ANOVA$DFn[6],
                             exp1_anova$ANOVA$DFd[6],
                             conf.level = 0.90) #90% CI is the  convention for PES
interaction_effect_CI
```

```
## $LL
## [1] 0
##
## $UL
## [1] 0.1073579
```

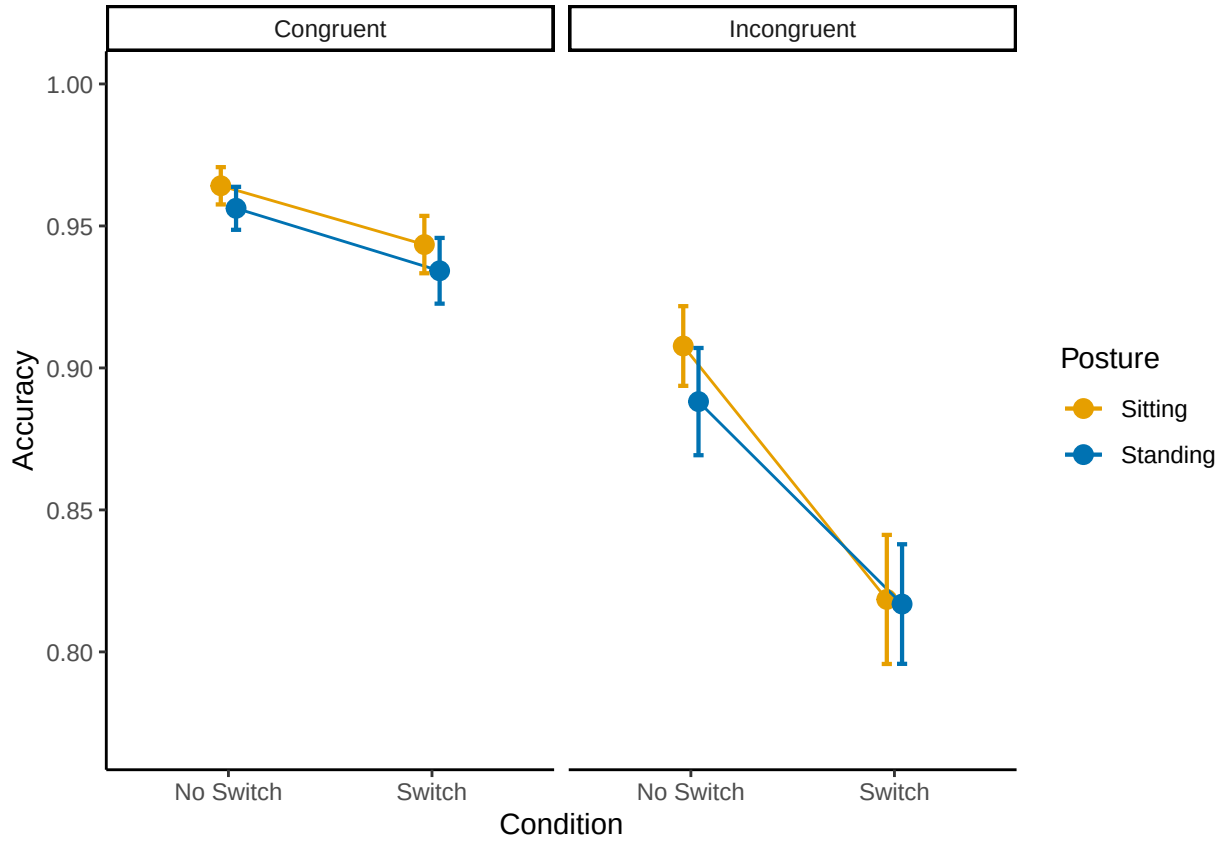
```
congruent.labs <- c("Congruent", "Incongruent")
names(congruent.labs) <- c("1", "2")

#make plot like Smith et al's
acc_plot <-
  superbPlot(ts_acc_mean_wide,
             WSFactors = c("Condition(2)", "Congruent(2)", "Posture(2)"),
             variables = colnames(ts_acc_mean_wide)[2:9],
             errorbar = "SE", #Tempted to change to CI, should stay SE to be consistent with SMith
             plotStyle = "line",
             factorOrder = c("Condition","Posture","Congruent"),
             adjustments = list(purpose = "difference"))+
  theme_classic() +
  ylim(0.77, 1) + #Trying to make ylim same as the Smith w/o cutting off error bars
  facet_wrap(vars(Congruent), labeller = labeller(Congruent = congruent.labs)) +
```

```
  scale_x_discrete(labels=c("1" = "No Switch", "2" = "Switch"))+
  scale_color_manual(values=c("#E69F00", "#0072B2"),
                     labels = c("Sitting", "Standing")) +
  labs(y = "Accuracy")
```

```
## superb::FYI: Here is how the within-subject variables are understood:
```

```
##  Condition Congruent Posture                      variable
##          1         1       1    sitting_congruent_noswitch
##          2         1       1      sitting_congruent_switch
##          1         2       1  sitting_incongruent_noswitch
##          2         2       1    sitting_incongruent_switch
##          1         1       2   standing_congruent_noswitch
##          2         1       2     standing_congruent_switch
##          1         2       2 standing_incongruent_noswitch
##          2         2       2   standing_incongruent_switch
```

```
ggsave(acc_plot,
       file = "plots/acc_plot.pdf",
       units = "in",
       width = 6.62,
       height = 5.50,
       dpi = 600)

acc_plot
```



RT for correct trials only

```
#look at reaction time for correct trials?
ts_correct_only <- task_switching_raw3 %>%
  filter(correct_bin == 1)

ts_rt_mean <- ts_correct_only %>%
  group_by(participant,
           posture,
           congruentTrialType,
           switchTrialType) %>%
  summarize(mean_rt    = mean(reactionTime))
```

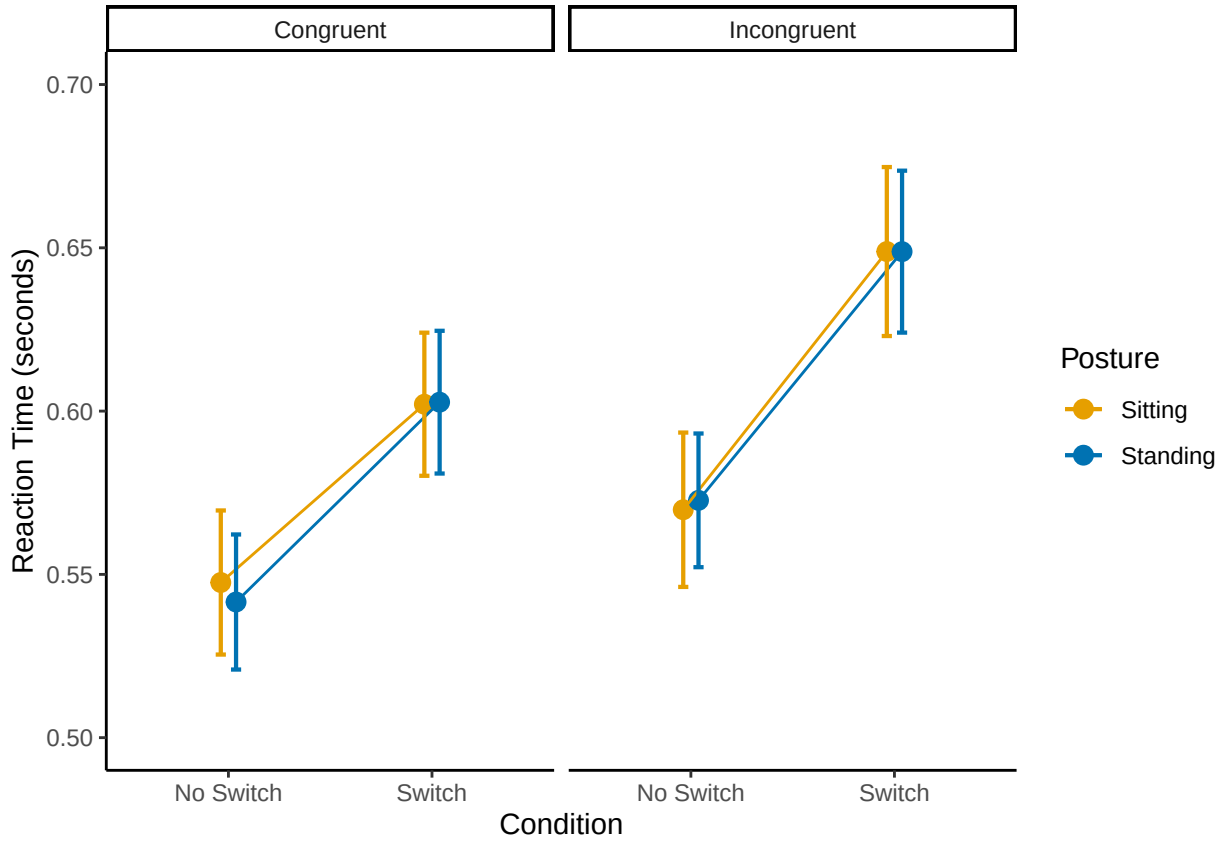
```
## `summarise()` has grouped output by 'participant', 'posture', 'congruentTrialType'. You can
## override using the `.groups` argument.
```

```
#Convert data to wide format
ts_rt_mean_wide <- ts_rt_mean %>%
  pivot_wider(names_from = c(posture,
                             congruentTrialType,
                             switchTrialType),
              values_from =   mean_rt)

RT_plot <-
  superbPlot(ts_rt_mean_wide,
             WSFactors = c("Condition(2)", "Congruent(2)", "Posture(2)"),
             variables = colnames(ts_acc_mean_wide)[2:9],
             errorbar = "SE",
             plotStyle = "line",
             factorOrder = c("Condition","Posture","Congruent"),
             adjustments = list(purpose = "difference"))+
  theme_classic()+
  facet_wrap(vars(Congruent), labeller = labeller(Congruent = congruent.labs)) +
  scale_x_discrete(labels=c("1" = "No Switch", "2" = "Switch")) +
  scale_color_manual(values=c("#E69F00", "#0072B2"), labels = c("Sitting", "Standing")) +
  ylim(0.50, 0.70) +
  labs(y = "Reaction Time (seconds)")
```

```
## superb::FYI: Here is how the within-subject variables are understood:
##  Condition Congruent Posture                      variable
##          1         1       1    sitting_congruent_noswitch
##          2         1       1      sitting_congruent_switch
##          1         2       1  sitting_incongruent_noswitch
##          2         2       1    sitting_incongruent_switch
##          1         1       2   standing_congruent_noswitch
##          2         1       2     standing_congruent_switch
##          1         2       2 standing_incongruent_noswitch
##          2         2       2   standing_incongruent_switch
```

```
ggsave(RT_plot,
       file = "plots/RT_plot.pdf",
       units = "in",
       width = 6.62,
       height = 5.50,
       dpi = 600)
```

```
RT_plot
```




```
exp1_anova_rt <- ezANOVA(ts_rt_mean,
                         dv = mean_rt,
                         wid = participant,
                         within = .(posture, congruentTrialType, switchTrialType),
                         type = 3,
                         detailed = TRUE,
                         return_aov = T
)
```

```
## Warning: Converting "participant" to factor for ANOVA.
```

```
## Warning: Converting "posture" to factor for ANOVA.
```

```
## Warning: Converting "congruentTrialType" to factor for ANOVA.
```

```
## Warning: Converting "switchTrialType" to factor for ANOVA.
```

```
exp1_anova_rt2 <- aov_ez(data = ts_rt_mean,
                         dv = 'mean_rt',
                         id = 'participant',
                         within = c('posture', 'congruentTrialType', 'switchTrialType'),
                         type = 3
)

exp1_stats_rt <- ezStats(ts_rt_mean,
                         dv = mean_rt,
```

```
                          wid = participant,
                          within = .(posture, congruentTrialType, switchTrialType),
                          type = 3
)
```

```
## Warning: Converting "participant" to factor for ANOVA.
```

```
## Warning: Converting "posture" to factor for ANOVA.
```

```
## Warning: Converting "congruentTrialType" to factor for ANOVA.
```

```
## Warning: Converting "switchTrialType" to factor for ANOVA.
```

```
write.csv(exp1_stats_rt[ ,-7],
          file = "output/Task_Switching_Descriptives_RT.csv", row.names = F)

#data.frame(exp1_anova$ANOVA)
output_rt <- aovEffectSize(exp1_anova_rt, effectSize = "pes")
output_rt <- data.frame(output_rt$ANOVA) %>%
  mutate(MSE = c(NA, exp1_anova_rt2$anova_table$MSE), .before = F)
write.csv(output_rt, "output/Task_switching_ANOVA_RT.csv")
output_rt
```

```
##                                     Effect DFn DFd          SSn        SSd          MSE
## 1                              (Intercept)   1  50 1.428705e+02 4.29367155           NA
## 2                                  posture   1  50 3.979595e-05 0.43347417 0.0086694834
## 3                        congruentTrialType   1  50 1.363938e-01 0.14478068 0.0028956136
## 4                           switchTrialType   1  50 4.682022e-01 0.16485963 0.0032971927
## 5                 posture:congruentTrialType   1  50 4.266607e-04 0.06545830 0.0013091659
## 6                    posture:switchTrialType   1  50 8.700576e-05 0.05211061 0.0010422122
## 7         congruentTrialType:switchTrialType   1  50 9.914733e-03 0.04607197 0.0009214393
## 8 posture:congruentTrialType:switchTrialType   1  50 5.769395e-04 0.06995820 0.0013991640
##              F            p p..05          pes
## 1 1.663733e+03 4.809845e-40     * 9.708239e-01
## 2 4.590349e-03 9.462532e-01       9.179855e-05
## 3 4.710359e+01 9.823661e-09     * 4.850860e-01
## 4 1.420003e+02 3.195952e-16     * 7.395837e-01
## 5 3.259027e-01 5.706388e-01       6.475845e-03
## 6 8.348180e-02 7.738279e-01       1.666853e-03
## 7 1.076005e+01 1.893419e-03     * 1.770909e-01
## 8 4.123459e-01 5.237146e-01       8.179462e-03
```

Generate RT analysis/plots for trimmed data

```
#Second exclusion criteria (should this be moved up?)
#How many trials faster than 100 ms? Only a single one
sum(ts_correct_only$reactionTime < 0.100)
```

```
## [1] 1
```

```
dim(ts_correct_only)
```

```
## [1] 17699    20
```

```
too.fast.gone <- ts_correct_only %>% filter(reactionTime >= 0.100)
#Sanity check, one trial is dropped. Now have 17,698 trials
dim(too.fast.gone)
```

```
## [1] 17698    20
```

```
#perhaps double check trimmed output with trimr package?
#Jon: Yeah, that's a very good idea

#need to reformat data for trimr
data.trimr <- too.fast.gone %>%
  select(participant, posture, switchTrialType, congruentTrialType, reactionTime, correct_bin) %>%
  unite("condition", posture:congruentTrialType) %>%
  rename(rt = reactionTime, accuracy = correct_bin) %>%
  mutate(participant = as.factor(participant))
trimmingOutput.trimr <- modifiedRecursive(data.trimr,
                                          minRT = .100,
                                          returnType = "mean",
                                          digits = 4)
#this goes ahead and generates means (change returnType to "raw" to see trimmed raw data)


trimmingOutput = pjRecursiveTrim2(dataSet = too.fast.gone,
                                  dv = "reactionTime",
                                  splitvars = c("participant",
                                                "posture",
                                                "switchTrialType",
                                                "congruentTrialType"))
trimmedData=trimmingOutput[[1]]
totalN = trimmingOutput[[2]]
rejected = trimmingOutput[[3]]
percentTrimmed = trimmingOutput[[4]] #this is very close to the percentage trimmed for stroop
#2.14% of trials
percentTrimmed
```

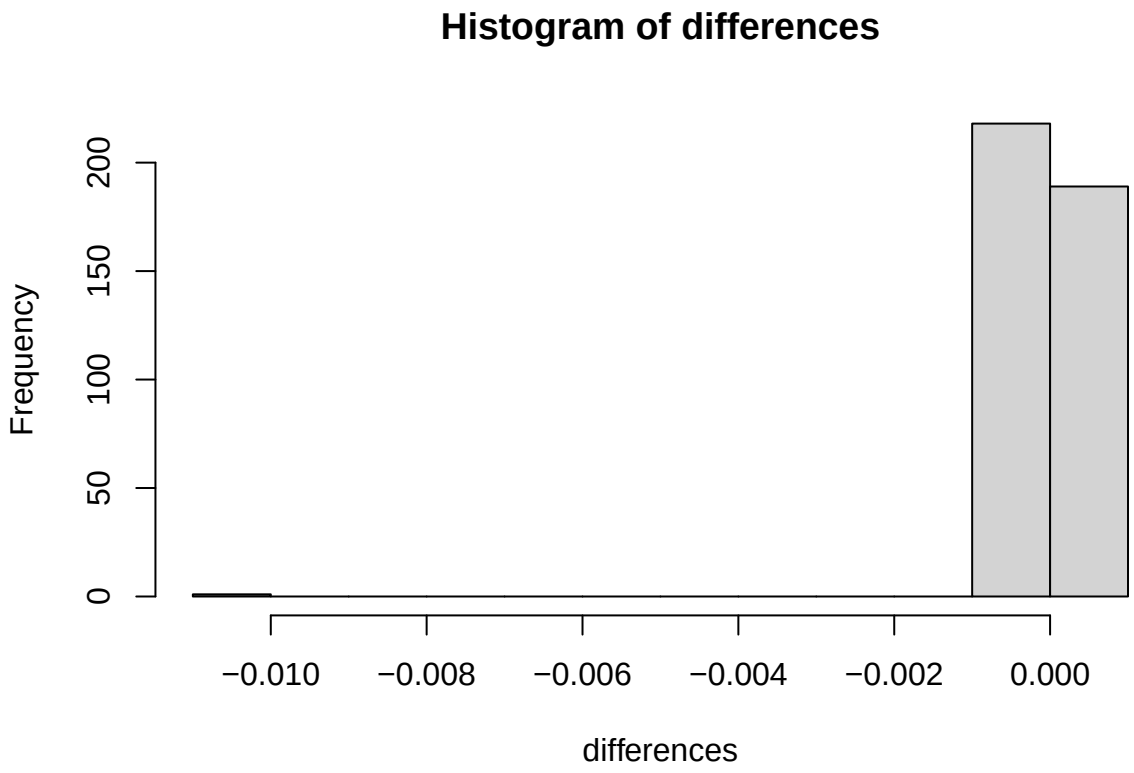
```
## [1] 2.141485
```

```
Ncells = trimmingOutput[[5]] # 51 participants * 8 conditions

#now use trimmedData for same analyses as above

trimmed_rt_mean <- trimmedData %>%
  group_by(participant,
           posture,
           congruentTrialType,
           switchTrialType) %>%
  summarize(mean_rt    = mean(reactionTime))
```

```
## `summarise()` has grouped output by 'participant', 'posture', 'congruentTrialType'. You can
## override using the `.groups` argument.
```

```
##compare these means with means from trimr
a <- trimmed_rt_mean %>%
  mutate(condition = paste(posture, switchTrialType, congruentTrialType, sep = "_"))
b <- trimmingOutput.trimr %>%
  pivot_longer(standing_noswitch_incongruent:sitting_noswitch_incongruent,
               names_to = "condition",
               values_to = "rt")
combined <- merge(a,b)
differences <- combined$mean_rt - combined$rt
```

```
hist(differences)
```

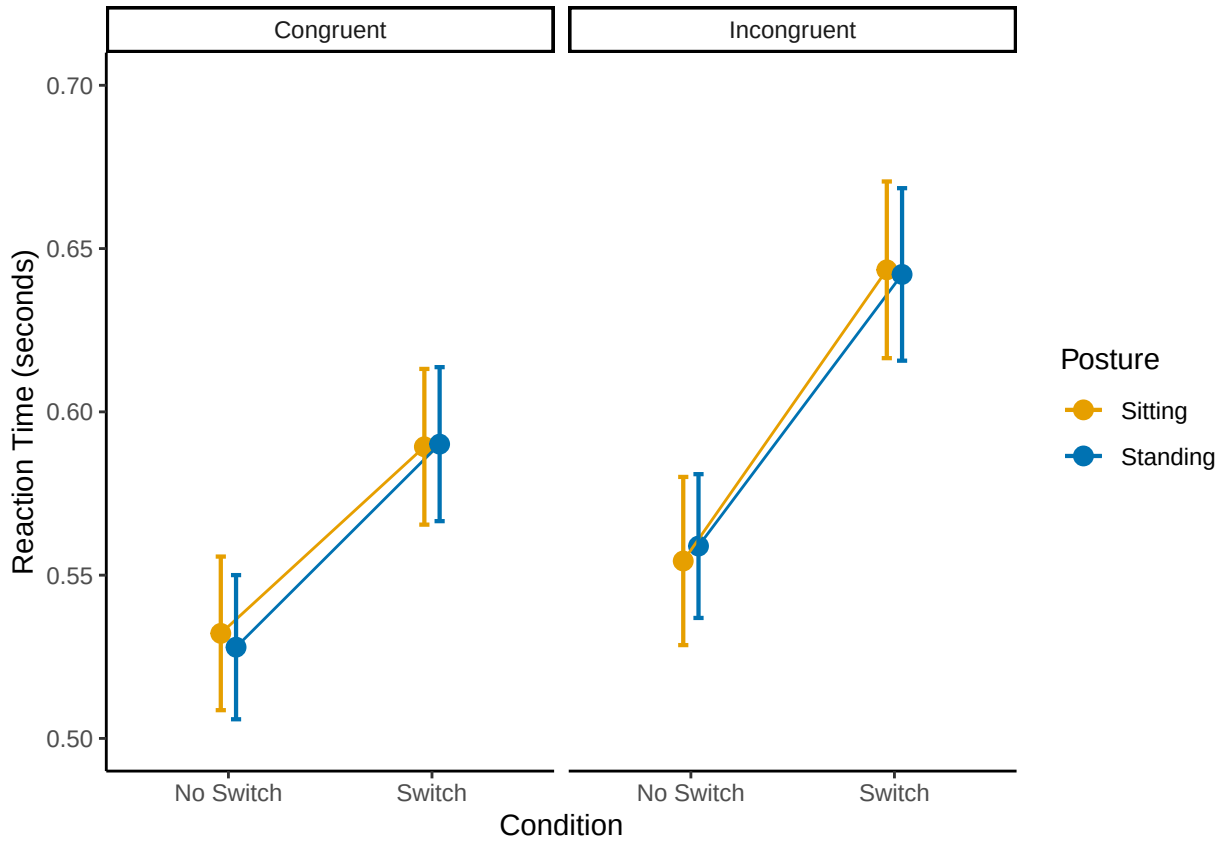



```
#Convert data to wide format
trimmed_rt_mean_wide <- trimmed_rt_mean %>%
  pivot_wider(names_from = c(posture,
                             congruentTrialType,
                             switchTrialType),
              values_from =   mean_rt)

trimmed_RT_plot <-
  superbPlot(trimmed_rt_mean_wide,
             WSFactors = c("Condition(2)", "Congruent(2)", "Posture(2)"),
             variables = colnames(ts_acc_mean_wide)[2:9],
             errorbar = "SE",
             plotStyle = "line",
             factorOrder = c("Condition","Posture","Congruent"),
             adjustments = list(purpose = "difference"))+
  theme_classic()+
  facet_wrap(vars(Congruent), labeller = labeller(Congruent = congruent.labs)) +
  scale_x_discrete(labels=c("1" = "No Switch", "2" = "Switch"))+
  scale_color_manual(values=c("#E69F00", "#0072B2"), labels = c("Sitting", "Standing")) +
  ylim(0.50, 0.70) +
  labs(y = "Reaction Time (seconds)")
```

```
## superb::FYI: Here is how the within-subject variables are understood:
##  Condition Congruent Posture                       variable
```

```
##          1         1       1    sitting_congruent_noswitch
##          2         1       1      sitting_congruent_switch
##          1         2       1  sitting_incongruent_noswitch
##          2         2       1    sitting_incongruent_switch
##          1         1       2   standing_congruent_noswitch
##          2         1       2     standing_congruent_switch
##          1         2       2 standing_incongruent_noswitch
##          2         2       2   standing_incongruent_switch
```

```r
ggsave(trimmed_RT_plot,
       file = "plots/trimmed_RT_plot.pdf",
       units = "in",
       width = 6.62,
       height = 5.50,
       dpi = 600)

trimmed_RT_plot
```




```r
exp1_anova_trimmed_rt <- ezANOVA(trimmed_rt_mean,
                                 dv = mean_rt,
                                 wid = participant,
                                 within = .(posture, congruentTrialType, switchTrialType),
                                 type = 3,
                                 detailed = TRUE,
                                 return_aov = T
)
```

```
## Warning: Converting "participant" to factor for ANOVA.
## Warning: Converting "posture" to factor for ANOVA.
## Warning: Converting "congruentTrialType" to factor for ANOVA.
## Warning: Converting "switchTrialType" to factor for ANOVA.
```

```
exp1_anova_trimmed_rt2 <- aov_ez(data = trimmed_rt_mean,
                                 dv = 'mean_rt',
                                 id = 'participant',
                                 within = c('posture', 'congruentTrialType', 'switchTrialType'),
                                 type = 3
)

exp1_stats_trimmed_rt <- ezStats(trimmed_rt_mean,
                                 dv = mean_rt,
                                 wid = participant,
                                 within = .(posture, congruentTrialType, switchTrialType),
                                 type = 3
)
```

```
## Warning: Converting "participant" to factor for ANOVA.
## Warning: Converting "posture" to factor for ANOVA.
## Warning: Converting "congruentTrialType" to factor for ANOVA.
## Warning: Converting "switchTrialType" to factor for ANOVA.
```

```
write.csv(exp1_stats_trimmed_rt[ ,-7],
          file = "output/Task_Switching_Descriptives_trimmed_RT.csv",
          row.names = F)

#data.frame(exp1_anova$ANOVA)
output_trimmed_rt <- aovEffectSize(exp1_anova_trimmed_rt, effectSize = "pes")
output_trimmed_rt <- data.frame(output_trimmed_rt$ANOVA) %>%
  mutate(MSE = c(NA, exp1_anova_trimmed_rt2$anova_table$MSE), .before = F)
write.csv(output_trimmed_rt, "output/Task_switching_ANOVA_trimmed_RT.csv")
output_trimmed_rt
```

```
##                                       Effect DFn DFd          SSn        SSd         MSE
## 1                                  (Intercept)   1  50 1.371527e+02 4.88081881          NA
## 2                                      posture   1  50 4.059328e-07 0.49610238 0.009922048
## 3                          congruentTrialType   1  50 1.617346e-01 0.16511068 0.003302214
## 4                             switchTrialType   1  50 5.423233e-01 0.20831102 0.004166220
## 5                  posture:congruentTrialType   1  50 2.766142e-04 0.07961345 0.001592269
## 6                     posture:switchTrialType   1  50 5.774668e-06 0.07595412 0.001519082
## 7          congruentTrialType:switchTrialType   1  50 1.793015e-02 0.06261657 0.001252331
## 8 posture:congruentTrialType:switchTrialType   1  50 7.751416e-04 0.07761821 0.001552364
##               F            p p..05          pes
## 1 1.405018e+03 2.884861e-38     * 9.656362e-01
## 2 4.091220e-05 9.949220e-01       8.182433e-07
## 3 4.897763e+01 6.035585e-09     * 4.948353e-01
## 4 1.301715e+02 1.584202e-15     * 7.224867e-01
## 5 1.737233e-01 6.786078e-01       3.462435e-03
## 6 3.801419e-03 9.510829e-01       7.602259e-05
## 7 1.431742e+01 4.140395e-04     * 2.226056e-01
```

```
## 8 4.993297e-01 4.830749e-01       9.887849e-03
```

Reproduce ANOVA for Smith et al. task-switching data

```
#load acc data
Smith_Exp2_acc <- read_excel("Smith Data/StandingData.xlsx",
                             sheet = "Exp2Acc")

head(Smith_Exp2_acc)
```

```
## # A tibble: 6 x 9
##   subj  sit_congruent_noswitch sit_congruent_swi~ sit_incongruent~ sit_incongruent~ stand_congruent~
##   <chr>                  <dbl>              <dbl>            <dbl>            <dbl>            <dbl>
## 1 1                      1                  1                0.957            0.951            0.98
## 2 2                      0.976              0.978            0.981            0.796            0.98
## 3 3                      0.977              0.979            0.98             0.935            0.980
## 4 4                      0.893              0.884            0.816            0.549            0.980
## 5 5                      1                  0.98             0.925            0.933            0.978
## 6 6                      1                  0.95             0.957            0.868            1
## # ... with 3 more variables: stand_congruent_switch <dbl>, stand_incongruent_noswitch <dbl>,
## #   stand_incongruent_switch <dbl>
```

```
#Drop last row with comment
Smith_Exp2_acc <- Smith_Exp2_acc[1:30,]

#Restructure from wide to narrow, using tidyr
Smith_exp2_acc_narrow <- Smith_Exp2_acc %>%
  gather(v, accuracy, colnames(Smith_Exp2_acc)[2:9]) %>%
  separate(v, c("posture", "con", "switch")) %>%
  arrange(subj)


Smith_exp2_acc_anova <- ezANOVA(Smith_exp2_acc_narrow,
                                dv = accuracy,
                                wid = subj,
                                within = .(posture, con, switch),
                                type = 3,
                                detailed = TRUE,
                                return_aov=F
)
```

```
## Warning: Converting "subj" to factor for ANOVA.
```

```
## Warning: Converting "posture" to factor for ANOVA.
```

```
## Warning: Converting "con" to factor for ANOVA.
```

```
## Warning: Converting "switch" to factor for ANOVA.
```

```
Smith_exp2_acc_anova
```

```
## $ANOVA
##               Effect DFn DFd          SSn        SSd            F            p p<.05          ges
## 1        (Intercept)   1  29 2.048909e+02 0.24225540 2.452716e+04 5.184222e-44     * 0.9965856538
## 2            posture   1  29 1.215410e-02 0.12309940 2.863286e+00 1.013416e-01       0.0170197030
## 3                con   1  29 2.719991e-01 0.11703974 6.739569e+01 4.729349e-09     * 0.2792700999
## 4             switch   1  29 1.403032e-01 0.06464470 6.294084e+01 9.482835e-09     * 0.1665777615
```

```
## 5        posture:con   1  29 2.734424e-03 0.04708210 1.684256e+00 2.045882e-01       0.0038802688
## 6     posture:switch   1  29 7.099180e-03 0.03715534 5.540959e+00 2.556408e-02     * 0.0100120392
## 7         con:switch   1  29 3.248637e-02 0.04037101 2.333617e+01 4.059829e-05     * 0.0442321480
## 8 posture:con:switch   1  29 5.244392e-04 0.03031748 5.016491e-01 4.844309e-01       0.0007465437
```

```
output_Smith_exp2_acc <- aovEffectSize(Smith_exp2_acc_anova, effectSize = "pes")
output_Smith_exp2_acc <- data.frame(output_Smith_exp2_acc$ANOVA)
write.csv(output_Smith_exp2_acc, "output/Smith_Exp2_ANOVA_acc.csv")
output_Smith_exp2_acc
```

```
##               Effect DFn DFd          SSn        SSd             F            p p..05        pes
## 1        (Intercept)   1  29 2.048909e+02 0.24225540 2.452716e+04 5.184222e-44     * 0.99881903
## 2            posture   1  29 1.215410e-02 0.12309940 2.863286e+00 1.013416e-01       0.08986162
## 3                con   1  29 2.719991e-01 0.11703974 6.739569e+01 4.729349e-09     * 0.69915667
## 4             switch   1  29 1.403032e-01 0.06464470 6.294084e+01 9.482835e-09     * 0.68457979
## 5        posture:con   1  29 2.734424e-03 0.04708210 1.684256e+00 2.045882e-01       0.05488989
## 6     posture:switch   1  29 7.099180e-03 0.03715534 5.540959e+00 2.556408e-02     * 0.16041707
## 7         con:switch   1  29 3.248637e-02 0.04037101 2.333617e+01 4.059829e-05     * 0.44588988
## 8 posture:con:switch   1  29 5.244392e-04 0.03031748 5.016491e-01 4.844309e-01       0.01700410
```

```
#plot acc effect sizes for our results and Smith together
#Check that ANOVA tables (rows) match
output_acc$Effect
```

```
## [1] "(Intercept)"                                "posture"
## [3] "congruentTrialType"                         "switchTrialType"
## [5] "posture:congruentTrialType"                 "posture:switchTrialType"
## [7] "congruentTrialType:switchTrialType"         "posture:congruentTrialType:switchTrialType"
```

```
output_Smith_exp2_acc$Effect
```

```
## [1] "(Intercept)"        "posture"            "con"                "switch"
## [5] "posture:con"        "posture:switch"     "con:switch"         "posture:con:switch"
```

```
#Drop intercept in the ANOVA
ts.acc.pes <- data.frame(matrix(nrow = 7, ncol = 3))
ts.acc.pes[1] <- output_acc$Effect[2:8]
ts.acc.pes[2] <- output_acc$pes[2:8]
ts.acc.pes[3] <- output_Smith_exp2_acc$pes[2:8]
ts.acc.pes[4] <- c("Red", rep("Black", times =2), rep("Red", times = 2), "Black", "Red")
colnames(ts.acc.pes) <- c("Effect", "Replication", "Original", "col")


# colnames(ts.acc.pes) <- c("Effect", "Current", "Original", "col")
#Scatter plot of original vs. rep effects
#Need to get CIs:
#Go through a data.frame repeating fct get.ci.partial.eta.squared by row
#try group_by() + map ?
output_Smith_exp2_acc
```

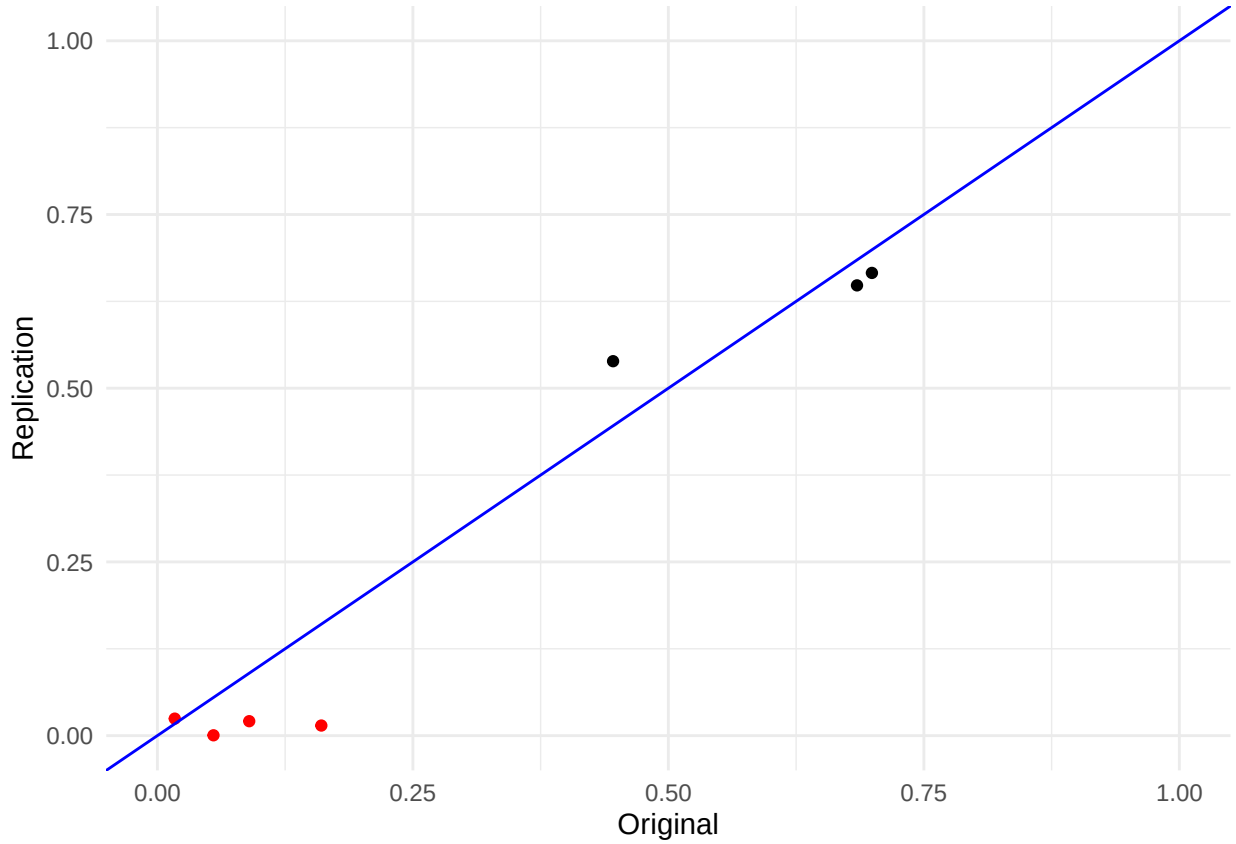
```
##               Effect DFn DFd          SSn        SSd             F            p p..05        pes
## 1        (Intercept)   1  29 2.048909e+02 0.24225540 2.452716e+04 5.184222e-44     * 0.99881903
## 2            posture   1  29 1.215410e-02 0.12309940 2.863286e+00 1.013416e-01       0.08986162
## 3                con   1  29 2.719991e-01 0.11703974 6.739569e+01 4.729349e-09     * 0.69915667
## 4             switch   1  29 1.403032e-01 0.06464470 6.294084e+01 9.482835e-09     * 0.68457979
## 5        posture:con   1  29 2.734424e-03 0.04708210 1.684256e+00 2.045882e-01       0.05488989
## 6     posture:switch   1  29 7.099180e-03 0.03715534 5.540959e+00 2.556408e-02     * 0.16041707
```

```
## 7         con:switch   1  29 3.248637e-02 0.04037101 2.333617e+01 4.059829e-05     * 0.44588988
## 8 posture:con:switch   1  29 5.244392e-04 0.03031748 5.016491e-01 4.844309e-01       0.01700410
```

```
str(output_Smith_exp2_acc)
```

```
## 'data.frame':    8 obs. of  9 variables:
##  $ Effect: chr  "(Intercept)" "posture" "con" "switch" ...
##  $ DFn   : num  1 1 1 1 1 1 1 1
##  $ DFd   : num  29 29 29 29 29 29 29 29
##  $ SSn   : num  2.05e+02 1.22e-02 2.72e-01 1.40e-01 2.73e-03 ...
##  $ SSd   : num  0.2423 0.1231 0.117 0.0646 0.0471 ...
##  $ F     : num  24527.16 2.86 67.4 62.94 1.68 ...
##  $ p     : num  5.18e-44 1.01e-01 4.73e-09 9.48e-09 2.05e-01 ...
##  $ p..05 : chr  "*" "" "*" "*" ...
##  $ pes   : num  0.9988 0.0899 0.6992 0.6846 0.0549 ...
```

```
#Possible to label on graph? Might have to use a legend with symbols? idk
#This will probably be too busy

#Experiment 2, accuracy (all ANOVA results except the intercept)
ggplot(ts.acc.pes, aes(x = Original, y = Replication, colour = col)) +
  geom_point() +
 # geom_smooth(method = lm, se = F) + #Confidence interval is cutoff b/c values are bounded from 0 to 1
  scale_colour_identity() +
  xlim(0, 1.00) +
  ylim(0, 1.00) +
  geom_abline(slope = 1, intercept = 0, col = "blue") +
  theme_minimal()
```




```
#Exact proportion of current to original effect: ~9%
ts.acc.pes$Current[6]/ts.acc.pes$Original[6]
```

```
## numeric(0)
```

```
#Compare current vs. original effect sizes
interaction.original <-
  get.ci.partial.eta.squared(output_Smith_exp2_acc$F[6],
                             output_Smith_exp2_acc$DFn[6],
                             output_Smith_exp2_acc$DFd[6],
                             conf.level = 0.90) #Typical convention for partial-eta


#Posture x congruency interaction
rep.exp1.peta2 <- 0.002  #Approx
rep.exp1.CI <-
  get.ci.partial.eta.squared(0.081,
                             2,
                             98,
                             conf.level = 0.90)

Smith.exp1.peta2 <- 0.27
Smith.exp1.CI <-
  get.ci.partial.eta.squared(4.73,
                             2,
                             26,
                             conf.level = 0.90)
```

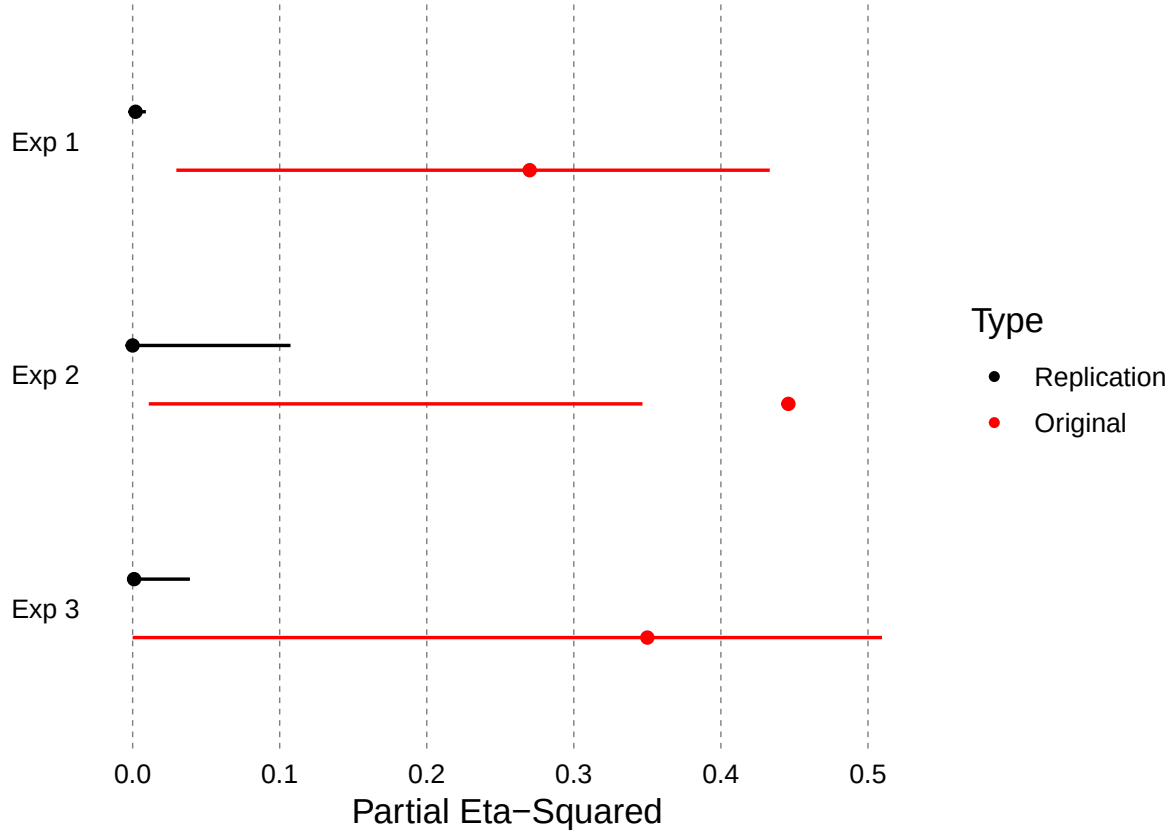
```r
#Posture x set size interaction
rep.exp3.peta2 <- 0.001 #Approx
rep.exp3.CI <-
  get.ci.partial.eta.squared(0.031,
                             1,
                             49,
                             conf.level = 0.90)

Smith.exp3.peta2 <- 0.35
Smith.exp3.CI <-
  get.ci.partial.eta.squared(1,
                             11,
                             5.90,
                             conf.level = 0.90)


ts.acc.pes.int <- data.frame(matrix(nrow = 6, ncol = 6))
colnames(ts.acc.pes.int) <- c("Data", "Type", "Effect.size", "CI.Lower", "CI.Upper", "name")
ts.acc.pes.int[6] <- c(rep("Exp 1", times = 2),
                       rep("Exp 2", times = 2),
                       rep("Exp 3", times = 2)
                       )

ts.acc.pes.int[2] <- rep(c("Replication", "Original"), times = 3)
# ts.acc.pes.int[6]     <- c(rep("RT1", times = 2),
#                            rep("Acc", times = 2),
#                            rep("RT2", times = 2)
#                           )

ts.acc.pes.int[1,3:5] <- c(rep.exp1.peta2, data.frame(rep.exp1.CI))
ts.acc.pes.int[2,3:5] <- c(Smith.exp1.peta2, data.frame(Smith.exp1.CI))
ts.acc.pes.int[3,3:5] <- c(ts.acc.pes$Current[6], data.frame(interaction_effect_CI))
ts.acc.pes.int[4,3:5] <- c(ts.acc.pes$Original[6], data.frame(interaction.original))
ts.acc.pes.int[5,3:5] <- c(rep.exp3.peta2, data.frame(rep.exp3.CI))
ts.acc.pes.int[6,3:5] <- c(Smith.exp3.peta2, data.frame(Smith.exp3.CI))

#Graph comparison of key effects for all three experiments- Similar to forest plot in sig
#filtering paper?
forest.colors <- c("red", "black")

ts.acc.pes.int$Data <- as.factor(ts.acc.pes.int$Data)
ts.acc.pes.int$Type <- as.factor(ts.acc.pes.int$Type)

str(ts.acc.pes.int)
```

```
## 'data.frame':    6 obs. of  6 variables:
##  $ Data       : Factor w/ 0 levels: NA NA NA NA NA NA
##  $ Type       : Factor w/ 2 levels "Original","Replication": 2 1 2 1 2 1
##  $ Effect.size: num  0.002 0.27 0 0.446 0.001 ...
##  $ CI.Lower   : num  0 0.0297 0.1074 0.011 0 ...
##  $ CI.Upper   : num  0.00903 0.43321 0 0.34666 0.03895 ...
##  $ name       : chr  "Exp 1" "Exp 1" "Exp 2" "Exp 2" ...
```

```
forest.comp <- mod.forestplot(df = ts.acc.pes.int,
                              estimate = Effect.size,
                              ci.lower = CI.Lower,
                              ci.upper = CI.Upper,
                              colour = Type,
                              xlab = "Partial Eta-Squared"
) +
  scale_color_manual(values = forest.colors)
```

```
## Scale for 'colour' is already present. Adding another scale for 'colour', which will replace the
## existing scale.
```

```
forest.comp
```




```
#For a mini-meta-analysis
# Extracting (sampling) var or SE from PES? CIs around PES are calculated in papers and software using
# Probably not possible (unknown sampling distribution)
# https://www.google.com/books/edition/The_SAGE_Encyclopedia_of_Research_Design/Pn1ZEAAAQBAJ?hl=en&gbpv
# Convert to Cohen's d, one appropriate for a within design?
# Use dz? easystats

# Straub et al. used dav (Mdiff/Saverage), Cummings (2014) then corrected dz using Hedges gz
# For N > 20+ I think dz and gz are equvialent. Need to look up
# https://easystats.github.io/effectsize/reference/t_to_r.html

# Comparison among all calculations
# https://www.tqmp.org/RegularArticles/vol17-1/p051/p051.pdf
```