Task Switching Replication

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2021-12-10

#Read in and Check Raw Data

```
#Import current data
  task_switching_raw <- read.csv(paste0(workingdir, "/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
  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

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```
#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 = "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 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 acc < 80%)
  length(unique(ts_acc_mean$participant))
```
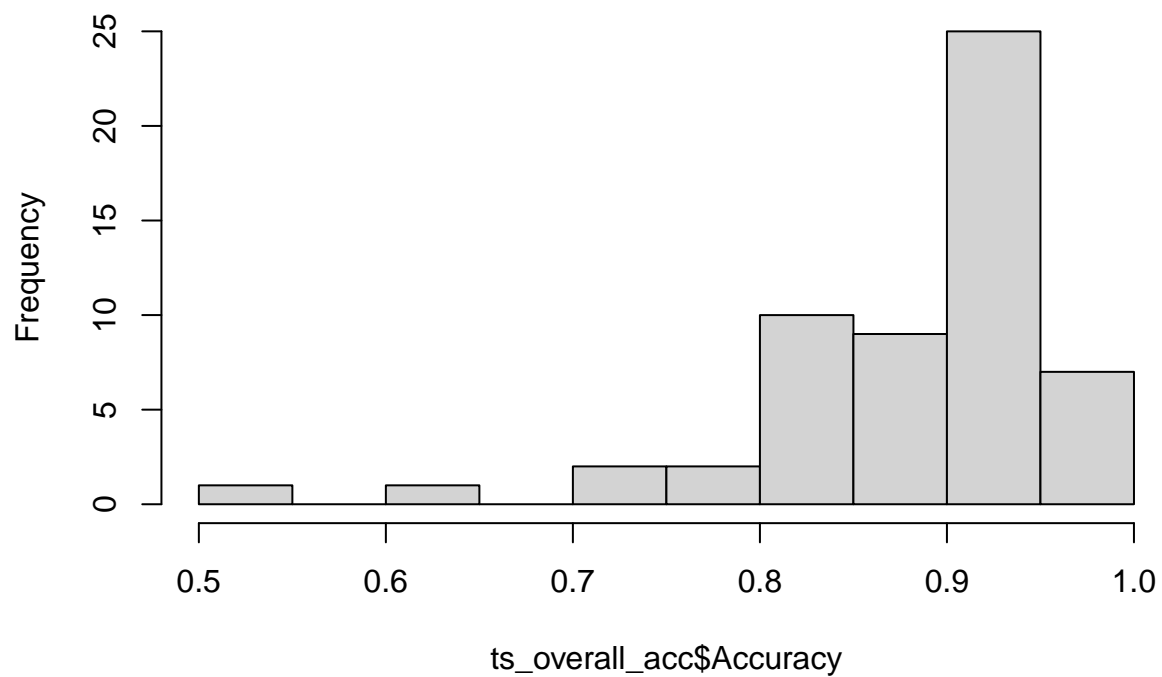
```
## [1] 51
```

Plots and Analyses

Accuracy

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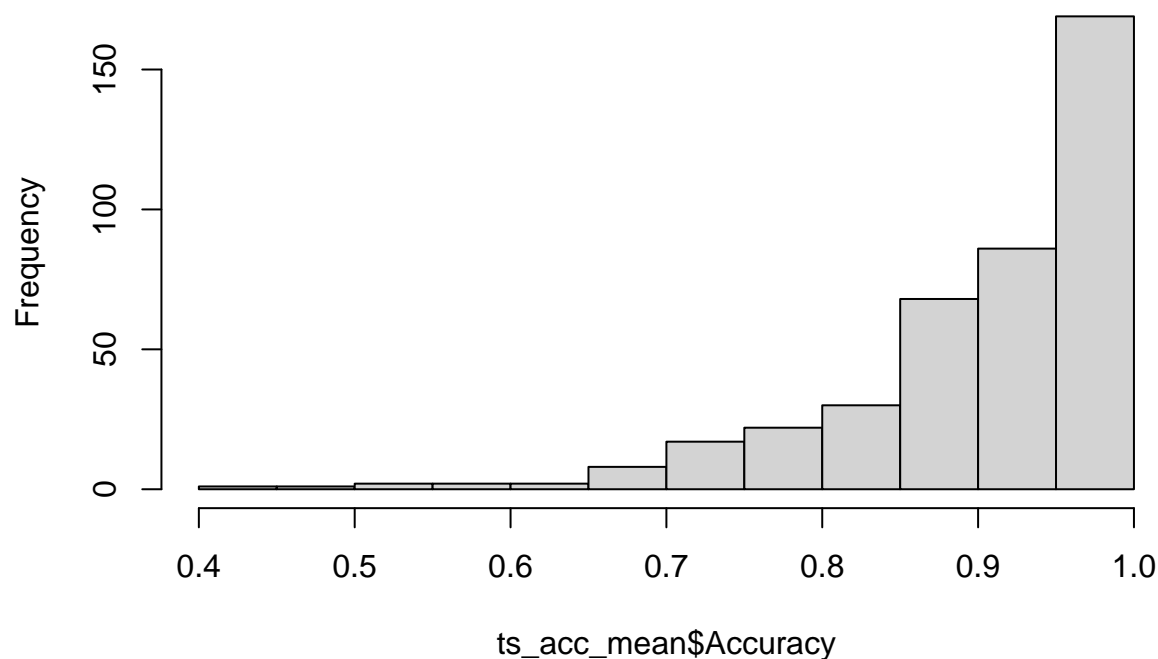
Histogram of ts_overall_acc$Accuracy


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

Histogram of 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
                      )

#data.frame(exp1_anova$ANOVA)
output_acc <- aovEffectSize(exp1_anova, effectSize = "pes")
output_acc <- data.frame(output_acc$ANOVA)
write.csv(output_acc, "Task_switching_ANOVA_acc.csv")
output_acc
```

```
##                                              Effect DFn DFd          SSn        SSd            F
## 1                                       (Intercept)   1  50 3.331616e+02 0.84392719 1.973876e+04
## 2                                           posture   1  50 9.386943e-03 0.44204149 1.061772e+00
## 3                                congruentTrialType   1  50 8.577579e-01 0.43034136 9.966017e+01
## 4                                   switchTrialType   1  50 2.633377e-01 0.14305407 9.204131e+01
## 5                        posture:congruentTrialType   1  50 1.038526e-04 0.20920092 2.482125e-02
## 6                           posture:switchTrialType   1  50 1.767731e-03 0.12000107 7.365482e-01
## 7                congruentTrialType:switchTrialType   1  50 8.851220e-02 0.07573624 5.843451e+01
## 8 posture:congruentTrialType:switchTrialType   1  50 2.360230e-03 0.09401427 1.255251e+00
##            p p..05         pes
```

```
## 1 1.301952e-66    * 0.9974733137
## 2 3.077703e-01      0.0207938669
## 3 1.702444e-13    * 0.6659097700
## 4 6.367282e-13    * 0.6479897331
## 5 8.754478e-01      0.0004961787
## 6 3.948644e-01      0.0145171124
## 7 5.925302e-10    * 0.5388921804
## 8 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
```

```
# This almost works for getting CIs around all effects....
# test.model <-
#    aov_car(Accuracy ~
#            posture*congruentTrialType*switchTrialType +
#            Error(participant/posture*congruentTrialType *switchTrialType),
#            ts_acc_mean, anova_table = (es = "pes"),
#            return = "aov",
#            include_aov = T,
#            type = 3)
# # test.model
# anova_stats(test.model)

#The CIs around effect sizes are calculated using Type I sums of squares?
#' ## Type of Sums of Squares
#' The sums of squares (or *F* statistics) used for the computation of the
#' effect sizes is based on those returned by `anova(model)` (whatever those may
#' be - for `aov` and `aovlist` these are *type-1* sums of squares; for
#' `lmerMod` (and `lmerModLmerTest`) these are *type-3* sums of squares)
# test.pes<-
# effectsize::eta_squared(test.model,
#                    alternative = "two.sided",
#                    ci = 0.90,
#                    partial = T,
#                    verbose = T)
#
#https://mran.microsoft.com/snapshot/2018-06-30/web/packages/sjstats/vignettes/anova-statistics.html

#Below function won't work with an afex or aov object for an rm ANOVA
#car::Anova(..., type = 3)
```

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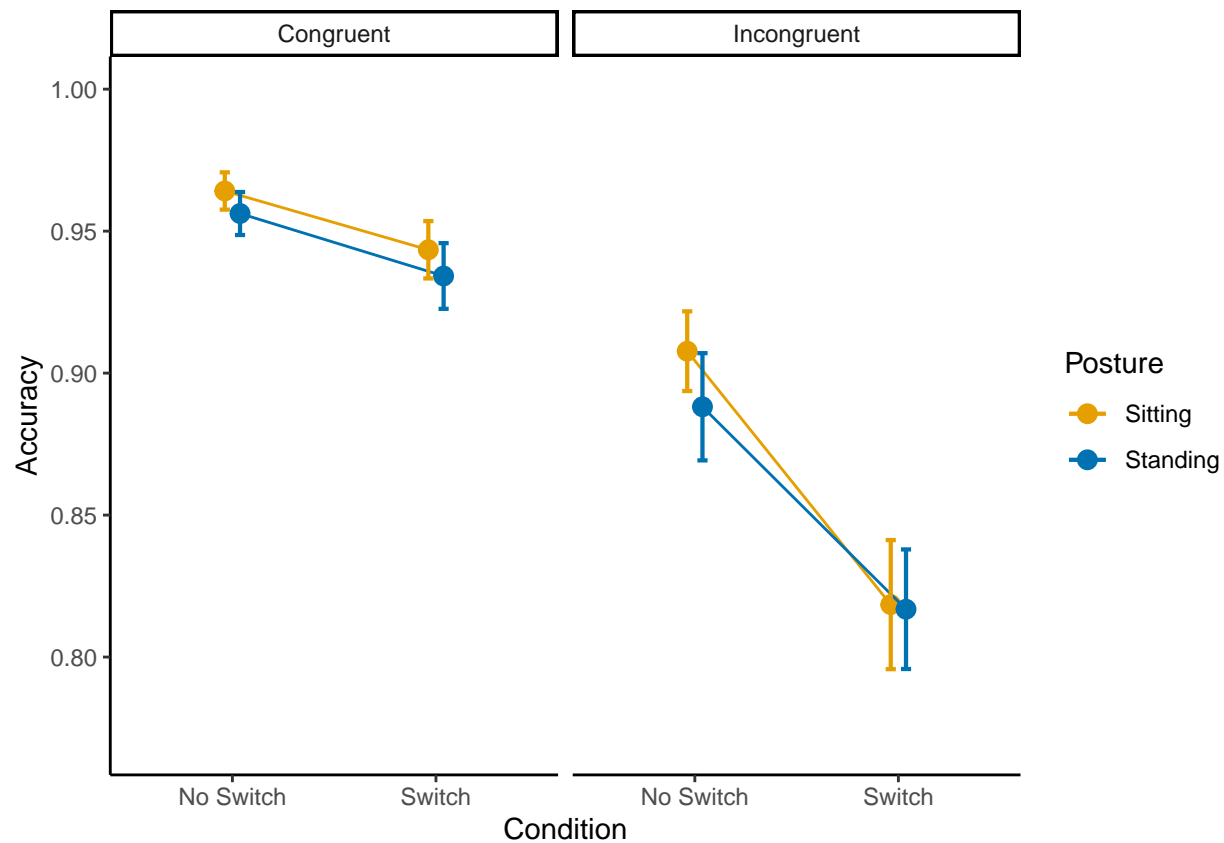
```
ggsave(acc_plot,
       file = "plots/acc_plot.pdf",
       units = "in",
       width = 6.62,
       height = 5.50,
       dpi = 600)

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
```

```
#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")) +
labs(y = "Reaction Time (ms)")
```

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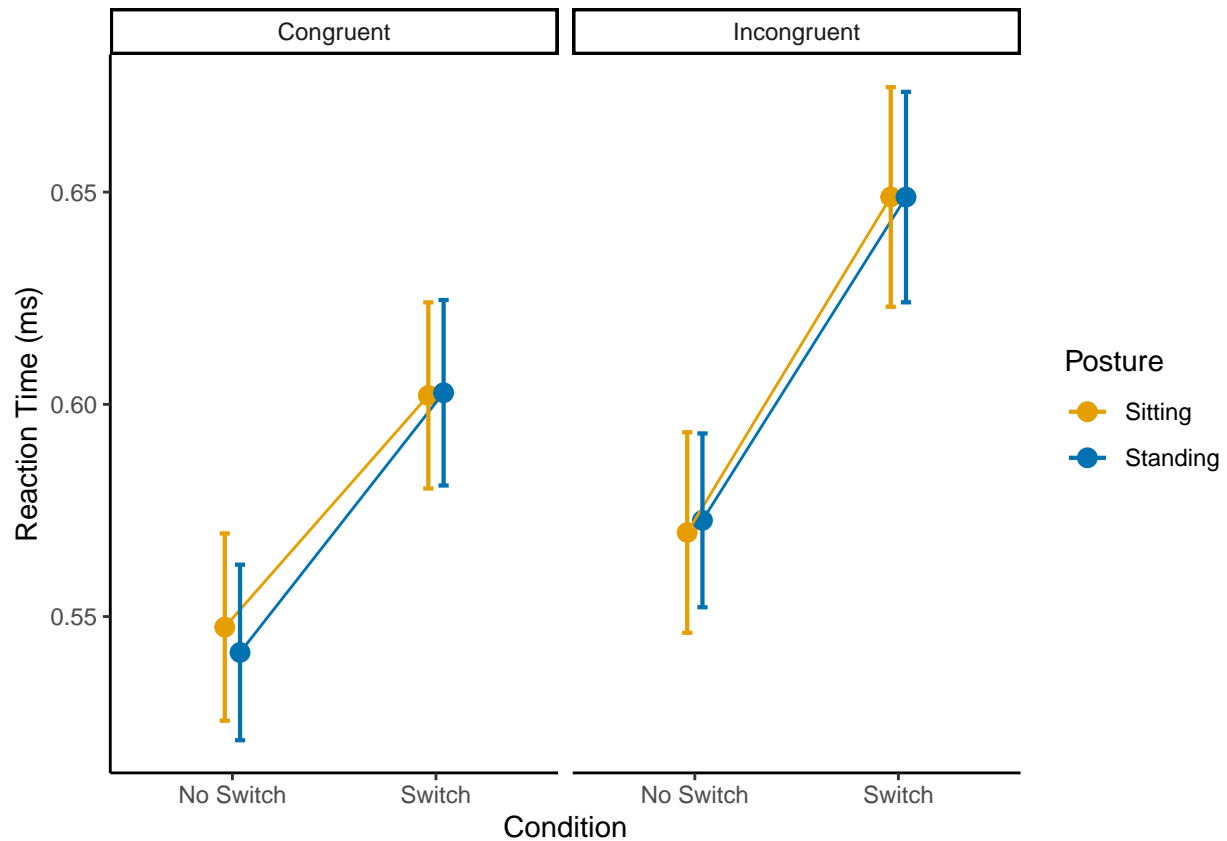
```
ggsave(RT_plot,
      file = "plots/RT_plot.pdf",
      units = "in",
      width = 6.62,
      height = 5.50,
      dpi = 600)

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.

```
#data.frame(exp1_anova$ANOVA)
output_rt <- aovEffectSize(exp1_anova, effectSize = "pes")
output_rt <- data.frame(output_rt$ANOVA)
write.csv(output_rt, "Task_switching_ANOVA_RT.csv")
output_rt
```

Effect DFn DFd   SSn   SSd   F

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