Task Switching Replication

Jon Bakdash & Laura Marusich

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#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
   low_acc_subs <- ts_overall_acc %>% filter(Accuracy < 0.80) %>%
     pull(participant)

#Drop participants w/<=80% acc
  #8, 49, 44, 2, 15, 51

     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

```
#Convert data to wide format
  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 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
length(unique(ts_acc_mean$participant))
```
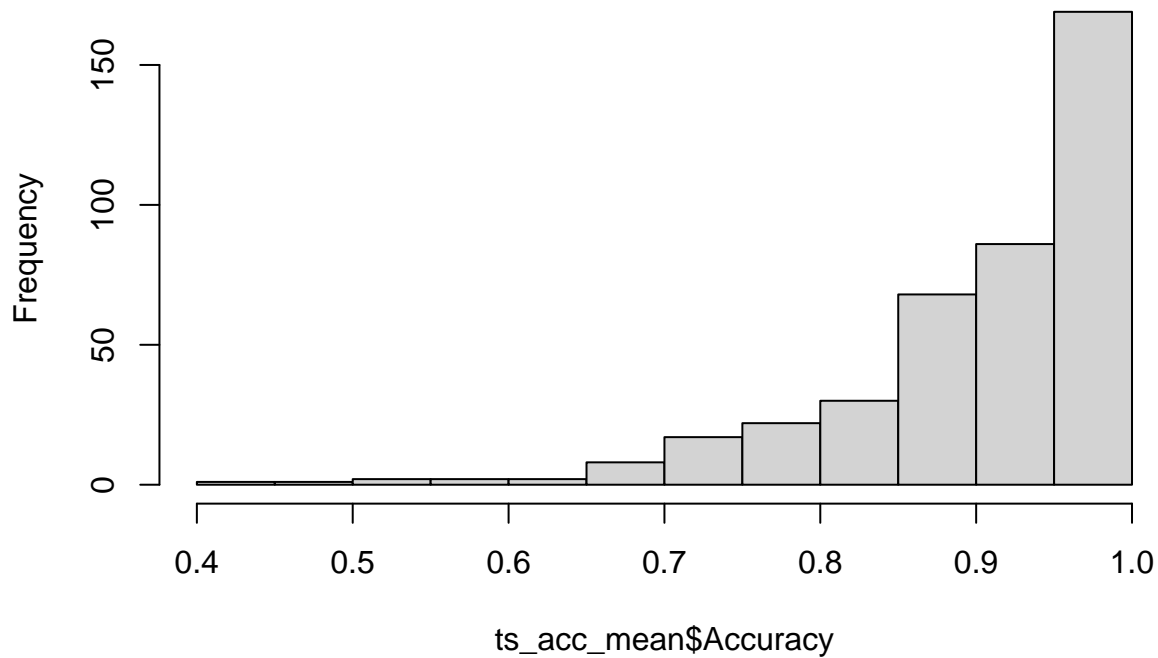
```
## [1] 51
```

Plots and Analyses

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

Histogram of ts_overall_acc$Accuracy
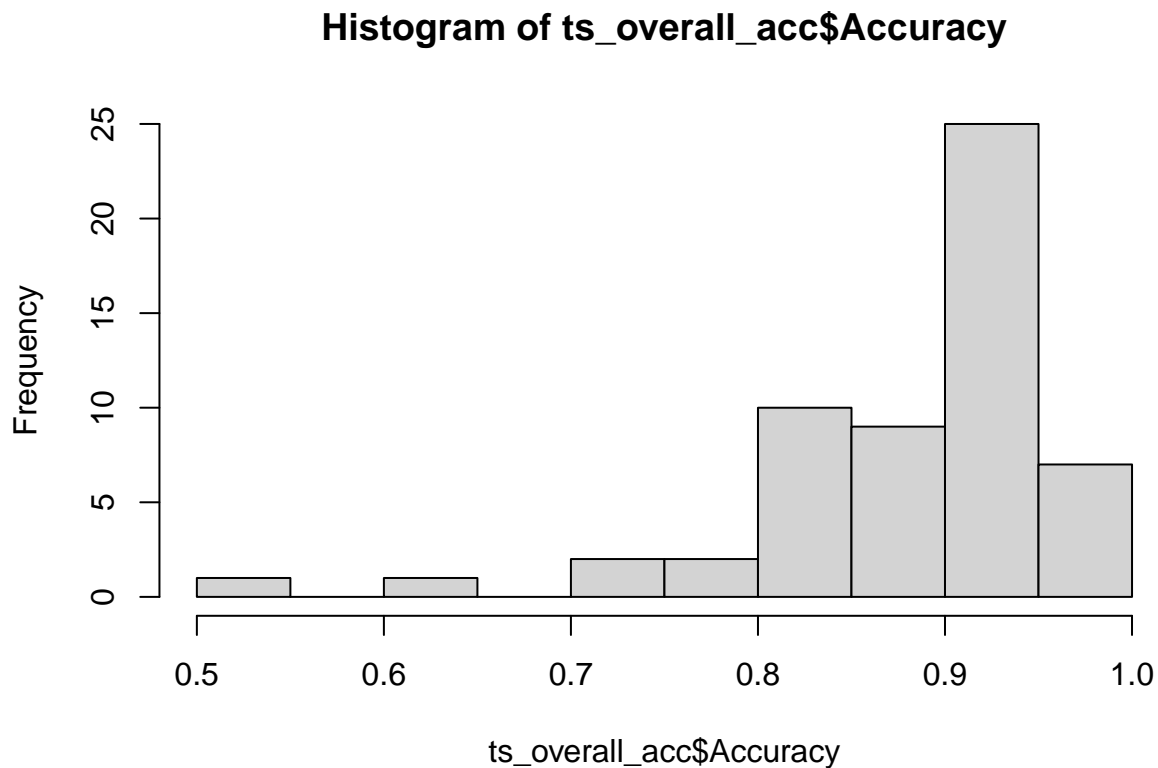

```
#Accuracy for all cells
hist(ts_acc_mean$Accuracy)
```

Histogram of ts_acc_mean$Accuracy


```r
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$ANOVA)
output1 <- aovEffectSize(exp1_anova, effectSize = "pes")
output1 <- data.frame(output1$ANOVA)

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

#make plot like Smith et al's
superbPlot(ts_acc_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 = "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
```
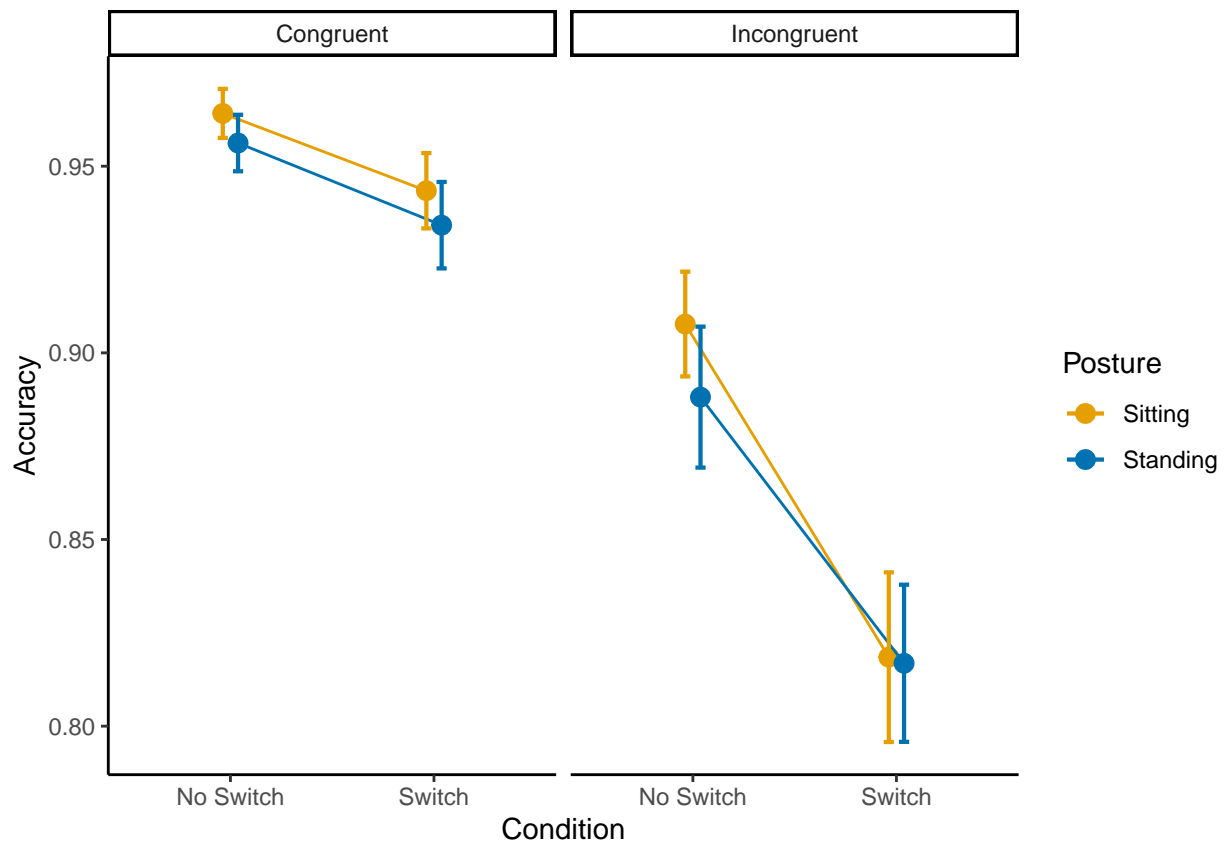


```
# write.csv(output, "output_ez.csv")
#importantly there was a significant condition [switch] × posture interaction,
#F(1, 29) = 5.54, p = .026, 2p = .16.
#posture:switchTrialType   1  52 6.705827e-03 0.15814085 2.205015e+00
#6.016033e-01       1.117445e-04
#p = 0.14
#GES = 0.07
# exp1_anova.b <-  aov(Accuracy ~
#                     posture*congruentTrialType*switchTrialType +
#                     Error(participant/posture*congruentTrialType*switchTrialType),
#                     ts_acc_mean)
# #str(ts_acc_mean)
```

```r
# summary(exp1_anova.b)
# output <- anova_stats(exp1_anova.b)
# write.csv(output, "output_aov.csv")
```

```r
#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

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


  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")
```

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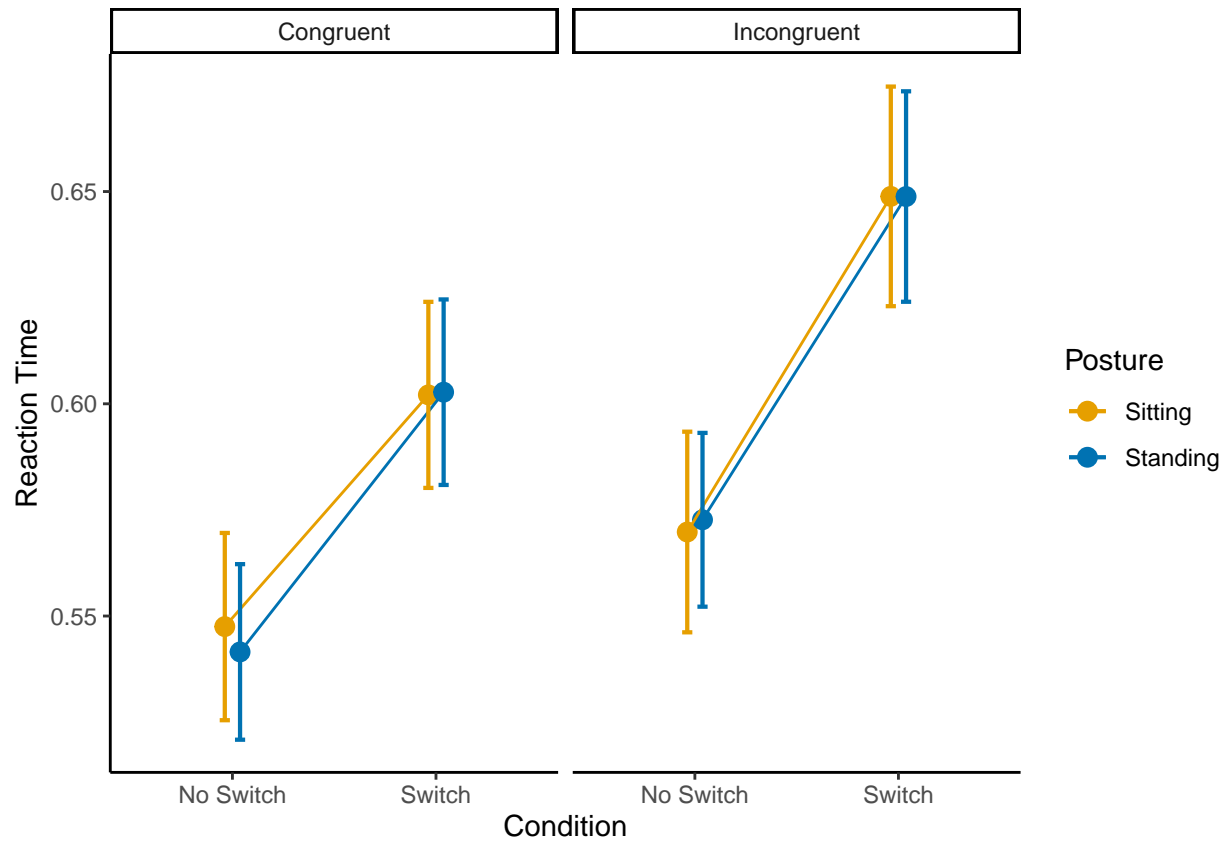
```
exp1_anova_rt <- ezANOVA(ts_rt_mean,
                        dv = mean_rt,
                        wid = participant,
                        within = .(posture, congruentTrialType, switchTrialType),
                        type = 3,
                        detailed = TRUE,
                     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