# Task Switching Replication

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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
   #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
## 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 = "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 ...
```

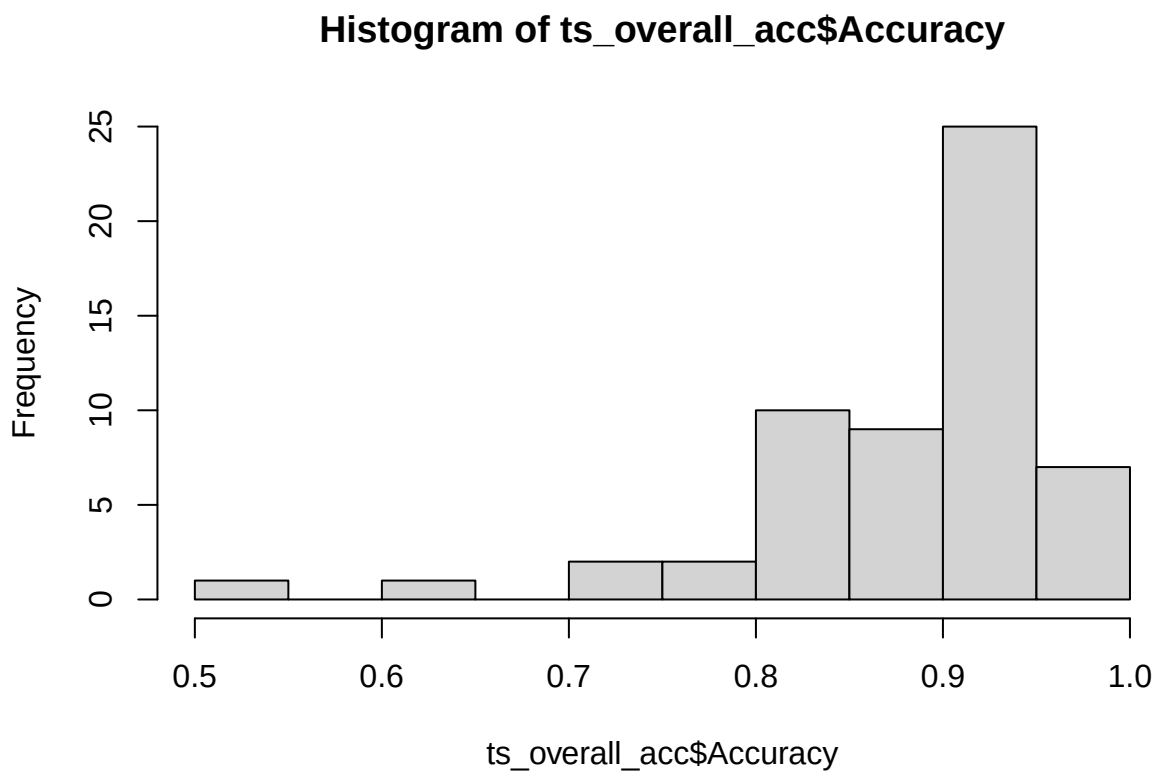
```
  #Total N = 51 (6 dropped for acc < 80%)
  length(unique(ts_acc_mean$participant))
```

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

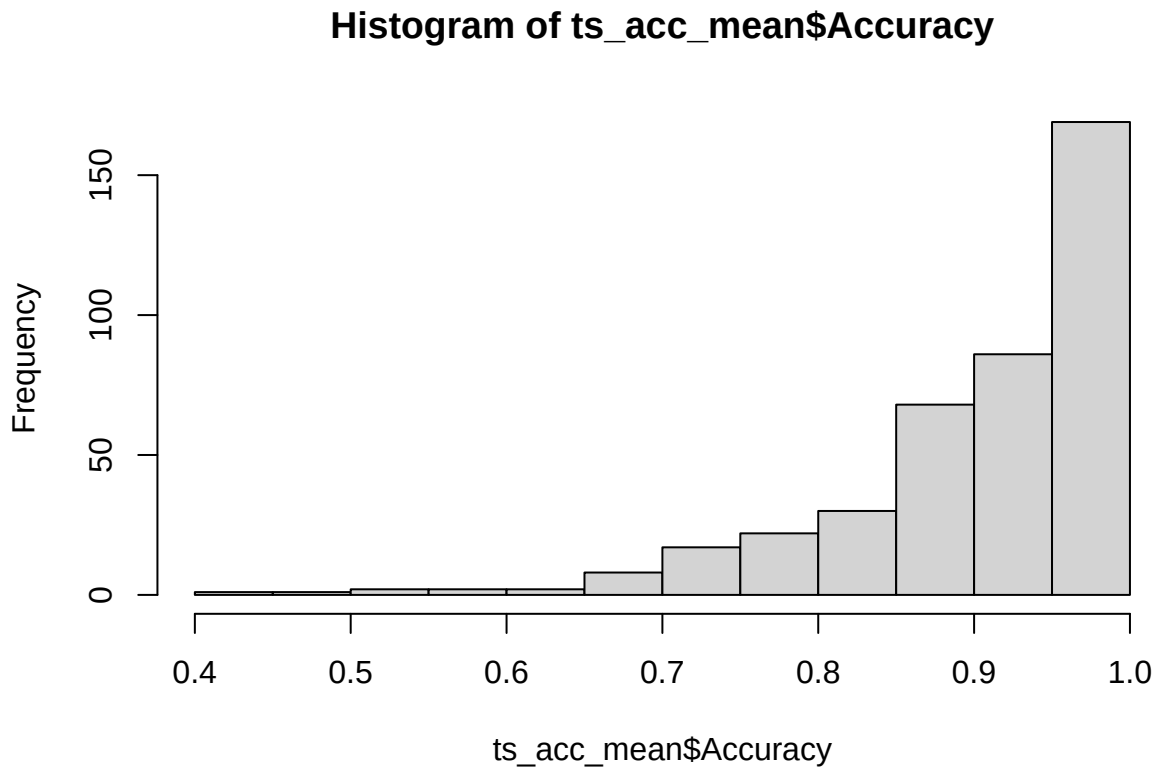
## Plots and Analyses

### Accuracy

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



```r
#Accuracy for all cells
  hist(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$ANOVA)
output_acc <- aovEffectSize(exp1_anova, effectSize = "pes")
output_acc <- data.frame(output_acc$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
```

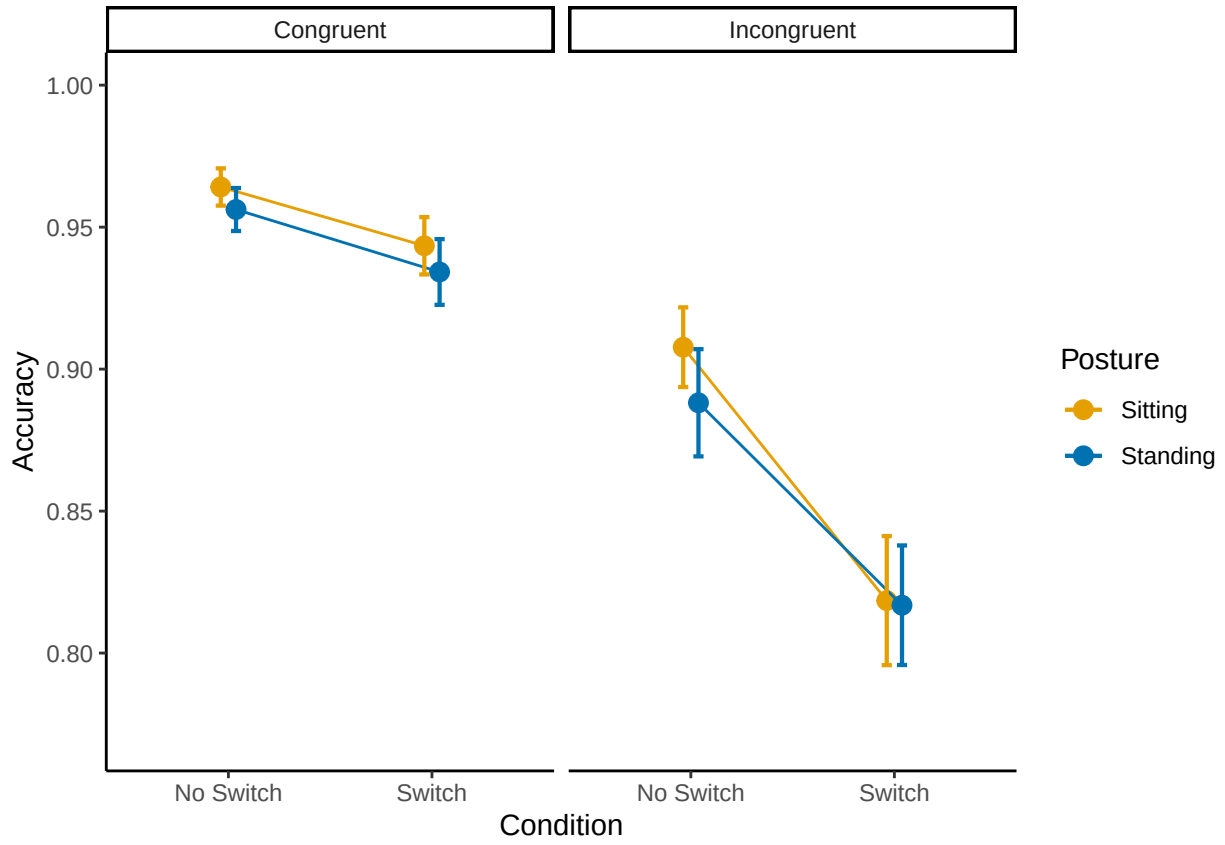
```
## $LL
## [1] 0
##
## $UL
## [1] 0.1073579
```

```
# 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))
```

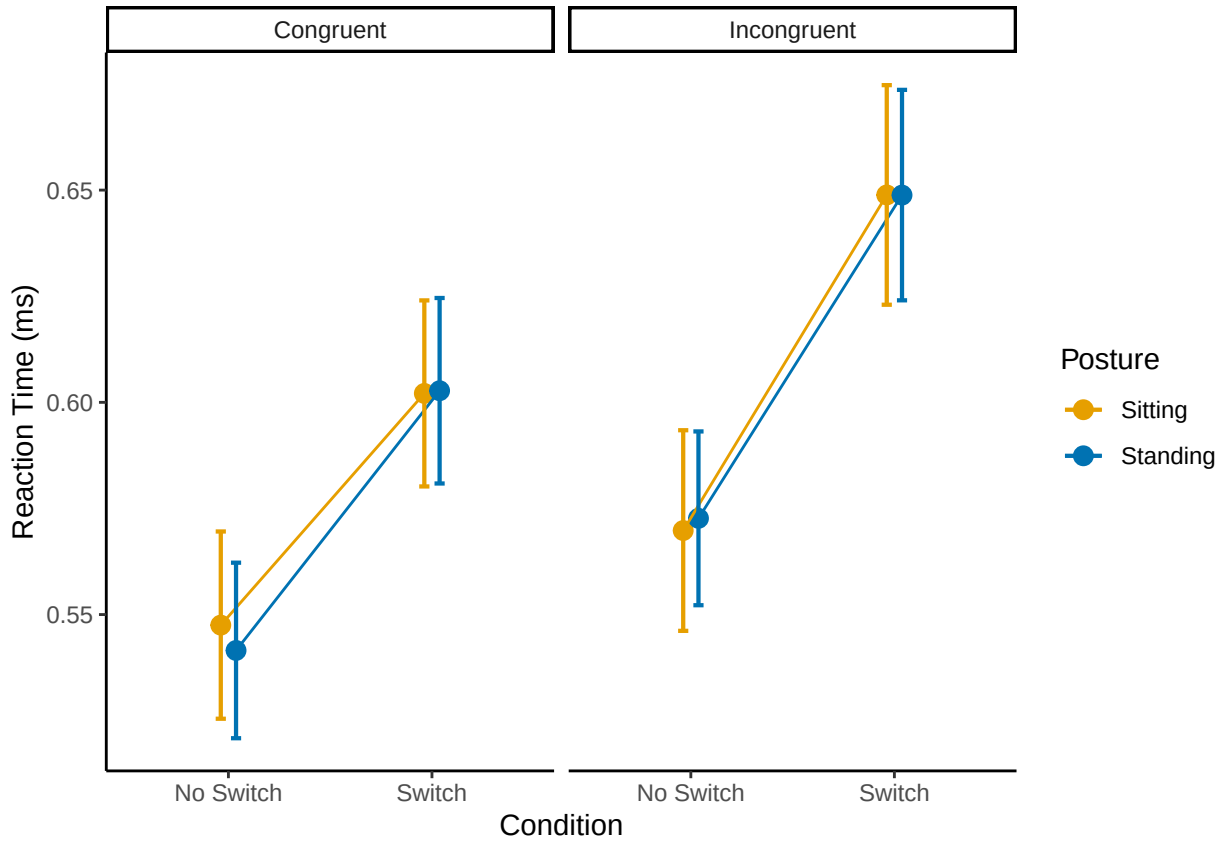
```
## `summarise()` has grouped output by 'participant', 'posture', 'congruentTrialType'. You can override
## using the `.groups` argument.
```

```
#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")) +
  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$ANOVA)
output_rt <- aovEffectSize(exp1_anova_rt, effectSize = "pes")
output_rt <- data.frame(output_rt$ANOVA)
write.csv(output_rt, "Task_switching_ANOVA_RT.csv")
output_rt
```

```
##                                    Effect DFn DFd          SSn        SSd             F
## 1                             (Intercept)   1  50 1.428705e+02 4.29367155 1.663733e+03
## 2                                 posture   1  50 3.979595e-05 0.43347417 4.590349e-03
## 3                       congruentTrialType   1  50 1.363938e-01 0.14478068 4.710359e+01
## 4                          switchTrialType   1  50 4.682022e-01 0.16485963 1.420003e+02
## 5                 posture:congruentTrialType   1  50 4.266607e-04 0.06545830 3.259027e-01
```

```
## 6                    posture:switchTrialType   1  50 8.700576e-05 0.05211061 8.348180e-02
## 7         congruentTrialType:switchTrialType   1  50 9.914733e-03 0.04607197 1.076005e+01
## 8 posture:congruentTrialType:switchTrialType   1  50 5.769395e-04 0.06995820 4.123459e-01
##              p p..05          pes
## 1 4.809845e-40     * 9.708239e-01
## 2 9.462532e-01       9.179855e-05
## 3 9.823661e-09     * 4.850860e-01
## 4 3.195952e-16     * 7.395837e-01
## 5 5.706388e-01       6.475845e-03
## 6 7.738279e-01       1.666853e-03
## 7 1.893419e-03     * 1.770909e-01
## 8 5.237146e-01       8.179462e-03
```

### Reproduce ANOVA for Smith et al. task-switching data

```
#load acc data
Smith_Exp2_acc <- read_excel("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, "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
```

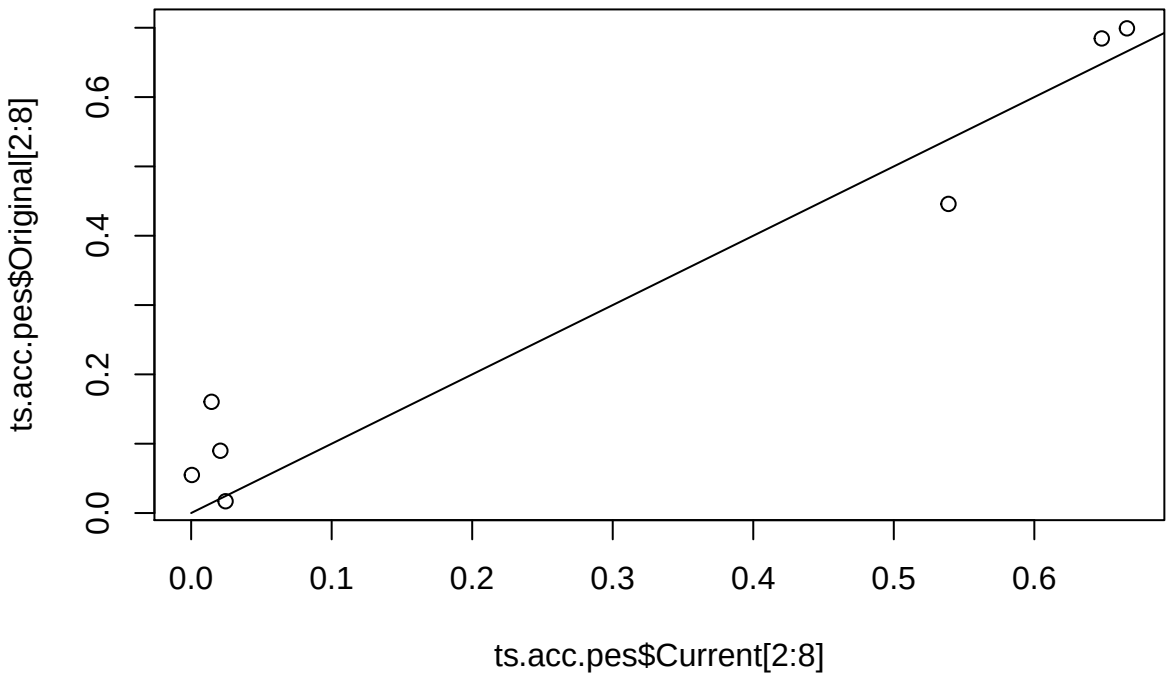
```
#plot acc effect sizes for our results and Smith together
#Check that ANOVA tables (rows) match
output_acc$Effect
```

```
## [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"
```

```
ts.acc.pes <- data.frame(matrix(nrow = 8, ncol = 3))
ts.acc.pes[1] <- output_acc$Effect
ts.acc.pes[2] <- output_acc$pes
ts.acc.pes[3] <- output_Smith_exp2_acc$pes

colnames(ts.acc.pes) <- c("Effect", "Current", "Original")
plot(ts.acc.pes$Current[2:8], ts.acc.pes$Original[2:8])
lines(x = c(0,1), y = c(0,1))
```




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

```
## [1] 0.09049606
```

```
#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)

ts.acc.pes.int <- data.frame(matrix(nrow = 2, ncol = 5))
colnames(ts.acc.pes.int) <- c("Exp", "Effect.size", "CI.Lower", "CI.Upper", "name")
ts.acc.pes.int[1] <- c("Current", "Original")
ts.acc.pes.int[1,2:4] <- c(ts.acc.pes$Current[6], data.frame(interaction_effect_CI))
ts.acc.pes.int[2,2:4] <- c(ts.acc.pes$Original[6], data.frame(interaction.original))
ts.acc.pes.int[1:2,5] <- c("Accuracy", "Accuracy")
#Graph comparison of key effects for all three experiments- Similar to forest plot in sig
#filtering paper?
forest.colors <- c("black", "red")

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

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

```
## 'data.frame':    2 obs. of  5 variables:
```

```
##  $ Exp        : Factor w/ 2 levels "Current","Original": 1 2
##  $ Effect.size: num  0.0145 0.1604
##  $ CI.Lower   : num  0 0.011
##  $ CI.Upper   : num  0.107 0.347
##  $ name       : chr  "Accuracy" "Accuracy"
```

```
forest.comp <- mod.forestplot(df = ts.acc.pes.int,
                              estimate = Effect.size,
                              ci.lower = CI.Lower,
                              ci.upper = CI.Upper,
                              colour = Exp,
                              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
```