

Smith Replication: Primary Data Analysis

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2022-11-07

Session Information

```
# References for R packages
# install.packages(devtools)
# require(devtools)
# devtools::install_github("crsh/papaja")
# require(papaja)
#
# papaja::r_refs(file = "results/r-package-refs.bib") #<-- writes bib file w/refs

#Save package versions
#renv::snapshot()

sessionInfo()

## R version 4.2.1 (2022-06-23 ucrt)
## Platform: x86_64-w64-mingw32/x64 (64-bit)
## Running under: Windows 10 x64 (build 19044)
##
## Matrix products: default
##
## locale:
## [1] LC_COLLATE=English_United States.utf8  LC_CTYPE=English_United States.utf8
## [3] LC_MONETARY=English_United States.utf8 LC_NUMERIC=C
## [5] LC_TIME=English_United States.utf8
##
## attached base packages:
## [1] stats      graphics  grDevices  utils      datasets  methods   base
##
## other attached packages:
## [1] labeling_0.4.2      MBESS_4.9.2          highr_0.9            farver_2.1.1
## [5] ggstance_0.3.5       scales_1.2.0         rlang_1.0.4          cowplot_1.1.1
## [9] readxl_1.4.0         reshape2_1.4.4       superb_0.95.0        psychReport_3.0.1
## [13] apaTables_2.0.8      psych_2.2.5          BayesFactor_0.9.12-4.4 coda_0.19-4
## [17] ez_4.4-0             afex_1.1-1           lme4_1.1-30          Matrix_1.4-1
## [21] forcats_0.5.1        stringr_1.4.0        dplyr_1.0.9          purrr_0.3.4
## [25] readr_2.1.2          tidyr_1.2.0          tibble_3.1.8         ggplot2_3.3.6
## [29] tidyverse_1.3.2      plyr_1.8.7           rmarkdown_2.14       knitr_1.39
## [33] pacman_0.5.1
##
## loaded via a namespace (and not attached):
## [1] TH.data_1.1-1        googledrive_2.0.0    minqa_1.2.4          colorspace_2.0-3
```

```
## [5] ellipsis_0.3.2      estimability_1.4    fs_1.5.2            rstudioapi_0.13
## [9] MatrixModels_0.5-0  fansi_1.0.3         mvtnorm_1.1-3       lubridate_1.8.0
## [13] xml2_1.3.3          codetools_0.2-18    splines_4.2.1       mnormt_2.1.0
## [17] jsonlite_1.8.0      lsr_0.5.2           nloptr_2.0.3        broom_1.0.0
## [21] dbplyr_2.2.1        shiny_1.7.2         compiler_4.2.1       httr_1.4.3
## [25] emmeans_1.7.5       backports_1.4.1     assertthat_0.2.1    fastmap_1.1.0
## [29] gargle_1.2.0        cli_3.3.0           later_1.3.0         htmltools_0.5.3
## [33] tools_4.2.1         lmerTest_3.1-3      gtable_0.3.0        glue_1.6.2
## [37] Rcpp_1.0.9          carData_3.0-5       cellranger_1.1.0    vctrs_0.4.1
## [41] nlme_3.1-157        xfun_0.31           rbibutils_2.2.8     rvest_1.0.2
## [45] mime_0.12           lifecycle_1.0.1     googlesheets4_1.0.0 MASS_7.3-57
## [49] zoo_1.8-11          shinyBS_0.61.1      promises_1.2.0.1    hms_1.1.1
## [53] parallel_4.2.1      sandwich_3.0-2      yaml_2.3.5          pbapply_1.5-0
## [57] stringi_1.7.8       boot_1.3-28         Rdpack_2.4          pkgconfig_2.0.3
## [61] evaluate_0.15       lattice_0.20-45     tidyselect_1.1.2    magrittr_2.0.3
## [65] R6_2.5.1            generics_0.1.3      multcomp_1.4-20     DBI_1.1.3
## [69] foreign_0.8-82      pillar_1.8.0        haven_2.5.0         withr_2.5.0
## [73] mgcv_1.8-40         survival_3.3-1      abind_1.4-5         modelr_0.1.8
## [77] crayon_1.5.1        car_3.1-0           utf8_1.2.2          tzdb_0.3.0
## [81] grid_4.2.1          reprex_2.0.1        digest_0.6.29       xtable_1.8-4
## [85] httpuv_1.6.5        numDeriv_2016.8-1.1 munsell_0.5.0
```

Unconventional Analysis:

Time-Outs (≥ 1500 ms to respond) are treated as errors. The primary results are reported using this atypical approach to be consistent with the original paper by Smith et al. Near the end we also present a *Conventional* Analysis which drops the time-outs for Percent Error (PE) results.

Experiment 1 - Stroop

Import and clean data

```
stroop_files = list.files(path = "data/Experiment 1 Data/", full.names = T)
stroop_files = stroop_files[str_detect(stroop_files, pattern="(?.*SJ)(?=.*.txt)")]

mergedStroopData <- ldply(stroop_files,
  read.delim,
  header=FALSE,
  stringsAsFactors = FALSE,
  sep = "") #for each item in the list apply the function read.delim

names(mergedStroopData) = c("sj",
  "cb",
  "blockNumber",
  "blockType",
  "trialNum",
  "congruency",
  "posture",
  "wordStim",
  "inkColour",
  "rt",
  "cResp",
  "resp",
```

```

"ac")
#...remove problem subjects
#.. No subjects pre-identified as needing to be removed (see ethics protocol)

#...check number of observations per condition
ftable(posture+congruency~sj, mergedStroopData)

```

##	posture	SITTING			STANDING		
##	congruency	congruent	incongruent	neutral	congruent	incongruent	neutral
## sj							
## 1		60	60	60	60	60	60
## 2		60	60	60	60	60	60
## 3		60	60	60	60	60	60
## 4		60	60	60	60	60	60
## 5		60	60	60	60	60	60
## 6		60	60	60	60	60	60
## 7		60	60	60	60	60	60
## 8		60	60	60	60	60	60
## 9		60	60	60	60	60	60
## 10		60	60	60	60	60	60
## 11		60	60	60	60	60	60
## 12		60	60	60	60	60	60
## 13		60	60	60	60	60	60
## 14		60	60	60	60	60	60
## 15		60	60	60	60	60	60
## 16		60	60	60	60	60	60
## 17		60	60	60	60	60	60
## 18		60	60	60	60	60	60
## 19		60	60	60	60	60	60
## 20		60	60	60	60	60	60
## 21		60	60	60	60	60	60
## 22		120	120	120	120	120	120
## 24		60	60	60	60	60	60
## 25		60	60	60	60	60	60
## 26		60	60	60	60	60	60
## 27		60	60	60	60	60	60
## 28		60	60	60	60	60	60
## 29		60	60	60	60	60	60
## 30		60	60	60	60	60	60
## 31		60	60	60	60	60	60
## 32		60	60	60	60	60	60
## 33		60	60	60	60	60	60
## 34		60	60	60	60	60	60
## 35		60	60	60	60	60	60
## 36		60	60	60	60	60	60
## 37		60	60	60	60	60	60
## 38		60	60	60	60	60	60
## 39		60	60	60	60	60	60
## 40		60	60	60	60	60	60
## 41		60	60	60	60	60	60
## 42		60	60	60	60	60	60
## 43		60	60	60	60	60	60
## 44		60	60	60	60	60	60
## 45		60	60	60	60	60	60

## 46	60	60	60	60	60	60
## 47	60	60	60	60	60	60
## 48	60	60	60	60	60	60
## 49	60	60	60	60	60	60
## 50	60	60	60	60	60	60

```
ftable(blockType~sj, mergedStroopData)
```

##	blockType	experimental	practice
##	sj		
## 1		288	72
## 2		288	72
## 3		288	72
## 4		288	72
## 5		288	72
## 6		288	72
## 7		288	72
## 8		288	72
## 9		288	72
## 10		288	72
## 11		288	72
## 12		288	72
## 13		288	72
## 14		288	72
## 15		288	72
## 16		288	72
## 17		288	72
## 18		288	72
## 19		288	72
## 20		288	72
## 21		288	72
## 22		576	144
## 24		288	72
## 25		288	72
## 26		288	72
## 27		288	72
## 28		288	72
## 29		288	72
## 30		288	72
## 31		288	72
## 32		288	72
## 33		288	72
## 34		288	72
## 35		288	72
## 36		288	72
## 37		288	72
## 38		288	72
## 39		288	72
## 40		288	72
## 41		288	72
## 42		288	72
## 43		288	72
## 44		288	72
## 45		288	72
## 46		288	72

```
## 47          288      72
## 48          288      72
## 49          288      72
## 50          288      72
```

```
#...need to fix SJ - same one was used with two counterbalances
```

```
mergedStroopData$sj = paste(mergedStroopData$sj,"_",mergedStroopData$cb,sep="")
```

```
#...check for missing data
```

```
mergedStroopData[!complete.cases(mergedStroopData),]
```

##	sj	cb	blockNumber	blockType	trialNum	congruency	posture	wordStim	inkColour	rt	cResp
## 646	10_2	2	8	experimental	34	incongruent	STANDING	RED	green	0	2
## 1081	12_2	2	1	practice	1	neutral	SITTING	XXXXX	green	0	2
## 1117	12_2	2	2	experimental	1	incongruent	SITTING	GREEN	red	0	1
## 1445	13_1	1	1	practice	5	incongruent	STANDING	GREEN	red	0	1
## 1801	14_2	2	1	practice	1	neutral	SITTING	XXX	green	0	2
## 2162	15_1	1	1	practice	2	congruent	STANDING	GREEN	green	0	2
## 2163	15_1	1	1	practice	3	neutral	STANDING	XXXXX	green	0	2
## 2615	16_2	2	3	experimental	23	incongruent	SITTING	RED	green	0	2
## 2720	16_2	2	6	practice	20	neutral	STANDING	XXX	red	0	1
## 2737	16_2	2	7	experimental	1	incongruent	STANDING	GREEN	red	0	1
## 2885	17_1	1	1	practice	5	incongruent	STANDING	RED	green	0	2
## 3360	18_2	2	4	experimental	12	incongruent	SITTING	GREEN	red	0	1
## 3457	18_2	2	7	experimental	1	incongruent	STANDING	RED	green	0	2
## 3601	19_1	1	1	practice	1	congruent	STANDING	RED	red	0	1
## 4370	20_2	2	2	experimental	14	neutral	SITTING	XXXXX	red	0	1
## 4505	20_2	2	6	practice	5	incongruent	STANDING	GREEN	red	0	1
## 4681	21_1	1	1	practice	1	congruent	STANDING	RED	red	0	1
## 4682	21_1	1	1	practice	2	neutral	STANDING	XXX	red	0	1
## 4692	21_1	1	1	practice	12	incongruent	STANDING	RED	green	0	2
## 5041	22_1	1	1	practice	1	incongruent	STANDING	GREEN	red	0	1
## 5042	22_1	1	1	practice	2	incongruent	STANDING	RED	green	0	2
## 5043	22_1	1	1	practice	3	neutral	STANDING	XXX	red	0	1
## 5422	22_2	2	1	practice	22	incongruent	SITTING	GREEN	red	0	1
## 5428	22_2	2	1	practice	28	incongruent	SITTING	RED	green	0	2
## 5501	22_2	2	3	experimental	29	neutral	SITTING	XXXXX	red	0	1
## 5530	22_2	2	4	experimental	22	incongruent	SITTING	RED	green	0	2
## 5533	22_2	2	4	experimental	25	incongruent	SITTING	RED	green	0	2
## 5608	22_2	2	6	practice	28	incongruent	STANDING	GREEN	red	0	1
## 5621	22_2	2	7	experimental	5	neutral	STANDING	XXXXX	green	0	2
## 5644	22_2	2	7	experimental	28	neutral	STANDING	XXX	green	0	2
## 5668	22_2	2	8	experimental	16	incongruent	STANDING	GREEN	red	0	1
## 5684	22_2	2	8	experimental	32	neutral	STANDING	XXXXX	red	0	1
## 5741	22_2	2	10	experimental	17	neutral	STANDING	XXX	green	0	2
## 5761	24_2	2	1	practice	1	congruent	SITTING	RED	red	0	1
## 5763	24_2	2	1	practice	3	congruent	SITTING	GREEN	green	0	2
## 5768	24_2	2	1	practice	8	neutral	SITTING	XXX	green	0	2
## 5770	24_2	2	1	practice	10	incongruent	SITTING	RED	green	0	2
## 5772	24_2	2	1	practice	12	congruent	SITTING	GREEN	green	0	2
## 5773	24_2	2	1	practice	13	neutral	SITTING	XXX	red	0	1
## 5775	24_2	2	1	practice	15	incongruent	SITTING	GREEN	red	0	1
## 5776	24_2	2	1	practice	16	neutral	SITTING	XXXXX	green	0	2
## 5797	24_2	2	2	experimental	1	neutral	SITTING	XXXXX	green	0	2
## 5798	24_2	2	2	experimental	2	incongruent	SITTING	RED	green	0	2

## 6018	24_2	2	8	experimental	6	congruent	STANDING	RED	red	0	1
## 6121	25_1	1	1	practice	1	neutral	STANDING	XXX	red	0	1
## 6482	26_2	2	1	practice	2	neutral	SITTING	XXXXX	red	0	1
## 6518	26_2	2	2	experimental	2	incongruent	SITTING	RED	green	0	2
## 6841	27_1	1	1	practice	1	congruent	STANDING	RED	red	0	1
## 6842	27_1	1	1	practice	2	neutral	STANDING	XXXXX	green	0	2
## 6843	27_1	1	1	practice	3	neutral	STANDING	XXXXX	red	0	1
## 7202	28_2	2	1	practice	2	incongruent	SITTING	GREEN	red	0	1
## 7921	3_1	1	1	practice	1	congruent	STANDING	GREEN	green	0	2
## 7957	3_1	1	2	experimental	1	neutral	STANDING	XXXXX	red	0	1
## 8858	31_1	1	7	experimental	2	congruent	SITTING	RED	red	0	1
## 9253	32_2	2	8	experimental	1	neutral	STANDING	XXX	green	0	2
## 9361	33_1	1	1	practice	1	congruent	STANDING	RED	red	0	1
## 9364	33_1	1	1	practice	4	incongruent	STANDING	GREEN	red	0	1
## 9386	33_1	1	1	practice	26	congruent	STANDING	GREEN	green	0	2
## 9390	33_1	1	1	practice	30	neutral	STANDING	XXX	red	0	1
## 9505	33_1	1	5	experimental	1	neutral	STANDING	XXXXX	red	0	1
## 10441	36_2	2	1	practice	1	congruent	SITTING	GREEN	green	0	2
## 10444	36_2	2	1	practice	4	incongruent	SITTING	GREEN	red	0	1
## 10447	36_2	2	1	practice	7	incongruent	SITTING	RED	green	0	2
## 10448	36_2	2	1	practice	8	neutral	SITTING	XXX	green	0	2
## 10535	36_2	2	3	experimental	23	incongruent	SITTING	GREEN	red	0	1
## 10639	36_2	2	6	practice	19	neutral	STANDING	XXXXX	green	0	2
## 10785	36_2	2	10	experimental	21	congruent	STANDING	GREEN	green	0	2
## 11294	38_2	2	4	experimental	26	incongruent	SITTING	RED	green	0	2
## 11387	38_2	2	7	experimental	11	neutral	STANDING	XXX	green	0	2
## 11418	38_2	2	8	experimental	6	incongruent	STANDING	RED	green	0	2
## 11421	38_2	2	8	experimental	9	incongruent	STANDING	GREEN	red	0	1
## 12202	4_2	2	9	experimental	34	incongruent	STANDING	GREEN	red	0	1
## 12241	40_2	2	1	practice	1	incongruent	SITTING	RED	green	0	2
## 13603	43_1	1	8	experimental	31	incongruent	SITTING	RED	green	0	2
## 13688	44_2	2	1	practice	8	incongruent	SITTING	RED	green	0	2
## 13689	44_2	2	1	practice	9	incongruent	SITTING	GREEN	red	0	1
## 13694	44_2	2	1	practice	14	incongruent	SITTING	GREEN	red	0	1
## 13695	44_2	2	1	practice	15	neutral	SITTING	XXXXX	red	0	1
## 13696	44_2	2	1	practice	16	incongruent	SITTING	RED	green	0	2
## 13702	44_2	2	1	practice	22	congruent	SITTING	GREEN	green	0	2
## 13709	44_2	2	1	practice	29	incongruent	SITTING	GREEN	red	0	1
## 13713	44_2	2	1	practice	33	incongruent	SITTING	RED	green	0	2
## 13715	44_2	2	1	practice	35	incongruent	SITTING	GREEN	red	0	1
## 13716	44_2	2	1	practice	36	congruent	SITTING	GREEN	green	0	2
## 13717	44_2	2	2	experimental	1	congruent	SITTING	RED	red	0	1
## 13721	44_2	2	2	experimental	5	incongruent	SITTING	GREEN	red	0	1
## 14041	45_1	1	1	practice	1	congruent	STANDING	GREEN	green	0	2
## 14379	45_1	1	10	experimental	15	neutral	SITTING	XXXXX	green	0	2
## 14864	47_1	1	3	experimental	32	congruent	STANDING	RED	red	0	1
## 14901	47_1	1	4	experimental	33	neutral	STANDING	XXX	green	0	2
## 14958	47_1	1	6	practice	18	incongruent	SITTING	RED	green	0	2
## 15121	48_2	2	1	practice	1	congruent	SITTING	GREEN	green	0	2
## 15842	5_1	1	1	practice	2	incongruent	STANDING	GREEN	red	0	1
## 15843	5_1	1	1	practice	3	congruent	STANDING	RED	red	0	1
## 15845	5_1	1	1	practice	5	congruent	STANDING	GREEN	green	0	2
## 15846	5_1	1	1	practice	6	incongruent	STANDING	RED	green	0	2
## 15847	5_1	1	1	practice	7	neutral	STANDING	XXX	green	0	2

## 16107	5_1	1	8 experimental	15 neutral	SITTING	XXX	red	0	1
## 16201	50_2	2	1 practice	1 incongruent	SITTING	GREEN	red	0	1
## 16565	6_2	2	1 practice	5 congruent	SITTING	RED	red	0	1
## 16957	7_1	1	2 experimental	1 neutral	STANDING	XXX	green	0	2
## 17282	8_2	2	1 practice	2 incongruent	SITTING	GREEN	red	0	1
## 17643	9_1	1	1 practice	3 congruent	STANDING	GREEN	green	0	2
## 17644	9_1	1	1 practice	4 incongruent	STANDING	RED	green	0	2
##	resp	ac							
## 646	0	NA							
## 1081	0	NA							
## 1117	0	NA							
## 1445	0	NA							
## 1801	0	NA							
## 2162	0	NA							
## 2163	0	NA							
## 2615	0	NA							
## 2720	0	NA							
## 2737	0	NA							
## 2885	0	NA							
## 3360	0	NA							
## 3457	0	NA							
## 3601	0	NA							
## 4370	0	NA							
## 4505	0	NA							
## 4681	0	NA							
## 4682	0	NA							
## 4692	0	NA							
## 5041	0	NA							
## 5042	0	NA							
## 5043	0	NA							
## 5422	0	NA							
## 5428	0	NA							
## 5501	0	NA							
## 5530	0	NA							
## 5533	0	NA							
## 5608	0	NA							
## 5621	0	NA							
## 5644	0	NA							
## 5668	0	NA							
## 5684	0	NA							
## 5741	0	NA							
## 5761	0	NA							
## 5763	0	NA							
## 5768	0	NA							
## 5770	0	NA							
## 5772	0	NA							
## 5773	0	NA							
## 5775	0	NA							
## 5776	0	NA							
## 5797	0	NA							
## 5798	0	NA							
## 6018	0	NA							
## 6121	0	NA							
## 6482	0	NA							

## 6518	0 NA
## 6841	0 NA
## 6842	0 NA
## 6843	0 NA
## 7202	0 NA
## 7921	0 NA
## 7957	0 NA
## 8858	0 NA
## 9253	0 NA
## 9361	0 NA
## 9364	0 NA
## 9386	0 NA
## 9390	0 NA
## 9505	0 NA
## 10441	0 NA
## 10444	0 NA
## 10447	0 NA
## 10448	0 NA
## 10535	0 NA
## 10639	0 NA
## 10785	0 NA
## 11294	0 NA
## 11387	0 NA
## 11418	0 NA
## 11421	0 NA
## 12202	0 NA
## 12241	0 NA
## 13603	0 NA
## 13688	0 NA
## 13689	0 NA
## 13694	0 NA
## 13695	0 NA
## 13696	0 NA
## 13702	0 NA
## 13709	0 NA
## 13713	0 NA
## 13715	0 NA
## 13716	0 NA
## 13717	0 NA
## 13721	0 NA
## 14041	0 NA
## 14379	0 NA
## 14864	0 NA
## 14901	0 NA
## 14958	0 NA
## 15121	0 NA
## 15842	0 NA
## 15843	0 NA
## 15845	0 NA
## 15846	0 NA
## 15847	0 NA
## 16107	0 NA
## 16201	0 NA
## 16565	0 NA


```
## 16957    0 NA
## 17282    0 NA
## 17643    0 NA
## 17644    0 NA
```

```
##...THERE IS MISSING DATA, BUT IT IS EXPECTED:
##...There are trials where the the experiment times out
##...can be identified as RT == 0
##...trials where a response was not made have an RT =0, resp=0 and ac = NA

##...get the number of time outs
dim(mergedStroopData[!complete.cases(mergedStroopData),])[1]
```

```
## [1] 104
```

```
##...how are the missing trials distributed???
timeOutStroopData = mergedStroopData[!complete.cases(mergedStroopData),]

ftable(posture~congruency, timeOutStroopData)
```

```
##           posture SITTING STANDING
## congruency
## congruent           10          14
## incongruent         29          18
## neutral             13          20
```

```
ftable(blockType~sj, timeOutStroopData)
```

```
##           blockType experimental practice
## sj
## 10_2           1           0
## 12_2           1           1
## 13_1           0           1
## 14_2           0           1
## 15_1           0           2
## 16_2           2           1
## 17_1           0           1
## 18_2           2           0
## 19_1           0           1
## 20_2           1           1
## 21_1           0           3
## 22_1           0           3
## 22_2           8           3
## 24_2           3           8
## 25_1           0           1
## 26_2           1           1
## 27_1           0           3
## 28_2           0           1
## 3_1            1           1
## 31_1           1           0
## 32_2           1           0
## 33_1           1           4
## 36_2           2           5
## 38_2           4           0
## 4_2            1           0
## 40_2           0           1
```

```

## 43_1          1      0
## 44_2          2     10
## 45_1          1      1
## 47_1          2      1
## 48_2          0      1
## 5_1           1      5
## 50_2          0      1
## 6_2           0      1
## 7_1           1      0
## 8_2           0      1
## 9_1           0      2

#...this code changes the "time-out" trials as errors
#...see Davoli et al.
mergedStroopData$ac[mergedStroopData$rt==0] = 0

#...remove practice trials
mergedStroopData <- mergedStroopData[!mergedStroopData$blockType=="practice",]

#...check that only experimental trials are left
unique(mergedStroopData$blockType)

## [1] "experimental"

totalStroopTrials = dim(mergedStroopData)[1]
observationDataStroop = data.frame(ftable(blockType~sj, mergedStroopData))[,c(1,3)]

#...remove trials faster than 100ms
# mergedStroopData= mergedStroopData[!mergedStroopData$rt==0,] #...greater than 1500ms
mergedStroopData= mergedStroopData[!(mergedStroopData$rt<=100 & mergedStroopData$rt > 0),]
validStroopRTTrials = dim(mergedStroopData)[1]
observationDataStroop$validTrials = data.frame(ftable(blockType~sj, mergedStroopData))[,c(3)]

print(paste("percent invalid trials = ",
            ((totalStroopTrials-validStroopRTTrials)/totalStroopTrials)*100))

## [1] "percent invalid trials = 0.006944444444444444"

#Drops "time-out" trials
mergedStroopData.conventional <- mergedStroopData %>%
  filter(rt != 0 & resp != 0)

write.csv(mergedStroopData, file = "results/exp1_merged_stroop_data.csv",
          row.names = F)

#Conventional analysis drops the time out trials, rather than treating as errors
write.table(mergedStroopData.conventional, file = "results/exp1_merged_stroop_data_conv.txt",
            row.names = F)

stroopCorrect = mergedStroopData[mergedStroopData$ac == 1, ]

# mergedDataSet = mergedDataSet[mergedDataSet$ac ==1,]
errorsRemoved = dim(stroopCorrect)[1] #...total remaining trials
observationDataStroop$correctTrials = data.frame(ftable(blockType~sj, stroopCorrect))[,c(3)]
trimInfo = data.frame(totalStroopTrials, validStroopRTTrials,errorsRemoved)
head(trimInfo)

```

```
## totalStroopTrials validStroopRTTrials errorsRemoved
## 1 14400 14399 13852
#...percent of error trials lost
print(paste("percent errors removed = ",
            (((validStroopRTTrials-errorsRemoved)/totalStroopTrials)*100)))

## [1] "percent errors removed = 3.79861111111111"
#####
#...CHECK 20% CRITERION
#####
observationDataStroop$percentLoss =
  ((observationDataStroop$Freq-observationDataStroop$correctTrials)/
   observationDataStroop$Freq)*100

observationDataStroop$percentLoss

## [1] 3.472222 1.736111 0.347222 6.944444 1.736111 4.166667 4.513889 1.736111
## [9] 1.041667 1.736111 1.736111 3.125000 2.083333 4.513889 1.736111 10.069444
## [17] 8.680556 0.347222 2.083333 4.513889 4.861111 1.388889 1.388889 3.472222
## [25] 16.666667 1.736111 15.972222 1.041667 0.000000 5.555556 2.083333 8.680556
## [33] 0.347222 3.125000 1.736111 2.083333 4.166667 2.777778 2.430556 7.638889
## [41] 1.041667 4.166667 2.777778 1.041667 5.555556 3.125000 10.069444 1.736111
## [49] 3.472222 3.819444

sum(observationDataStroop$percentLoss>20)

## [1] 0
#...None!

#...RUN TRIMMING PROCEDURE
tempList = pjRecursiveTrim2(stroopCorrect, #...dataset
                             "rt", #...dependent variables
                             c("sj",
                               "cb",
                               "congruency",
                               "posture")) #.independent variables

trimmedStroopData=tempList[[1]]
totalStroopN = tempList[[2]]
rejectedStroop = tempList[[3]]
percentTrimmedStroop = tempList[[4]]
NcellsStroop = tempList[[5]]

#...get the trimming info
trimOutputStroop= data.frame(totalStroopN, rejectedStroop,percentTrimmedStroop,NcellsStroop)
head(trimOutputStroop)

## totalStroopN rejectedStroop percentTrimmedStroop NcellsStroop
## 1 13852 292 2.107999 300

stroopRT = plyr::ddply(trimmedStroopData,
                      .(sj, cb,congruency,posture),
                      summarise,
```

```

meanRT = mean(rt))

head(stroopRT)

##      sj cb congruency posture meanRT
## 1 1_1 1 congruent SITTING 471.6458
## 2 1_1 1 congruent STANDING 400.0638
## 3 1_1 1 incongruent SITTING 430.0455
## 4 1_1 1 incongruent STANDING 439.8444
## 5 1_1 1 neutral SITTING 454.5455
## 6 1_1 1 neutral STANDING 408.4565

#...get error data
stroopPE = plyr::ddply(mergedStroopData,
                      .(sj, cb, congruency, posture),
                      summarise,
                      meanPE = 100 - (mean(ac)*100))

head(stroopPE)

##      sj cb congruency posture meanPE
## 1 1_1 1 congruent SITTING 0.000000
## 2 1_1 1 congruent STANDING 0.000000
## 3 1_1 1 incongruent SITTING 4.166667
## 4 1_1 1 incongruent STANDING 6.250000
## 5 1_1 1 neutral SITTING 6.250000
## 6 1_1 1 neutral STANDING 4.166667

#...combine the RT and error data
stroopCombined = cbind(stroopRT, meanPE = stroopPE$meanPE)

head(stroopCombined)

##      sj cb congruency posture meanRT meanPE
## 1 1_1 1 congruent SITTING 471.6458 0.000000
## 2 1_1 1 congruent STANDING 400.0638 0.000000
## 3 1_1 1 incongruent SITTING 430.0455 4.166667
## 4 1_1 1 incongruent STANDING 439.8444 6.250000
## 5 1_1 1 neutral SITTING 454.5455 6.250000
## 6 1_1 1 neutral STANDING 408.4565 4.166667

#...set as factors
stroopCombined$sj = factor(stroopCombined$sj)
stroopCombined$cb = factor(stroopCombined$cb)

```

Reaction time results

```

rtModelStroop <- ezANOVA(stroopCombined,
                        dv = .(meanRT),
                        wid=.(sj),
                        within=.(posture, congruency),
                        detailed=TRUE,
                        type=3,
                        return_aov=TRUE)

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

```

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

```
rtModelStroop$ANOVA
```

	Effect	DFn	DFd	SSn	SSd	F	p	p<.05	ges
## 1	(Intercept)	1	49	6.530862e+07	1322013.63	2.420643e+03	2.233955e-43	*	0.9748634585
## 2	posture	1	49	8.221421e+02	156217.37	2.578776e-01	6.138604e-01		0.0004879807
## 3	congruency	2	98	7.093105e+04	154676.49	2.247026e+01	9.278220e-09	*	0.0404190166
## 4	posture:congruency	2	98	8.430066e+01	51054.35	8.090852e-02	9.223396e-01		0.0000500584

```
rtStroopMSE = rtModelStroop$ANOVA$SSd/rtModelStroop$ANOVA$DFd
```

```
##...print ANOVA in nice format
```

```
paste(rtModelStroop$ANOVA$Effect,": F(",
      rtModelStroop$ANOVA$DFn,
      ", ",
      rtModelStroop$ANOVA$DFd,
      ") = ",
      round(rtModelStroop$ANOVA$F,3),
      ", MSE = ",
      round(rtStroopMSE,3),
      ", p = ",
      round(rtModelStroop$ANOVA$p,3),
      ", partialEtaSq = ",
      round(rtModelStroop$ANOVA$SSn/(rtModelStroop$ANOVA$SSn+rtModelStroop$ANOVA$SSd),4),
      sep="")
```

```
## [1] "(Intercept): F(1, 49) = 2420.643, MSE = 26979.87, p = 0, partialEtaSq = 0.9802"
```

```
## [2] "posture: F(1, 49) = 0.258, MSE = 3188.11, p = 0.614, partialEtaSq = 0.0052"
```

```
## [3] "congruency: F(2, 98) = 22.47, MSE = 1578.332, p = 0, partialEtaSq = 0.3144"
```

```
## [4] "posture:congruency: F(2, 98) = 0.081, MSE = 520.963, p = 0.922, partialEtaSq = 0.0016"
```

```
##...CALCULATE THE BAYES FACTORS FOR THE RT ANALYSIS
```

```
stroopBF = stroopCombined
stroopBF$posture = factor(stroopBF$posture)
stroopBF$congruency = factor(stroopBF$congruency)
bfValues1 = anovaBF(meanRT~congruency*posture+sj,
                    data = stroopBF,
                    whichRandom = "sj",
                    method="laplace")
```

```
bfValues1
```

```
## Bayes factor analysis
```

```
## -----
```

```
## [1] congruency + sj : 35335703 ±NA%
```

```
## [2] posture + sj : 0.1461731 ±NA%
```

```
## [3] congruency + posture + sj : 5410998 ±NA%
```

```
## [4] congruency + posture + congruency:posture + sj : 346149.8 ±NA%
```

```
##
```

```
## Against denominator:
```

```
## meanRT ~ sj
```

```
## ---
```

```
## Bayes factor type: BFlinearModel, JZS
```

```
##...get the Bayes factor for the Null Interaction
```

```
bfValues1[3]/bfValues1[4]
```

```

## Bayes factor analysis
## -----
## [1] congruency + posture + sj : 15.63195 ±NA%
##
## Against denominator:
##   meanRT ~ congruency + posture + congruency:posture + sj
## ---
## Bayes factor type: BFlinearModel, JZS
1/(bfValues1[3]/bfValues1[4])

## Bayes factor analysis
## -----
## [1] congruency + posture + congruency:posture + sj : 0.06397154 ±NA%
##
## Against denominator:
##   meanRT ~ congruency + posture + sj
## ---
## Bayes factor type: BFlinearModel, JZS
# Difference scores and paired t-tests
#... stroop effect (incongruent - congruent) FOR Standing
standingStroop = stroopCombined[stroopCombined$posture=="STANDING", ]
standingStroop = standingStroop[standingStroop$congruency!="neutral", ]
t.test(standingStroop$meanRT[standingStroop$congruency=="congruent"],
       standingStroop$meanRT[standingStroop$congruency=="incongruent"],
       paired=TRUE )

##
## Paired t-test
##
## data: standingStroop$meanRT[standingStroop$congruency == "congruent"] and standingStroop$meanRT[standingStroop$congruency == "incongruent"]
## t = -4.3805, df = 49, p-value = 6.226e-05
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##   -53.81756 -19.96796
## sample estimates:
## mean difference
##   -36.89276

#... stroop effect (incongruent - congruent) FOR SITTING
sittingStroop = stroopCombined[stroopCombined$posture=="SITTING", ]
sittingStroop = sittingStroop[sittingStroop$congruency!="neutral", ]
t.test(sittingStroop$meanRT[sittingStroop$congruency=="congruent"],
       sittingStroop$meanRT[sittingStroop$congruency=="incongruent"],
       paired=TRUE )

##
## Paired t-test
##
## data: sittingStroop$meanRT[sittingStroop$congruency == "congruent"] and sittingStroop$meanRT[sittingStroop$congruency == "incongruent"]
## t = -5.1209, df = 49, p-value = 5.104e-06
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##   -52.27703 -22.81052
## sample estimates:

```

```
## mean difference
##      -37.54377
```

Percent error results

```
errModelStroop <- ezANOVA(stroopCombined,
                          dv = .(meanPE),
                          wid=.(sj),
                          within=.(posture,congruency),
                          detailed=TRUE,
                          type=3,
                          return_aov = TRUE)
```

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

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

```
errStroopMSE = errModelStroop$ANOVA$SSd/errModelStroop$ANOVA$DFd
```

```
exp1_ANOVA_acc_uncon <-
paste(errModelStroop$ANOVA$Effect,": F(",
      errModelStroop$ANOVA$DFn,
      ", ",
      errModelStroop$ANOVA$DFd,
      ") = ",
      round(errModelStroop$ANOVA$F,3),
      ", MSE = ",
      round(errStroopMSE,3),
      ", p = ",
      round(errModelStroop$ANOVA$p,3),
      ", partialEtaSq = ",
      round(errModelStroop$ANOVA$SSn/(errModelStroop$ANOVA$SSn+errModelStroop$ANOVA$SSd),4),
      sep="")
exp1_ANOVA_acc_uncon
```

```
## [1] "(Intercept): F(1, 49) = 57.526, MSE = 75.297, p = 0, partialEtaSq = 0.54"
## [2] "posture: F(1, 49) = 0.007, MSE = 16.562, p = 0.934, partialEtaSq = 1e-04"
## [3] "congruency: F(2, 98) = 11.598, MSE = 9.222, p = 0, partialEtaSq = 0.1914"
## [4] "posture:congruency: F(2, 98) = 1.59, MSE = 6.228, p = 0.209, partialEtaSq = 0.0314"
```

```
write.csv(exp1_ANOVA_acc_uncon, "results/exp1_ANOVA_PE_uncon.csv")
```

```
#BF for errors
```

```
bfValues1.error = anovaBF(meanPE~congruency*posture+sj,
                          data = stroopBF,
                          whichRandom = "sj",
                          method="laplace")
```

```
bfValues1.error
```

```
## Bayes factor analysis
```

```
## -----
```

```
## [1] congruency + sj : 776.6647 ±NA%
## [2] posture + sj : 0.1172445 ±NA%
## [3] congruency + posture + sj : 91.51836 ±NA%
## [4] congruency + posture + congruency:posture + sj : 13.90884 ±NA%
```

```

##
## Against denominator:
##   meanPE ~ sj
## ---
## Bayes factor type: BFlinearModel, JZS
#...get the Bayes factor for the Null Interaction
bfValues1.error[3]/bfValues1.error[4]

## Bayes factor analysis
## -----
## [1] congruency + posture + sj : 6.579869 ±NA%
##
## Against denominator:
##   meanPE ~ congruency + posture + congruency:posture + sj
## ---
## Bayes factor type: BFlinearModel, JZS
1/(bfValues1.error[3]/bfValues1.error[4])

## Bayes factor analysis
## -----
## [1] congruency + posture + congruency:posture + sj : 0.1519787 ±NA%
##
## Against denominator:
##   meanPE ~ congruency + posture + sj
## ---
## Bayes factor type: BFlinearModel, JZS
#...ERRORs
#... stroop effect (incongruent - congruent) FOR Standing
t.test(standingStroop$meanPE[standingStroop$congruency=="congruent"],
       standingStroop$meanPE[standingStroop$congruency=="incongruent"],
       paired=TRUE )

##
## Paired t-test
##
## data: standingStroop$meanPE[standingStroop$congruency == "congruent"] and standingStroop$meanPE[stan
## t = -2.0681, df = 49, p-value = 0.04393
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  -2.79325655 -0.04007678
## sample estimates:
## mean difference
##      -1.416667

#... stroop effect (incongruent - congruent) FOR SITTING
t.test(sittingStroop$meanPE[sittingStroop$congruency=="congruent"],
       sittingStroop$meanPE[sittingStroop$congruency=="incongruent"],
       paired=TRUE )

##
## Paired t-test
##
## data: sittingStroop$meanPE[sittingStroop$congruency == "congruent"] and sittingStroop$meanPE[sittin
## t = -4.6535, df = 49, p-value = 2.51e-05

```



```
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
## -3.758593 -1.491407
## sample estimates:
## mean difference
## -2.625
```

Make plots for Stroop

```
#...pull out summary statistics per condition averaged across subjects for graph
```

```
graphRT = describeBy(stroopCombined$meanRT,
                      list(stroopCombined$posture, stroopCombined$congruency),
                      mat=TRUE,
                      digits = 1)
```

```
graphPE = describeBy(stroopCombined$meanPE,
                      list(stroopCombined$posture, stroopCombined$congruency),
                      mat=TRUE,
                      digits = 1)
```

```
head(graphRT)
```

```
##      item  group1      group2 vars  n mean    sd median trimmed mad   min   max range skew
## X11     1  SITTING  congruent    1 50 450.8  56.3  443.0   446.5 45.5 348.3 598.3 250.0  0.7
## X12     2  STANDING  congruent    1 50 448.5  60.6  440.3   442.2 48.6 341.3 624.4 283.0  1.0
## X13     3  SITTING  incongruent    1 50 488.3  91.9  471.8   476.7 74.4 351.1 803.1 452.0  1.2
## X14     4  STANDING  incongruent    1 50 485.4 100.6  458.7   470.5 79.0 358.3 861.5 503.2  1.8
## X15     5  SITTING    neutral    1 50 465.6  66.3  456.6   460.1 49.7 357.8 702.6 344.7  1.0
## X16     6  STANDING    neutral    1 50 460.9  67.6  452.7   453.6 51.5 346.2 695.4 349.2  1.4
##      kurtosis  se
## X11         0.2  8.0
## X12         0.9  8.6
## X13         1.7 13.0
## X14         3.8 14.2
## X15         1.9  9.4
## X16         2.7  9.6
```

```
#...get rid of irrelevant columns
```

```
graphRT = graphRT[,c("group1", "group2", "mean", "se")]
graphPE = graphPE[,c("group1", "group2", "mean", "se")]
```

```
#...rename the variables
```

```
names(graphRT) = c("posture", "congruency", "mean", "se")
names(graphPE) = c("posture", "congruency", "mean", "se")
```

```
#...make sure posture is in UPPERCASE
```

```
graphRT$posture = str_to_upper(graphRT$posture)
```

```
#..calculate the within subjects confidence intervals based on loftus and masson
#..the confidence intervals are based on the interaction term.
```

```
inxn.rt.MSE = rtStroopMSE[4]
inxn.err.MSE = errStroopMSE[4]
```

```
graphRT$se = sqrt((inxn.rt.MSE)/length(unique(stroopCombined$sj)))
```

```

graphPE$se= sqrt((inxn.err.MSE)/length(unique(stroopCombined$sj)))

critT = qt(p=.025,df=length(unique(stroopCombined$sj))-2,lower.tail =FALSE)

#---add the min and max for the confidence intervals
graphRT$min = graphRT$mean - (graphRT$se*critT)
graphRT$max = graphRT$mean + (graphRT$se*critT)

####GET AC DATA FROM twoAnimalWordsPRPac.R
graphRT$ac = paste("(",format(round(graphPE$mean,digits=1),nsmall = 1),"),",sep="")
head(graphRT)

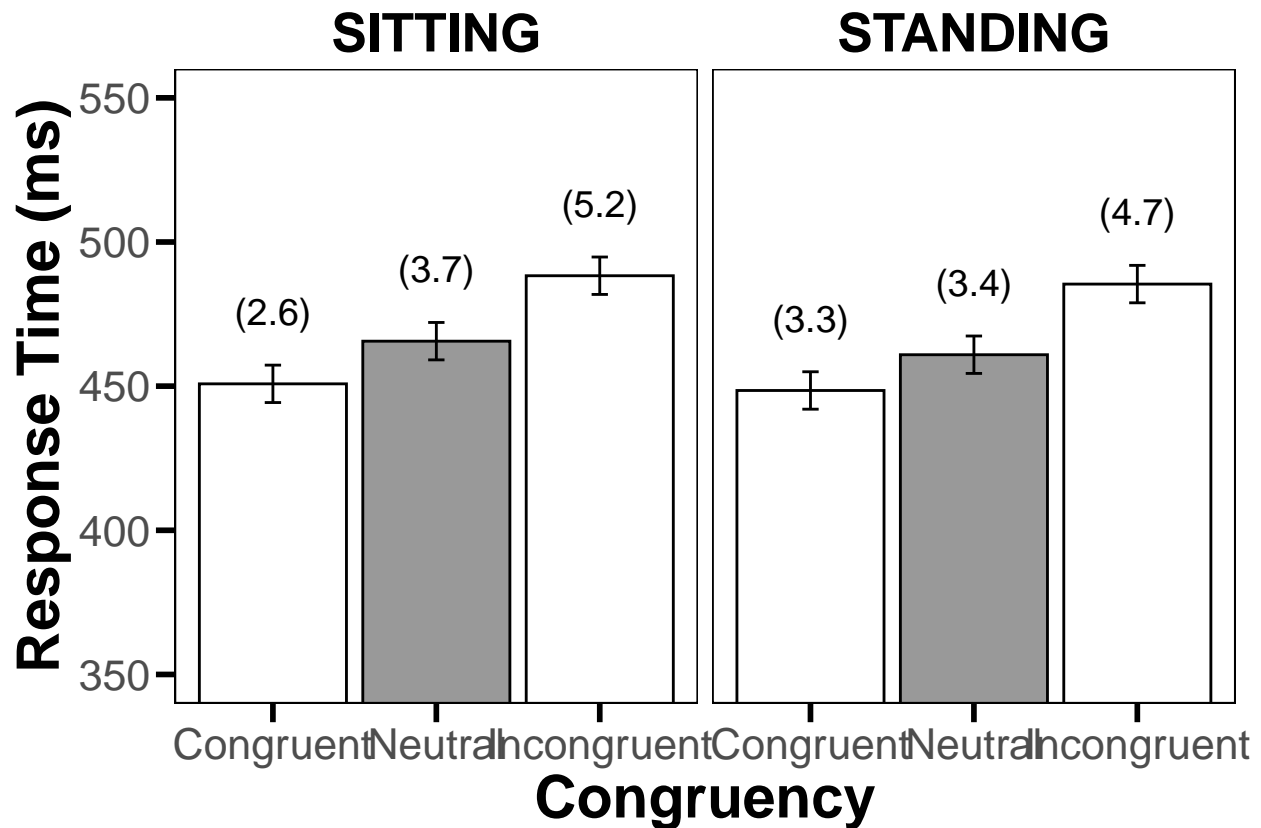
##      posture congruency mean      se      min      max      ac
## X11  SITTING   congruent 450.8 3.227887 444.3099 457.2901 (2.6)
## X12  STANDING   congruent 448.5 3.227887 442.0099 454.9901 (3.3)
## X13  SITTING  incongruent 488.3 3.227887 481.8099 494.7901 (5.2)
## X14  STANDING  incongruent 485.4 3.227887 478.9099 491.8901 (4.7)
## X15  SITTING    neutral 465.6 3.227887 459.1099 472.0901 (3.7)
## X16  STANDING    neutral 460.9 3.227887 454.4099 467.3901 (3.4)

#...used for positioning the accuracy data on the graph
graphRT$vAdj = 25 #down
graphRT$vAdj[graphRT$congruency=="incongruent"]=25 #up
graphRT$hAdj = 0 #right
#graphRT$hAdj[graphRT$posture=="SITTING"]=-60 #left
graphRT$congruency = factor(graphRT$congruency,labels = c("Congruent","Incongruent","Neutral"))
graphRT$congruency = factor(graphRT$congruency,levels=c("Congruent","Neutral","Incongruent"))

interactionPlot <- ggplot(graphRT, aes(congruency, mean, group=posture)) +
  theme(legend.position = "none")+
  scale_fill_manual(values=c("#FFFFFF","#999999","#FFFFFF","#999999")) +
  coord_cartesian(ylim=c(350,550),expand=TRUE) +
  scale_y_continuous(breaks = round(seq(350, 550, by = 50),0)) +
  geom_text(aes(label=ac),nudge_x=graphRT$hAdj,nudge_y =graphRT$vAdj, size=5) +
  geom_bar(stat="identity", aes(fill=interaction(congruency)),colour="black")+
  geom_errorbar(aes(ymin=min,ymax=max,group=interaction(posture,congruency)), width=.1)+
  labs(x = "Congruency", y = "Response Time (ms)") +
  theme(axis.ticks = element_line(size = 1, colour = "black", linetype = "solid"),
        axis.ticks.length = unit(.25,"cm"),
        #axis.line = element_line(size = 1, colour = "black", linetype = "solid"),
        panel.background = element_rect(fill = "white", colour = "white", size = 1),
        axis.text=element_text(size=16),
        axis.title=element_text(size=22,face="bold"),
        strip.text = element_text(size = 20, face = "bold",colour = "black", angle = 0),
        panel.border = element_rect(colour = "black", fill = NA, size = 0.50),
        strip.background = element_rect(fill=NA,colour="NA",size = 2))+
  facet_grid(~posture)

interactionPlot

```



```
ggsave(interactionPlot,
  file = "results/plots/fig1_exp1_stroop_interaction_plot.pdf",
  units = "in",
  width = 8.5,
  height = 5,
  dpi = 600)
```

```
exp1.table <-
apa.2way.table(congruency,
  posture,
  meanRT,
  stroopCombined,
  show.conf.interval = TRUE,
  landscape=TRUE,
  filename = "results/plots/exp1_table.doc")
exp1.table
```

```
##
##
## Means and standard deviations for meanRT as a function of a 3(congruency) X 2(posture) design
##
##           M           M_95%_CI      SD
## posture:SITTING
##   congruency
```

```
##      congruent 450.77 [434.78, 466.76] 56.26
##      incongruent 488.31 [462.20, 514.42] 91.87
##      neutral 465.62 [446.78, 484.47] 66.31
##
## posture:STANDING
##      congruency
##      congruent 448.51 [431.30, 465.72] 60.56
##      incongruent 485.40 [456.81, 513.99] 100.61
##      neutral 460.86 [441.64, 480.08] 67.64
##
## Note. M and SD represent mean and standard deviation, respectively.
## LL and UL indicate the lower and upper limits of the
## 95% confidence interval for the mean, respectively.
## The confidence interval is a plausible range of population means
## that could have created a sample mean (Cumming, 2014).
```

Experiment 2 - Task-switching

Import and clean data

```
###read in data
ts_path <- "/data/Experiment 2 Data/task-switching-replication-recoded-2.csv"
task_switching_raw <- read.csv(paste0(workingdir, ts_path))
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
```

```
### check data
```

```
#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)

#Change RTs from seconds to milliseconds
task_switching_raw2 <- task_switching_raw2 %>%
  mutate(reactionTime = reactionTime * 1000)

#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))

#Summary of time-out trials
timeOutTaskSwitch = task_switching_raw3 %>%
  filter(is.na(reactionTime))

fable(posture~congruentTrialType, timeOutTaskSwitch)

```

```
##                posture sitting standing
## congruentTrialType
## congruent                82          92
## incongruent              98         117
```

```
fable(posture~congruentTrialType~switchTrialType, timeOutTaskSwitch)
```

```
##                congruentTrialType congruent incongruent
## switchTrialType
## noswitch                76          88
## switch                  98         127
```

```
fable(congruentTrialType ~ participant, timeOutTaskSwitch)
```

```
##                congruentTrialType congruent incongruent
## participant
## 1                8                7
## 3                2                3
## 4                3                8
## 7                1                2
## 9                2                0
## 10               1                1
## 11               0                1
## 12               1                2
## 13               4                2
## 14               3                0
## 16               3                4
## 17               1                1
## 18               3                2
## 19               14               21
## 20               1                2
## 21               3                10
## 22               1                1
## 23               6                5
## 24               5                3
## 25               2                3
## 26               1                2
## 27               3                5
## 28               4                4
## 29               4                6
## 30               5                6
## 31               11               13
## 32               7                2
## 33               1                4
## 34               3                1
## 35               2                2
## 36               2                2
## 37               1                4
## 38               6                3
## 39               2                5
## 41               3                3
## 42               5                12
## 43               4                5
## 45               0                8
## 46               5                5
```

## 47	2	0
## 48	10	7
## 50	2	3
## 52	1	0
## 53	1	1
## 54	3	3
## 55	13	27
## 56	6	2
## 57	3	2

```
fable(switchTrialType ~ participant, timeOutTaskSwitch)
```

##	switchTrialType	noswitch	switch
## participant			
## 1	6	9	
## 3	4	1	
## 4	7	4	
## 7	2	1	
## 9	0	2	
## 10	1	1	
## 11	1	0	
## 12	0	3	
## 13	1	5	
## 14	0	3	
## 16	1	6	
## 17	1	1	
## 18	3	2	
## 19	19	16	
## 20	2	1	
## 21	6	7	
## 22	1	1	
## 23	4	7	
## 24	1	7	
## 25	3	2	
## 26	1	2	
## 27	5	3	
## 28	3	5	
## 29	6	4	
## 30	5	6	
## 31	13	11	
## 32	5	4	
## 33	1	4	
## 34	2	2	
## 35	1	3	
## 36	2	2	
## 37	1	4	
## 38	4	5	
## 39	3	4	
## 41	3	3	
## 42	6	11	
## 43	5	4	
## 45	3	5	
## 46	5	5	
## 47	0	2	
## 48	8	9	

```
## 50          0      5
## 52          1      0
## 53          0      2
## 54          2      4
## 55         11     29
## 56          4      4
## 57          1      4
```

```
#Drop "time-out" trials
task_switching_raw.conventional <- task_switching_raw3 %>%
  filter(!is.na(reactionTime))

write.csv(task_switching_raw.conventional, file = "results/exp2_merged_ts_conv.csv",
  row.names = F)

#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),
    PE = (1 - Accuracy) * 100)
```

`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 %>%
  select(-Accuracy) %>%
  pivot_wider(names_from = c(posture,
    congruentTrialType,
    switchTrialType),
    values_from = PE)

ts_acc_mean <- ts_acc_mean %>%
  ungroup() %>%
  mutate(across(posture:switchTrialType, as.factor))

str(ts_acc_mean)
```

```
## tibble [408 x 6] (S3: tbl_df/tbl/data.frame)
## $ participant      : int [1:408] 1 1 1 1 1 1 1 1 3 3 ...
## $ 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 [1:408] 0.96 0.978 0.957 0.88 0.981 ...
## $ PE               : num [1:408] 4 2.17 4.35 12 1.89 ...
```

```
#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",
                           "/Experiment 2 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
```

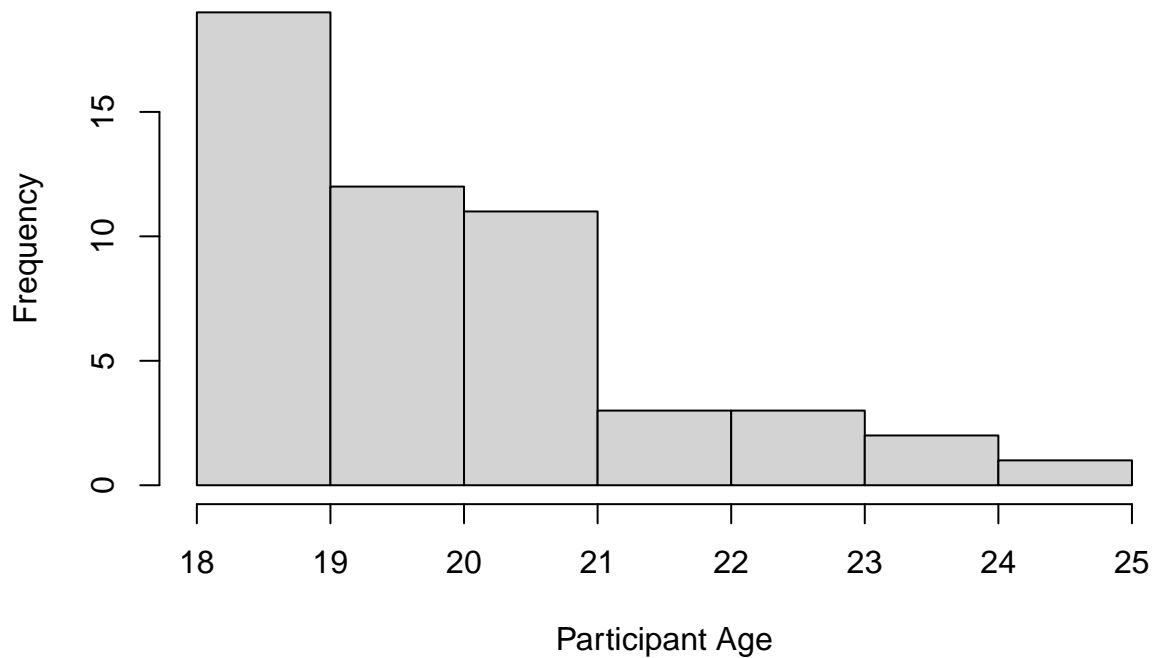
```
demo_df <- demo_df %>%
  mutate(Gender.New = ifelse(Gender.Pick %in% c("Man", "Woman"), Gender.Pick, Gender.Text),
         Eng.First = toupper(Eng.First))
```

```
#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")
```

Histogram of Participant Ages



```
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
```

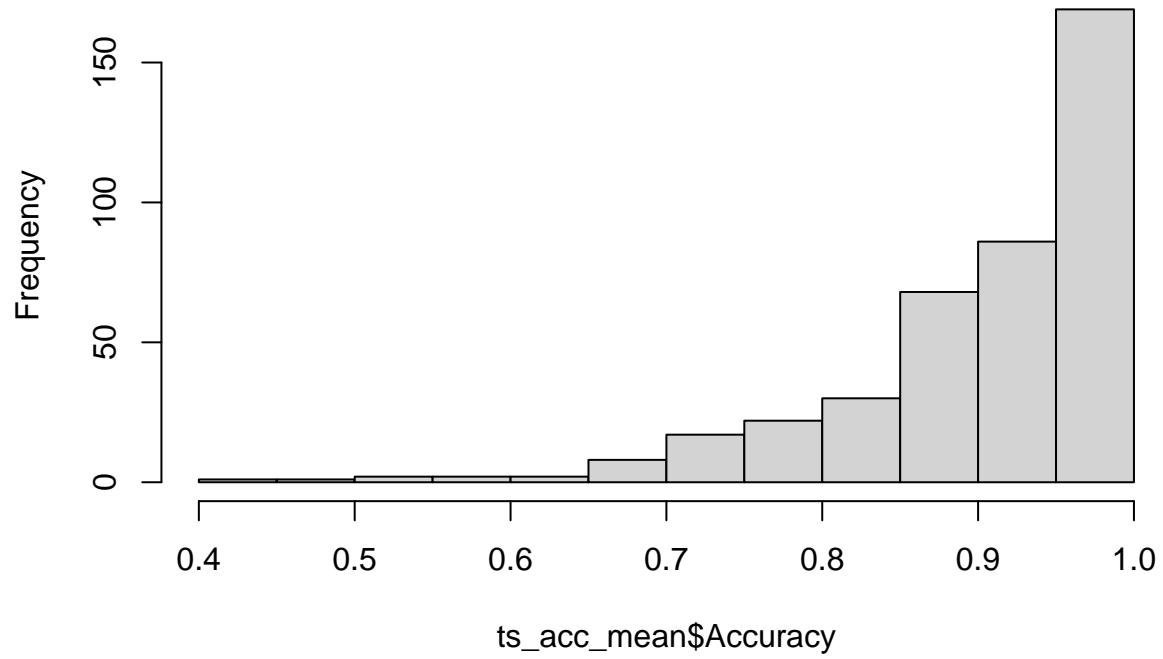
```
#language breakdown
lang_table <- demo_df %>%
  group_by(Eng.First) %>%
  summarize(n=n())
lang_table
```

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

Accuracy results

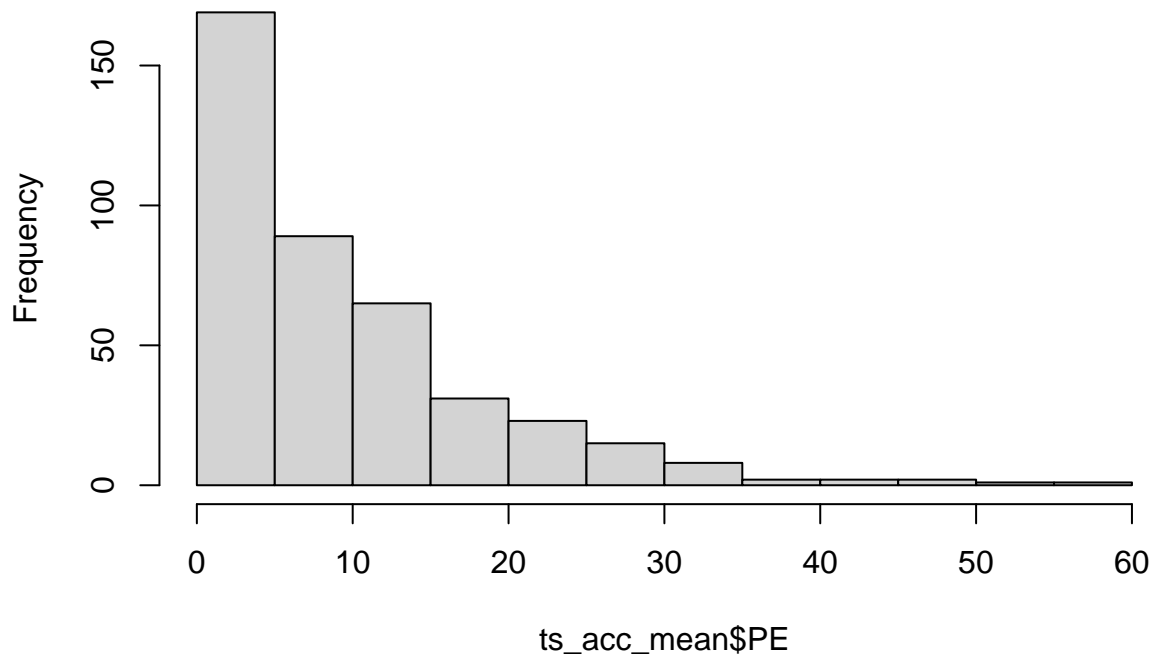
```
#Accuracy for all cells
hist(ts_acc_mean$Accuracy)
```

Histogram of ts_acc_mean\$Accuracy



```
hist(ts_acc_mean$PE)
```

Histogram of ts_acc_mean\$PE



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

```
acc.stats.TS <- ezStats(ts_acc_mean,
                       dv = PE,
                       wid = participant,
                       within = .(posture, congruentTrialType, switchTrialType),
                       type = 3
)
```

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

```
write.csv(acc.stats.TS[, -7], file = "results/exp2_Descriptives_ACC.csv",
          row.names = F)
```

```
write.csv(accModelTS$anova_table, "results/exp2_ANOVA_PE_uncon.csv")
accModelTS
```

```
## Anova Table (Type 3 tests)
```

```
##
```

```
## Response: PE
```

```
##              Effect    df    MSE        F    pes p.value
## 1              posture 1, 50 88.41      1.06 .021   .308
## 2      congruentTrialType 1, 50 86.07 99.66 *** .666   <.001
## 3      switchTrialType 1, 50 28.61 92.04 *** .648   <.001
## 4      posture:congruentTrialType 1, 50 41.84      0.02 <.001   .875
## 5      posture:switchTrialType 1, 50 24.00      0.74 .015   .395
## 6      congruentTrialType:switchTrialType 1, 50 15.15 58.43 *** .539   <.001
## 7 posture:congruentTrialType:switchTrialType 1, 50 18.80      1.26 .024   .268
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '+' 0.1 ' ' 1
```

```
#Calculate confidence interval: PES for posture x switch/condition interaction
#using ANOVA results (partial eta-squared)
interaction_effect_CI <- get.ci.partial.eta.squared(accModelTS$anova_table$F[5],
                                                    accModelTS$anova_table$num Df[5],
                                                    accModelTS$anova_table$den Df[5],
                                                    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() +
  theme(axis.text=element_text(size=14),
        panel.background = element_rect(fill = "white", colour = "white", size = 1),
        axis.title = element_text(size=14, face="bold"),
        strip.text = element_text(size = 14, face = "bold", colour = "black", angle = 0),
        legend.text = element_text(size = 13),
        legend.title = element_text(size= 14, face = "bold")) +
  ylim(0, 22) + #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 = "Percent Error")
```

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

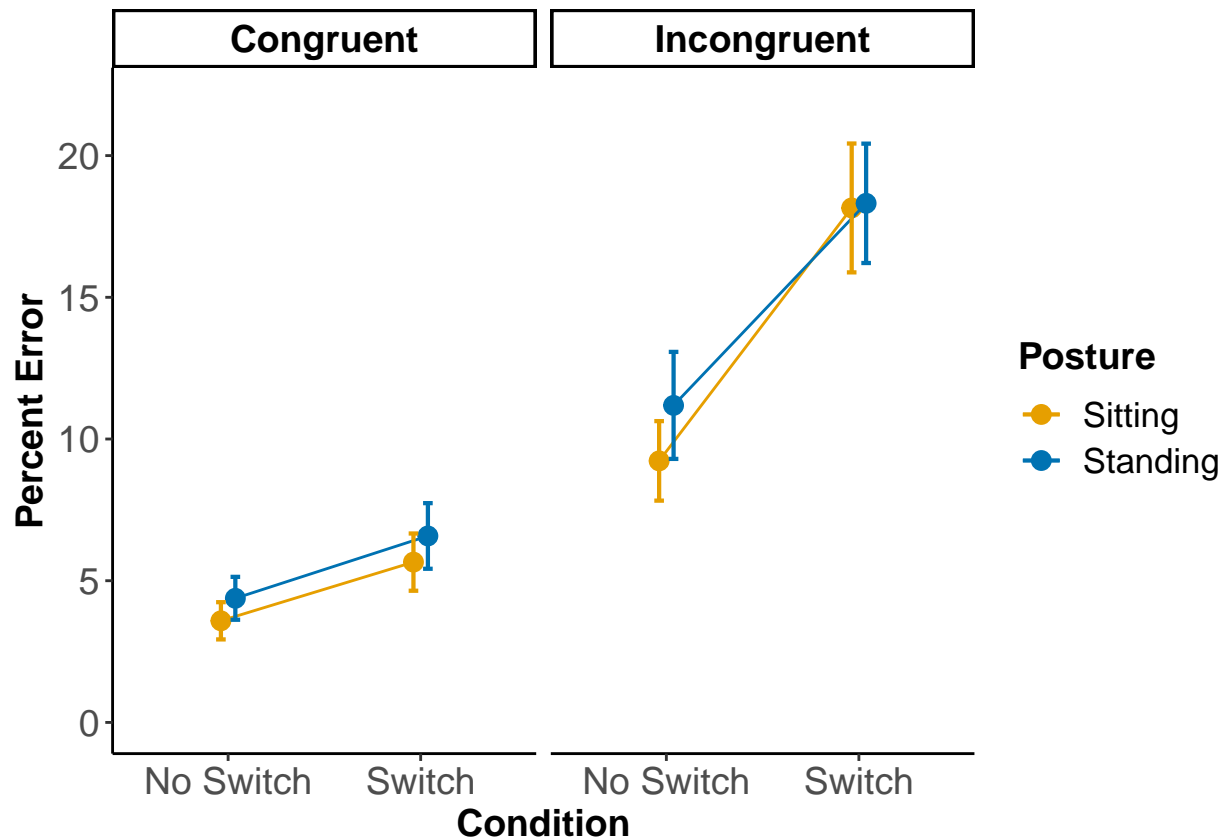
```
## Condition Congruent Posture          variable
##          1          1          1    sitting_congruent_noswitch
```

```
##      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
```

#Note this is Figure 3, not figure 2 (drawn below)

```
ggsave(acc_plot,
       file = "results/plots/fig3_exp2_ts_acc_plot.pdf",
       units = "in",
       width = 6.62,
       height = 5.50,
       dpi = 600)
```

acc_plot



#...CALCULATE THE BAYES FACTORS FOR THE ACC ANALYSIS

```
taskswitchBF = data.frame(ts_acc_mean)
```

```
taskswitchBF$participant = factor(ts_acc_mean$participant)
```

```
taskswitchBF$posture = factor(ts_acc_mean$posture)
```

```
taskswitchBF$congruentTrialType = factor(taskswitchBF$congruentTrialType)
```

```
taskswitchBF$switchTrialType = factor(taskswitchBF$switchTrialType)
```

```
#str(taskswitchBF)
```

```

bfValues2 = anovaBF(Accuracy~ posture*switchTrialType+participant,
                    data = taskswitchBF,
                    whichRandom = "participant",
                    method="laplace")

bfValues2

## Bayes factor analysis
## -----
## [1] posture + participant : 0.1836549 ±NA%
## [2] switchTrialType + participant : 5429475 ±NA%
## [3] posture + switchTrialType + participant : 1064550 ±NA%
## [4] posture + switchTrialType + posture:switchTrialType + participant : 168897.1 ±NA%
##
## Against denominator:
## Accuracy ~ participant
## ---
## Bayes factor type: BFlinearModel, JZS

#...get the Bayes factor for the Null Interaction (vs. model w/no interaction)
bfValues2[3]/bfValues2[4]

## Bayes factor analysis
## -----
## [1] posture + switchTrialType + participant : 6.302952 ±NA%
##
## Against denominator:
## Accuracy ~ posture + switchTrialType + posture:switchTrialType + participant
## ---
## Bayes factor type: BFlinearModel, JZS

1/(bfValues2[3]/bfValues2[4])

## Bayes factor analysis
## -----
## [1] posture + switchTrialType + posture:switchTrialType + participant : 0.1586558 ±NA%
##
## Against denominator:
## Accuracy ~ posture + switchTrialType + participant
## ---
## Bayes factor type: BFlinearModel, JZS

```

Reaction time results

```

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

#Second exclusion criteria
#How many trials faster than 100 ms? Only a single one
sum(ts_correct_only$reactionTime < 100)

## [1] 1

dim(ts_correct_only)

## [1] 17699 20

```



```

ts_correct_only2 <- ts_correct_only %>% filter(reactionTime >= 100)
#Sanity check, one trial is dropped. Now have 17,698 trials
dim(ts_correct_only2)

## [1] 17698    20

trimOutputTS = pjRecursiveTrim2(dataSet = ts_correct_only2,
                                dv = "reactionTime",
                                splitvars = c("participant",
                                                "posture",
                                                "switchTrialType",
                                                "congruentTrialType"))

trimmedTSData=trimOutputTS[[1]]
totalN.TS = trimOutputTS[[2]]
rejectedTS = trimOutputTS[[3]]
percentTrimmedTS = trimOutputTS[[4]] #this is very close to the percentage trimmed for stroop
#2.14% of trials
percentTrimmedTS

## [1] 2.141485

NcellsTS = trimOutputTS[[5]] # 51 participants * 8 conditions

trimmed_rt_mean_TS <- trimmedTSData %>%
  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
trimmed_rt_mean_TS_wide <- trimmed_rt_mean_TS %>%
  pivot_wider(names_from = c(posture,
                              congruentTrialType,
                              switchTrialType),
              values_from = mean_rt)

trimmed_RT_plot <-
  superbPlot(trimmed_rt_mean_TS_wide,
             WSFactors = c("Condition(2)", "Congruent(2)", "Posture(2)"),
             variables = colnames(trimmed_rt_mean_TS_wide)[2:9],
             errorbar = "SE",
             plotStyle = "line",
             factorOrder = c("Condition", "Posture", "Congruent"),
             adjustments = list(purpose = "difference"))+
  theme_classic() +
  theme(axis.text=element_text(size=14),
        panel.background = element_rect(fill = "white", colour = "white", size = 1),
        axis.title = element_text(size=14, face="bold"),
        strip.text = element_text(size = 14, face = "bold", colour = "black", angle = 0),
        legend.text = element_text(size = 13),
        legend.title = element_text(size= 14, face = "bold")) +
  facet_wrap(vars(Congruent), labeller = labeller(Congruent = congruent.labs)) +

```

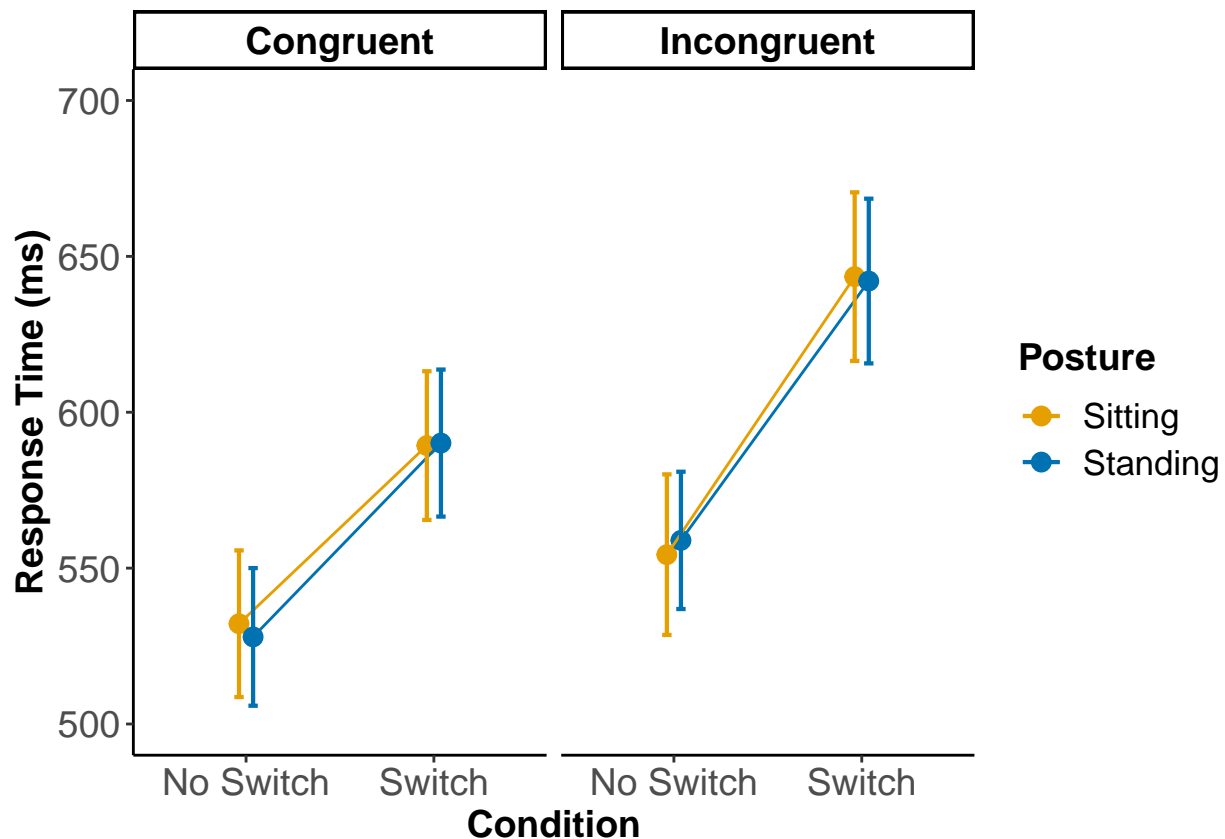
```
scale_x_discrete(labels=c("1" = "No Switch", "2" = "Switch"))+
scale_color_manual(values=c("#E69F00", "#0072B2"), labels = c("Sitting", "Standing")) +
ylim(500, 700) +
labs(y = "Response Time (ms)")
```

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(trimmed_RT_plot,
  file = "results/plots/fig2_exp2_ts_trimmed_RT_plot.pdf",
  units = "in",
  width = 6.62,
  height = 5.50,
  dpi = 600)
```

trimmed_RT_plot



```
rtModelTS <- aov_ez(data = trimmed_rt_mean_TS,
  dv = 'mean_rt',
```

```

        id = 'participant',
        within = c('posture',
                   'congruentTrialType',
                   'switchTrialType'),
        type = 3,
        anova_table = list(es = "pes"))

rt.stats.TS <- ezStats(trimmed_rt_mean_TS,
                      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(rt.stats.TS[, -7],
         file = "results/exp2_Descriptives_trimmed_RT.csv",
         row.names = F)

write.csv(rtModelTS$anova_table, file = "results/exp2_ANOVA_trimmed_RT.csv")
rtModelTS

```

```
## Anova Table (Type 3 tests)
```

```
##
## Response: mean_rt
```

	Effect	df	MSE	F	pes	p.value
## 1	posture	1, 50	9922.05	0.00	<.001	.995
## 2	congruentTrialType	1, 50	3302.21	48.98 ***	.495	<.001
## 3	switchTrialType	1, 50	4166.22	130.17 ***	.722	<.001
## 4	posture:congruentTrialType	1, 50	1592.27	0.17	.003	.679
## 5	posture:switchTrialType	1, 50	1519.08	0.00	<.001	.951
## 6	congruentTrialType:switchTrialType	1, 50	1252.33	14.32 ***	.223	<.001
## 7	posture:congruentTrialType:switchTrialType	1, 50	1552.36	0.50	.010	.483

```

## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '+' 0.1 ' ' 1

```

```

trimmed_rt_mean_TS2 <- data.frame(trimmed_rt_mean_TS)
trimmed_rt_mean_TS2$participant = factor(trimmed_rt_mean_TS2$participant)
trimmed_rt_mean_TS2$posture = factor(trimmed_rt_mean_TS2$posture)
trimmed_rt_mean_TS2$congruentTrialType = factor(trimmed_rt_mean_TS2$congruentTrialType)
trimmed_rt_mean_TS2$switchTrialType = factor(trimmed_rt_mean_TS2$switchTrialType)

```

```

bfValues2.RT = anovaBF(mean_rt ~ posture*switchTrialType+participant,
                      data = trimmed_rt_mean_TS2,
                      whichRandom = "participant",
                      method="laplace")

```

```
bfValues2.RT
```

```
## Bayes factor analysis
```

```
## -----
```

```
## [1] posture + participant : 0.1007388 ±NA%
## [2] switchTrialType + participant : 4.227658e+24 ±NA%
## [3] posture + switchTrialType + participant : 4.265145e+23 ±NA%
## [4] posture + switchTrialType + posture:switchTrialType + participant : 6.012989e+22 ±NA%
##
## Against denominator:
## mean_rt ~ participant
## ---
## Bayes factor type: BFlinearModel, JZS

#...get the Bayes factor for the Null Interaction (vs. model w/no interaction)
bfValues2.RT[3]/bfValues2.RT[4]

## Bayes factor analysis
## -----
## [1] posture + switchTrialType + participant : 7.093219 ±NA%
##
## Against denominator:
## mean_rt ~ posture + switchTrialType + posture:switchTrialType + participant
## ---
## Bayes factor type: BFlinearModel, JZS

1/(bfValues2.RT[3]/bfValues2.RT[4])

## Bayes factor analysis
## -----
## [1] posture + switchTrialType + posture:switchTrialType + participant : 0.1409797 ±NA%
##
## Against denominator:
## mean_rt ~ posture + switchTrialType + participant
## ---
## Bayes factor type: BFlinearModel, JZS
```

Experiment 3 - Visual search

Import and clean data

```
vs_files = list.files(path = "data/Experiment 3 Data/", full.names = T)
vs_files = vs_files[str_detect(vs_files,pattern="(?!.*SJ)(?!.*.txt)")]

merged.VS.data <- ldply(vs_files,
                        read.delim,
                        header=FALSE,
                        stringsAsFactors = FALSE,
                        sep = "") #for each item in the list apply the function read.delim

##..ADD HEADERS
names(merged.VS.data) = c("sj",
                          "cb",
                          "blockNumber",
                          "blockType",
                          "trialNum",
                          "target",
                          "targetImage",
                          "distractor",
```

```
"distractorImage",  
"posture",  
"setSize",  
"rt",  
"resp",  
"cresp",  
"ac")
```

```
#...look at unique values from both columns  
unique(merged.VS.data[c('sj')])
```

```
##      sj  
## 1      1  
## 265    10  
## 529    11  
## 793    12  
## 1057   13  
## 1321   14  
## 1585   15  
## 1849   16  
## 2113   17  
## 2377   18  
## 2641   19  
## 2905    2  
## 3169   20  
## 3433   21  
## 3697   22  
## 3961   23  
## 4225   24  
## 4489   25  
## 4753   26  
## 5017   27  
## 5281   28  
## 5545   29  
## 5809    3  
## 6073   30  
## 6337   31  
## 6601   32  
## 6865   33  
## 7129   34  
## 7393   35  
## 7657   36  
## 7921   37  
## 8185   38  
## 8449   39  
## 8713    4  
## 8977   40  
## 9241   41  
## 9505   42  
## 9769   43  
## 10033  44  
## 10297  45  
## 10561  46  
## 10825  47
```

```
## 11089 48
## 11353 49
## 11617 5
## 11881 50
## 12145 6
## 12409 7
## 12673 8
## 12937 9
```

```
unique(merged.VS.data[c('blockType')])
```

```
##      blockType
## 1      practice
## 9 experimental
```

```
##..DOES EACH SUBJECT HAVE THE SAME NUMBER OF TRIALS
```

```
fable(blockType~sj, merged.VS.data)
```

```
##      blockType experimental practice
## sj
## 1              256            8
## 2              256            8
## 3              256            8
## 4              256            8
## 5              256            8
## 6              256            8
## 7              256            8
## 8              256            8
## 9              256            8
## 10             256            8
## 11             256            8
## 12             256            8
## 13             256            8
## 14             256            8
## 15             256            8
## 16             256            8
## 17             256            8
## 18             256            8
## 19             256            8
## 20             256            8
## 21             256            8
## 22             256            8
## 23             256            8
## 24             256            8
## 25             256            8
## 26             256            8
## 27             256            8
## 28             256            8
## 29             256            8
## 30             256            8
## 31             256            8
## 32             256            8
## 33             256            8
## 34             256            8
## 35             256            8
```

```
## 36          256          8
## 37          256          8
## 38          256          8
## 39          256          8
## 40          256          8
## 41          256          8
## 42          256          8
## 43          256          8
## 44          256          8
## 45          256          8
## 46          256          8
## 47          256          8
## 48          256          8
## 49          256          8
## 50          256          8
```

```
###DO WE HAVE EQUAL OBSERVATIONS FOR EACH COUNTERBALANCE
ftable(blockType~cb, merged.VS.data)
```

```
##      blockType experimental practice
## cb
## 1          6400          200
## 2          6400          200
```

```
###LOOK FOR MISSING DATA
merged.VS.data[!complete.cases(merged.VS.data),]
```

```
## [1] sj          cb          blockNumber    blockType      trialNum      target
## [7] targetImage    distractor    distractorImage posture      setSize      rt
## [13] resp          cresp        ac
## <0 rows> (or 0-length row.names)
```

```
### GET RID OF PRACTICE TRIALS
merged.VS.data <- merged.VS.data[!merged.VS.data$blockType=="practice",]
```

```
### CHECK TRIALS PER CONDITION
ftable(posture+target+distractor+setSize~sj, merged.VS.data)
```

```
##      posture      SITTING      STANDING
##      target      h          s      h          s
##      distractor  e      u      e      u      e      u      e      u
##      setSize    4      8      4      8      4      8      4      8
## sj
## 1      16 16 16 16 16 16 16 16 16 16 16 16 16 16 16 16
## 2      16 16 16 16 16 16 16 16 16 16 16 16 16 16 16 16
## 3      16 16 16 16 16 16 16 16 16 16 16 16 16 16 16 16
## 4      16 16 16 16 16 16 16 16 16 16 16 16 16 16 16 16
## 5      16 16 16 16 16 16 16 16 16 16 16 16 16 16 16 16
## 6      16 16 16 16 16 16 16 16 16 16 16 16 16 16 16 16
## 7      16 16 16 16 16 16 16 16 16 16 16 16 16 16 16 16
## 8      16 16 16 16 16 16 16 16 16 16 16 16 16 16 16 16
## 9      16 16 16 16 16 16 16 16 16 16 16 16 16 16 16 16
## 10     16 16 16 16 16 16 16 16 16 16 16 16 16 16 16 16
## 11     16 16 16 16 16 16 16 16 16 16 16 16 16 16 16 16
## 12     16 16 16 16 16 16 16 16 16 16 16 16 16 16 16 16
## 13     16 16 16 16 16 16 16 16 16 16 16 16 16 16 16 16
```

```
## 14      16 16 16 16 16 16 16 16      16 16 16 16 16 16 16 16
## 15      16 16 16 16 16 16 16 16      16 16 16 16 16 16 16 16
## 16      16 16 16 16 16 16 16 16      16 16 16 16 16 16 16 16
## 17      16 16 16 16 16 16 16 16      16 16 16 16 16 16 16 16
## 18      16 16 16 16 16 16 16 16      16 16 16 16 16 16 16 16
## 19      16 16 16 16 16 16 16 16      16 16 16 16 16 16 16 16
## 20      16 16 16 16 16 16 16 16      16 16 16 16 16 16 16 16
## 21      16 16 16 16 16 16 16 16      16 16 16 16 16 16 16 16
## 22      16 16 16 16 16 16 16 16      16 16 16 16 16 16 16 16
## 23      16 16 16 16 16 16 16 16      16 16 16 16 16 16 16 16
## 24      16 16 16 16 16 16 16 16      16 16 16 16 16 16 16 16
## 25      16 16 16 16 16 16 16 16      16 16 16 16 16 16 16 16
## 26      16 16 16 16 16 16 16 16      16 16 16 16 16 16 16 16
## 27      16 16 16 16 16 16 16 16      16 16 16 16 16 16 16 16
## 28      16 16 16 16 16 16 16 16      16 16 16 16 16 16 16 16
## 29      16 16 16 16 16 16 16 16      16 16 16 16 16 16 16 16
## 30      16 16 16 16 16 16 16 16      16 16 16 16 16 16 16 16
## 31      16 16 16 16 16 16 16 16      16 16 16 16 16 16 16 16
## 32      16 16 16 16 16 16 16 16      16 16 16 16 16 16 16 16
## 33      16 16 16 16 16 16 16 16      16 16 16 16 16 16 16 16
## 34      16 16 16 16 16 16 16 16      16 16 16 16 16 16 16 16
## 35      16 16 16 16 16 16 16 16      16 16 16 16 16 16 16 16
## 36      16 16 16 16 16 16 16 16      16 16 16 16 16 16 16 16
## 37      16 16 16 16 16 16 16 16      16 16 16 16 16 16 16 16
## 38      16 16 16 16 16 16 16 16      16 16 16 16 16 16 16 16
## 39      16 16 16 16 16 16 16 16      16 16 16 16 16 16 16 16
## 40      16 16 16 16 16 16 16 16      16 16 16 16 16 16 16 16
## 41      16 16 16 16 16 16 16 16      16 16 16 16 16 16 16 16
## 42      16 16 16 16 16 16 16 16      16 16 16 16 16 16 16 16
## 43      16 16 16 16 16 16 16 16      16 16 16 16 16 16 16 16
## 44      16 16 16 16 16 16 16 16      16 16 16 16 16 16 16 16
## 45      16 16 16 16 16 16 16 16      16 16 16 16 16 16 16 16
## 46      16 16 16 16 16 16 16 16      16 16 16 16 16 16 16 16
## 47      16 16 16 16 16 16 16 16      16 16 16 16 16 16 16 16
## 48      16 16 16 16 16 16 16 16      16 16 16 16 16 16 16 16
## 49      16 16 16 16 16 16 16 16      16 16 16 16 16 16 16 16
## 50      16 16 16 16 16 16 16 16      16 16 16 16 16 16 16 16
```

```
#... UNLIKE THE STROOP, PARTICIPANTS WERE ALLOWED TO TAKE LONGER THAN 1500MS BUT WERE GIVEN A WARNING
#... TRIALS LONGER THAN 1500 MS will be considered errors (i.e., they will be dropped in RT but kept in
#... Set values in the ac column to 0 on trials where a response is > = 1500
```

```
#...check that only experimental trials are left
unique(merged.VS.data$blockType)
```

```
## [1] "experimental"
```

```
write.table(merged.VS.data, file = "results/exp3_merged_vs_data.txt", row.names = F)
```

```
#...count trials
```

```
totalTrialsVS = dim(merged.VS.data)[1]
```

```
observationDataVS = data.frame(ftable(blockType~sj, merged.VS.data))[,c(1,3)]
```

```
#...get the number of extreme trials <100 - anticipatory or fast responses
```

```
merged.VS.data= merged.VS.data[!merged.VS.data$rt<=100,]
```



```

validRTTrialsVS = dim(merged.VS.data)[1]
observationDataVS$validTrials = data.frame(ftable(blockType~sj, merged.VS.data))[c(3)]

print(paste("percent invalid trials = ", ((totalTrialsVS-validRTTrialsVS)/totalTrialsVS)*100))

## [1] "percent invalid trials =  0"

##...get the number of time outs
timeOutVS = merged.VS.data %>% filter(rt >= 1500)
dim(timeOutVS)[1]

## [1] 168

ftable(posture~setSize, timeOutVS)

##           posture SITTING STANDING
## setSize
## 4              32              13
## 8              56              67

ftable(posture~sj, timeOutVS)

##           posture SITTING STANDING
## sj
## 2              9              12
## 3              2              0
## 4              6              2
## 5              3              1
## 6              0              1
## 7              1              2
## 9              4              6
## 10             7              3
## 11             3              2
## 12             2              7
## 13             4              1
## 15             1              2
## 17             2              0
## 18             0              1
## 19             3              2
## 20             1              2
## 22             2              2
## 24             0              2
## 25             2              4
## 27             0              2
## 28             0              1
## 29             5              6
## 30             2              0
## 31             3              0
## 33             0              1
## 35             3              2
## 36             0              1
## 37             0              1
## 39             2              3
## 40             3              3
## 41             0              2
## 42             2              1

```

```

## 44          4          2
## 45          3          0
## 46          3          0
## 47          0          1
## 48          1          0
## 49          3          2
## 50          2          0

ftable(blockType~setSize, timeOutVS)

##          blockType experimental
## setSize
## 4                      45
## 8                      123

merged.VS.data.conventional <- merged.VS.data %>% filter(rt < 1500)
write.csv(merged.VS.data.conventional,
          file = "results/exp3_merged_vs_data_conv.csv",
          row.names = F)

#...this code changes the 1550ms+ trials into errors
merged.VS.data.orig <- merged.VS.data
merged.VS.data$ac[merged.VS.data$rt>=1500] = 0

vsCorrect = merged.VS.data[merged.VS.data$ac ==1,]

errorsRemovedVS = dim(vsCorrect)[1]
observationDataVS$correctTrials = data.frame(ftable(blockType~sj, vsCorrect))[c(3)]

trimInfo = data.frame(totalTrialsVS, validRTTrialsVS, errorsRemovedVS)
head(trimInfo)

## totalTrialsVS validRTTrialsVS errorsRemovedVS
## 1          12800          12800          12397

#####
#...CHECK 20% CRITERION
#####
observationDataVS$percentLoss = ((observationDataVS$Freq-observationDataVS$correctTrials)/observationDataVS$Freq)*100
sum(observationDataVS$percentLoss>20)

## [1] 0

#...None!

#...RUN TRIMMING PROCEDURE
tempList = pjRecursiveTrim2(vsCorrect, #...dataset
                           "rt", #...dependent variables
                           c("sj",
                             "cb",
                             "setSize",
                             "posture")) #.independent variables

trimmedData=tempList[[1]]
totalN = tempList[[2]]
rejected = tempList[[3]]

```

```

percentTrimmed = tempList[[4]]
Ncells = tempList[[5]]

print(paste("Percent of outliers removed: ",round(percentTrimmed,3)))

## [1] "Percent of outliers removed:  1.339"

###...get the trimming info
output.out= data.frame(totalN, rejected,percentTrimmed,Ncells)
head(output.out)

##   totalN rejected percentTrimmed Ncells
## 1  12397      166      1.339034     200

###...get mean error data
vsPE = plyr::ddply(merged.VS.data,
                  .(sj,cb,setSize, posture),
                  summarise,
                  meanPE = 100 - (mean(ac)*100))
head(vsPE)

##   sj cb setSize  posture meanPE
## 1  1  1      4  SITTING 0.0000
## 2  1  1      4  STANDING 0.0000
## 3  1  1      8  SITTING 0.0000
## 4  1  1      8  STANDING 0.0000
## 5  2  1      4  SITTING 4.6875
## 6  2  1      4  STANDING 4.6875

vsRT = plyr::ddply(trimmedData,
                  .(sj, cb, setSize,posture),
                  summarise,
                  meanRT = mean(rt))

###...combine the RT and error data
vsCombined = cbind(vsRT,meanPE =vsPE$meanPE)
str(vsCombined)

## 'data.frame':   200 obs. of  6 variables:
## $ sj      : int  1 1 1 1 2 2 2 2 3 3 ...
## $ cb      : int  1 1 1 1 1 1 1 1 1 1 ...
## $ setSize: int  4 4 8 8 4 4 8 8 4 4 ...
## $ posture: chr  "SITTING" "STANDING" "SITTING" "STANDING" ...
## $ meanRT : num  677 593 736 620 792 ...
## $ meanPE : num  0 0 0 0 4.69 ...

###...set as factors
vsCombined$sj = factor(vsCombined$sj)
vsCombined$cb = factor(vsCombined$cb)
vsCombined$setSize = factor(vsCombined$setSize)
vsCombined$postureFactor = factor(vsCombined$posture)
summary(vsCombined$cb)

##   1   2
## 100 100

```

Reaction time results

```
rtModelVS <- ezANOVA(vsCombined,
                     dv = .(meanRT),
                     wid=.(sj),
                     within=.(postureFactor,setSize),
                     detailed=TRUE,
                     type=3,
                     return_aov=TRUE)

rtModelVS$ANOVA

##              Effect DFn DFd          SSn          SSd          F          p p<.05
## 1      (Intercept)    1  49 1.084958e+08 1189588.17 4.469020e+03 8.326740e-50      *
## 2      postureFactor    1  49 2.052064e+04 153738.29 6.540411e+00 1.369090e-02      *
## 3          setSize    1  49 3.574624e+05  46863.03 3.737628e+02 1.414816e-24      *
## 4 postureFactor:setSize    1  49 2.246613e+01  35654.35 3.087534e-02 8.612429e-01
##              ges
## 1 9.870285e-01
## 2 1.418774e-02
## 3 2.004492e-01
## 4 1.575613e-05

rt.VS.MSE <- rtModelVS$ANOVA$SSd/rtModelVS$ANOVA$DFd

#...print ANOVA in nice format
paste(rtModelVS$ANOVA$Effect,": F(",
      rtModelVS$ANOVA$DFn,
      ", ",
      rtModelVS$ANOVA$DFd,
      ") = ",
      round(rtModelVS$ANOVA$F,3),
      ", MSE = ",
      round(rt.VS.MSE,3),
      ", p = ",
      round(rtModelVS$ANOVA$p,3),
      ", partialEtaSq = ",
      round(rtModelVS$ANOVA$SSn/(rtModelVS$ANOVA$SSn+rtModelVS$ANOVA$SSd),4),sep="")

## [1] "(Intercept): F(1, 49) = 4469.02, MSE = 24277.31, p = 0, partialEtaSq = 0.9892"
## [2] "postureFactor: F(1, 49) = 6.54, MSE = 3137.516, p = 0.014, partialEtaSq = 0.1178"
## [3] "setSize: F(1, 49) = 373.763, MSE = 956.388, p = 0, partialEtaSq = 0.8841"
## [4] "postureFactor:setSize: F(1, 49) = 0.031, MSE = 727.64, p = 0.861, partialEtaSq = 6e-04"

#...CALCULATE THE BAYES FACTORS FOR THE RT ANALYSIS
bfValues3 = anovaBF(meanRT~setSize*postureFactor+sj,
                    data = vsCombined,
                    whichRandom = "sj",
                    method="laplace")

bfValues3

## Bayes factor analysis
## -----
## [1] setSize + sj : 2.916459e+26 ±NA%
## [2] postureFactor + sj : 1.51507 ±NA%
## [3] setSize + postureFactor + sj : 1.321058e+28 ±NA%
```

```

## [4] setSize + postureFactor + setSize:postureFactor + sj : 2.585184e+27 ±NA%
##
## Against denominator:
##   meanRT ~ sj
## ---
## Bayes factor type: BFlinearModel, JZS
#...get the Bayes factor for the Null Interaction
bfValues3[3]/bfValues3[4]

## Bayes factor analysis
## -----
## [1] setSize + postureFactor + sj : 5.110113 ±NA%
##
## Against denominator:
##   meanRT ~ setSize + postureFactor + setSize:postureFactor + sj
## ---
## Bayes factor type: BFlinearModel, JZS
1/(bfValues3[3]/bfValues3[4])

## Bayes factor analysis
## -----
## [1] setSize + postureFactor + setSize:postureFactor + sj : 0.1956904 ±NA%
##
## Against denominator:
##   meanRT ~ setSize + postureFactor + sj
## ---
## Bayes factor type: BFlinearModel, JZS
#####
# GET DIFFERENCE SCORES - SEARCH RATE
#####

wideData = dcast(vsCombined, #the name of the dataframe you want to reshape
                 sj+cb #row variables
                 ~posture+setSize, #row variables ~ column variables
                 value.var = "meanRT")
head(wideData)

##   sj cb SITTING_4 SITTING_8 STANDING_4 STANDING_8
## 1  1  1  676.5238  735.5397   593.1129   619.6406
## 2  2  1  792.4590  931.9474   815.7213   993.5000
## 3  3  1  721.2787  827.2222   654.1639   774.5238
## 4  4  1  695.7119  741.9298   660.2632   653.0172
## 5  5  1  693.6034  839.2903   705.1967   759.7419
## 6  6  1  625.3750  694.0484   592.4531   687.5645

wideData$sittingEffect = (wideData$SITTING_8-wideData$SITTING_4)/4
wideData$standingEffect = (wideData$STANDING_8-wideData$STANDING_4)/4
wideData$interaction = wideData$sittingEffect - wideData$standingEffect

searchratestand = mean(wideData$standingEffect) #...search rate in standing condition
searchratesit = mean(wideData$sittingEffect) #...search rate in the sitting condition

searchratestand

## [1] 21.30589

```

```

searchratesit

## [1] 20.97073

#One-sample t-tests
t.test(wideData$standingEffect)

##
## One Sample t-test
##
## data: wideData$standingEffect
## t = 16.69, df = 49, p-value < 2.2e-16
## alternative hypothesis: true mean is not equal to 0
## 95 percent confidence interval:
## 18.74050 23.87127
## sample estimates:
## mean of x
## 21.30589

t.test(wideData$sittingEffect)

##
## One Sample t-test
##
## data: wideData$sittingEffect
## t = 13.055, df = 49, p-value < 2.2e-16
## alternative hypothesis: true mean is not equal to 0
## 95 percent confidence interval:
## 17.74261 24.19884
## sample estimates:
## mean of x
## 20.97073

#...Exact Binomial SIGN TEST
binom.test(length(wideData$interaction[wideData$interaction>=0]),
            length(unique(vsCombined$sj)))

##
## Exact binomial test
##
## data: length(wideData$interaction[wideData$interaction >= 0]) and length(unique(vsCombined$sj))
## number of successes = 25, number of trials = 50, p-value = 1
## alternative hypothesis: true probability of success is not equal to 0.5
## 95 percent confidence interval:
## 0.355273 0.644727
## sample estimates:
## probability of success
## 0.5

```

Percent error results

```

errModelVS <- ezANOVA(vsCombined,
                      dv = .(meanPE),
                      wid=.(sj),
                      within=.(postureFactor,setSize),
                      detailed=TRUE,

```

```

type=3,
return_aov = TRUE)

```

```
errModelVS
```

```

## $ANOVA
##           Effect DFn DFd          SSn          SSd          F          p p<.05          ges
## 1      (Intercept)    1  49 1982.531738 1158.9478 83.8209098 3.463466e-12      * 0.504342884
## 2      postureFactor    1  49   3.527832  227.7954  0.7588554 3.879351e-01      0.001807368
## 3          setSize    1  49 129.504395  343.5181 18.4727266 8.162026e-05      * 0.062324860
## 4 postureFactor:setSize    1  49   20.520020  218.1274  4.6096032 3.676850e-02      * 0.010422027
##
## $aov
##
## Call:
## aov(formula = formula(aov_formula), data = data)
##
## Grand Mean: 3.148438
##
## Stratum 1: sj
##
## Terms:
##           Residuals
## Sum of Squares    1158.948
## Deg. of Freedom         49
##
## Residual standard error: 4.863332
##
## Stratum 2: sj:postureFactor
##
## Terms:
##           postureFactor Residuals
## Sum of Squares          3.52783 227.79541
## Deg. of Freedom          1         49
##
## Residual standard error: 2.156128
## 1 out of 2 effects not estimable
## Estimated effects are balanced
##
## Stratum 3: sj:setSize
##
## Terms:
##           setSize Residuals
## Sum of Squares 129.5044  343.5181
## Deg. of Freedom    1         49
##
## Residual standard error: 2.647749
## 1 out of 2 effects not estimable
## Estimated effects are balanced
##
## Stratum 4: sj:postureFactor:setSize
##
## Terms:
##           postureFactor:setSize Residuals

```

```

## Sum of Squares                20.52002 218.12744
## Deg. of Freedom                1         49
##
## Residual standard error: 2.109877
## Estimated effects are balanced

err.VS.MSE <- errModelVS$ANOVA$SSd/errModelVS$ANOVA$DFd

exp3_ANOVA_PE_uncon <-
paste(errModelVS$ANOVA$Effect,": F(",
      errModelVS$ANOVA$DFn,
      ", ",
      errModelVS$ANOVA$DFd,
      ") = ",
      round(errModelVS$ANOVA$F,3),
      ", MSE = ",
      round(err.VS.MSE,3),
      ", p = ",
      round(errModelVS$ANOVA$p,3),
      ", partialEtaSq = ",
      round(errModelVS$ANOVA$SSn/(errModelVS$ANOVA$SSn+errModelVS$ANOVA$SSd),4),sep="")

write.csv(exp3_ANOVA_PE_uncon, "results/exp3_ANOVA_PE_uncon.csv")

wideData = dcast(vsCombined, #the name of the dataframe you want to reshape
                 sj+cb #row variables
                 ~posture+setSize, #row variables ~ column variables
                 value.var = "meanPE")

head(wideData)

##   sj  cb SITTING_4 SITTING_8 STANDING_4 STANDING_8
## 1  1  1    0.0000    0.0000    0.0000    0.0000
## 2  2  1    4.6875   10.9375    4.6875   15.6250
## 3  3  1    1.5625    1.5625    0.0000    0.0000
## 4  4  1    6.2500   10.9375    4.6875    6.2500
## 5  5  1    3.1250    3.1250    1.5625    1.5625
## 6  6  1    0.0000    1.5625    0.0000    1.5625

wideData$sittingEffect = (wideData$SITTING_8-wideData$SITTING_4)/4
wideData$standingEffect = (wideData$STANDING_8-wideData$STANDING_4)/4
wideData$interaction = wideData$sittingEffect - wideData$standingEffect

searchratestand = mean(wideData$standingEffect) #...search rate in standing condition
searchratesit = mean(wideData$sittingEffect) #...search rate in the sitting condition

searchratestand

## [1] 0.5625

searchratesit

## [1] 0.2421875

#One-sample t-tests
t.test(wideData$standingEffect)

##

```



```

## One Sample t-test
##
## data: wideData$standingEffect
## t = 4.0858, df = 49, p-value = 0.0001623
## alternative hypothesis: true mean is not equal to 0
## 95 percent confidence interval:
## 0.2858399 0.8391601
## sample estimates:
## mean of x
## 0.5625
t.test(wideData$sittingEffect)

##
## One Sample t-test
##
## data: wideData$sittingEffect
## t = 2.4588, df = 49, p-value = 0.01752
## alternative hypothesis: true mean is not equal to 0
## 95 percent confidence interval:
## 0.04424588 0.44012912
## sample estimates:
## mean of x
## 0.2421875
###...CALCULATE THE BAYES FACTORS FOR THE RT ANALYSIS
bfValues3.error = anovaBF(meanPE~setSize*postureFactor+sj,
                           data = vsCombined,
                           whichRandom = "sj",
                           method="laplace")
bfValues3.error

## Bayes factor analysis
## -----
## [1] setSize + sj : 4888.005 ±NA%
## [2] postureFactor + sj : 0.1823325 ±NA%
## [3] setSize + postureFactor + sj : 937.7872 ±NA%
## [4] setSize + postureFactor + setSize:postureFactor + sj : 997.3734 ±NA%
##
## Against denominator:
## meanPE ~ sj
## ---
## Bayes factor type: BFlinearModel, JZS
###...get the Bayes factor for the Null Interaction
bfValues3.error[3]/bfValues3.error[4]

## Bayes factor analysis
## -----
## [1] setSize + postureFactor + sj : 0.9402568 ±NA%
##
## Against denominator:
## meanPE ~ setSize + postureFactor + setSize:postureFactor + sj
## ---
## Bayes factor type: BFlinearModel, JZS

```

```
1/(bfValues3.error[3]/bfValues3.error[4])
```

```
## Bayes factor analysis
## -----
## [1] setSize + postureFactor + setSize:postureFactor + sj : 1.063539 ±NA%
##
## Against denominator:
## meanPE ~ setSize + postureFactor + sj
## ---
## Bayes factor type: BFlinearModel, JZS
```

Make plots for visual search

```
graphRT3 = describeBy(vsCombined$meanRT,
                      list(vsCombined$posture,vsCombined$setSize),
                      mat=TRUE,
                      digits = 1)
graphPE3 = describeBy(vsCombined$meanPE,
                      list(vsCombined$posture,vsCombined$setSize),
                      mat=TRUE,
                      digits = 1)

graphRT3 = graphRT3[,c("group1","group2","mean","se")]
graphPE3 = graphPE3[,c("group1","group2","mean","se")]

names(graphRT3) = c("posture","setSize","mean","se")
names(graphPE3) = c("posture","setSize","mean","se")

graphRT3$posture = str_to_upper(graphRT3$posture)

#####
#..calculate the within subjects confidence intervals based on loftus and masson
#..the confidence intervals are based on the interaction term.
#####

graphRT3$se = sqrt((rt.VS.MSE[4])/length(unique(vsCombined$sj)))
graphPE3$se= sqrt((err.VS.MSE[4])/length(unique(vsCombined$sj)))

#####
#..calculate the within subjects confidence intervals based on loftus and masson
#..the confidence intervals are based on the interaction term.
#####

critT3 = qt(p=.025,df=length(unique(vsCombined$sj))-2,lower.tail =FALSE)

#---add the min and max for the confidence intervals
graphRT3$min = graphRT3$mean - (graphRT3$se*critT3)
graphRT3$max = graphRT3$mean + (graphRT3$se*critT3)

####GET AC DATA FROM twoAnimalWordsPRPac.R
graphRT3$ac = paste("(",format(round(graphPE3$mean,digits=1),nsmall = 1),"),",sep="")
head(graphRT3)
```

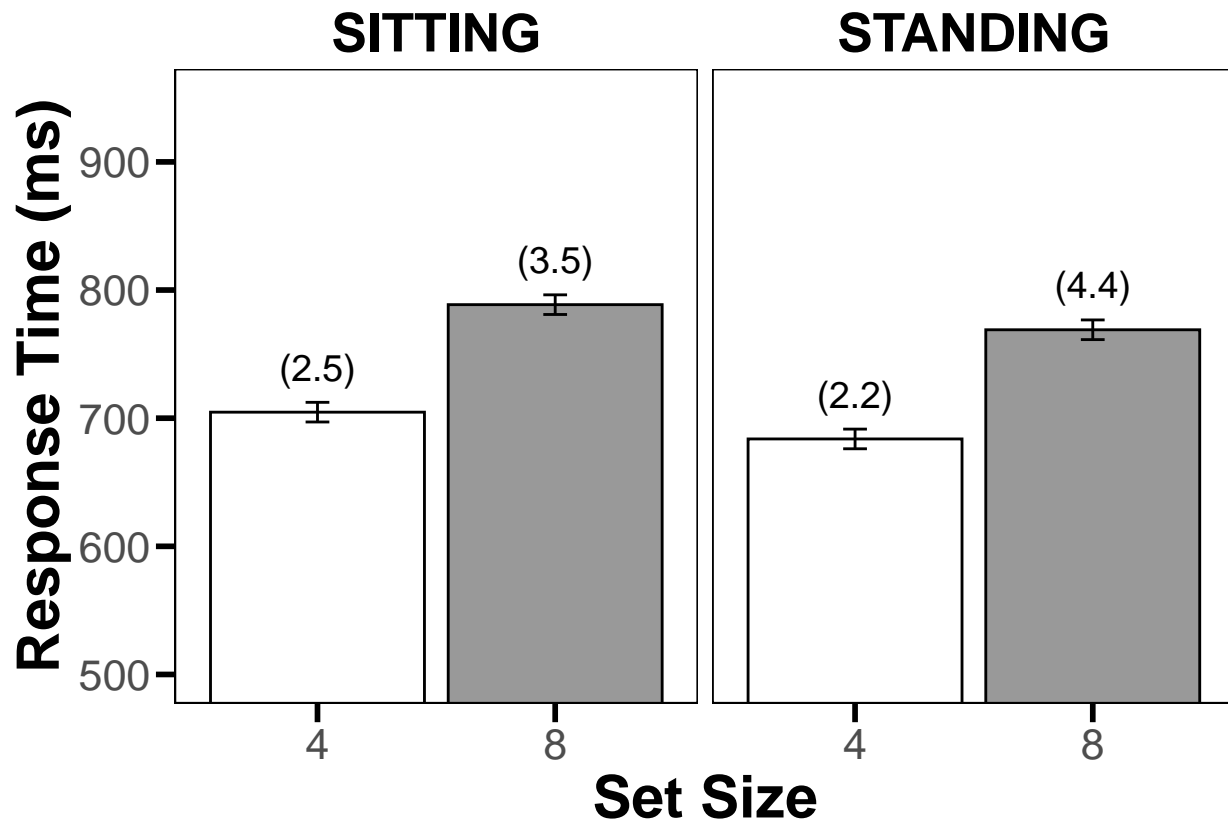
```
##      posture setSize mean      se      min      max      ac
## X11  SITTING      4 704.7 3.814813 697.0298 712.3702 (2.5)
## X12 STANDING      4 683.8 3.814813 676.1298 691.4702 (2.2)
## X13  SITTING      8 788.6 3.814813 780.9298 796.2702 (3.5)
## X14 STANDING      8 769.0 3.814813 761.3298 776.6702 (4.4)

graphRT3$vAdj = 35 #down
graphRT3$vAdj[graphRT3$setSize=="incongruent"]=35 #up
graphRT3$hAdj = 0 #right
#graphRT3$hAdj[graphRT3$posture=="SITTING"]=-60 #left

graphRT3$congruency = factor(graphRT3$setSize, labels = c("4", "8"))

interactionPlot3 <- ggplot(graphRT3, aes(setSize, mean, group=posture)) +
  theme(legend.position = "none")+
  scale_fill_manual(values=c("#FFFFFF", "#999999", "#FFFFFF", "#999999"))+
  coord_cartesian(ylim=c(500,950), expand=TRUE)+
  scale_y_continuous(breaks = round(seq(500, 950, by = 100), 0))+
  geom_text(aes(label=ac), nudge_x=graphRT3$hAdj, nudge_y =graphRT3$vAdj, size=5)+
  geom_bar(stat="identity", aes(fill=interaction(setSize)), colour="black")+
  geom_errorbar(aes(ymin=min, ymax=max, group=interaction(posture, setSize)), width=.1)+
  labs(x = "Set Size", y = "Response Time (ms)") +
  theme(axis.ticks = element_line(size = 1, colour = "black", linetype = "solid"),
        axis.ticks.length = unit(.25, "cm"),
        #axis.line = element_line(size = 1, colour = "black", linetype = "solid"),
        panel.background = element_rect(fill = "white", colour = "white", size = 1),
        axis.text=element_text(size=16),
        axis.title=element_text(size=22, face="bold"),
        strip.text = element_text(size = 20, face = "bold", colour = "black", angle = 0),
        panel.border = element_rect(colour = "black", fill = NA, size = 0.50),
        strip.background = element_rect(fill=NA, colour="NA", size = 2))+
  facet_grid(~posture)

interactionPlot3
```



```
ggsave(interactionPlot3,
  file = "results/plots/fig4_exp3_visual_search_interaction_plot.pdf",
  units = "in",
  width = 8.5,
  height = 5,
  dpi = 600)
```

Reproduce results from Smith et al.

```
# Data source: The data from all the experiments are available at:
# http://rabrams.net under the Resources tab.

### Experiment 1 (Stroop)

#load acc data
Smith_Exp1_acc <- read_excel("data/smith_data.xlsx",
  sheet = "Exp1Acc",
  n_max = 14) #Sample size in Smith

#load rt data
Smith_Exp1_rt <- read_excel("data/smith_data.xlsx",
  sheet = "Exp1RT",
  n_max = 14)

#Restructure from wide to narrow, using tidyr
Smith_Exp1_acc_narrow <- Smith_Exp1_acc %>%
```

```

pivot_longer(cols = sit_neut:sta_con, names_to = "condition", values_to = "acc") %>%
separate(col = condition, into = c("posture", "con"))

Smith_Exp1_rt_narrow <- Smith_Exp1_rt %>%
pivot_longer(cols = sit_neut:sta_con, names_to = "condition", values_to = "rt") %>%
separate(col = condition, into = c("posture", "con"))

Smith_Exp1 <- merge(Smith_Exp1_acc_narrow, Smith_Exp1_rt_narrow)

Smith_exp1_anova_acc <- aov_ez(data = Smith_Exp1,
                             dv = 'acc',
                             id = 'subj',
                             within = c('posture', 'con'),
                             anova_table = list(es = "pes", correction = "none"),
                             type = 3)
kable(nice(Smith_exp1_anova_acc), caption = "ANOVA results for Smith Exp 1 - accuracy")

```

Table 2: ANOVA results for Smith Exp 1 - accuracy

Effect	df	MSE	F	pes	p.value
posture	1, 13	4.59	0.51	.038	.488
con	2, 26	3.19	3.76 *	.224	.037
posture:con	2, 26	2.18	1.47	.101	.250

```

Smith_exp1_anova_rt <- aov_ez(data = Smith_Exp1,
                             dv = 'rt',
                             id = 'subj',
                             within = c('posture', 'con'),
                             anova_table = list(es = "pes", correction = "none"),
                             type = 3)
kable(nice(Smith_exp1_anova_rt), caption = "ANOVA results for Smith Exp 1 - RT")

```

Table 3: ANOVA results for Smith Exp 1 - RT

Effect	df	MSE	F	pes	p.value
posture	1, 13	816.34	0.09	.007	.768
con	2, 26	150.32	3.45 *	.210	.047
posture:con	2, 26	128.10	4.73 *	.267	.018

```

### Experiment 2 (Task-switching)

#load acc data
Smith_Exp2_acc <- read_excel("data/smith_data.xlsx",
                             sheet = "Exp2Acc",
                             n_max = 30)

#load rt data
Smith_Exp2_rt <- read_excel("data/smith_data.xlsx",
                             sheet = "Exp2RT",
                             n_max = 30)

```

```

#Restructure from wide to narrow, using tidyr
Smith_Exp2_acc_narrow <- Smith_Exp2_acc %>%
  pivot_longer(cols = sit_congruent_noswitch:stand_incongruent_switch,
    names_to = "condition", values_to = "acc") %>%
  separate(col = condition, into = c("posture", "con", "switch"))

Smith_Exp2_rt_narrow <- Smith_Exp2_rt %>%
  pivot_longer(cols = sit_congruent_noswitch:stand_incongruent_switch,
    names_to = "condition", values_to = "rt") %>%
  separate(col = condition, into = c("posture", "con", "switch"))

Smith_Exp2 <- merge(Smith_Exp2_acc_narrow, Smith_Exp2_rt_narrow)

Smith_exp2_anova_acc <- aov_ez(data = Smith_Exp2,
  dv = 'acc',
  id = 'subj',
  within = c('posture', 'con', 'switch'),
  anova_table = list(es = "pes", correction = "none"),
  type = 3)
kable(nice(Smith_exp2_anova_acc), caption = "ANOVA results for Smith Exp 2 - accuracy")

```

Table 4: ANOVA results for Smith Exp 2 - accuracy

Effect	df	MSE	F	pes	p.value
posture	1, 29	0.00	2.86	.090	.101
con	1, 29	0.00	67.40 ***	.699	<.001
switch	1, 29	0.00	62.94 ***	.685	<.001
posture:con	1, 29	0.00	1.68	.055	.205
posture:switch	1, 29	0.00	5.54 *	.160	.026
con:switch	1, 29	0.00	23.34 ***	.446	<.001
posture:con:switch	1, 29	0.00	0.50	.017	.484

```

Smith_exp2_anova_rt <- aov_ez(data = Smith_Exp2,
  dv = 'rt',
  id = 'subj',
  within = c('posture', 'con', 'switch'),
  anova_table = list(es = "pes", correction = "none"),
  type = 3)
kable(nice(Smith_exp2_anova_rt), caption = "ANOVA results for Smith Exp 2 - RT")

```

Table 5: ANOVA results for Smith Exp 2 - RT

Effect	df	MSE	F	pes	p.value
posture	1, 29	0.02	0.03	.001	.856
con	1, 29	0.00	40.95 ***	.585	<.001
switch	1, 29	0.00	115.10 ***	.799	<.001
posture:con	1, 29	0.00	0.49	.017	.489
posture:switch	1, 29	0.00	0.10	.004	.751
con:switch	1, 29	0.00	4.77 *	.141	.037
posture:con:switch	1, 29	0.00	0.67	.023	.420

```

### Experiment 3 (Visual Search)

#load acc data
Smith_Exp3_acc <- read_excel("data/smith_data.xlsx",
                             sheet = "Exp3Acc",
                             n_max = 12) %>%

  select(subj:sit8)

#load rt data
Smith_Exp3_rt <- read_excel("data/smith_data.xlsx",
                             sheet = "Exp3RT",
                             n_max = 12) %>%

  select(subj:sit8)

#Restructure from wide to narrow, using tidyr
Smith_Exp3_acc_narrow <- Smith_Exp3_acc %>%
  pivot_longer(cols = stand4:sit8, names_to = "condition", values_to = "acc") %>%
  separate(col = condition, into = c("posture", "set.size"), sep = -1)

Smith_Exp3_rt_narrow <- Smith_Exp3_rt %>%
  pivot_longer(cols = stand4:sit8, names_to = "condition", values_to = "rt") %>%
  separate(col = condition, into = c("posture", "set.size"), sep = -1)

Smith_Exp3 <- merge(Smith_Exp3_acc_narrow, Smith_Exp3_rt_narrow)

Smith_exp3_anova_acc <- aov_ez(data = Smith_Exp3,
                               dv = 'acc',
                               id = 'subj',
                               within = c('posture', 'set.size'),
                               anova_table = list(es = "pes", correction = "none"),
                               type = 3)
kable(nice(Smith_exp3_anova_acc), caption = "ANOVA results for Smith Exp 3 - accuracy")

```

Table 6: ANOVA results for Smith Exp 3 - accuracy

Effect	df	MSE	F	pes	p.value
posture	1, 11	4.61	0.76	.065	.401
set.size	1, 11	1.75	3.44 +	.238	.090
posture:set.size	1, 11	1.38	7.96 *	.420	.017

```

Smith_exp3_anova_rt <- aov_ez(data = Smith_Exp3,
                               dv = 'rt',
                               id = 'subj',
                               within = c('posture', 'set.size'),
                               anova_table = list(es = "pes", correction = "none"),
                               type = 3)
kable(nice(Smith_exp3_anova_rt), caption = "ANOVA results for Smith Exp 3 - RT")

```

Table 7: ANOVA results for Smith Exp 3 - RT

Effect	df	MSE	F	pes	p.value
posture	1, 11	2323.81	0.23	.021	.639
set.size	1, 11	473.24	81.88 ***	.882	<.001
posture:set.size	1, 11	298.96	5.91 *	.350	.033

Overall summary plots: Smith and replication

```
smith_anovas <- lst(Smith_exp1_anova_acc$anova_table,
  Smith_exp1_anova_rt$anova_table,
  Smith_exp2_anova_acc$anova_table,
  Smith_exp2_anova_rt$anova_table,
  Smith_exp3_anova_acc$anova_table,
  Smith_exp3_anova_rt$anova_table)

repl_anovas <- lst(aov_ez(data = stroopCombined,
  dv = "meanPE",
  id = "sj",
  within = c("posture", "congruency"),
  type = 3,
  anova_table = list(es = "pes")),
  aov_ez(data = stroopCombined,
  dv = "meanRT",
  id = "sj",
  within = c("posture", "congruency"),
  type = 3,
  anova_table = list(es = "pes")),
  accModelTS,
  rtModelTS,
  aov_ez(data = vsCombined,
  dv = "meanPE",
  id = "sj",
  within = c("postureFactor", "setSize"),
  type = 3,
  anova_table = list(es = "pes")),
  aov_ez(data = vsCombined,
  dv = "meanRT",
  id = "sj",
  within = c("postureFactor", "setSize"),
  type = 3,
  anova_table = list(es = "pes")))

for (i in 1:6){

  smith_anovas[[i]] <- smith_anovas[[i]] %>%
    rownames_to_column() %>%
    as.data.frame() %>%
    rowwise() %>%
    mutate(LL = get.ci.partial.eta.squared(F, `num Df`, `den Df`, conf.level = 0.9)$LL,
      UL = get.ci.partial.eta.squared(F, `num Df`, `den Df`, conf.level = 0.9)$UL)
```



```

repl_anovas[[i]] <- repl_anovas[[i]]$anova_table %>%
  rownames_to_column() %>%
  as.data.frame() %>%
  rowwise() %>%
  mutate(LL = get.ci.partial.eta.squared(F, `num Df`, `den Df`, conf.level = 0.9)$LL,
         UL = get.ci.partial.eta.squared(F, `num Df`, `den Df`, conf.level = 0.9)$UL)
}

###Exp1 (Stroop)
smith.stroop <- smith_anovas[[1]] %>%
  ungroup() %>%
  bind_rows(smith_anovas[[2]]) %>%
  select(Effect = rowname, pes, LL, UL) %>%
  mutate(dv = rep(c("acc", "rt"), each = 3), col = rep(c("black", "black", "red"), 2))

repl.stroop <- repl_anovas[[1]] %>%
  ungroup() %>%
  bind_rows(repl_anovas[[2]]) %>%
  select(Effect = rowname, pes, LL, UL) %>%
  mutate(dv = rep(c("acc", "rt"), each = 3), col = rep(c("black", "black", "red"), 2),
         Effect = smith.stroop$Effect)

stroop.effects <- merge(smith.stroop, repl.stroop,
                       by = c("Effect", "dv"), suffixes = c("Smith", "Replication"))

stroop.plot <- ggplot(data = stroop.effects, aes(x = pesSmith, y = pesReplication, shape = dv)) +
  geom_point(size = 2.5, col = stroop.effects$colSmith) +
  xlim(0, 1.00) +
  ylim(0, 1.00) +
  geom_abline(slope = 1, intercept = 0, col = "blue") +
  theme_classic() +
  theme(legend.position = c(0.2, 0.85),
        legend.background = element_rect(colour = "black",
                                           linetype = "solid",
                                           fill = "lightgray"),
        legend.title = element_blank(),
        legend.margin = margin(-3, 5, 0, 0)) +
  labs(y = "Replication", x = "Smith et al.", title = "Stroop")

###Exp2 (Task-switching)
smith.ts <- smith_anovas[[3]] %>%
  ungroup() %>%
  bind_rows(smith_anovas[[4]]) %>%
  select(Effect = rowname, pes, LL, UL) %>%
  mutate(dv = rep(c("acc", "rt"), each = 7),
         col = rep(c("black", "black", "black", "black", "red", "black", "black"), 2))

repl.ts <- repl_anovas[[3]] %>%
  ungroup() %>%
  bind_rows(repl_anovas[[4]]) %>%
  select(Effect = rowname, pes, LL, UL) %>%

```

```

mutate(dv = rep(c("acc","rt"), each = 7),
       col = rep(c("black","black","black","black","red","black","black"),2),
       Effect = smith.ts$Effect)

ts.effects <- merge(smith.ts, repl.ts,
                   by = c("Effect","dv"), suffixes = c("Smith","Replication"))

ts.plot <- ggplot(data = ts.effects, aes(x = pesSmith, y = pesReplication, shape = dv)) +
  geom_point(size = 2.5, col = ts.effects$colSmith) +
  xlim(0, 1.00) +
  ylim(0, 1.00) +
  geom_abline(slope = 1, intercept = 0, col = "blue") +
  theme_classic() +
  theme(legend.position = c(0.2, 0.85),
        legend.background = element_rect(colour = "black",
                                           linetype = "solid",
                                           fill = "lightgray"),
        legend.title = element_blank(),
        legend.margin=margin(-3,5,0,0)) +
  labs(y = "Replication", x = "Smith et al.", title = "Task-Switching")

###Exp3 (Visual Search)
smith.vs <- smith_anovas[[5]] %>%
  ungroup() %>%
  bind_rows(smith_anovas[[6]]) %>%
  select(Effect = rowname, pes, LL, UL) %>%
  mutate(dv = rep(c("acc","rt"), each = 3),
         col = rep(c("black","black","red"),2))

repl.vs <- repl_anovas[[5]] %>%
  ungroup() %>%
  bind_rows(repl_anovas[[6]]) %>%
  select(Effect = rowname, pes, LL, UL) %>%
  mutate(dv = rep(c("acc","rt"), each = 3),
         col = rep(c("black","black","red"),2),
         Effect = smith.vs$Effect)

vs.effects <- merge(smith.vs, repl.vs,
                   by = c("Effect","dv"), suffixes = c("Smith",
                                                         "Replication"))

vs.plot <- ggplot(data = vs.effects, aes(x = pesSmith, y = pesReplication, shape = dv)) +
  geom_point(size = 2.5, col = vs.effects$colSmith) +
  xlim(0, 1) +
  ylim(0, 1) +
  geom_abline(slope = 1, intercept = 0, col = "blue") +
  theme_classic() +
  theme(legend.position = c(0.2, 0.85),
        legend.background = element_rect(colour = "black",

```

```

                                linetype = "solid",
                                fill = "lightgray"),
  legend.title = element_blank(),
  legend.margin=margin(-3,5,0,0)) +
labs(y = "Replication", x = "Smith et al.", title = "Visual Search")

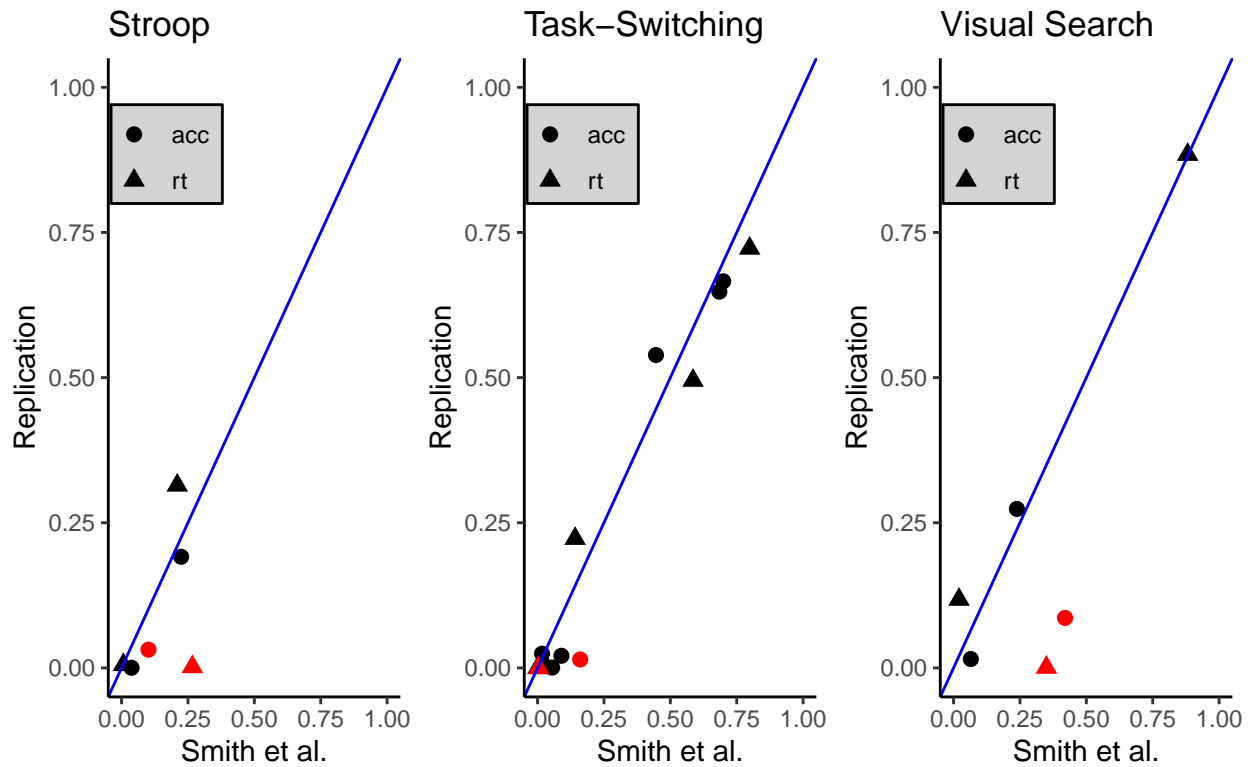
all.plot <- plot_grid(stroop.plot, ts.plot, vs.plot, ncol = 3)

title <- ggdraw() +
  draw_label(
    "Effect Size Comparisons",
    fontface = 'bold',
    x = 0,
    hjust = 0
  ) +
  theme(
    # add margin on the left of the drawing canvas,
    # so title is aligned with left edge of first plot
    plot.margin = margin(0, 0, 0, 7)
  )
all.plot <- plot_grid(
  title, all.plot,
  ncol = 1,
  # rel_heights values control vertical title margins
  rel_heights = c(0.1, 1)
)

all.plot

```

Effect Size Comparisons



```
ggsave(all.plot,
       file = "results/plots/supp_all_effects_plot.pdf",
       units = "in",
       width = 9.5,
       height = 4.50,
       dpi = 600)

### Forest plot
#Graph comparison of key effects for all three experiments
forest.colors <- c("black", "red")

forest.data <- data.frame(Experiment = rep(c("Smith", "Replication"), 3),
                          name = rep(c("Stroop", "Task-switching", "Visual Search"), each = 2),
                          dv = rep(c("rt", "acc", "rt"), each = 2),
                          pes = numeric(6),
                          LL = numeric(6),
                          UL = numeric(6))

forest.data[1,4:6] <- smith_anovas[[2]][3,c(6,8,9)]
forest.data[2,4:6] <- repl_anovas[[2]][3,c(6,8,9)]

forest.data[3,4:6] <- smith_anovas[[3]][5,c(6,8,9)]
forest.data[4,4:6] <- repl_anovas[[3]][5,c(6,8,9)]

forest.data[5,4:6] <- smith_anovas[[6]][3,c(6,8,9)]
forest.data[6,4:6] <- repl_anovas[[6]][3,c(6,8,9)]
```

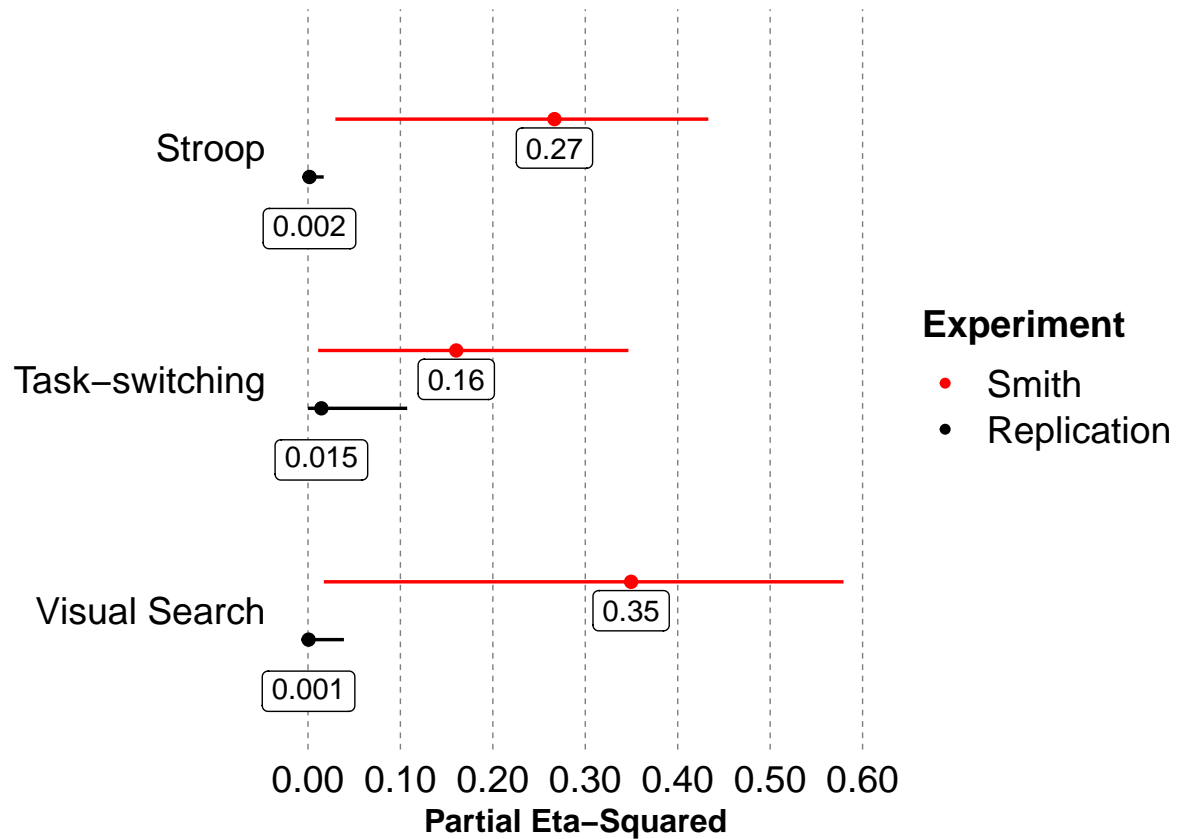
```

forest.comp <- mod.forestplot(df = forest.data,
                             estimate = pes,
                             ci.lower = LL,
                             ci.upper = UL,
                             colour = Experiment,
                             xlab = "Partial Eta-Squared"
) +
  scale_color_manual(values = forest.colors) +
  scale_x_continuous(labels = label_number(accuracy = 0.01), breaks = seq(0.00, 0.60, 0.10)) +
  #Too busy w/numbers for effects?
  geom_label(data = subset(forest.data, Experiment == "Smith"),
             aes(label = round(pes, digits = 2))) +
  geom_label(data = subset(forest.data, Experiment == "Replication"),
             aes(label = round(pes, digits = 3)),
             vjust = 2.50) +
  theme(axis.text=element_text(size=14),
        panel.background = element_rect(fill = "white", colour = "white", size = 1),
        axis.title = element_text(size=12, face="bold"),
        strip.text = element_text(size = 12, face = "bold",colour = "black", angle = 0),
        legend.text = element_text(size = 14),
        legend.title = element_text(size= 14, face = "bold")) +
  coord_cartesian(clip="off") #Disable clipping to draw outside plot area

```

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

```
forest.comp
```



```
ggsave(forest.comp,
  file = "results/plots/fig5_forest_plot.pdf",
  units = "in",
  width = 7,
  height = 5,
  dpi = 600)

#Compare proportions: replication divided by original effect sizes
replication.effects <- subset(forest.data, Experiment == "Replication")
original.effects <- subset(forest.data, Experiment == "Smith")

#As a percentage
prop.effects <- (replication.effects$pes/original.effects$pes)*100
#< 1%, ~9%, and <1%
prop.effects

## [1] 0.6181838 9.0496059 0.1801278

#Average proportion is 3.28%
mean(prop.effects)

## [1] 3.282639
```

Appendix: Analysis with conventional dropping of timeout trials (only affects PE analysis)

Experiment 1: Stroop

```
e1.conv.PE = plyr::ddply(mergedStroopData.conventional,
                        .(sj, cb, congruency, posture),
                        summarise,
                        meanPE = 100 - (mean(ac)*100)) %>%
  ungroup() %>%
  mutate(across(sj:posture, factor))

e1.conv.errmodel <- ezANOVA(e1.conv.PE,
                            dv = .(meanPE),
                            wid=.(sj),
                            within=.(posture, congruency),
                            detailed=TRUE,
                            type=3,
                            return_aov = TRUE)

e1.conv.MSE = e1.conv.errmodel$ANOVA$SSd/e1.conv.errmodel$ANOVA$DFd

exp1_ANOVA_PE_con <-
paste(e1.conv.errmodel$ANOVA$Effect, ": F(",
      e1.conv.errmodel$ANOVA$DFn,
      ", ",
      e1.conv.errmodel$ANOVA$DFd,
      ") = ",
      round(e1.conv.errmodel$ANOVA$F, 3),
      ", MSE = ",
      round(e1.conv.MSE, 3),
      ", p = ",
      round(e1.conv.errmodel$ANOVA$p, 3),
      ", partialEtaSq = ",
      round(e1.conv.errmodel$ANOVA$SSn/(e1.conv.errmodel$ANOVA$SSn+e1.conv.errmodel$ANOVA$SSd), 4),
      sep="")
exp1_ANOVA_PE_con

## [1] "(Intercept): F(1, 49) = 54.682, MSE = 69.145, p = 0, partialEtaSq = 0.5274"
## [2] "posture: F(1, 49) = 0.028, MSE = 14.823, p = 0.868, partialEtaSq = 6e-04"
## [3] "congruency: F(2, 98) = 8.813, MSE = 9.641, p = 0, partialEtaSq = 0.1524"
## [4] "posture:congruency: F(2, 98) = 1.533, MSE = 5.865, p = 0.221, partialEtaSq = 0.0303"

write.csv(exp1_ANOVA_PE_con, "results/exp1_ANOVA_PE_con.csv")

#BF for errors
e1.conv.BF = anovaBF(meanPE~congruency*posture+sj,
                     data = e1.conv.PE,
                     whichRandom = "sj",
                     method="laplace")

e1.conv.BF

## Bayes factor analysis
```

```
## -----
## [1] congruency + sj : 136.8983 ±NA%
## [2] posture + sj : 0.1188895 ±NA%
## [3] congruency + posture + sj : 16.39088 ±NA%
## [4] congruency + posture + congruency:posture + sj : 2.363896 ±NA%
##
## Against denominator:
## meanPE ~ sj
## ---
## Bayes factor type: BFlinearModel, JZS
#...get the Bayes factor for the Null Interaction
e1.conv.BF[3]/e1.conv.BF[4]

## Bayes factor analysis
## -----
## [1] congruency + posture + sj : 6.933838 ±NA%
##
## Against denominator:
## meanPE ~ congruency + posture + congruency:posture + sj
## ---
## Bayes factor type: BFlinearModel, JZS
1/(e1.conv.BF[3]/e1.conv.BF[4])

## Bayes factor analysis
## -----
## [1] congruency + posture + congruency:posture + sj : 0.1442203 ±NA%
##
## Against denominator:
## meanPE ~ congruency + posture + sj
## ---
## Bayes factor type: BFlinearModel, JZS
```

Experiment 2: Task-Switching

```
e2.conv.PE <- task_switching_raw.conventional %>%
  group_by(participant,
            posture,
            congruentTrialType,
            switchTrialType) %>%
  summarize(meanPE = mean((1 - correct_bin) * 100)) %>%
  ungroup() %>%
  mutate(across(participant:switchTrialType, factor))
```

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

```
e2.conv.errmodel <- ezANOVA(e2.conv.PE,
  dv = .(meanPE),
  wid = .(participant),
  within = .(posture, congruentTrialType, switchTrialType),
  detailed = TRUE,
  type = 3,
  return_aov = TRUE)
```



```

e2.conv.MSE = e2.conv.errmodel$ANOVA$SSd/e2.conv.errmodel$ANOVA$DFd

exp2_ANOVA_PE_con <-
paste(e2.conv.errmodel$ANOVA$Effect,": F(",
      e2.conv.errmodel$ANOVA$DFn,
      ", ",
      e2.conv.errmodel$ANOVA$DFd,
      ") = ",
      round(e1.conv.errmodel$ANOVA$F,3),
      ", MSE = ",
      round(e2.conv.MSE,3),
      ", p = ",
      round(e2.conv.errmodel$ANOVA$p,3),
      ", partialEtaSq = ",
      round(e2.conv.errmodel$ANOVA$SSn/(e2.conv.errmodel$ANOVA$SSn+e2.conv.errmodel$ANOVA$SSd),4),
      sep="")
exp2_ANOVA_PE_con

## [1] "(Intercept): F(1, 50) = 54.682, MSE = 124.788, p = 0, partialEtaSq = 0.8018"
## [2] "posture: F(1, 50) = 0.028, MSE = 77.648, p = 0.425, partialEtaSq = 0.0128"
## [3] "congruentTrialType: F(1, 50) = 8.813, MSE = 76.694, p = 0, partialEtaSq = 0.6854"
## [4] "switchTrialType: F(1, 50) = 1.533, MSE = 21.856, p = 0, partialEtaSq = 0.6665"
## [5] "posture:congruentTrialType: F(1, 50) = 54.682, MSE = 38.811, p = 0.939, partialEtaSq = 1e-04"
## [6] "posture:switchTrialType: F(1, 50) = 0.028, MSE = 18.608, p = 0.243, partialEtaSq = 0.0272"
## [7] "congruentTrialType:switchTrialType: F(1, 50) = 8.813, MSE = 13.78, p = 0, partialEtaSq = 0.560"
## [8] "posture:congruentTrialType:switchTrialType: F(1, 50) = 1.533, MSE = 13.555, p = 0.491, partial

write.csv(exp2_ANOVA_PE_con, "results/exp2_ANOVA_PE_con.csv")

#BF for errors
e2.conv.BF = anovaBF(meanPE~congruentTrialType*posture+participant,
                     data = e2.conv.PE,
                     whichRandom = "participant",
                     method="laplace")

## Warning: data coerced from tibble to data frame
e2.conv.BF

## Bayes factor analysis
## -----
## [1] posture + participant : 0.1450097 ±NA%
## [2] congruentTrialType + participant : 1.472075e+31 ±NA%
## [3] posture + congruentTrialType + participant : 2.552796e+30 ±NA%
## [4] posture + congruentTrialType + posture:congruentTrialType + participant : 3.597384e+29 ±NA%
##
## Against denominator:
## meanPE ~ participant
## ---
## Bayes factor type: BFlinearModel, JZS
#...get the Bayes factor for the Null Interaction
e2.conv.BF[3]/e2.conv.BF[4]

## Bayes factor analysis
## -----

```

```
## [1] posture + congruentTrialType + participant : 7.096257 ±NA%
##
## Against denominator:
##   meanPE ~ posture + congruentTrialType + posture:congruentTrialType + participant
## ---
## Bayes factor type: BFlinearModel, JZS
1/(e2.conv.BF[3]/e2.conv.BF[4])

## Bayes factor analysis
## -----
## [1] posture + congruentTrialType + posture:congruentTrialType + participant : 0.1409194 ±NA%
##
## Against denominator:
##   meanPE ~ posture + congruentTrialType + participant
## ---
## Bayes factor type: BFlinearModel, JZS
```

Experiment 3: Visual Search

```
e3.conv.PE = plyr::ddply(merged.VS.data.conventional,
                        .(sj, setSize, posture),
                        summarise,
                        meanPE = 100 - (mean(ac)*100)) %>%
  ungroup() %>%
  mutate(across(sj:posture, factor))

e3.conv.errmodel <- ezANOVA(e3.conv.PE,
                           dv = .(meanPE),
                           wid=.(sj),
                           within=.(posture, setSize),
                           detailed=TRUE,
                           type=3,
                           return_aov = TRUE)

e3.conv.MSE = e3.conv.errmodel$ANOVA$SSd/e3.conv.errmodel$ANOVA$DFd

exp3_ANOVA_PE_con <-
paste(e3.conv.errmodel$ANOVA$Effect,": F(",
      e3.conv.errmodel$ANOVA$DFn,
      ", ",
      e3.conv.errmodel$ANOVA$DFd,
      ") = ",
      round(e3.conv.errmodel$ANOVA$F,3),
      ", MSE = ",
      round(e3.conv.MSE,3),
      ", p = ",
      round(e3.conv.errmodel$ANOVA$p,3),
      ", partialEtaSq = ",
      round(e3.conv.errmodel$ANOVA$SSn/(e3.conv.errmodel$ANOVA$SSn+e3.conv.errmodel$ANOVA$SSd),4),
      sep="")

exp3_ANOVA_PE_con

## [1] "(Intercept): F(1, 49) = 55.236, MSE = 12.588, p = 0, partialEtaSq = 0.5299"
```

```
## [2] "posture: F(1, 49) = 3.311, MSE = 2.43, p = 0.075, partialEtaSq = 0.0633"
## [3] "setSize: F(1, 49) = 2.312, MSE = 3.628, p = 0.135, partialEtaSq = 0.0451"
## [4] "posture:setSize: F(1, 49) = 0.623, MSE = 2.794, p = 0.434, partialEtaSq = 0.0125"

write.csv(exp3_ANOVA_PE_con, "results/exp3_ANOVA_PE_con.csv")

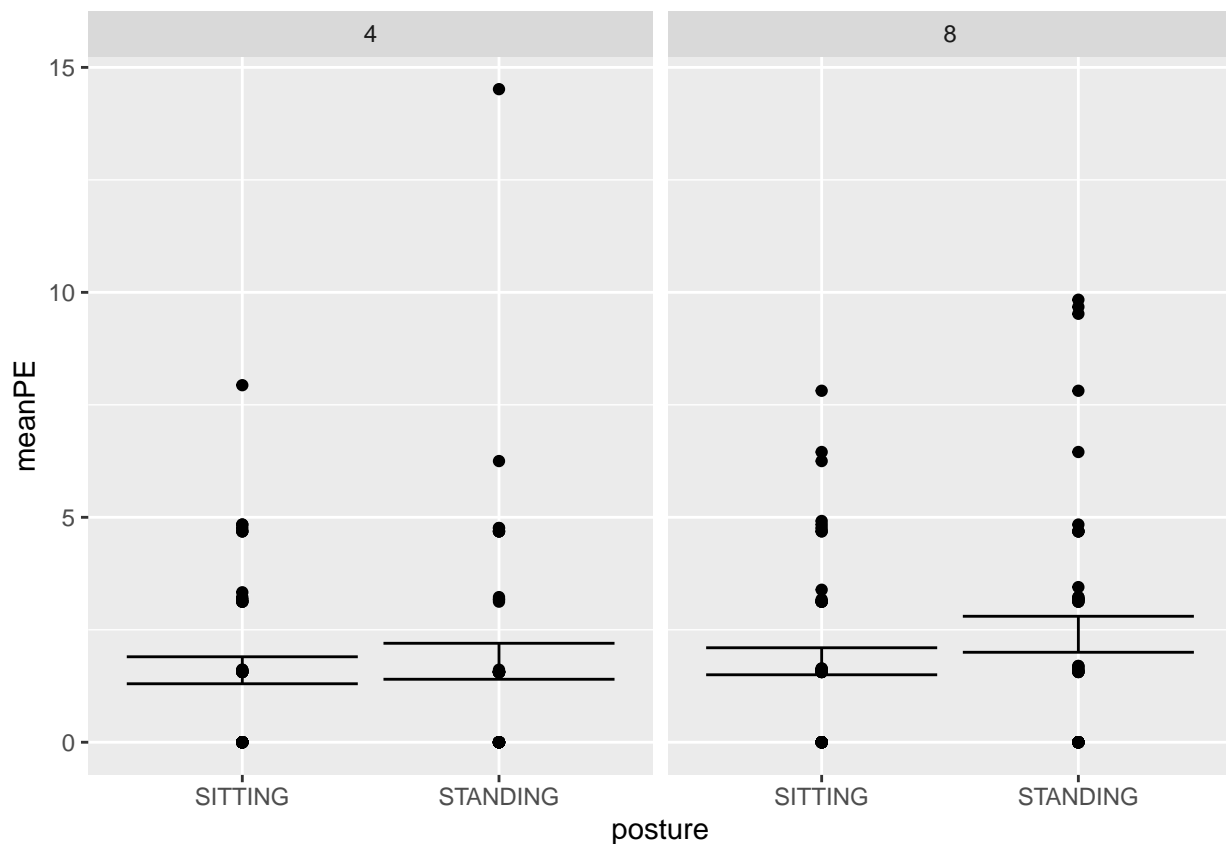
graphPE3.con = describeBy(e3.conv.PE$meanPE,
                           list(e3.conv.PE$posture, e3.conv.PE$setSize),
                           mat=TRUE,
                           digits = 1)

graphPE3.con = graphPE3.con[,c("group1", "group2", "mean", "sd", "se")]

names(graphPE3.con) = c("posture", "setSize", "meanPE", "sd", "se")

e3.PE.conv.plot <-
ggplot(data = e3.conv.PE, aes(x = posture,
                              y = meanPE)) +
  geom_point() +
  facet_wrap(~setSize) +
  geom_errorbar(data = graphPE3.con, aes(ymin = meanPE - se, ymax = meanPE + se))

e3.PE.conv.plot
```

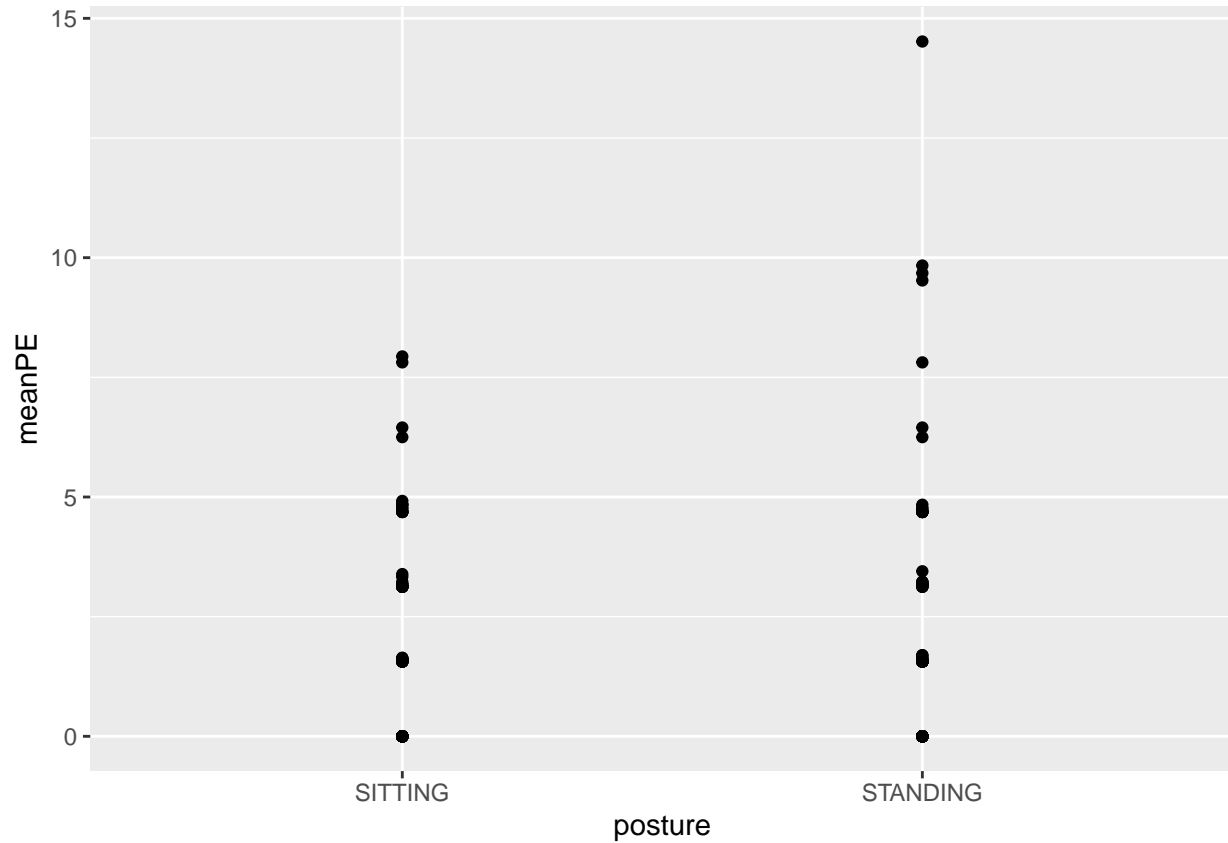


```
#Standing has a single cell mean, set size = 4, nearly 15 percent error
e3.PE.conv.plot2 <-
ggplot(data = e3.conv.PE, aes(x = posture,
```

```

                                y = meanPE)) +
  geom_point()
e3.PE.conv.plot2

```



```

#hist(e3.conv.PE$meanPE)

#BF for errors
e3.conv.BF = anovaBF(meanPE~setSize*posture+sj,
                      data = e3.conv.PE,
                      whichRandom = "sj",
                      method="laplace")

e3.conv.BF

## Bayes factor analysis
## -----
## [1] setSize + sj                : 0.5212586  ±NA%
## [2] posture + sj             : 0.4937759  ±NA%
## [3] setSize + posture + sj  : 0.2659863  ±NA%
## [4] setSize + posture + setSize:posture + sj : 0.06740099 ±NA%
##
## Against denominator:
##   meanPE ~ sj
## ---
## Bayes factor type: BFlinearModel, JZS

```

```
#...get the Bayes factor for the Null Interaction
e3.conv.BF[3]/e3.conv.BF[4]
```

```
## Bayes factor analysis
## -----
## [1] setSize + posture + sj : 3.946327 ±NA%
##
## Against denominator:
## meanPE ~ setSize + posture + setSize:posture + sj
## ---
## Bayes factor type: BFlinearModel, JZS
1/(e3.conv.BF[3]/e3.conv.BF[4])
```

```
## Bayes factor analysis
## -----
## [1] setSize + posture + setSize:posture + sj : 0.2534002 ±NA%
##
## Against denominator:
## meanPE ~ setSize + posture + sj
## ---
## Bayes factor type: BFlinearModel, JZS
```

Effect of different RT cutoffs on PE interaction

```
#compare different criteria for removing long trials
criteria <- seq(1000, 2000, by = 100)
ncriteria <- length(criteria)
criteria.dat <- merged.VS.data.orig
```

```
for (i in criteria){
  criteria.dat <- criteria.dat %>%
    mutate("drop{i}" := ifelse(rt >= i | ac == 0, 0, 1))
}
```

```
vsPEcriteria = criteria.dat %>%
  group_by(sj, cb, setSize, posture) %>%
  summarize(across(starts_with("drop"), ~ 100 - (mean(.x)*100)))
```

```
## `summarise()` has grouped output by 'sj', 'cb', 'setSize'. You can override using the `.groups`
## argument.
```

```
#...set as factors
vsPEcriteria$sj = factor(vsPEcriteria$sj)
vsPEcriteria$cb = factor(vsPEcriteria$cb)
vsPEcriteria$setSize = factor(vsPEcriteria$setSize)
vsPEcriteria$postureFactor = factor(vsPEcriteria$posture)

criteria.results <- data.frame(cutoff = criteria,
                              es = numeric(ncriteria),
                              p.vals = numeric(ncriteria),
                              ci.LL = numeric(ncriteria),
                              ci.UL = numeric(ncriteria))

for (i in 1:length(criteria)){
```

```

tempcol <- paste0("drop",criteria[i])
tempmod <- aov_ez(data = vsPEcriteria,
                  dv = tempcol,
                  id = 'sj',
                  within = c('posture', 'setSize'),
                  anova_table = list(es = "pes", correction = "none"),
                  type = 3)

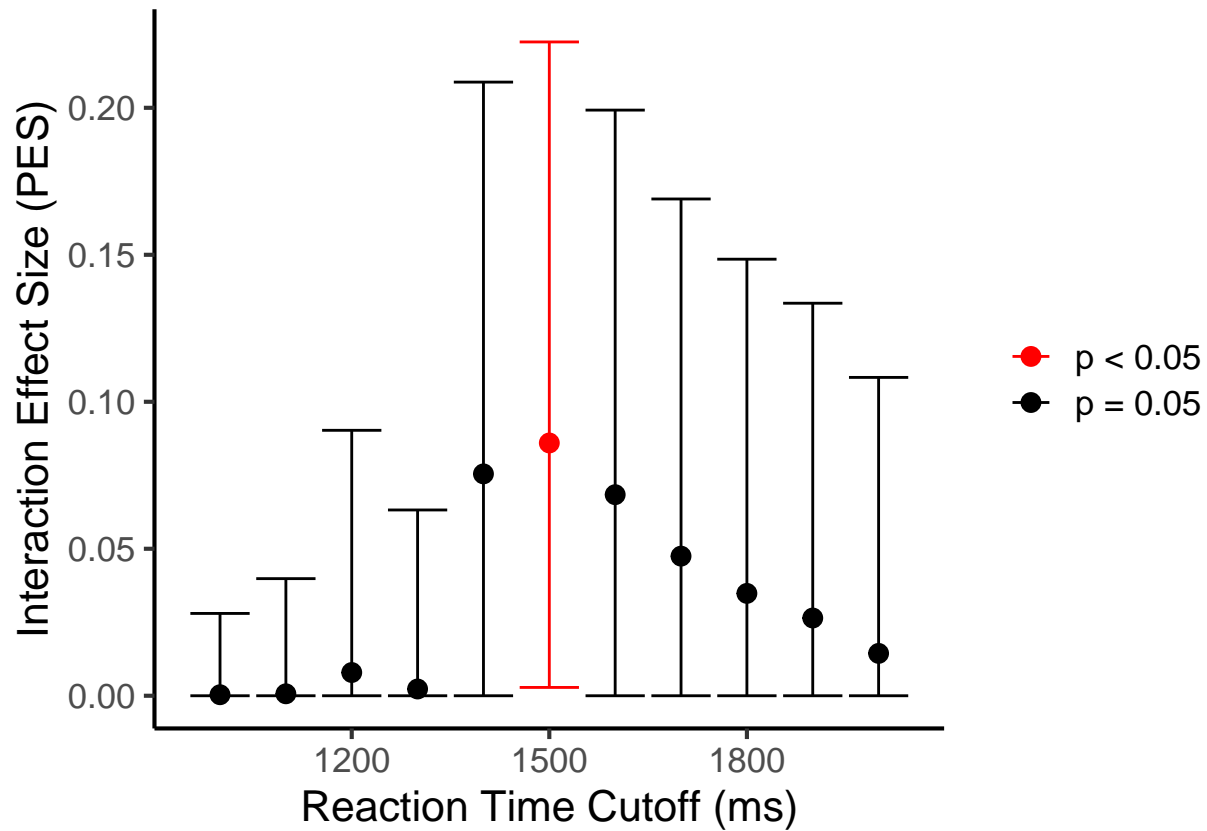
criteria.results$es[i] <- tempmod$anova_table$pes[3]
criteria.results$p.vals[i] <- tempmod$anova_table$`Pr(>F)`[3]
criteria.results$ci.LL[i] <- get.ci.partial.eta.squared(F.value=tempmod$anova_table$F[3],
                                                       df1=tempmod$anova_table$num Df`[3],
                                                       df2 = tempmod$anova_table$den Df`[3])$LL
criteria.results$ci.UL[i] <- get.ci.partial.eta.squared(F.value=tempmod$anova_table$F[3],
                                                       df1=tempmod$anova_table$num Df`[3],
                                                       df2 = tempmod$anova_table$den Df`[3])$UL
}

criteria.results$sig <- ifelse(criteria.results$p.vals < 0.05, "p < 0.05", "p \u2265 0.05")

exp3_rt_cutoff <-
ggplot(criteria.results, aes(criteria, es, col = sig)) +
  geom_point(size = 3) +
  geom_errorbar(aes(ymin = ci.LL, ymax = ci.UL)) +
  scale_color_manual(values = c("red","black")) +
  theme_classic(base_size = 16) +
  theme(legend.title = element_blank()) +
  labs(y = "Interaction Effect Size (PES)", x = "Reaction Time Cutoff (ms)")

exp3_rt_cutoff

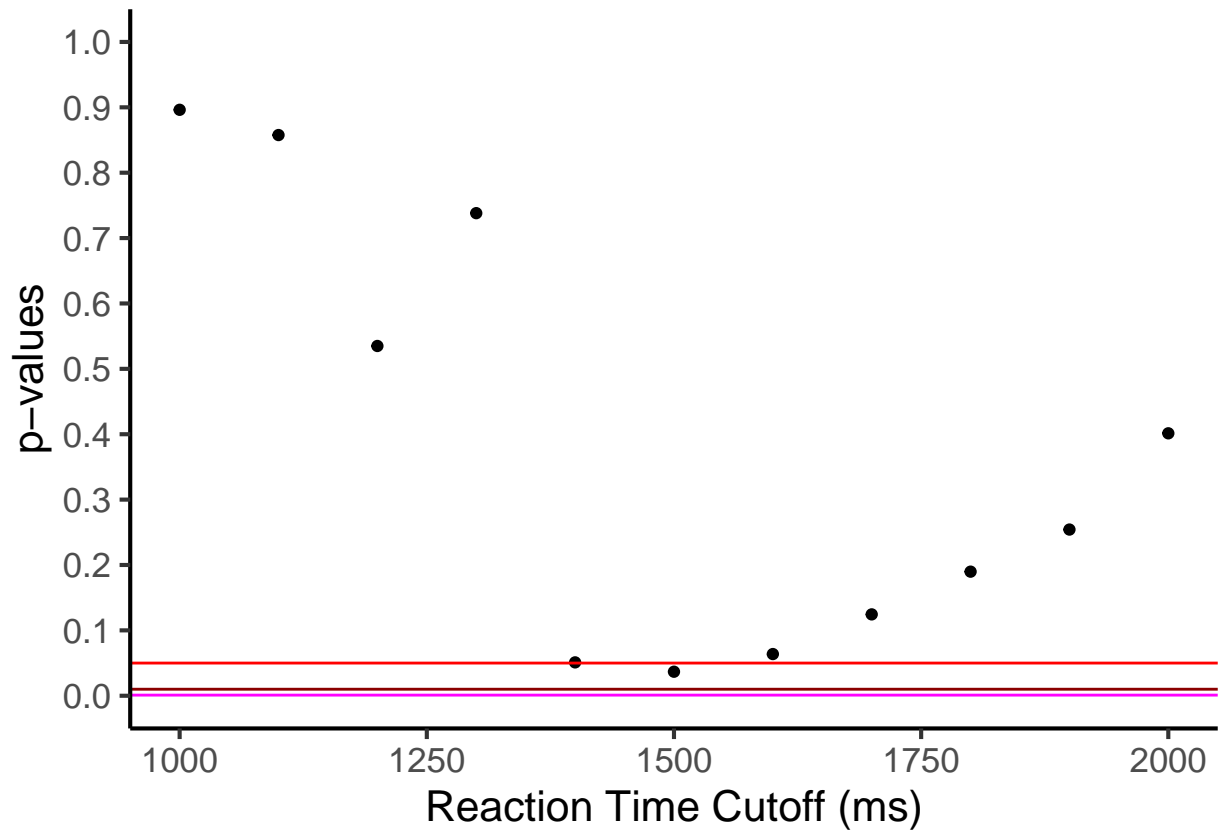
```



```
ggsave(exp3_rt_cutoff,
       file = "results/plots/supp_exp3_RT_cutoff.pdf",
       units = "in",
       width = 9,
       height = 6,
       dpi = 600)

#Not in the supp: Distribution of p-values
exp3_rt_cutoff.pvals <-
ggplot(criteria.results, aes(criteria, p.vals)) +
  geom_point(size = 1.5) +
  scale_color_manual(values = c("red", "black")) +
  theme_classic(base_size = 16) +
  theme(legend.title = element_blank()) +
  scale_y_continuous(limits = c(0, 1), breaks = seq(0, 1, 0.1)) +
  labs(y = "p-values", x = "Reaction Time Cutoff (ms)")

exp3_rt_cutoff.pvals + geom_hline(yintercept = 0.05, color = "red") +
  geom_hline(yintercept = 0.01, color = "darkred") +
  geom_hline(yintercept = 0.001, color = "magenta")
```



```
#plot(criteria.results$p.vals, criteria.results$es)
```