```r
library(tidyverse)
```

```
Warning: package 'ggplot2' was built under R version 4.4.3
```

```
-- Attaching core tidyverse packages ---------------------- tidyverse 2.0.0 --
v dplyr     1.1.4     v readr     2.1.5
v forcats   1.0.0     v stringr   1.5.1
v ggplot2   3.5.2     v tibble    3.2.1
v lubridate 1.9.4     v tidyr     1.3.1
v purrr     1.0.4
-- Conflicts -------------------------------------- tidyverse_conflicts() --
x dplyr::filter() masks stats::filter()
x dplyr::lag()    masks stats::lag()
i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to becom
```

```r
library(flextable)
```

```
Warning: package 'flextable' was built under R version 4.4.3
```

```
Attaching package: 'flextable'
```

```
The following object is masked from 'package:purrr':

    compose
```

```r
#library(tinytex)
library(gtsummary)
```

```
Warning: package 'gtsummary' was built under R version 4.4.3
```

```
Attaching package: 'gtsummary'
```

```
The following object is masked from 'package:flextable':

    continuous_summary
```

```r
library(lm.beta)
library(broom)
```

Warning: package 'broom' was built under R version 4.4.3

```r
library(effects)
```

Loading required package: carData
lattice theme set by effectsTheme()
See ?effectsTheme for details.

```r
library(ggplot2)
library(svglite)
```

Warning: package 'svglite' was built under R version 4.4.3

```r
library(scales)
```

Attaching package: 'scales'

The following object is masked from 'package:purrr':

    discard

The following object is masked from 'package:readr':

    col_factor

```r
library(ggeffects)
```

Warning: package 'ggeffects' was built under R version 4.4.3

```r
library(corrplot)
```

Warning: package 'corrplot' was built under R version 4.4.3

corrplot 0.95 loaded

```r
library(quarto)
```

Warning: package 'quarto' was built under R version 4.4.3

```r
library(rmarkdown)
library(glue)
library(gt)
library(kableExtra)
```

Warning: package 'kableExtra' was built under R version 4.4.3

Attaching package: 'kableExtra'

The following objects are masked from 'package:flextable':

    as_image, footnote

The following object is masked from 'package:dplyr':

    group_rows

```r
library(rstatix)
```

Warning: package 'rstatix' was built under R version 4.4.3

Attaching package: 'rstatix'

The following object is masked from 'package:stats':

    filter

```r
MTdat_change <- read_csv("~/thesis/thesis files/data/MTdat_change.csv")
```

New names:
Rows: 508 Columns: 25
-- Column specification

```
--------------------------------------------------------- Delimiter: "," chr
(2): diagnosis_grp, time_period dbl (23): ...1, megateam_id, rand_group, age,
gender, overall_total_timeplay...
i Use `spec()` to retrieve the full column specification for this data. i
Specify the column types or set `show_col_types = FALSE` to quiet this message.
* `` -> `...1`
```

```r
MTdat <- read_csv("~/thesis/thesis files/data/MTdat.csv")
```

```
New names:
Rows: 708 Columns: 478
-- Column specification
--------------------------------------------------------- Delimiter: "," chr
(60): diagnosis_grp, redcap_event_name, Comments_0, stimuli_0, CTT_SD_... dbl
(396): ...1, megateam_id, visit, gender, dob_year, dob_month, medstatus... lgl
(11): missing_0, status_0, missing_1, status_1, Comments_2, status_2, ... dttm
(1): snapiv_parent_timestamp date (10): consent_date, date, nback_date_0,
nback_date_1, nback_date_2, tt...
i Use `spec()` to retrieve the full column specification for this data. i
Specify the column types or set `show_col_types = FALSE` to quiet this message.
* `` -> `...1`
* `...30.x` -> `...56`
* `...33.x` -> `...59`
* `...30.y` -> `...114`
* `...33.y` -> `...117`
* `...30` -> `...172`
* `...33` -> `...175`
* `...1` -> `...203`
* `...116` -> `...404`
```

```r
#5094301 assign this pt ADHD in dxtx var based on PICS and randomisation noted as ADHD.
#5485402 and 5465302 assign this pt ASD in dxtx var based on networkdemo and randomisation ma

MTdat$adhd_dxtx <- ifelse(MTdat$megateam_id == 5094301, 1, MTdat$adhd_dxtx)
MTdat$asd_dxtx <- ifelse(MTdat$megateam_id %in% c(5465302,5485402), 1, MTdat$asd_dxtx)

#count snap 1-9 for inattentive and 10-18 for hyperactive. speciicaly items rated 2 and 3.

demo <- MTdat %>%
  select(megateam_id, visit, rand_group, diagnosis_grp, gender, consent_date, dob, age, medst
  mutate(gender = case_when(gender == 1 ~ 1,
                            gender == 2 ~ 2,
```

```
                                    gender == 3 ~ 3,
                                    gender == 4 ~ 3)) %>%
  mutate(gender = factor(gender, levels = c(1, 2, 3), labels = c("Cisgender Boy", "Cisgender
         rand_group = factor(rand_group, levels = c(1, 2), labels = c("Mega Team", "TAU")),
         medstatus = factor(medstatus),
         adhd_dxtx = factor(adhd_dxtx),
         asd_dxtx = factor(asd_dxtx),
         odd_dxtx = factor(odd_dxtx),
         schizobpetc_dxtx = factor(schizobpetc_dxtx),
         ocd_dxtx = factor(ocd_dxtx),
         tics_dxtx = factor(tics_dxtx),
         other_dxtx = factor(other_dxtx))

demotbl <- demo %>%
  filter(visit == 1) %>%
  select(age, diagnosis_grp, gender, rand_group, medstatus, adhd_dxtx, asd_dxtx, odd_dxtx, t
  tbl_strata(
    strata = diagnosis_grp,
    ~.x %>%
      tbl_summary(by = rand_group,
                  missing = "no",
                  label = list(medstatus = "Takes Stimulant Medication",
                               adhd_dxtx = "ADHD",
                               asd_dxtx = "Autism",
                               odd_dxtx = "ODD",
                               schizobpetc_dxtx = "Anxiety",
                               ocd_dxtx = "OCD",
                               tics_dxtx = "Tics",
                               converted_calculated_ss = "IQ",
                               bl_snap_comb_sum = "Baseline ADHD Symptoms",
                               scq_score = "Baseline Autism Symptoms",
                               other_dxtx = "Other"),
                  type = where(is.numeric) ~ "continuous",
                  value = list(medstatus ~ "1",
                               adhd_dxtx ~ "1",
                               asd_dxtx ~ "1",
                               odd_dxtx ~ "1",
                               schizobpetc_dxtx ~ "1",
                               ocd_dxtx ~ "1",
                               tics_dxtx ~ "1",
                               other_dxtx ~ "1"),
                  statistic = list(
```

```
                      all_continuous() ~ "{mean} ({sd})",
                      all_dichotomous() ~ "{n} ({p}%)"
                 ))%>%
      add_p()) %>%
  modify_footnote(all_stat_cols() ~ NA) %>%
  #modify_table_styling(columns = label, rows = label %in% c("age", "IQ", "Baseline ADHD Symp
  #modify_table_styling(columns = label,rows = label %in% c("gender", "Takes Stimulant Medica
  as_flex_table() %>%
  add_footer_lines("M (SD); n (%)") %>%
  theme_apa() %>%
  align(j = 1, align = "left", part = "all") %>%
  line_spacing(space = 1, part = "all")
```

The following errors were returned during `as_flex_table()`:
x For variable `overall_total_timeplayed` (`rand_group`) and "statistic" and
  "p.value" statistics: grouping factor must have exactly 2 levels
The following errors were returned during `as_flex_table()`:
x For variable `overall_total_timeplayed` (`rand_group`) and "statistic" and
  "p.value" statistics: grouping factor must have exactly 2 levels
The following warnings were returned during `as_flex_table()`:
! For variable `age` (`rand_group`) and "estimate", "statistic", "p.value",
  "conf.low", and "conf.high" statistics: cannot compute exact p-value with
  ties
! For variable `age` (`rand_group`) and "estimate", "statistic", "p.value",
  "conf.low", and "conf.high" statistics: cannot compute exact confidence
  intervals with ties
! For variable `bl_raw_GEC` (`rand_group`) and "estimate", "statistic",
  "p.value", "conf.low", and "conf.high" statistics: cannot compute exact
  p-value with ties
! For variable `bl_raw_GEC` (`rand_group`) and "estimate", "statistic",
  "p.value", "conf.low", and "conf.high" statistics: cannot compute exact
  confidence intervals with ties
! For variable `bl_snap_comb_sum` (`rand_group`) and "estimate", "statistic",
  "p.value", "conf.low", and "conf.high" statistics: cannot compute exact
  p-value with ties
! For variable `bl_snap_comb_sum` (`rand_group`) and "estimate", "statistic",
  "p.value", "conf.low", and "conf.high" statistics: cannot compute exact
  confidence intervals with ties
! For variable `bl_target_acc_1` (`rand_group`) and "estimate", "statistic",
  "p.value", "conf.low", and "conf.high" statistics: cannot compute exact
  p-value with ties
! For variable `bl_target_acc_1` (`rand_group`) and "estimate", "statistic",

```
  "p.value", "conf.low", and "conf.high" statistics: cannot compute exact
  confidence intervals with ties
! For variable `bl_target_acc_2` (`rand_group`) and "estimate", "statistic",
  "p.value", "conf.low", and "conf.high" statistics: cannot compute exact
  p-value with ties
! For variable `bl_target_acc_2` (`rand_group`) and "estimate", "statistic",
  "p.value", "conf.low", and "conf.high" statistics: cannot compute exact
  confidence intervals with ties
! For variable `converted_calculated_ss` (`rand_group`) and "estimate",
  "statistic", "p.value", "conf.low", and "conf.high" statistics: cannot
  compute exact p-value with ties
! For variable `converted_calculated_ss` (`rand_group`) and "estimate",
  "statistic", "p.value", "conf.low", and "conf.high" statistics: cannot
  compute exact confidence intervals with ties
! For variable `scq_score` (`rand_group`) and "estimate", "statistic",
  "p.value", "conf.low", and "conf.high" statistics: cannot compute exact
  p-value with ties
! For variable `scq_score` (`rand_group`) and "estimate", "statistic",
  "p.value", "conf.low", and "conf.high" statistics: cannot compute exact
  confidence intervals with ties
```

```r
#demotbl

outcomes <- MTdat %>%
  select(megateam_id, visit, rand_group, diagnosis_grp, itssrt, target_acc_1, target_acc_2,
  mutate(rand_group = factor(rand_group, levels = c(1, 2), labels = c("Mega Team", "TAU")))


#open text code the other_dxtx and pull out the LDs


#check for group level differences at 5 week breakdown

data_summ <- MTdat_change %>%
  filter(time_period == "change1") %>%
  mutate(overall_total_timeplayed = if_else(rand_group == 2, 0, overall_total_timeplayed)) %>%
  mutate(rand_group = case_when(rand_group == 1 ~ "Mega Team",
                                rand_group == 2 ~ "Control")) %>%
  mutate(rand_group = factor(rand_group))

MTdat_change$time_period <- factor(MTdat_change$time_period, levels = c("change1", "changetot
```

```
MTdatch5_adhd <- MTdat_change %>%
  filter(diagnosis_grp == "ADHD") %>%
  filter(time_period == "change1") %>%
  mutate(overall_total_timeplayed = if_else(rand_group == 2, 0, overall_total_timeplayed)) %>
  mutate(rand_group = case_when(rand_group == 1 ~ 1,
                                rand_group == 2 ~ 0)) %>%
  mutate(rand_group = factor(rand_group)) %>%
  mutate(medstatus = factor(medstatus, levels = c(0,1))) %>%
  mutate(gender = case_when(gender == 1 ~ 0,
                            gender == 2 ~ 1,
                            gender == 3 ~ 2)) %>%
  mutate(gender = factor(gender, levels = c(0, 1, 2)))

#print("Stop Task 5 Week improvement")

s5_mod_all <- lm(cs_itssrt ~ medstatus*rand_group + bl_snap_comb_sum*rand_group + bl_scq*rand

s5_F <- signif(glance(s5_mod_all)$statistic[[1]], 2)

s5_p <- glance(s5_mod_all)$p.value[[1]]


s5_r2 <- signif(glance(s5_mod_all)$r.squared[[1]], 2)

s5_beta <- lm.beta(s5_mod_all)


#mean(s5_mod_all$residuals)

#shows specific predictor's standardized beta coefficient
s5_beta_s <- signif(s5_beta$standardized.coefficients[["rand_group1:bl_itssrt"]], 2)

#shows specific predictor's pvalue
s5_p_s <- signif(summary(s5_mod_all)$coefficients["rand_group1:bl_itssrt",4], 2)
#summary(s5_mod_all)

#print("BRIEF 5 Week improvement")

b5_mod_all <- lm(cs_GEC ~ medstatus*rand_group + bl_snap_comb_sum*rand_group + bl_scq*rand_gr

b5_beta <- lm.beta(b5_mod_all)
```

```r
b5_F <- signif(glance(b5_mod_all)$statistic[[1]], 2)

b5_p <- signif(glance(b5_mod_all)$p.value[[1]], 2)

b5_r2 <- signif(glance(b5_mod_all)$r.squared[[1]], 2)


#summary(b5_mod_all)

#print("1-back 5 Week improvement")

ob5_mod_all <- lm(cs_targacc1 ~ medstatus*rand_group + bl_snap_comb_sum*rand_group + bl_scq*

ob5_beta <- lm.beta(ob5_mod_all)

ob5_F <- signif(glance(ob5_mod_all)$statistic[[1]], 2)

ob5_p <- signif(glance(ob5_mod_all)$p.value[[1]], 2)

ob5_r2 <- signif(glance(ob5_mod_all)$r.squared[[1]], 2)


#shows specific predictor's standardized beta coefficient
ob5_beta_tp <- signif(ob5_beta$standardized.coefficients[["overall_total_timeplayed"]],2)

#shows specific predictor's pvalue
ob5_p_tp <- signif(summary(ob5_mod_all)$coefficients["overall_total_timeplayed",4], 2)

#summary(ob5_mod_all)


#print("2-back 5 Week improvement")

tb5_mod_all <- lm(cs_targacc2 ~ medstatus*rand_group + bl_snap_comb_sum*rand_group + bl_scq*

tb5_beta <- lm.beta(tb5_mod_all)

tb5_F <- signif(glance(tb5_mod_all)$statistic[[1]], 2)

tb5_p <- signif(glance(tb5_mod_all)$p.value[[1]], 2)

tb5_r2 <- signif(glance(tb5_mod_all)$r.squared[[1]], 2)
```

```r
#summary(tb5_mod_all)

#plot(allEffects(tb6_mod_all))


#print("SNAP 5 Week improvement")

ad5_mod_all <- lm(cs_snap ~ medstatus*rand_group + bl_snap_comb_sum*rand_group + bl_scq*rand_

ad5_beta <- lm.beta(ad5_mod_all)

ad5_F <- signif(glance(ad5_mod_all)$statistic[[1]], 2)

ad5_p <- signif(glance(ad5_mod_all)$p.value[[1]], 2)

ad5_r2 <- signif(glance(ad5_mod_all)$r.squared[[1]], 2)

#summary(ad5_mod_all)

#print("Tower 5 Week improvement")

t5_mod_all <- lm(cs_tas ~ medstatus*rand_group + bl_snap_comb_sum*rand_group + bl_scq*rand_g

t5_beta <- lm.beta(t5_mod_all)

t5_F <- signif(glance(t5_mod_all)$statistic[[1]], 2)

t5_p <- signif(glance(t5_mod_all)$p.value[[1]], 2)

t5_r2 <- signif(glance(t5_mod_all)$r.squared[[1]], 2)

#shows specific predictor's standardized beta coefficient
t5_beta_ad <- signif(t5_beta[["standardized.coefficients"]][["rand_group1:bl_snap_comb_sum"]]

#shows specific predictor's pvalue
t5_p_ad <- signif(summary(t5_mod_all)[["coefficients"]][["rand_group1:bl_snap_comb_sum",4]],

#shows specific predictor's standardized beta coefficient
t5_beta_b <- signif(t5_beta[["standardized.coefficients"]][["rand_group1:bl_raw_GEC"]],2)
```

```
#shows specific predictor's pvalue
t5_p_b <- signif(summary(t5_mod_all)[["coefficients"]][["rand_group1:bl_raw_GEC",4]], 2)

#summary(t5_mod_all)

#print("WJ 5 Week improvement")

w5_mod_all <- lm(cs_fluency ~ medstatus*rand_group + bl_snap_comb_sum*rand_group + bl_scq*ra

w5_beta <- lm.beta(w5_mod_all)

w5_F <- signif(glance(w5_mod_all)$statistic[[1]], 2)

w5_p <- signif(glance(w5_mod_all)$p.value[[1]], 2)

w5_r2 <- signif(glance(w5_mod_all)$r.squared[[1]], 2)

#summary(w5_mod_all)

MTdatch6_adhd <- MTdat_change %>%
  filter(diagnosis_grp == "ADHD") %>%
  filter(time_period == "changetotal") %>%
  mutate(overall_total_timeplayed = if_else(rand_group == 2, 0, overall_total_timeplayed)) %
  mutate(rand_group = case_when(rand_group == 1 ~ 1,
                                rand_group == 2 ~ 0)) %>%
  mutate(rand_group = factor(rand_group)) %>%
  mutate(medstatus = factor(medstatus, levels = c(0,1))) %>%
  mutate(gender = case_when(gender == 1 ~ 0,
                            gender == 2 ~ 1,
                            gender == 3 ~ 2)) %>%
  mutate(gender = factor(gender, levels = c(0, 1, 2)))

#print("Stop Task 6 month improvement")

s6_mod_all <- lm(cs_itssrt ~ medstatus*rand_group + bl_snap_comb_sum*rand_group + bl_scq*ran

s6_beta <- lm.beta(s6_mod_all)

s6_F <- signif(glance(s6_mod_all)$statistic[[1]], 2)

s6_p <- signif(glance(s6_mod_all)$p.value[[1]], 2)
```

```r
s6_r2 <- signif(glance(s6_mod_all)$r.squared[[1]], 2)

#shows specific predictor's standardized beta coefficient
s6_beta_ob <- signif(s6_beta$standardized.coefficients[["rand_group1:bl_target_acc_1"]], 2)

#shows specific predictor's pvalue
s6_p_ob <- signif(summary(s6_mod_all)$coefficients["rand_group1:bl_target_acc_1",4], 2)

#summary(s6_mod_all)

#print("BRIEF 6 month improvement")

b6_mod_all <- lm(cs_GEC ~ medstatus*rand_group + bl_snap_comb_sum*rand_group + bl_scq*rand_g

b6_beta <- lm.beta(b6_mod_all)

#summary(b6_mod_all)

b6_F <- signif(glance(b6_mod_all)$statistic[[1]], 2)

b6_p <- signif(glance(b6_mod_all)$p.value[[1]], 2)

b6_r2 <- signif(glance(b6_mod_all)$r.squared[[1]], 2)

#print("1-Back 6 month improvement")

ob6_mod_all <- lm(cs_targacc1 ~ medstatus*rand_group + bl_snap_comb_sum*rand_group + bl_scq*

ob6_beta <- lm.beta(ob6_mod_all)

#summary(ob6_mod_all)

ob6_F <- signif(glance(ob6_mod_all)$statistic[[1]], 2)

ob6_p <- signif(glance(ob6_mod_all)$p.value[[1]], 2)

ob6_r2 <- signif(glance(ob6_mod_all)$r.squared[[1]], 2)

#print("2-Back 6 month improvement")

tb6_mod_all <- lm(cs_targacc2 ~ medstatus*rand_group + bl_snap_comb_sum*rand_group + bl_scq*
```

```r
tb6_beta <- lm.beta(tb6_mod_all)

tb6_F <- signif(glance(tb6_mod_all)$statistic[[1]], 2)

tb6_p <- signif(glance(tb6_mod_all)$p.value[[1]], 2)

tb6_r2 <- signif(glance(tb6_mod_all)$r.squared[[1]], 2)

#summary(tb6_mod_all)

#shows specific predictor's standardized beta coefficient
tb6_beta_ob <- signif(tb6_beta[["standardized.coefficients"]][["rand_group1:bl_target_acc_1"]

#shows specific predictor's pvalue
tb6_p_ob <- signif(summary(tb6_mod_all)[["coefficients"]][["rand_group1:bl_target_acc_1",4]]


#print("SNAP 6 month improvement")

ad6_mod_all <- lm(cs_snap ~ medstatus*rand_group + bl_snap_comb_sum*rand_group + bl_scq*rand_

ad6_beta <- lm.beta(ad6_mod_all)

ad6_F <- signif(glance(ad6_mod_all)$statistic[[1]], 2)

ad6_p <- signif(glance(ad6_mod_all)$p.value[[1]], 2)

ad6_r2 <- signif(glance(ad6_mod_all)$r.squared[[1]], 2)

#summary(ad6_mod_all)

#print("Tower 6 month improvement")

t6_mod_all <- lm(cs_tas ~ medstatus*rand_group + bl_snap_comb_sum*rand_group + bl_scq*rand_g

t6_beta <- lm.beta(t6_mod_all)

#summary(t6_mod_all)

t6_F <- signif(glance(t6_mod_all)$statistic[[1]], 2)

t6_p <- signif(glance(t6_mod_all)$p.value[[1]], 2)
```

```r
t6_r2 <- signif(glance(t6_mod_all)$r.squared[[1]], 2)

#print("WJ 6 month improvement")

w6_mod_all <- lm(cs_fluency ~ medstatus*rand_group + bl_snap_comb_sum*rand_group + bl_scq*ra

w6_beta <- lm.beta(w6_mod_all)

w6_F <- signif(glance(w6_mod_all)$statistic[[1]], 2)

w6_p <- signif(glance(w6_mod_all)$p.value[[1]], 2)

w6_r2 <- signif(glance(w6_mod_all)$r.squared[[1]], 2)

#summary(w6_mod_all)



#another option to format pvalues https://scriptsandstatistics.wordpress.com/2019/09/22/forma

pvals <- c(ad5_p, ad6_p, b5_p, b6_p, ob5_p, ob5_p_tp, ob6_p, s5_p, s5_p_s, s6_p, s6_p_ob, t5_

pvals <- p_format(pvals, digits = 2, accuracy = 0.001, add.p = TRUE, space = TRUE)

names(pvals) <- c("ad5_p", "ad6_p", "b5_p", "b6_p", "ob5_p", "ob5_p_tp", "ob6_p", "s5_p", "s5


MT_cor <- MTdatch5_adhd %>%
  select(!c(megateam_id, rand_group, diagnosis_grp, time_period, ...1)) %>%
  mutate(gender = as.numeric(gender),
         medstatus = as.numeric(medstatus))

MT_cor <- cor(na.omit(MT_cor))
test = cor.mtest(MT_cor, conf.level = 0.95)

#corrplot(MT_cor, p.mat = test$p, type = "lower", insig='blank', addCoef.col = "black", col =


MT_cor <- MTdatch6_adhd %>%
  select(!c(megateam_id, rand_group, diagnosis_grp, time_period, ...1)) %>%
  mutate(gender = as.numeric(gender),
         medstatus = as.numeric(medstatus))
```

```r
MT_cor <- cor(na.omit(MT_cor))
test = cor.mtest(MT_cor, conf.level = 0.95)
#corrplot(MT_cor, p.mat = test$p, type = "lower", insig='blank', addCoef.col = "black", col =


# summary(ad5_mod_all)
# plot(allEffects(ad5_mod_all))
#
# summary(ad6_mod_all)
# plot(allEffects(ad6_mod_all))
#
# summary(b5_mod_all)
# plot(allEffects(b5_mod_all))
#
# summary(b6_mod_all)
# plot(allEffects(b6_mod_all))
#
# summary(s5_mod_all)
# plot(allEffects(s5_mod_all))
#
# summary(s6_mod_all)
# plot(allEffects(s6_mod_all))
#
# summary(ob5_mod_all)
# plot(allEffects(ob5_mod_all))
#
# summary(ob6_mod_all)
# plot(allEffects(ob6_mod_all))
#
# summary(tb5_mod_all)
# plot(allEffects(tb5_mod_all))
# summary(tb6_mod_all)
# plot(allEffects(tb6_mod_all))
#
# summary(t5_mod_all)
# plot(allEffects(t5_mod_all))
#
# summary(t6_mod_all)
# plot(allEffects(t6_mod_all))
#
# summary(w5_mod_all)
# plot(allEffects(w5_mod_all))
```

```
#
# summary(w6_mod_all)
# plot(allEffects(w6_mod_all))

#checking regression assumptions - all pass
# plot(ad5_mod_all)
# plot(ad6_mod_all)
# plot(b5_mod_all)
# plot(b6_mod_all)
# plot(s5_mod_all)
# plot(s6_mod_all)
# plot(ob5_mod_all)
# plot(ob6_mod_all)
# plot(tb5_mod_all)
# plot(tb6_mod_all)
# plot(t5_mod_all)
# plot(t6_mod_all)
# plot(w5_mod_all)
# plot(w6_mod_all)

# hist(MTdatch5_adhd$bl_itssrt)
# hist(MTdatch5_adhd$bl_target_acc_1)
# hist(MTdatch5_adhd$bl_target_acc_2)
#
#
# hist(MTdatch5_asd$bl_itssrt)
# hist(MTdatch5_asd$bl_target_acc_1)
# hist(MTdatch5_asd$bl_target_acc_2)
#
# hist(MTdat$bl_itssrt)
# hist(MTdat$bl_target_acc_1)
# hist(MTdat$bl_target_acc_2)

# hist(MTdat$scq_score)
# hist(MTdatch5_asd$bl_scq)
# hist(MTdatch5_adhd$bl_scq)
```

```
MTdatch5_asd <- MTdat_change %>%
  filter(diagnosis_grp == "Autism") %>%
  filter(time_period == "change1") %>%
  mutate(overall_total_timeplayed = if_else(rand_group == 2, 0, overall_total_timeplayed)) %:
  mutate(rand_group = case_when(rand_group == 1 ~ 1,
```

```r
                              rand_group == 2 ~ 0)) %>%
  mutate(rand_group = factor(rand_group)) %>%
  mutate(medstatus = factor(medstatus, levels = c(0,1))) %>%
  mutate(gender = case_when(gender == 1 ~ 0,
                            gender == 2 ~ 1,
                            gender == 3 ~ 2)) %>%
  mutate(gender = factor(gender, levels = c(0, 1, 2)))

#print("Stop Task 5 Week improvement")

s5_mod_asd <- lm(cs_itssrt ~ bl_scq*rand_group + bl_snap_comb_sum*rand_group + bl_itssrt*rand

s5_F2 <- signif(glance(s5_mod_asd)$statistic[[1]], 2)

s5_p2 <- signif(glance(s5_mod_asd)$p.value[[1]], 2)

s5_r22 <- signif(glance(s5_mod_asd)$r.squared[[1]], 2)

s5_beta2 <- lm.beta(s5_mod_asd)

#mean(s5_mod_asd$residuals)

#summary(s5_mod_asd)

#shows specific predictor's standardized beta coefficient
s5_beta_s2 <- signif(s5_beta2$standardized.coefficients[["bl_itssrt"]], 2)
s5_beta_ad2 <- signif(s5_beta2$standardized.coefficients[["bl_snap_comb_sum"]], 2)

#shows specific predictor's pvalue
s5_p_s2 <- signif(summary(s5_mod_asd)$coefficients["bl_itssrt",4], 2)
s5_p_ad2 <- signif(summary(s5_mod_asd)$coefficients["bl_snap_comb_sum",4], 2)

#summary(s5_mod_asd)

#print("BRIEF 5 Week improvement")

b5_mod_asd <- lm(cs_GEC ~ bl_scq*rand_group + bl_itssrt*rand_group + bl_target_acc_1*rand_gro

b5_beta2 <- lm.beta(b5_mod_asd)
```

```r
b5_F2 <- signif(glance(b5_mod_asd)$statistic[[1]], 2)

b5_p2 <- signif(glance(b5_mod_asd)$p.value[[1]], 2)

b5_r22 <- signif(glance(b5_mod_asd)$r.squared[[1]], 2)

#summary(b5_mod_asd)

#print("1-back 5 Week improvement")

ob5_mod_asd <- lm(cs_targacc1 ~ bl_scq*rand_group + bl_itssrt*rand_group + bl_target_acc_1*ra

ob5_beta2 <- lm.beta(ob5_mod_asd)

ob5_F2 <- signif(glance(ob5_mod_asd)$statistic[[1]], 2)

ob5_p2 <- signif(glance(ob5_mod_asd)$p.value[[1]], 2)

ob5_r22 <- signif(glance(ob5_mod_asd)$r.squared[[1]], 2)

#summary(ob5_mod_asd)


MTdatch6_asd <- MTdat_change %>%
  filter(diagnosis_grp == "Autism") %>%
  filter(time_period == "changetotal") %>%
  mutate(overall_total_timeplayed = if_else(rand_group == 2, 0, overall_total_timeplayed)) %>%
  mutate(rand_group = case_when(rand_group == 1 ~ 1,
                                rand_group == 2 ~ 0)) %>%
  mutate(rand_group = factor(rand_group)) %>%
  mutate(medstatus = factor(medstatus, levels = c(0,1))) %>%
  mutate(gender = case_when(gender == 1 ~ 0,
                            gender == 2 ~ 1,
                            gender == 3 ~ 2)) %>%
  mutate(gender = factor(gender, levels = c(0, 1, 2)))

#print("Stop Task 5 Week improvement")

s6_mod_asd <- lm(cs_itssrt ~ bl_scq*rand_group + bl_snap_comb_sum*rand_group + bl_itssrt*ran


s6_F2 <- signif(glance(s6_mod_asd)$statistic[[1]], 2)
```

```r
s6_p2 <- signif(glance(s6_mod_asd)$p.value[[1]], 2)

s6_r22 <- signif(glance(s6_mod_asd)$r.squared[[1]], 2)

s6_beta2 <- lm.beta(s6_mod_asd)

#mean(s5_mod_all$residuals)

#shows specific predictor's standardized beta coefficient
s6_beta_s2 <- signif(s6_beta2$standardized.coefficients[["bl_itssrt"]], 2)

#shows specific predictor's pvalue
s6_p_s2 <- signif(summary(s6_mod_asd)$coefficients["bl_itssrt",4], 2)

#summary(s6_mod_asd)

#print("BRIEF 5 Week improvement")

b6_mod_asd <- lm(cs_GEC ~ bl_scq*rand_group + bl_itssrt*rand_group + bl_target_acc_1*rand_gr

b6_beta2 <- lm.beta(b6_mod_asd)

b6_F2 <- signif(glance(b6_mod_asd)$statistic[[1]], 2)

b6_p2 <- signif(glance(b6_mod_asd)$p.value[[1]], 2)

b6_r22 <- signif(glance(b6_mod_asd)$r.squared[[1]], 2)

#summary(b6_mod_asd)

#print("1-back 5 Week improvement")

ob6_mod_asd <- lm(cs_targacc1 ~ bl_scq*rand_group + bl_itssrt*rand_group + bl_target_acc_1*ra

ob6_beta2 <- lm.beta(ob6_mod_asd)

ob6_F2 <- signif(glance(ob6_mod_asd)$statistic[[1]], 2)

ob6_p2 <- signif(glance(ob6_mod_asd)$p.value[[1]], 2)

ob6_r22 <- signif(glance(ob6_mod_asd)$r.squared[[1]], 2)
```

```
#summary(ob6_mod_asd)


asd_pvals <- c(b5_p2, b6_p2, ob5_p2, ob6_p2, s5_p2, s6_p2, s5_p_s2, s5_p_ad2, s6_p_s2)

asd_pvals <- p_format(asd_pvals, digits = 2, accuracy = 0.001, add.p = TRUE, space = TRUE)

names(asd_pvals) <- c("b5_p2", "b6_p2", "ob5_p2", "ob6_p2", "s5_p2", "s6_p2", "s5_p_s2", "s5_
```

```
# summary(s5_mod_all)
# plot(allEffects(s5_mod_all))
#
# summary(b5_mod_all)
# plot(allEffects(b5_mod_all))
#
# summary(ob5_mod_all)
# plot(allEffects(ob5_mod_all))
#
# summary(s6_mod_all)
# plot(allEffects(s6_mod_all))
#
# summary(b6_mod_all)
# plot(allEffects(b6_mod_all))
#
# summary(ob6_mod_all)
# plot(allEffects(ob6_mod_all))
#
# summary(tb6_mod_all)
# plot(allEffects(tb6_mod_all))

#checking assumptions - a few cook's distance for stop were borderline..
# plot(b5_mod_asd)
# plot(b6_mod_asd)
# plot(s5_mod_asd)
# plot(s6_mod_asd)
# plot(ob5_mod_asd)
# plot(ob6_mod_asd)
```