

Structural abnormality in AD patients

Set up

```
packages <- c("here", "readxl", "dplyr", "ggplot2", "psych")

lapply(packages, library, character.only = TRUE)

## here() starts at /Users/YQ/OneDrive/Research/Shenzhen/AD/data_analysis/AD_GM

##
## Attaching package: 'dplyr'

## The following objects are masked from 'package:stats':
##
##   filter, lag

## The following objects are masked from 'package:base':
##
##   intersect, setdiff, setequal, union

##
## Attaching package: 'psych'

## The following objects are masked from 'package:ggplot2':
##
##   %+%, alpha

## [[1]]
## [1] "here"      "stats"      "graphics"   "grDevices" "utils"      "datasets"
## [7] "methods"   "base"
##
## [[2]]
## [1] "readxl"    "here"      "stats"      "graphics"   "grDevices" "utils"
## [7] "datasets" "methods"   "base"
##
## [[3]]
## [1] "dplyr"      "readxl"    "here"      "stats"      "graphics"   "grDevices"
## [7] "utils"      "datasets"  "methods"   "base"
##
## [[4]]
## [1] "ggplot2"    "dplyr"      "readxl"    "here"      "stats"      "graphics"
## [7] "grDevices" "utils"      "datasets"  "methods"   "base"
##
## [[5]]
## [1] "psych"      "ggplot2"    "dplyr"      "readxl"    "here"      "stats"
## [7] "graphics"   "grDevices" "utils"      "datasets"  "methods"   "base"
```

```
source("code/plot_cc.R")
```

Load data

```
Behavioral_data_ADT1 <- read_excel(here("datafile/tidy_datafile.xlsx"),
  sheet = 1)
Behavioral_data_ADT2 <- read_excel(here("datafile/tidy_datafile.xlsx"),
  sheet = 2)

## New names:
## * ' ' -> '...18'

Behavioral_data_HC <- read_excel(here("datafile/tidy_datafile.xlsx"),
  sheet = 3)

Behavioral_data_ADT1 <- as.data.frame(Behavioral_data_ADT1)
Behavioral_data_ADT1$`Research Group` <- "AD_T1"
Behavioral_data_ADT2 <- as.data.frame(Behavioral_data_ADT2[-18])
Behavioral_data_ADT2$`Research Group` <- "AD_T2"
Behavioral_data_HC <- as.data.frame(Behavioral_data_HC)

# compile behavioral data
Behavioral_data <- rbind.data.frame(Behavioral_data_ADT1[1:40,], Behavioral_data_ADT2[1:40,],
  Behavioral_data_HC[1:45,])

#View(Behavioral_data)
```

Demographic information and clinical scores in AD patients and HC

```
demo_table <- as.data.frame(matrix(0,5,8))
colnames(demo_table) <- c("AD-T1 mean", "AD-T1 range", "AD-T2 mean", "AD-T2 range",
  "HC mean", "HC range", "HC vs. AD-T1 p value",
  "HC vs. AD-T2 p value")

# Sex
table(Behavioral_data$`Sex:F=1;M=2`, Behavioral_data$`Research Group`)
```

```
##
##      AD_T1 AD_T2 HC
##    1     18    18 18
##    2     22    22 27
```

```
chit <- chisq.test(matrix(c(18, 22, 18, 27), ncol = 2))
chit$p.value
```

```
## [1] 0.8058652
```

```
demo_table[1,] <- c("18/22","", "18/22","", "18/27","", round(chit$p.value,2), "")
```

```
# Age, CDR, MMSE, MoCA
```

```
colnames(Behavioral_data)[c(1,3,5,9:12)]
```

```
## [1] "Subject ID" "Sex:F=1;M=2" "Research Group" "Age"
```

```
## [5] "Global CDR" "MMSE Total Score" "MoCA Total Score"
```

```
gr_diff <- describeBy(Behavioral_data[,c(1,3,5,9:12)], group = "Research Group",
  mat = TRUE, digits = 2)
```

```
ttt1 <- sapply(c(9:12), function(i)
```

```
  t.test(Behavioral_data[Behavioral_data$`Research Group` == "HC",i],
    Behavioral_data[Behavioral_data$`Research Group` == "AD_T1",i],
    na.action=na.omit))
```

```
ttt2 <- sapply(c(9:12), function(i)
```

```
  t.test(Behavioral_data[Behavioral_data$`Research Group` == "HC",i],
    Behavioral_data[Behavioral_data$`Research Group` == "AD_T2",i],
    na.action=na.omit))
```

```
demo_table[2:5,] <- cbind.data.frame(paste0(gr_diff[gr_diff$group1=="AD_T1", "mean"][-(1:3)],"±",
  gr_diff[gr_diff$group1=="AD_T1", "sd"][-(1:3)]),
  paste0(paste0(gr_diff[gr_diff$group1=="AD_T1", "min"][-(1:3)]),"-",
    paste0(gr_diff[gr_diff$group1=="AD_T1", "max"][-(1:3)])),
  paste0(gr_diff[gr_diff$group1=="AD_T2", "mean"][-(1:3)],"±",
    gr_diff[gr_diff$group1=="AD_T2", "sd"][-(1:3)]),
  paste0(paste0(gr_diff[gr_diff$group1=="AD_T2", "min"][-(1:3)]),"-",
    paste0(gr_diff[gr_diff$group1=="AD_T2", "max"][-(1:3)])),
  paste0(gr_diff[gr_diff$group1=="HC", "mean"][-(1:3)],"±",
    gr_diff[gr_diff$group1=="HC", "sd"][-(1:3)]),
  paste0(paste0(gr_diff[gr_diff$group1=="HC", "min"][-(1:3)]),"-",
    paste0(gr_diff[gr_diff$group1=="HC", "max"][-(1:3)])),
  rbind(round(ttt1[,1]$p.value,2),round(ttt1[,2]$p.value,2),
    round(ttt1[,3]$p.value,2),round(ttt1[,4]$p.value,2)),
  rbind(round(ttt2[,1]$p.value,3),round(ttt2[,2]$p.value,3),
    round(ttt2[,3]$p.value,3),round(ttt2[,4]$p.value,3)))
```

```
rownames(demo_table) <- c("Sex", colnames(Behavioral_data)[c(9:12)])
```

```
demo_table
```

##	AD-T1 mean	AD-T1 range	AD-T2 mean	AD-T2 range	HC mean
## Sex	18/22		18/22		18/27
## Age	74.66±7.23	56-88	75.73±7.25	57-89.3	74.78±4.95
## Global CDR	0.76±0.32	0.5-2	0.94±0.47	0.5-2	0±0
## MMSE Total Score	23.1±2.06	19-26	21±4.5	9-29	29.13±1.25
## MoCA Total Score	18.65±4.62	11-27	16.58±5.65	7-27	24.35±2.46
##	HC range	HC vs. AD-T1 p value	HC vs. AD-T2 p value		
## Sex		0.81			
## Age	66.6-84.8	0.92		0.489	

```
## Global CDR          0-0          0          0
## MMSE Total Score    24-30         0          0
## MoCA Total Score    18-29         0          0
```

```
#View(demo_table)
```

Plot group differences in grey matter volume

```
# Load data
```

```
gmv_diff <- read_excel(here("datafile/tidy_datafile.xlsx"), sheet = 4)
gmv_diff <- as.data.frame(gmv_diff)
```

```
#View(gmv_diff)
```

```
colnames(gmv_diff)
```

```
## [1] "subject ID"          "group"
## [3] "GMV"                 "WMV"
## [5] "CSF"                 "overlapped decrease area"
## [7] "continuing decrease area" "left STG"
## [9] "right STG"           "left caudate"
```

```
gmv_diff$group <- factor(gmv_diff$group, levels = c("HC", "AD-T1", "AD-T2"))
```

```
# Differences in global grey matter volume
```

```
tt <- "GMV"
```

```
t.test(gmv_diff[gmv_diff$group == "HC", tt], gmv_diff[gmv_diff$group == "AD-T1", tt])
```

```
##
## Welch Two Sample t-test
##
## data: gmv_diff[gmv_diff$group == "HC", tt] and gmv_diff[gmv_diff$group == "AD-T1", tt]
## t = 2.3091, df = 70.853, p-value = 0.02386
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  3.837647 52.418375
## sample estimates:
## mean of x mean of y
##  594.0011 565.8731
```

```
t.test(gmv_diff[gmv_diff$group == "HC", tt], gmv_diff[gmv_diff$group == "AD-T2", tt])
```

```
##
## Welch Two Sample t-test
##
## data: gmv_diff[gmv_diff$group == "HC", tt] and gmv_diff[gmv_diff$group == "AD-T2", tt]
## t = 3.5685, df = 68.386, p-value = 0.0006616
## alternative hypothesis: true difference in means is not equal to 0
```

```
## 95 percent confidence interval:
## 19.92006 70.44701
## sample estimates:
## mean of x mean of y
## 594.0011 548.8176
```

```
t.test(gmv_diff[gmv_diff$group == "AD-T1",tt],gmv_diff[gmv_diff$group == "AD-T2",tt],
       paired = TRUE)
```

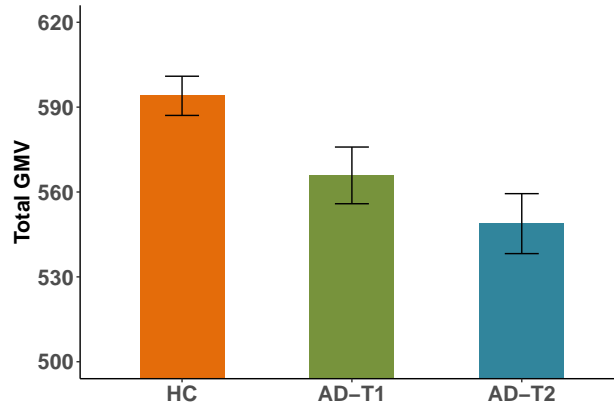
```
##
## Paired t-test
##
## data: gmv_diff[gmv_diff$group == "AD-T1", tt] and gmv_diff[gmv_diff$group == "AD-T2", tt]
## t = 6.5473, df = 39, p-value = 9.016e-08
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## 11.78650 22.32455
## sample estimates:
## mean of the differences
## 17.05553
```

```
colnames(gmv_diff)[c(1,2,3)]
```

```
## [1] "subject ID" "group" "GMV"
```

```
gmv_diff_global <- gmv_diff[,c(1,2,3)] %>%
  group_by(group) %>%
  summarise(
    n=n(),
    mean=mean(GMV),
    sd=sd(GMV)) %>%
  mutate( se=sd/sqrt(n)) %>%
  mutate( ic=se * qt((1-0.05)/2 + .5, n-1))

ggplot(gmv_diff_global, aes(x = group, y = mean, fill = group)) +
  scale_fill_manual(values = c( "#E46C0A", "#77933C", "#31859C")) +
  #geom_bar(position = "dodge", stat = "summary", fun = "mean", width = 0.5) +
  geom_bar(position = "dodge",stat="identity",width = 0.5) +
  geom_errorbar(aes(x=group, ymin=mean-se, ymax=mean+se),
    position = "dodge", width = 0.2) +
  labs(y = "Total GMV", x = "") +
  guides(color = "none", fill = "none") +
  theme(plot.title = element_text(hjust = 0.5, size = 16, face = "bold"),
    axis.text = element_text(size = 16, face = "bold"),
    axis.title.y = element_text(size = 16, face = "bold"))+
  theme(panel.border = element_blank(),
    panel.background = element_blank(),
    panel.grid = element_blank(),
    axis.line = element_line(colour = "black")) +
  coord_cartesian(ylim=c(500, 620)) +
  scale_y_continuous(breaks = seq(500, 620, 30))
```



```

ggsave(here("results/global_GMV.png"), width = 4, height = 3,
       units = c("in"), dpi = 200)

# Differences in overlapped decrease area
tt <- "overlapped decrease area"

t.test(gmv_diff[gmv_diff$group == "HC",tt],gmv_diff[gmv_diff$group == "AD-T1",tt])

##
## Welch Two Sample t-test
##
## data: gmv_diff[gmv_diff$group == "HC", tt] and gmv_diff[gmv_diff$group == "AD-T1", tt]
## t = 16.125, df = 78.612, p-value < 2.2e-16
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  0.1944975 0.2492816
## sample estimates:
## mean of x mean of y
## 1.0583614 0.8364719

t.test(gmv_diff[gmv_diff$group == "HC",tt],gmv_diff[gmv_diff$group == "AD-T2",tt])

##
## Welch Two Sample t-test
##
## data: gmv_diff[gmv_diff$group == "HC", tt] and gmv_diff[gmv_diff$group == "AD-T2", tt]
## t = 17.064, df = 82.506, p-value < 2.2e-16
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  0.2214327 0.2798673
## sample estimates:
## mean of x mean of y
## 1.0583614 0.8077114

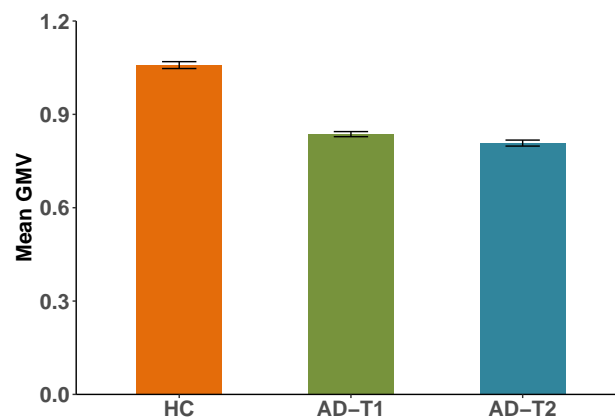
t.test(gmv_diff[gmv_diff$group == "AD-T1",tt],gmv_diff[gmv_diff$group == "AD-T2",tt],
       paired = TRUE)

```

```
##
## Paired t-test
##
## data:  gmv_diff[gmv_diff$group == "AD-T1", tt] and gmv_diff[gmv_diff$group == "AD-T2", tt]
## t = 6.5067, df = 39, p-value = 1.026e-07
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  0.01981997 0.03770103
## sample estimates:
## mean of the differences
##                0.0287605
```

```
gmv_diff_overlapped <- gmv_diff[,c(1,2,6)] %>%
  group_by(group) %>%
  summarise(
    n=n(),
    mean=mean(`overlapped decrease area`),
    sd=sd(`overlapped decrease area`)) %>%
  mutate( se=sd/sqrt(n)) %>%
  mutate( ic=se * qt((1-0.05)/2 + .5, n-1))

ggplot(gmv_diff_overlapped, aes(x = group, y = mean, fill = group)) +
  scale_fill_manual(values = c( "#E46C0A", "#77933C", "#31859C")) +
  #geom_bar(position = "dodge", stat = "summary", fun = "mean", width = 0.5) +
  geom_bar(position = "dodge", stat="identity", width = 0.5) +
  geom_errorbar(aes(x=group, ymin=mean-se, ymax=mean+se),
    position = "dodge", width = 0.2) +
  labs(y = "Mean GMV", x = "") +
  guides(color = "none", fill = "none") +
  theme(plot.title = element_text(hjust = 0.5, size = 16, face = "bold"),
    axis.text = element_text(size = 16, face = "bold"),
    axis.title.y = element_text(size = 16, face = "bold"))+
  theme(panel.border = element_blank(),
    panel.background = element_blank(),
    panel.grid = element_blank(),
    axis.line = element_line(colour = "black")) +
  scale_y_continuous(expand = c(0, 0), limits = c(0, 1.2),
    breaks = seq(0, 1.2, 0.3))
```



```

ggsave(here("results/overlapped_decrease_area.png"),
       width = 4, height = 3, units = c("in"), dpi = 200)

# Differences in GMV of continuing decrease area
tt <- "continuing decrease area"

t.test(gmv_diff[gmv_diff$group == "HC", tt], gmv_diff[gmv_diff$group == "AD-T1", tt])

##
## Welch Two Sample t-test
##
## data: gmv_diff[gmv_diff$group == "HC", tt] and gmv_diff[gmv_diff$group == "AD-T1", tt]
## t = 9.6526, df = 81.604, p-value = 3.809e-15
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## 0.07959764 0.12092725
## sample estimates:
## mean of x mean of y
## 0.9425395 0.8422770

t.test(gmv_diff[gmv_diff$group == "HC", tt], gmv_diff[gmv_diff$group == "AD-T2", tt])

##
## Welch Two Sample t-test
##
## data: gmv_diff[gmv_diff$group == "HC", tt] and gmv_diff[gmv_diff$group == "AD-T2", tt]
## t = 13.057, df = 79.797, p-value < 2.2e-16
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## 0.1352508 0.1838937
## sample estimates:
## mean of x mean of y
## 0.9425395 0.7829673

t.test(gmv_diff[gmv_diff$group == "AD-T1", tt], gmv_diff[gmv_diff$group == "AD-T2", tt],
       paired = TRUE)

##
## Paired t-test
##
## data: gmv_diff[gmv_diff$group == "AD-T1", tt] and gmv_diff[gmv_diff$group == "AD-T2", tt]
## t = 7.7901, df = 39, p-value = 1.808e-09
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## 0.04390998 0.07470961
## sample estimates:
## mean of the differences
## 0.05930979

gmv_diff_continuing <- gmv_diff[, c(1, 2, 7)] %>%
  group_by(group) %>%

```

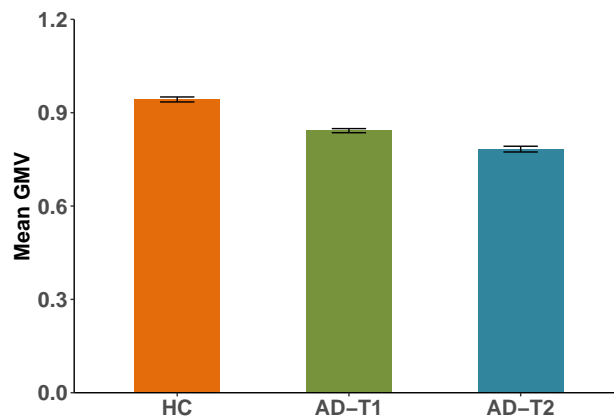


```

summarise(
  n=n(),
  mean=mean(`continuing decrease area`),
  sd=sd(`continuing decrease area`)) %>%
mutate( se=sd/sqrt(n)) %>%
mutate( ic=se * qt((1-0.05)/2 + .5, n-1))

ggplot(gmv_diff_continuing, aes(x = group, y = mean, fill = group)) +
  scale_fill_manual(values = c( "#E46C0A", "#77933C", "#31859C")) +
  #geom_bar(position = "dodge", stat = "summary", fun = "mean", width = 0.5) +
  geom_bar(position = "dodge", stat="identity", width = 0.5) +
  geom_errorbar(aes(x=group, ymin=mean-se, ymax=mean+se),
    position = "dodge", width = 0.2) +
  labs(y = "Mean GMV", x = "") +
  guides(color = "none", fill = "none") +
  theme(plot.title = element_text(hjust = 0.5, size = 16, face = "bold"),
    axis.text = element_text(size = 16, face = "bold"),
    axis.title.y = element_text(size = 16, face = "bold"))+
  theme(panel.border = element_blank(),
    panel.background = element_blank(),
    panel.grid = element_blank(),
    axis.line = element_line(colour = "black")) +
  scale_y_continuous(expand = c(0, 0), limits = c(0, 1.2),
    breaks = seq(0, 1.2, 0.3))

```



```

ggsave(here("results/continuing_decrease_area.png"),
  width =4, height = 3,units = c("in"), dpi = 200)

# Differences in AD-T1 vs. AD-T2
tt <- "left STG"

t.test(gmv_diff[gmv_diff$group == "AD-T1",tt],gmv_diff[gmv_diff$group == "AD-T2",tt],
  paired = TRUE)

##
## Paired t-test
##

```

```
## data: gmv_diff[gmv_diff$group == "AD-T1", tt] and gmv_diff[gmv_diff$group == "AD-T2", tt]
## t = 5.0549, df = 39, p-value = 1.053e-05
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## 0.05879781 0.13724142
## sample estimates:
## mean of the differences
## 0.09801961
```

```
gmv_diff_cc <- gmv_diff[gmv_diff$group != "HC",c(1,2,8)] %>%
  group_by(group) %>%
  summarise(
    n=n(),
    mean=mean(`left STG`),
    sd=sd(`left STG`)) %>%
  mutate( se=sd/sqrt(n)) %>%
  mutate( ic=se * qt((1-0.05)/2 + .5, n-1))

plot_cc(gmv_diff_cc, tt)

tt <- "right STG"
t.test(gmv_diff[gmv_diff$group == "AD-T1",tt],gmv_diff[gmv_diff$group == "AD-T2",tt],
       paired = TRUE)
```

```
##
## Paired t-test
##
## data: gmv_diff[gmv_diff$group == "AD-T1", tt] and gmv_diff[gmv_diff$group == "AD-T2", tt]
## t = 7.6929, df = 39, p-value = 2.444e-09
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## 0.06684568 0.11453668
## sample estimates:
## mean of the differences
## 0.09069118
```

```
gmv_diff_cc <- gmv_diff[gmv_diff$group != "HC",c(1,2,9)] %>%
  group_by(group) %>%
  summarise(
    n=n(),
    mean=mean(`right STG`),
    sd=sd(`right STG`)) %>%
  mutate( se=sd/sqrt(n)) %>%
  mutate( ic=se * qt((1-0.05)/2 + .5, n-1))

plot_cc(gmv_diff_cc, tt)

tt <- "left caudate"
t.test(gmv_diff[gmv_diff$group == "AD-T1",tt],gmv_diff[gmv_diff$group == "AD-T2",tt],
       paired = TRUE)
```

```
##
```

```
## Paired t-test
##
## data:  gmv_diff[gmv_diff$group == "AD-T1", tt] and gmv_diff[gmv_diff$group == "AD-T2", tt]
## t = 9.3611, df = 39, p-value = 1.604e-11
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  0.08148337 0.12640179
## sample estimates:
## mean of the differences
##                0.1039426

gmv_diff_cc <- gmv_diff[gmv_diff$group != "HC",c(1,2,10)] %>%
group_by(group) %>%
summarise(
  n=n(),
  mean=mean(`left caudate`),
  sd=sd(`left caudate`)) %>%
mutate( se=sd/sqrt(n)) %>%
mutate( ic=se * qt((1-0.05)/2 + .5, n-1))

plot_cc(gmv_diff_cc, tt)
```

Correlations between changes in gray matter and changes in MoCA

```
which(Behavioral_data_ADT1$`Subject ID`[1:40] !=
      Behavioral_data_ADT2$`Subject ID`[1:40])

## integer(0)

NeuralData_ADT1 <- read.table(here("datafile/first_C1_C2_C3_continue_overlap.txt"),
                             header = F)

colnames(NeuralData_ADT1) <- c("LSTG", "RSTG", "Lcaudate", "continue", "overlap")

NeuralData_ADT2 <- read.table(here("datafile/second_C1_C2_C3_continue_overlap.txt"),
                             header = F)

colnames(NeuralData_ADT2) <- c("LSTG", "RSTG", "Lcaudate", "continue", "overlap")

Behavioral_Neural_ADT1 <- cbind.data.frame(Behavioral_data_ADT1[c(1:40),c(1,11:13)],
                                           NeuralData_ADT1)

Behavioral_Neural_ADT2 <- cbind.data.frame(Behavioral_data_ADT2[c(1:40),c(1,11:13)],
                                           NeuralData_ADT2)

Behavioral_data_diff <- Behavioral_Neural_ADT1[1:40,c(2:9)] -
  Behavioral_Neural_ADT2[1:40,c(2:9)]

sum_cor <- as.data.frame(matrix(0, length(2:4)*length(colnames(NeuralData_ADT1)),
                               4))
dim(sum_cor)
```

```
## [1] 15 4
```

```
k <- 0
for(i in 1:3) {
  for (j in 4:8) {
    k <- k+1
    tmp <- Behavioral_data_diff[!is.na(Behavioral_data_diff[,i]),]
    tt <- cor.test(tmp[,i], tmp[,j])
    sum_cor[k,1:2] <- colnames(tmp)[c(i,j)]
    sum_cor[k,3:4] <- c(round(tt$estimate,2),round(tt$p.value,2))
  }
}
```

```
sum_cor
```

```
##           V1      V2   V3  V4
## 1 MMSE Total Score   LSTG 0.00 0.99
## 2 MMSE Total Score   RSTG -0.02 0.89
## 3 MMSE Total Score Lcaudate 0.17 0.29
## 4 MMSE Total Score continue 0.01 0.94
## 5 MMSE Total Score overlap 0.15 0.36
## 6 MoCA Total Score   LSTG 0.25 0.12
## 7 MoCA Total Score   RSTG 0.44 0.01
## 8 MoCA Total Score Lcaudate 0.35 0.03
## 9 MoCA Total Score continue 0.16 0.34
## 10 MoCA Total Score overlap 0.28 0.08
## 11      MoCA-MIS   LSTG 0.00 0.98
## 12      MoCA-MIS   RSTG 0.06 0.73
## 13      MoCA-MIS Lcaudate -0.17 0.32
## 14      MoCA-MIS continue -0.17 0.31
## 15      MoCA-MIS overlap -0.09 0.61
```

```
p.adjust(sum_cor$V4[6:8])
```

```
## [1] 0.12 0.03 0.06
```

```
# plot
Behavioral_data_diff$`MoCA Total Score`
```

```
## [1] 8 -2 -2 NA 3 -1 6 NA -2 -2 -3 9 2 2 6 5 9 2 3 -3 4 6 7 2 -1
## [26] -4 9 1 3 2 -2 -2 7 3 1 9 4 -1 2 1
```

```
ggplot(Behavioral_data_diff,aes(x = `MoCA Total Score`, y = RSTG)) +
  geom_point(color = "red", size = 3, position = "jitter",alpha = 0.7) +
  geom_smooth(color = "black", size = 2, method = "lm", se = FALSE) +
  theme(legend.position = "none") +
  theme(plot.title = element_blank()) +
  labs(y = "Changes in right STG GMV", x = "Changes in MoCA scores") +
  theme(axis.text = element_text(size = 16, face = "bold"),
        axis.title = element_text(size = 18, face = "bold")) +
  theme(panel.background = element_blank(),
        panel.border = element_blank(),
```

```

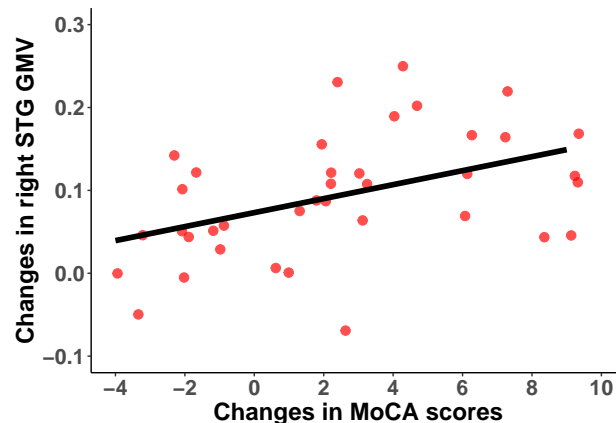
    panel.grid = element_blank(),
    axis.line = element_line(colour = "black")) +
  coord_cartesian(xlim=c(-4,10), ylim=c(-0.1, 0.3)) +
  scale_x_continuous(breaks = seq(-4, 10, 2)) +
  scale_y_continuous(breaks = seq(-0.1, 0.4, 0.1))

```

```
## 'geom_smooth()' using formula 'y ~ x'
```

```
## Warning: Removed 2 rows containing non-finite values (stat_smooth).
```

```
## Warning: Removed 2 rows containing missing values (geom_point).
```



```
ggsave(here("results/MoCA_RSTG.png"), width = 5, height = 4, units = c("in"), dpi = 200)
```

```
## 'geom_smooth()' using formula 'y ~ x'
```

```
## Warning: Removed 2 rows containing non-finite values (stat_smooth).
```

```
## Removed 2 rows containing missing values (geom_point).
```

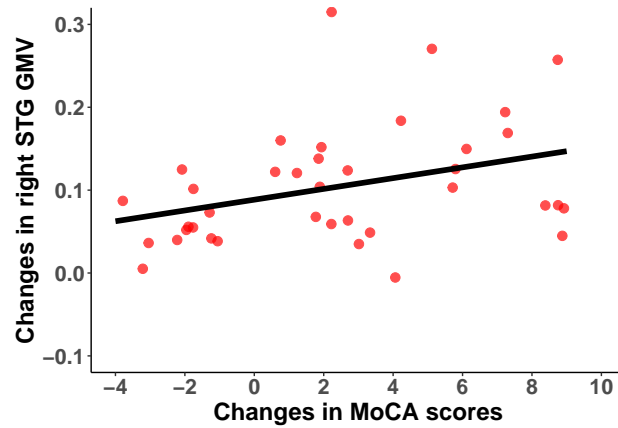
```

ggplot(Behavioral_data_diff, aes(x = `MoCA Total Score`, y = Lcaudate)) +
  geom_point(color = "red", size = 3, position = "jitter", alpha = 0.7) +
  geom_smooth(color = "black", size = 2, method = "lm", se = FALSE) +
  labs(y = "Changes in right STG GMV", x = "Changes in MoCA scores") +
  theme(legend.position = "none") +
  theme(plot.title = element_blank()) +
  theme(axis.text = element_text(size = 16, face = "bold"),
        axis.title = element_text(size = 18, face = "bold")) +
  theme(panel.background = element_blank(),
        panel.border = element_blank(),
        panel.grid = element_blank(),
        axis.line = element_line(colour = "black")) +
  coord_cartesian(xlim=c(-4,10), ylim=c(-0.1, 0.3)) +
  scale_x_continuous(breaks = seq(-4, 10, 2)) +
  scale_y_continuous(breaks = seq(-0.1, 0.4, 0.1))

```

```
## 'geom_smooth()' using formula 'y ~ x'
```

```
## Warning: Removed 2 rows containing non-finite values (stat_smooth).  
## Removed 2 rows containing missing values (geom_point).
```



```
ggsave(here("results/MoCA_Lcaudate.png"), width = 5, height = 4,  
        units = c("in"), dpi = 200)
```

```
## 'geom_smooth()' using formula 'y ~ x'
```

```
## Warning: Removed 2 rows containing non-finite values (stat_smooth).  
## Removed 2 rows containing missing values (geom_point).
```