Structural abnormality in AD patients

detach("package:here", unload=TRUE) setwd("/Users/YQ/OneDrive/Research/Shenzhen/AD/data_analysis/AD_GM")
here::set_here(path = "/Users/YQ/OneDrive/Research/Shenzhen/AD/data_analysis/AD_GM")

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
```

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

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

```r
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"
```

```r
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"),
```

```r
        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))
```
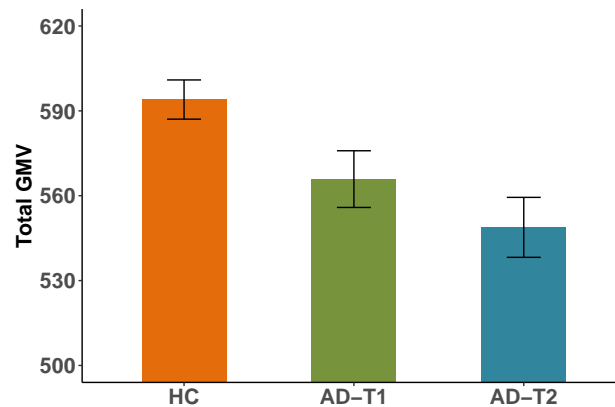


```r
    ggsave(here("results/global_GMV.png"), width =4, height = 3,
           units = c("in"), dpi = 200)
```

```r
# 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
```

```r
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
```
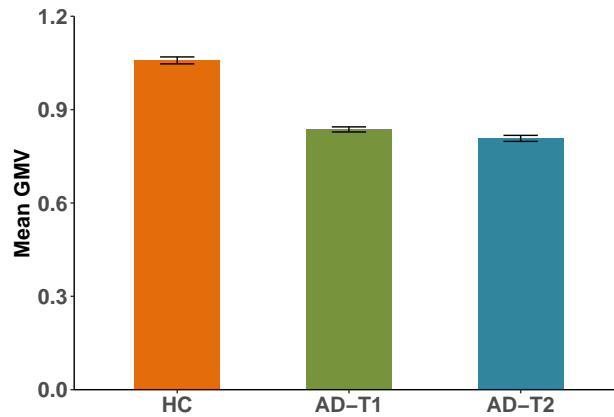
```
## 95 percent confidence interval:
##  0.2214327 0.2798673
## sample estimates:
## mean of x mean of y
## 1.0583614 0.8077114
```

```r
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
```

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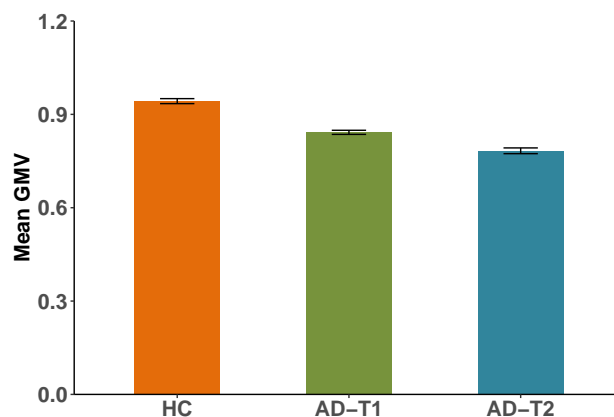
```
## 
##  Paired t-test
## 
## data:  gmv_diff[gmv_diff$group == "AD-T1", tt] and gmv_diff[gmv_diff$group == "AD-T2", tt]
## t = 7.7901, df = 39, p-value = 1.808e-09
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  0.04390998 0.07470961
##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

```r
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
```

```r
# 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
```

```r
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).
```
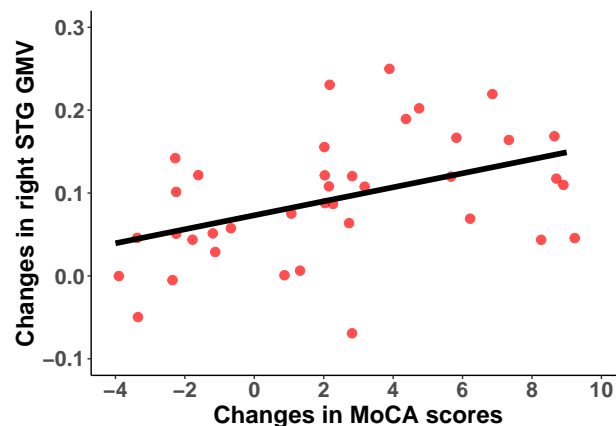


```r
ggsave(here("results/MoCA_RSTG.png"), width =5, height = 4,units = c("in"), dpi = 200)
```

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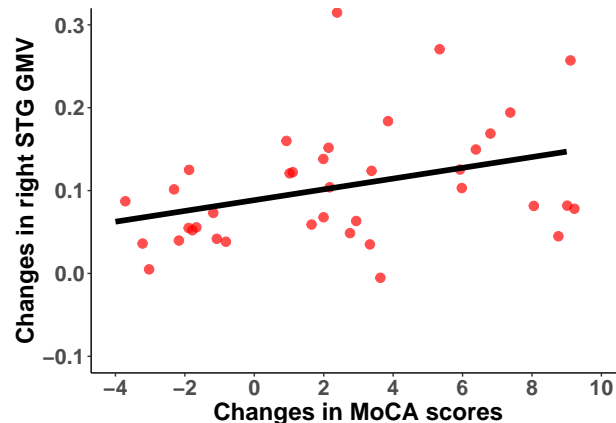```

```
## 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).
```