Brain structure differences and brain-behavior correlations

Setup

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

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

# load functions
source("code/pplot.R")
source("code/diff_volume.R")
```

Load datafile

```
G_WMV_all <- readxl::read_excel(here('datafile/datafile.xlsx'), sheet = 1)

G_WMV_all <- as.data.frame(G_WMV_all)

#View(G_WMV_all)
```

Demographic information

```
# samples from different scanners
table(G_WMV_all$Scanner)
```

```
##
##  1  2
## 35  9
```

```
table(G_WMV_all$Gender,G_WMV_all$Scanner)
```

```
##
##      1  2
##   0  8  1
##   1 27  8
```

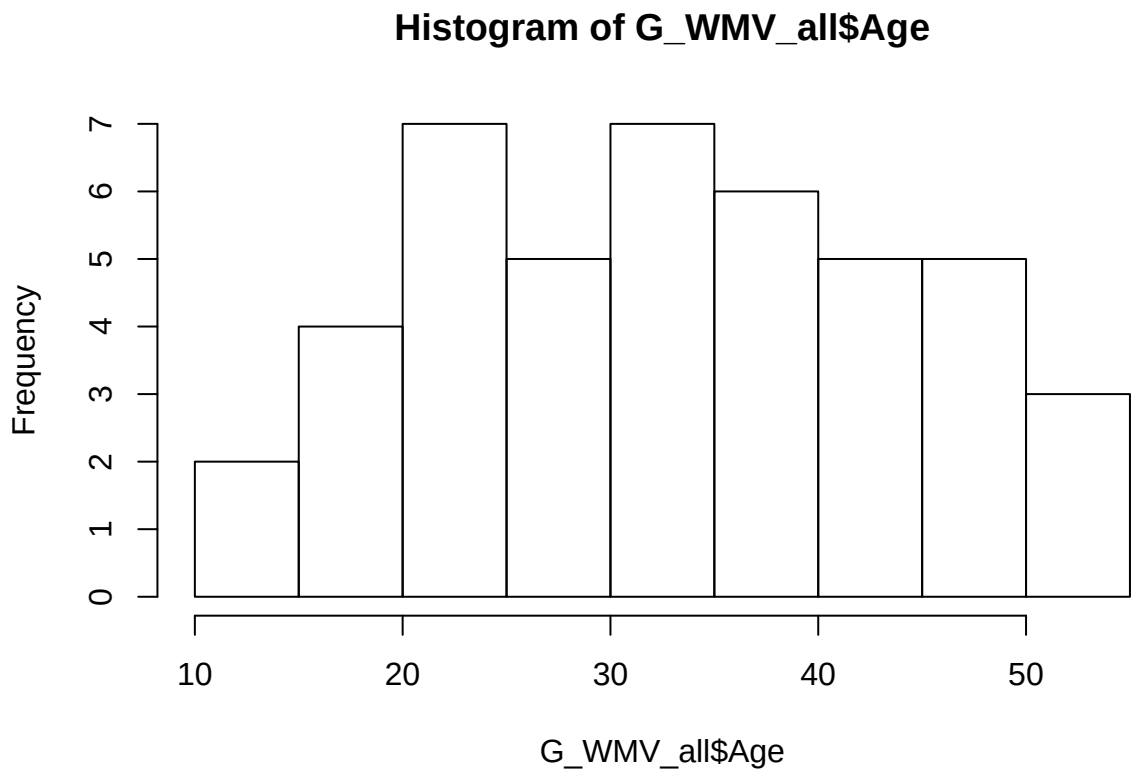
```
summary(G_WMV_all$Age[G_WMV_all$Scanner == 1])
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   12.00   26.00   35.00   34.86   43.50   52.00
```

```
summary(G_WMV_all$Age[G_WMV_all$Scanner == 2])
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   19.00   20.00   26.00   27.89   35.00   38.00
```

```
# age & gender for ASD and nonASD
hist(G_WMV_all$Age)
```




```
G_WMV_all %>%
    group_by(Group) %>%
    summarise(mean = mean(Age), sd = sd(Age), min=min(Age), max = max(Age))
```

```
## `summarise()` ungrouping output (override with `.groups` argument)
```

```
## # A tibble: 2 x 5
##   Group   mean    sd   min   max
##   <chr>  <dbl> <dbl> <dbl> <dbl>
## 1 ASD     36.8  9.20    24    51
## 2 nonASD  29.4 11.5     12    52
```

```r
chisq.test(table(G_WMV_all$Group,G_WMV_all$Gender))
```

```
##
##  Pearson's Chi-squared test with Yates' continuity correction
##
## data:  table(G_WMV_all$Group, G_WMV_all$Gender)
## X-squared = 0.19672, df = 1, p-value = 0.6574
```

```r
t.test(G_WMV_all$Age[G_WMV_all$Group == "ASD"],
       G_WMV_all$Age[G_WMV_all$Age != 12 & G_WMV_all$Group == "nonASD"])
```

```
##
##  Welch Two Sample t-test
##
## data:  G_WMV_all$Age[G_WMV_all$Group == "ASD"] and G_WMV_all$Age[G_WMV_all$Age != 12 & G_WMV_all$Grou
## t = 1.7321, df = 34.038, p-value = 0.0923
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -0.9285715 11.6507937
## sample estimates:
## mean of x mean of y
##  36.75000  31.38889
```

```r
# ADOS or CARS
G_WMV_all_ASD <- G_WMV_all[G_WMV_all$Group == "ASD", ]

k <- dim(G_WMV_all_ASD[!is.na(G_WMV_all_ASD$ADOS_Total),])[1] # 9

kk <- dim(G_WMV_all_ASD[!is.na(G_WMV_all_ASD$CARS_Total),])[1] # 21

print(paste0("n = ", k, " children with ASD had ADOS"))
```

```
## [1] "n = 9 children with ASD had ADOS"
```

```r
print(paste0("n = ", kk, " children with ASD had CARS"))
```

```
## [1] "n = 21 children with ASD had CARS"
```

```r
# overlap
overlab_subj <- intersect(G_WMV_all_ASD$Subject[!is.na(G_WMV_all_ASD$ADOS_Total)],
      G_WMV_all_ASD$Subject[!is.na(G_WMV_all_ASD$CARS_Total)])

print(paste0("n = ", length(overlab_subj), " children with ASD had both ADOS and CARS"))
```

```
## [1] "n = 6 children with ASD had both ADOS and CARS"
```

```r
# mean, sd, range of ADOS/CARS
mean(G_WMV_all_ASD$ADOS_com_soc[!is.na(G_WMV_all_ASD$ADOS_com_soc)])
```

```
## [1] 14.11111
```

```
sd(G_WMV_all_ASD$ADOS_com_soc[!is.na(G_WMV_all_ASD$ADOS_com_soc)])
```

```
## [1] 3.140241
```

```
range(G_WMV_all_ASD$ADOS_com_soc[!is.na(G_WMV_all_ASD$ADOS_com_soc)])
```

```
## [1]  9 19
```

```
mean(G_WMV_all_ASD$ADOS_stereo[!is.na(G_WMV_all_ASD$ADOS_com_soc)])
```

```
## [1] 2.111111
```

```
sd(G_WMV_all_ASD$ADOS_stereo[!is.na(G_WMV_all_ASD$ADOS_com_soc)])
```

```
## [1] 1.364225
```

```
range(G_WMV_all_ASD$ADOS_stereo[!is.na(G_WMV_all_ASD$ADOS_com_soc)])
```

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

```
table(G_WMV_all_ASD$Gender[!is.na(G_WMV_all_ASD$ADOS_Total)])
```

```
##
## 0 1
## 1 8
```

```
mean(G_WMV_all_ASD$CARS_Total[!is.na(G_WMV_all_ASD$CARS_Total)])
```

```
## [1] 33.95238
```

```
sd(G_WMV_all_ASD$CARS_Total[!is.na(G_WMV_all_ASD$CARS_Total)])
```

```
## [1] 4.329852
```

```
range(G_WMV_all_ASD$CARS_Total[!is.na(G_WMV_all_ASD$CARS_Total)])
```

```
## [1] 30 42
```

```
table(G_WMV_all_ASD$Gender[!is.na(G_WMV_all_ASD$CARS_Total)])
```

```
##
##  0  1
##  6 15
```

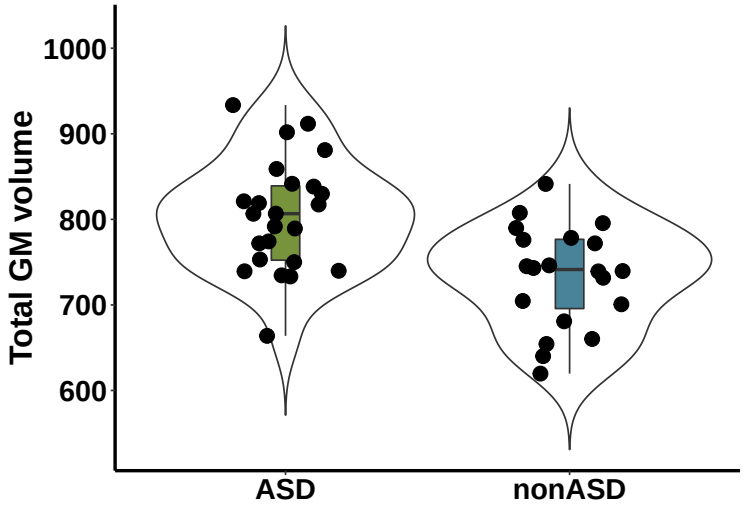
```r
# sample with Gesell data
#colnames(G_WMV_all)[13:18]

gesell_diff <- as.data.frame(matrix(0, 6, 6))

gesell_gr <- describeBy(G_WMV_all[,c(2,3,13:18)],group = "Group", mat = TRUE, digits = 2 )

# rownames(gesell_diff) <- rownames(gesell_gr[gesell_gr$group1=="nonASD", ])[-(1:3)]

ttt <- sapply(c(13:18), function(i) t.test(G_WMV_all[G_WMV_all$Group == "ASD",i],
                        G_WMV_all[G_WMV_all$Group == "nonASD",i]))

gesell_diff <- cbind(paste0(gesell_gr[gesell_gr$group1=="ASD", "mean"][-(1:2)],"±",
                        gesell_gr[gesell_gr$group1=="ASD", "sd"][-(1:2)]),
                  paste0(paste0(gesell_gr[gesell_gr$group1=="ASD", "min"][-(1:2)]),"-",
                        paste0(gesell_gr[gesell_gr$group1=="ASD", "max"][-(1:2)])),
                  paste0(gesell_gr[gesell_gr$group1=="nonASD", "mean"][-(1:2)],"±",
                        gesell_gr[gesell_gr$group1=="nonASD", "sd"][-(1:2)]),
                  paste0(paste0(gesell_gr[gesell_gr$group1=="nonASD", "min"][-(1:3)]),"-",
                        paste0(gesell_gr[gesell_gr$group1=="nonASD", "max"][-(1:3)])),
                  rbind(round(ttt[,1]$statistic,2),round(ttt[,2]$statistic,2),
                        round(ttt[,3]$statistic,2),round(ttt[,4]$statistic,2),
                        round(ttt[,5]$statistic,2),round(ttt[,6]$statistic,2)),
                  rbind(round(ttt[,1]$p.value,3),round(ttt[,2]$p.value,3),
                        round(ttt[,3]$p.value,3),round(ttt[,4]$p.value,3),
                        round(ttt[,5]$p.value,3),round(ttt[,6]$p.value,3))
                  )

colnames(gesell_diff) <- c("ASD mean", "ASD range", "nonASD mean", "nonASD range",
                "t value","p value")

gesell_diff <- as.data.frame(gesell_diff)

rownames(gesell_diff) <- c("Gesell_Total","Gesell_Adap", "Gesell_MtrGross",
                "Gesell_MtrFine","Gesell_Lang","Gesell_Social")

knitr::kable(gesell_diff)
```

	ASD mean	ASD range	nonASD mean	nonASD range	t value	p value
Gesell_Total	59.4±9.48	39.3-74.4	77.14±7.89	60.4-100	-6.01	0
Gesell_Adap	61.41±14.44	35.6-93.7	78.45±13.19	70-105.5	-3.6	0.001
Gesell_MtrGross	71±10.79	47.8-91	87.92±11.8	75.3-97	-4.3	0
Gesell_MtrFine	69.5±13.3	48.3-94.6	84.39±8.5	47-90.8	-4.04	0
Gesell_Lang	42.26±8.9	26.6-60.9	61.07±10.29	59.1-89.8	-5.59	0
Gesell_Social	51.68±10.52	31-66.7	73.87±8.52	60.4-100	-6.87	0

```
#writexl::write_xlsx(gesell_diff,here("results/gesell_diff.xlsx"))
```

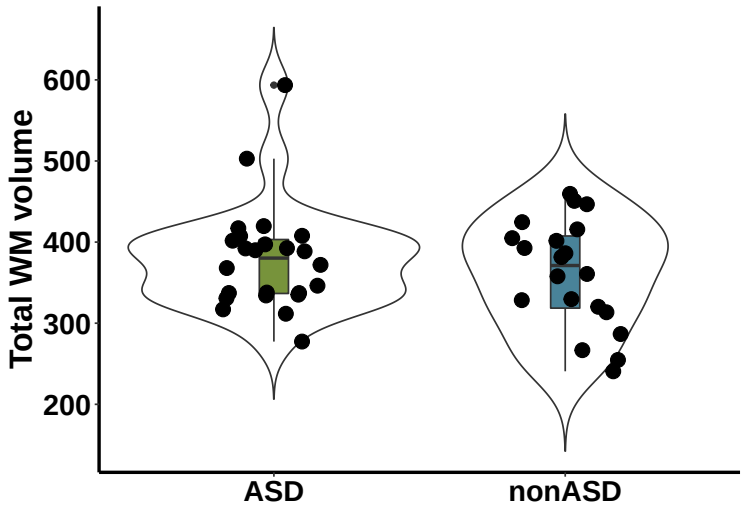
Differences in global volume of GM, WM, CSF, and TIV

```
# load data
G_WMV_all <- readxl::read_excel(here('datafile/datafile.xlsx'),sheet = 'GMV&WMV(all)')

G_WMV_all <- as.data.frame(G_WMV_all)

diff_volume("GM","Total GM volume")
```



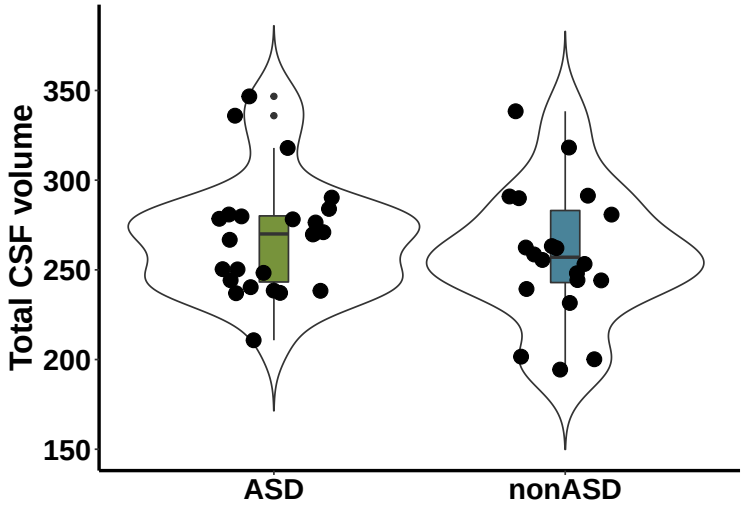
t value	p value	Cohen's d	95% CI
3.79	0	1.14	[0.48, 1.8]

```
diff_volume("WM","Total WM volume")
```



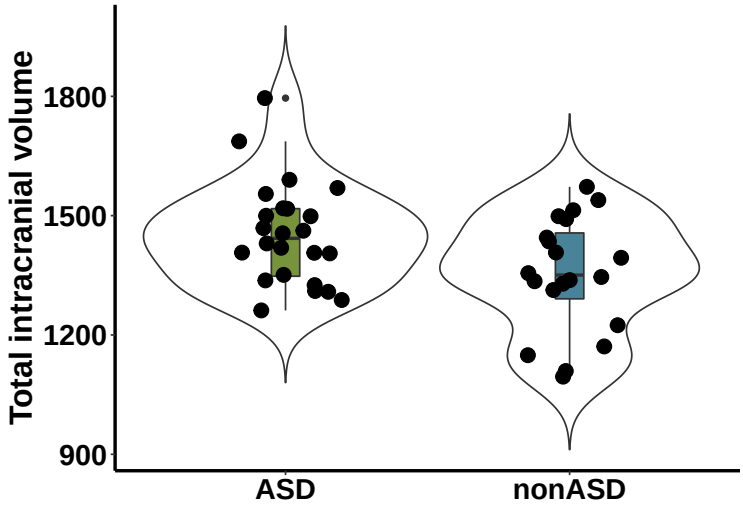
t value	p value	Cohen's d	95% CI
0.93	0.357	0.28	[-0.33, 0.9]

```
diff_volume("CSF", "Total CSF volume")
```



t value	p value	Cohen's d	95% CI
0.94	0.351	0.29	[-0.32, 0.9]

```
diff_volume("TIV", "Total intracranial volume")
```



t value	p value	Cohen's d	95% CI
2.41	0.021	0.74	[0.11, 1.37]

Scatterplots for brain-behavior correlation

```
# load data
G_WMV <- readxl::read_excel(here('datafile/datafile.xlsx'),sheet = 2)
```

```
## New names:
```

```
G_WMV <- as.data.frame(G_WMV)

# Gesell social
subtest <- "Gesell_social"
gmv <- "gesell_social_mask"

cor.test(G_WMV[ G_WMV$Group == "nonASD",subtest],
     G_WMV[ G_WMV$Group == "nonASD", gmv])
```

```
##
##  Pearson's product-moment correlation
##
## data:  G_WMV[G_WMV$Group == "nonASD", subtest] and G_WMV[G_WMV$Group == "nonASD", gmv]
## t = 2.9899, df = 12, p-value = 0.01128
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  0.187971 0.879178
## sample estimates:
##      cor
## 0.653386
```

```
length(G_WMV[G_WMV$Group == "nonASD", subtest])
```

```
## [1] 14
```

```
cor.test(G_WMV[G_WMV$Group == "ASD",subtest], G_WMV[G_WMV$Group == "ASD", gmv])
```

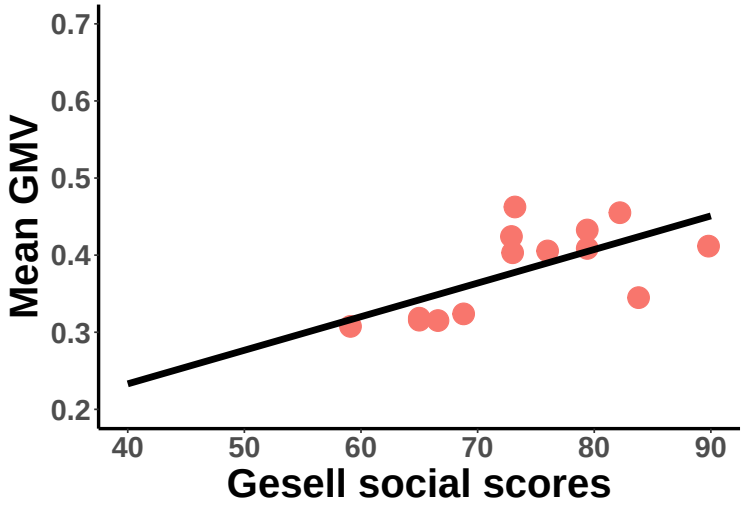
```
##
##  Pearson's product-moment correlation
##
## data:  G_WMV[G_WMV$Group == "ASD", subtest] and G_WMV[G_WMV$Group == "ASD", gmv]
## t = 0.057223, df = 19, p-value = 0.955
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  -0.4209453  0.4423072
## sample estimates:
##        cor
## 0.01312679
```

```
length(G_WMV[G_WMV$Group == "ASD", subtest])
```

```
## [1] 21
```

```
pplot(subtest, gmv, "Gesell social scores")
```

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




```
# Gesell language
subtest <- "Gesell_language"
gmv <- "gesell_language_mask"  # gesell_language_frontal_mask gesell_language_left_cerebellum, gesell_l

cor.test(G_WMV[G_WMV$Group == "nonASD",subtest], G_WMV[G_WMV$Group == "nonASD", gmv])
```

```
##
##  Pearson's product-moment correlation
##
## data:  G_WMV[G_WMV$Group == "nonASD", subtest] and G_WMV[G_WMV$Group == "nonASD", gmv]
## t = 2.2702, df = 12, p-value = 0.04242
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  0.0247414 0.8356715
## sample estimates:
##       cor
## 0.5481255
```

```
# removing the highest score
cor.test(G_WMV[G_WMV$Gesell_language != 90.8 & G_WMV$Group == "nonASD",subtest],
     G_WMV[G_WMV$Gesell_language != 90.8 & G_WMV$Group == "nonASD", gmv])
```

```
##
##  Pearson's product-moment correlation
##
## data:  G_WMV[G_WMV$Gesell_language != 90.8 & G_WMV$Group == "nonASD",  and G_WMV[G_WMV$Gesell_languag
## t = 3.0105, df = 11, p-value = 0.01185
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
```

```
##  0.1923673 0.8925616
## sample estimates:
##       cor
## 0.6721142
```

```
length(G_WMV[G_WMV$Group == "nonASD", subtest])
```

```
## [1] 14
```

```
cor.test(G_WMV[G_WMV$Group == "ASD",subtest], G_WMV[G_WMV$Group == "ASD", gmv])
```

```
##
##  Pearson's product-moment correlation
##
## data:  G_WMV[G_WMV$Group == "ASD", subtest] and G_WMV[G_WMV$Group == "ASD", gmv]
## t = -0.24239, df = 19, p-value = 0.8111
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  -0.4758053  0.3854014
## sample estimates:
##         cor
## -0.05552291
```

```
length(G_WMV[G_WMV$Group == "ASD", subtest])
```

```
## [1] 21
```

```
pplot(subtest, gmv, "Gesell language scores")
```

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