

Morphological alterations of language regions in ASD children

```
library(here)
here::set_here(path = ".")
detach("package:here", unload = TRUE)
```

Set up

```
packages <- c("here", "readxl", "multcomp", "magrittr", "dplyr", "nlme",
              "openxlsx", "car", "Hmisc", "ppcor", "modelr", "lmerTest",
              "ggpubr", "ggplot2", "psych", "tidyverse", "PMCMRplus", "data.table")

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

Load data

```
data_behavior <- read.xlsx("./Raw/subj_info_final.xlsx")
eTIV <- read.csv("./Raw/TIV_allsubj.txt", sep="")
colnames(eTIV)[1] <- "Name" #

data_behavior$Gender <- recode(data_behavior$Gender, "'F' = 0; 'M' = 1")

all_data <- merge(data_behavior, eTIV, by="Name")

# View(all_data)

# divide the ASD group into two subgroups
median_value <- median(all_data$Gesell_Lang[all_data$Dx == "ASD"])

all_data$subgroup[all_data$Dx == "ASD" & all_data$Gesell_Lang > median_value] <- "ASDMLD"
all_data$subgroup[all_data$Dx == "ASD" & all_data$Gesell_Lang < median_value] <- "ASDSLDD"
all_data$subgroup[all_data$Dx == "TD"] <- "TD"
print(unique(all_data$subgroup))

## [1] "TD"      "ASDMLD" "ASDSLDD"

# Adjust cols
all_data <- all_data[, c(1:4, 17, 5:16)]
all_data[, c(3, 6:16)] <- lapply(all_data[, c(3, 6:16)], function(x) as.numeric(gsub("[^0-9.-]", NA, x)))
write.xlsx(all_data, "./Table/Data/datafile_beh.xlsx", colnames = T)
head(all_data)
```

```
##      Name Gender Age Dx subgroup Gesell_Adpt Gesell_GrMot Gesell_FineMot
## 1   Caidian    1 4.07 TD      TD      98.0      104.0      98.0
## 2   Caiziyi    1 2.17 TD      TD      97.0      103.0      98.0
## 3   Caozimiao  1 1.52 ASD   ASDMLD  70.0      76.3      78.9
## 4   Chenboyang 1 3.50 ASD   ASDSLD  39.0      64.1      58.5
## 5   Chenhaiqi  1 2.83 ASD   ASDMLD  73.7      78.5      82.6
## 6   Chentianman 1 2.83 TD      TD      95.0      99.0     103.0
## Gesell_Lang Gesell_Social Gesell_Total ADOS_SA ADOS_RRB ADOS_Total CARS ABC
## 1      96.0      96.0      98.4      NA      NA      NA      NA 17
## 2      94.0      94.0      97.2      NA      NA      NA      NA 28
## 3      61.0      67.3      69.7      10      1      11      NA 56
## 4      23.6      32.4      43.5      15      3      18      45 87
## 5      44.6      66.7      71.2      16      2      18      34 78
## 6      95.0      95.0      97.4      NA      NA      NA      15 25
##      eTIV
## 1 1062922
## 2 1249739
## 3 768175
## 4 1299138
## 5 1161733
## 6 1160498
```

Demographic information

```
datafile <- read.xlsx("./Table/Data/datafile_beh.xlsx", sheet = 1)
demo_all <- as.data.frame(as.matrix(0, 8, 12))

datafile$subgroup <- factor(datafile$subgroup,
                             levels = c("TD", "ASDMLD", "ASDSLD"))

## TD and ASD groups
## Age
aa <- describeBy(datafile[,c("Dx", "Age")], group = "Dx")
bb <- as.data.frame(rbind(cbind(paste0(round(aa[[1]]$mean[2], 2), "±", round(aa[[1]]$sd[2], 2)),
                                paste0(round(aa[[1]]$min[2], 2), "-", round(aa[[1]]$max[2], 2))),
                          cbind(paste0(round(aa[[2]]$mean[2], 2), "±", round(aa[[2]]$sd[2], 2)),
                                paste0(round(aa[[2]]$min[2], 2), "-", round(aa[[2]]$max[2], 2))))))
colnames(bb) <- c("mean±sd", "range")
rownames(bb) <- c("ASD", "TD")
knitr::kable(bb)
```

	mean±sd	range
ASD	3.18±1.17	1.52-6.53
TD	3.39±1.49	1.5-5.87

```
## TD, ASDMLD, and ASDSLD groups
## Age, subgroup, Gesell, ADOS, CARS, ABC
print(colnames(datafile[,c(3, 5, 6, 16)]))
```

```
## [1] "Age"                "subgroup"          "Gesell_Adpt"       "Gesell_GrMot"
## [5] "Gesell_FineMot"      "Gesell_Lang"       "Gesell_Social"     "Gesell_Total"
## [9] "ADOS_SA"            "ADOS_RRB"          "ADOS_Total"        "CARS"
## [13] "ABC"
```

```
mean_all <- describeBy(datafile[,c(3,5,6:16)], group = "subgroup")
```

```
## Warning in FUN(newX[, i], ...): no non-missing arguments to min; returning Inf
## Warning in FUN(newX[, i], ...): no non-missing arguments to min; returning Inf
## Warning in FUN(newX[, i], ...): no non-missing arguments to min; returning Inf
```

```
## Warning in FUN(newX[, i], ...): no non-missing arguments to max; returning -Inf
## Warning in FUN(newX[, i], ...): no non-missing arguments to max; returning -Inf
## Warning in FUN(newX[, i], ...): no non-missing arguments to max; returning -Inf
```

```
# Mean±SD, Range
```

```
demo_all[1:12, 1:6] <-
  cbind(paste0(round(mean_all[[1]]$mean[c(1,3:13)],2), "+",
    round(mean_all[[1]]$sd[c(1,3:13)],2)),
    paste0(round(mean_all[[1]]$min[c(1,3:13)],2), "-",
    round(mean_all[[1]]$max[c(1,3:13)],2)),
    paste0(round(mean_all[[2]]$mean[c(1,3:13)],2), "+",
    round(mean_all[[2]]$sd[c(1,3:13)],2)),
    paste0(round(mean_all[[2]]$min[c(1,3:13)],2), "-",
    round(mean_all[[2]]$max[c(1,3:13)],2)),
    paste0(round(mean_all[[3]]$mean[c(1,3:13)],3), "+",
    round(mean_all[[3]]$sd[c(1,3:13)],3)),
    paste0(round(mean_all[[3]]$min[c(1,3:13)],3), "-",
    round(mean_all[[3]]$max[c(1,3:13)],3)))
```

```
rownames(demo_all) <- colnames(datafile[,c(3,6:16)])
```

```
colnames(demo_all)[1:6] <- c("TD_mean", "TD_range",
  "ASDMLD_mean", "ASDMLD_range",
  "ASDSLD_mean", "ASDSLD_range")
```

```
knitr::kable(demo_all)
```

	TD_mean	TD_range	ASDMLD_mean	ASDMLD_range	ASDSLD_mean	ASDSLD_range
Age	3.39±1.49	1.5-5.87	3.31±1.33	1.52-6.53	3.039±0.98	2-5.57
Gesell_Adpt	93.79±5.39	80-107	66.18±8.76	40.9-82	55.068±13.334	31.6-93.7
Gesell_GrMot	97.42±6.1	81.1-107	77.76±8.7	47.8-91	71.791±8.342	52-87.5
Gesell_FineMot	96.73±5.34	86-108	73.31±9.39	54.1-90.4	64.247±10.212	45.9-84.1
Gesell_Lang	91.47±5.55	75.7-101	55.07±7.76	44.6-70.7	37.112±5.908	23.6-44.2
Gesell_Social	93.76±4.52	80-103	60.46±7.4	31-70.2	48.156±7.779	30.2-64.2
Gesell_Total	94.34±4.22	85.1-100.8	66.72±5.61	49.1-79.4	55.254±7.112	39.3-68.74
ADOS_SA	NaN±NA	Inf-Inf	12.41±3.6	7-20	13.04±3.259	8-22
ADOS_RRB	NaN±NA	Inf-Inf	1.24±0.91	0-4	1.52±1.046	0-4
ADOS_Total	NaN±NA	Inf-Inf	13.2±4.72	0-23	14.56±3.906	9-24
CARS	14.33±1.15	13-15	31.92±2.02	30-38	35±4.967	25-45
ABC	25.3±8.56	8-43	66.65±14.26	53-107	74.971±19.806	54-130

```

## Group comparison
# Age, subgroup, Gesell, ADOS, CARS, ABC: t-test between each two groups
for(tt in colnames(datafile)[c(3,6:16)]) {
  # TD with no ADOS
  if (all(is.na(datafile[datafile$subgroup == "TD", tt]))) {

    myt3 <- t.test(datafile[datafile$subgroup == "ASDMLD", tt],
                  datafile[datafile$subgroup == "ASDSL", tt], na.action = T)
    demo_all[tt, 7:12] <- c(NA, NA, NA, NA, round(myt3$statistic, 2),
                          round(myt3$p.value, 3))

  } else {
    myt1 <- t.test(datafile[datafile$subgroup == "TD", tt],
                  datafile[datafile$subgroup == "ASDMLD", tt], na.action = T)
    myt2 <- t.test(datafile[datafile$subgroup == "TD", tt],
                  datafile[datafile$subgroup == "ASDSL", tt], na.action = T)
    myt3 <- t.test(datafile[datafile$subgroup == "ASDMLD", tt],
                  datafile[datafile$subgroup == "ASDSL", tt], na.action = T)

    demo_all[tt, 7:12] <- c(round(myt1$statistic, 2), round(myt1$p.value, 3),
                          round(myt2$statistic, 2), round(myt2$p.value, 3),
                          round(myt3$statistic, 2), round(myt3$p.value, 3))
  }
}

colnames(demo_all)[7:12] <- c("TDvsASDMLD_t", "TDvsASDMLD_p",
                          "TDvsASDSL_t", "TDvsASDSL_p",
                          "ASDmodvsASDsev_t", "ASDmodvsASDsev_p")

#View(demo_all)

## gender: Chi-square Test
median(datafile$Gesell_Lang[datafile$Dx == "ASD"])

```

```
## [1] 44.4
```

```

k <- table(datafile$subgroup, datafile$Gender)
tk <- chisq.test(k) # comparison across three groups
tk

```

```

##
## Pearson's Chi-squared test
##
## data: k
## X-squared = 5.7106, df = 2, p-value = 0.05754

```

```

datafile$subgroup <- as.character(datafile$subgroup)

# comparsion between each two groups
k1 <- table(datafile$subgroup[datafile$subgroup != "ASDSL"],
            datafile$Gender[datafile$subgroup != "ASDSL"])
tk1 <- chisq.test(k1)

```

```
k2 <- table(datafile$subgroup[datafile$subgroup != "ASDMLD"],
             datafile$Gender[datafile$subgroup != "ASDMLD"])
tk2 <- chisq.test(k2)

k3 <- table(datafile$subgroup[datafile$subgroup != "TD"],
             datafile$Gender[datafile$subgroup != "TD"])
tk3 <- chisq.test(k3)

demo_all["Sex", 1:12] <- c(paste0(k[1,1], "/", k[1,2]), " ",
                           paste0(k[2,1], "/", k[2,2]), " ",
                           paste0(k[3,1], "/", k[3,2]), " ",
                           round(tk1$statistic,3), round(tk1$p.value,3),
                           round(tk2$statistic,3), round(tk2$p.value,3),
                           round(tk3$statistic,3), round(tk3$p.value,3))

knitr::kable(demo_all["Sex", 1:12])
```

	TD_med	TD_range	ASDMLA	ASDMLA_incl	ASDMLA_sev	ASDMLA_inclvsASDse	ASDMLA_sevvsASDse	ASDMLA_inclvsASDse_p
Sex	5/32	2/32			9/25	0.461	0.497	1.15

```
# correcting for multiple comparisons using FDR
for (cc in 1:nrow(demo_all)){
  demo_all[cc,13:15] <- p.adjust(c(demo_all$TDvsASDMLD_p[cc],
                                   demo_all$TDvsASDSLSD_p[cc],
                                   demo_all$ASDmodvsASDsev_p[cc]), method = "fdr")
}

colnames(demo_all)[13:15] <-
  c("TDvsASDMLD_adj_p", "TDvsASDSLSD_adj_p",
    "ASDMLDvsASDSLSD_adj_p")

# Adjust rows and cols
demo_all <- demo_all[c(1,13,2:12),]
demo_all <- demo_all[,c(1:6,7:8,13,9:10,14,11:12,15)]

write.xlsx(demo_all, "./Table/Data/demographic_info_subgroups.xlsx",
           colNames = TRUE, rowNames = TRUE)
knitr::kable(demo_all[,7:15])
```

	TDvsASDMLP	TDvsASDMLP	TDvsASDMLP	TDvsASDMLP	TDvsASDMLP	TDvsASDMLP	TDvsASDMLP	TDvsASDMLP	TDvsASDMLP
Age	0.25	0.807	0.807	1.19	0.238	0.5115	0.96	0.341	0.5115
Sex	0.461	0.497	0.497	1.15	0.284	0.4260	3.904	0.048	0.1440
Gesell_Adj	15.82	0	0.000	15.79	0	0.0000	4.06	0	0.0000
Gesell_GrM	16.04	0	0.000	14.67	0	0.0000	2.88	0.005	0.0050
Gesell_Fine	13.77	0	0.000	16.58	0	0.0000	3.81	0	0.0000
Gesell_Lang	22.55	0	0.000	39.86	0	0.0000	10.73	0	0.0000
Gesell_Soc	22.65	0	0.000	29.86	0	0.0000	6.68	0	0.0000
Gesell_Tot	23.27	0	0.000	27.85	0	0.0000	7.38	0	0.0000

	TDvsASD	MLA_SDM	MLA_SDM	MLDvsASD	PDDvsASD	PDDvsASD	ASDvsASD	ASDvsASD	ASDvsASD
ADOS_SANA	NA	NA	NA	NA	NA	NA	-0.67	0.505	0.5050
ADOS_RR	NA	NA	NA	NA	NA	NA	-1.04	0.306	0.3060
ADOS_Total	NA	NA	NA	NA	NA	NA	-1.17	0.248	0.2480
CARS	-22.69	0	0.000	-19.11	0	0.0000	-3.28	0.002	0.0020
ABC	-14.66	0	0.000	-13.51	0	0.0000	-1.99	0.051	0.0510

```
## ADOS and CARS
```

```
subj_info_ASD <- datafile[datafile$Dx == "ASD", ]
dim(subj_info_ASD)
```

```
## [1] 68 17
```

```
k <- sum(!is.na(datafile$ADOS_Total[datafile$Dx == "ASD"]))
kk <- sum(!is.na(datafile$CARS[datafile$Dx == "ASD"]))
kkk <- sum(!is.na(datafile$CARS[datafile$Dx == "TD"]))

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

```
## [1] "n = 55 children with ASD had ADOS"
```

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

```
## [1] "n = 60 children with ASD had CARS"
```

```
print(paste0("n = ", kkk, " TD children had CARS"))
```

```
## [1] "n = 3 TD children had CARS"
```

Load cortical volume/thickness/surface data

```
wb <- createWorkbook()

ROIs <- c("parsorbitalis", "parstriangularis", "parsopercularis",
          "caudalmiddlefrontal", "supramarginal", "inferiorparietal",
          "transversetemporal", "superiortemporal", "middletemporal", "lingual")

for (feature in c("volume", "thickness", "area")) {

  # ASD group
  ASD_ROIL <- read.table(paste0("Raw/ROI_aparc_aseg/ASD/aparc_stats2table/lh.aparc_stats.",
                                feature, ".txt"), header = T)
  ASD_ROIR <- read.table(paste0("Raw/ROI_aparc_aseg/ASD/aparc_stats2table/rh.aparc_stats.",
                                feature, ".txt"), header = T)
  ASD_all <- cbind(ASD_ROIL[1], ASD_ROIL[, paste0("lh_", ROIs, "_", feature)],
                  ASD_ROIR[, paste0("rh_", ROIs, "_", feature)])
}
```

```

colnames(ASD_all)[1] <- "Name"

dim(ASD_all)

# TD group
TD_ROIL <- read.table(paste0("Raw/ROI_aparc_aseg/TD/aparc_stats2table/lh.aparc_stats.",
                             feature, ".txt"), header = T)
TD_ROIR <- read.table(paste0("Raw/ROI_aparc_aseg/TD/aparc_stats2table/rh.aparc_stats.",
                             feature, ".txt"), header = T)
TD_all <- cbind(TD_ROIL[,1], TD_ROIL[,paste0("lh_",ROIIs,"_", feature )],
               TD_ROIR[,paste0("rh_",ROIIs,"_", feature )])

colnames(TD_all)[1] <- "Name"

dim(TD_all)

ROI_all <- rbind.data.frame(ASD_all, TD_all)

datafile_new <- merge(datafile, ROI_all, by = "Name")

dim(datafile_new)

addWorksheet(wb,feature)
writeData(wb,feature,datafile_new)

}

# saveWorkbook(wb, paste0("./Table/Data/datafile_features.xlsx"))

print(colnames(datafile_new))

```

```

## [1] "Name" "Gender"
## [3] "Age" "Dx"
## [5] "subgroup" "Gesell_Adpt"
## [7] "Gesell_GrMot" "Gesell_FineMot"
## [9] "Gesell_Lang" "Gesell_Social"
## [11] "Gesell_Total" "ADOS_SA"
## [13] "ADOS_RRB" "ADOS_Total"
## [15] "CARS" "ABC"
## [17] "eTIV" "lh_parsorbitalis_area"
## [19] "lh_parstriangularis_area" "lh_parsopercularis_area"
## [21] "lh_caudalmiddlefrontal_area" "lh_supramarginal_area"
## [23] "lh_inferiorparietal_area" "lh_transversetemporal_area"
## [25] "lh_superiortemporal_area" "lh_middletemporal_area"
## [27] "lh_lingual_area" "rh_parsorbitalis_area"
## [29] "rh_parstriangularis_area" "rh_parsopercularis_area"
## [31] "rh_caudalmiddlefrontal_area" "rh_supramarginal_area"
## [33] "rh_inferiorparietal_area" "rh_transversetemporal_area"
## [35] "rh_superiortemporal_area" "rh_middletemporal_area"
## [37] "rh_lingual_area"

```

Descriptive analysis on cortical volume/thickness/surface

```
wb <- createWorkbook()

for (feature in c("volume", "thickness", "area")) {

  ROIs_all <- as.data.frame(as.matrix(0, 30,7))

  datafile_feature <- read.xlsx("./Table/Data/datafile_features.xlsx",sheet = feature)

  datafile_feature$subgroup <- factor(datafile_feature$subgroup,
    levels = c("TD", "ASDMLD","ASDSLD"))

  mean_ROIs <- describeBy(datafile_feature[,c(5,18:37)], group ="subgroup")

  ROIs_all[1:30, 1:7] <-
    rbind(cbind(group = rep("TD",10),
      colnames(datafile_feature)[18:27],
      paste0(round(mean_ROIs[[1]]$mean[c(2:11)],2), "±",
        round(mean_ROIs[[1]]$sd[c(2:11)],2)),
      paste0(round(mean_ROIs[[1]]$min[c(2:11)],2), "-",
        round(mean_ROIs[[1]]$max[c(2:11)],2)),
      colnames(datafile_feature)[28:37],
      paste0(round(mean_ROIs[[1]]$mean[c(12:21)],2), "±",
        round(mean_ROIs[[1]]$sd[c(12:21)],2)),
      paste0(round(mean_ROIs[[1]]$min[c(12:21)],2), "-",
        round(mean_ROIs[[1]]$max[c(12:21)],2))),
    cbind(group = rep("ASDMLD",10),
      colnames(datafile_feature)[18:27],
      paste0(round(mean_ROIs[[2]]$mean[c(2:11)],2), "±",
        round(mean_ROIs[[2]]$sd[c(2:11)],2)),
      paste0(round(mean_ROIs[[2]]$min[c(2:11)],2), "-",
        round(mean_ROIs[[2]]$max[c(2:11)],2)),
      colnames(datafile_feature)[28:37],
      paste0(round(mean_ROIs[[2]]$mean[c(12:21)],2), "±",
        round(mean_ROIs[[2]]$sd[c(12:21)],2)),
      paste0(round(mean_ROIs[[2]]$min[c(12:21)],2), "-",
        round(mean_ROIs[[2]]$max[c(12:21)],2))),
    cbind(group = rep("ASDSLD",10),
      colnames(datafile_feature)[18:27],
      paste0(round(mean_ROIs[[3]]$mean[c(2:11)],2), "±",
        round(mean_ROIs[[3]]$sd[c(2:11)],2)),
      paste0(round(mean_ROIs[[3]]$min[c(2:11)],2), "-",
        round(mean_ROIs[[3]]$max[c(2:11)],2)),
      colnames(datafile_feature)[28:37],
      paste0(round(mean_ROIs[[3]]$mean[c(12:21)],2), "±",
        round(mean_ROIs[[3]]$sd[c(12:21)],2)),
      paste0(round(mean_ROIs[[3]]$min[c(12:21)],2), "-",
        round(mean_ROIs[[3]]$max[c(12:21)],2))))

  colnames(ROIs_all) <- c("group", "LHROI", "mean±sd", "range", "RHROI",
    "mean±sd", "range")
}
```



```

    addWorksheet(wb,feature)
    writeData(wb,feature,ROIs_all)
}

# saveWorkbook(wb, paste0("./Table/Data/all_ROI_features.xlsx"))

# combine tables
volume <- read.xlsx("./Table/Data/all_ROI_features.xlsx", sheet = "volume")
thickness <- read.xlsx("./Table/Data/all_ROI_features.xlsx", sheet = "thickness")
area <- read.xlsx("./Table/Data/all_ROI_features.xlsx", sheet = "area")

#View(all_feature_info)
all_feature_info <- cbind(volume, thickness[,-1], area[,-1])

```

Within-group analysis

```

wb <- createWorkbook()

withinGroup_results <- data.frame(group=character(),roi=character(),
                                   F_value = numeric(), p_value=numeric(),
                                   adjusted_p_value=numeric())

for (feature in c("volume", "thickness", "area")) {
  i <- 0
  datafile_feature <- read.xlsx("./Table/Data/datafile_features.xlsx",sheet=feature)
  #View(datafile_feature)

  for (igroup in c("TD","ASDMLD","ASDSLDD")){
    # select data of one group
    tmp <- datafile_feature[datafile_feature$subgroup==igroup,]

    # standardize eTIV to z-score
    tmp$eTIV_z <- scale(tmp$eTIV)
    # Add a col (Hemisphere)
    lh_list <- grep("lh", colnames(tmp))
    rh_list <- grep("rh", colnames(tmp))
    colnames(tmp)[lh_list] <- ROIs
    colnames(tmp)[rh_list] <- ROIs
    ll <- setdiff(1:length(tmp), c(lh_list, rh_list))
    tmp1 <- rbind.data.frame(cbind(tmp[, ll], tmp[, lh_list], LR = "LH"),
                           cbind(tmp[, ll], tmp[, rh_list], LR = "RH"))

    for (iregion in ROIs){
      i <- i + 1

      f1 <- as.formula(paste0(iregion, "~ LR + Age + Gender + eTIV_z +
                              (1|Name)"))
    }
  }
}

```

```

model_withingroup <- lmer(fl, data = tmp1)
res <- anova(model_withingroup)

#print(paste0(igroup, " ", iregion, feature))

withinGroup_results[i,1:2] <- c(igroup, paste0(iregion, "_", feature))
withinGroup_results[i,3:4] <- c(round(res$`F value`[1],3),
                                round(res$`Pr(>F)`[1],3))

    } # end for 10 ROI
} # end for 3 groups

# View(withinGroup_results)
# dim(withinGroup_results)

# adjust p value
j <- 0
for (igroup in c("TD", "ASDMLD", "ASDSLD")){
  withinGroup_results[(10*j+1):(10*(j+1)),5] <- round(
    p.adjust(withinGroup_results$p_value[withinGroup_results$group==igroup], method="fdr"), 3)
  j <- j+1
}

#View(withinGroup_results)
addWorksheet(wb, feature)
writeData(wb, feature, withinGroup_results)
} # end for 3 features

# saveWorkbook(wb, "./Table/withingroup_results.xlsx")

knitr::kable(filter(withinGroup_results, adjusted_p_value < 0.05))

```

group	roi	F_value	p_value	adjusted_p_value
TD	parsorbitalis_area	64.331	0.000	0.000
TD	parstriangularis_area	22.989	0.000	0.000
TD	parsopercularis_area	17.889	0.000	0.000
TD	supramarginal_area	24.156	0.000	0.000
TD	inferiorparietal_area	98.087	0.000	0.000
TD	transversetemporal_area	168.909	0.000	0.000
TD	superiortemporal_area	33.297	0.000	0.000
TD	middletemporal_area	116.380	0.000	0.000
ASDMLD	parsorbitalis_area	81.334	0.000	0.000
ASDMLD	parstriangularis_area	39.847	0.000	0.000
ASDMLD	parsopercularis_area	25.441	0.000	0.000
ASDMLD	caudalmiddlefrontal_area	20.241	0.000	0.000
ASDMLD	supramarginal_area	34.866	0.000	0.000
ASDMLD	inferiorparietal_area	85.990	0.000	0.000
ASDMLD	transversetemporal_area	157.432	0.000	0.000
ASDMLD	superiortemporal_area	37.193	0.000	0.000
ASDMLD	middletemporal_area	38.497	0.000	0.000
ASDMLD	lingual_area	9.228	0.005	0.005
ASDSLD	parsorbitalis_area	38.979	0.000	0.000

group	roi	F_value	p_value	adjusted_p_value
ASDSLD	parstriangularis_area	30.927	0.000	0.000
ASDSLD	parsopercularis_area	32.848	0.000	0.000
ASDSLD	supramarginal_area	15.647	0.000	0.000
ASDSLD	inferiorparietal_area	60.781	0.000	0.000
ASDSLD	transversetemporal_area	163.491	0.000	0.000
ASDSLD	superiortemporal_area	35.412	0.000	0.000
ASDSLD	middletemporal_area	29.011	0.000	0.000

Sup: Within-group analysis (without females)

```

withinGroup_results_new <- data.frame(group=character(),roi=character(),
                                     F_value = numeric(), p_value=numeric(),
                                     adjusted_p_value=numeric())

for (feature in c("volume", "thickness", "area")) {
  i <- 0
  datafile_feature <- read.xlsx("./Table/Data/datafile_features.xlsx",sheet=feature)
  datafile_feature_new <- datafile_feature[datafile_feature$Gender==1,]

  #View(datafile_feature_new)

  for (igroup in c("TD","ASDMLD","ASDSLD")){

    tmp <- datafile_feature_new[datafile_feature_new$subgroup==igroup,]

    tmp$eTIV_z <- scale(tmp$eTIV)

    lh_list <- grep("lh", colnames(tmp))
    rh_list <- grep("rh", colnames(tmp))

    colnames(tmp)[lh_list] <- ROIs
    colnames(tmp)[rh_list] <- ROIs

    ll <- setdiff(1:length(tmp), c(lh_list, rh_list))

    tmp1 <- rbind.data.frame(cbind(tmp[, ll], tmp[, lh_list], LR = "LH"),
                           cbind(tmp[, ll], tmp[, rh_list], LR = "RH"))

    for (ivolume in ROIs){

      i <- i + 1

      fl <- as.formula(paste0(ivolume, "~ LR + Age + eTIV_z +
                              (1|Name)"))

      model_withingroup <- lmer(fl, data = tmp1)

```

```

    res <- anova(model_withingroup)

    #print(paste0(igroup, " ", ivolume, feature))

    withinGroup_results_new[i,1:2] <- c(igroup, paste0(ivolume, "_", feature))

    withinGroup_results_new[i,3:4] <- c(res$`F value`[1], res$`Pr(>F)`[1])

  }
}

# View(withinGroup_results_new)
dim(withinGroup_results_new)

# p
p.adjTD <- p.adjust(withinGroup_results_new$p_value[withinGroup_results_new$group=="TD"],
  method="fdr")

p.adjASDHL <- p.adjust(withinGroup_results_new$p_value[withinGroup_results_new$group=="ASDMLD"],
  method="fdr")

p.adjASDLL <- p.adjust(withinGroup_results_new$p_value[withinGroup_results_new$group=="ASDSLd"],
  method="fdr")

withinGroup_results_new[,5] <- round(c(p.adjTD, p.adjASDHL, p.adjASDLL), 3)
#View(withinGroup_results_new)

write.xlsx(withinGroup_results_new, paste0("./Table/Males_withingroup_", feature, ".xlsx"))
}

knitr::kable(filter(withinGroup_results_new, adjusted_p_value < 0.05 ))

```

group	roi	F_value	p_value	adjusted_p_value
TD	parsorbitalis_area	45.736332	0.0000001	0.000
TD	parstriangularis_area	18.564580	0.0001539	0.000
TD	parsopercularis_area	14.751240	0.0005676	0.001
TD	supramarginal_area	26.927796	0.0000125	0.000
TD	inferiorparietal_area	87.033835	0.0000000	0.000
TD	transversetemporal_area	147.326954	0.0000000	0.000
TD	superiortemporal_area	31.335903	0.0000039	0.000
TD	middletemporal_area	105.579020	0.0000000	0.000
ASDMLD	parsorbitalis_area	70.147083	0.0000000	0.000
ASDMLD	parstriangularis_area	39.255228	0.0000006	0.000
ASDMLD	parsopercularis_area	24.288857	0.0000264	0.000
ASDMLD	caudalmiddlefrontal_area	22.828204	0.0000406	0.000
ASDMLD	supramarginal_area	32.637707	0.0000028	0.000
ASDMLD	inferiorparietal_area	74.555208	0.0000000	0.000
ASDMLD	transversetemporal_area	172.481788	0.0000000	0.000
ASDMLD	superiortemporal_area	38.491607	0.0000007	0.000
ASDMLD	middletemporal_area	32.456902	0.0000029	0.000
ASDMLD	lingual_area	8.108087	0.0077531	0.008

group	roi	F_value	p_value	adjusted_p_value
ASDSLD	parsorbitalis_area	26.089808	0.0000316	0.000
ASDSLD	parstriangularis_area	18.187460	0.0002694	0.000
ASDSLD	parsopercularis_area	29.009588	0.0000157	0.000
ASDSLD	supramarginal_area	9.533484	0.0050346	0.006
ASDSLD	inferiorparietal_area	42.790306	0.0000009	0.000
ASDSLD	transversetemporal_area	117.415773	0.0000000	0.000
ASDSLD	superiortemporal_area	27.316938	0.0000234	0.000
ASDSLD	middletemporal_area	17.028815	0.0003825	0.001

Plots for laterality of 10 ROIs in three groups

```

mapping <- list("parsorbitalis" = "Pars orbitalis",
               "parstriangularis" = "Pars triangularis",
               "parsopercularis" = "Pars opercularis",
               "caudalmiddlefrontal" = "Caudal middle frontal gyrus",
               "supramarginal" = "Supramarginal gyrus",
               "inferiorparietal" = "Inferior parietal gyrus",
               "transversetemporal" = "Transverse temporal gyrus",
               "superiortemporal" = "Superior temporal gyrus",
               "middletemporal" = "Middle temporal gyrus",
               "lingual" = "Lingual gyrus")

Label <- c("Pars orbitalis", "Pars triangularis", "Pars opercularis",
          "Caudal middle frontal gyrus", "Supramarginal gyrus",
          "Inferior parietal gyrus", "Transverse temporal gyrus",
          "Superior temporal gyrus", "Middle temporal gyrus", "Lingual gyrus")

for (feature in c("volume", "thickness", "area")) {

  tmp <- read.xlsx("./Table/Data/datafile_features.xlsx", sheet = feature)

  lh_list <- grep("lh", colnames(tmp))
  rh_list <- grep("rh", colnames(tmp))

  colnames(tmp)[lh_list] <- ROIs
  colnames(tmp)[rh_list] <- ROIs

  ll <- setdiff(1:length(tmp), c(lh_list, rh_list))

  tmp1 <- rbind.data.frame(cbind(tmp[, ll], tmp[, lh_list], LR = "LH"),
                          cbind(tmp[, ll], tmp[, rh_list], LR = "RH"))

  #View(tmp1)
  # transform to long format
  tmp1_long <- gather(tmp1, ROI, value, ROIs[1]:ROIs[10],
                     factor_key=TRUE)

  for (igroup in c("TD", "ASDMLD", "ASDSLD")){

```

```

tmp2 <- tmp1_long[tmp1_long$subgroup == igroup,]
tmp2$LR <- factor(tmp2$LR)
tmp2$ROI <- factor(tmp2$ROI, levels = ROIs)

#View(tmp2)

summary_data <- tmp2 %>% group_by(ROI, LR) %>%
  summarise(mean = mean(value, na.rm = TRUE),
            N = sum(!is.na(value)),
            SE = sd(value, na.rm = TRUE)/sqrt(N))

summary_data$xlabel_name <- mapping[summary_data$ROI]
summary_data$xlabel_name <- factor(summary_data$xlabel_name,
                                   levels = Label)

p <- ggplot(summary_data, aes(x = xlabel_name, y = mean, fill=LR)) +
  geom_bar(stat = "identity", position = "dodge", width = 0.8,
          alpha = 0.9) +
  geom_errorbar(aes(ymin = mean - SE, ymax = mean + SE),
               position = position_dodge(width = 0.8), width = 0.4,
               alpha = 0.8) +
  scale_fill_manual(values = c("LH" = "#E69F00", "RH" = "#56B4E9")) +
  labs(fill = "Hemisphere", title=paste0(igroup, "_", feature)) +
  # scale_x_discrete(labels = function(x) str_wrap(x, width = 10)) + # x
  theme_bw() + #
  theme(axis.text.x = element_text(size = 8, face = 'bold', angle = 45, hjust = 1),
        axis.text.y = element_text(size = 14, face = "bold"),
        axis.title.x = element_blank(),
        axis.title.y = element_blank(),
        plot.title = element_text( size = 25, face = "bold", hjust = 0.5),
        panel.grid.major = element_blank(), #
        panel.grid.minor = element_blank(), #
        panel.background = element_rect(colour = "black", linewidth=1))+
  guides(fill = guide_legend(keywidth = 2, keyheight = 2))+
  theme(legend.text = element_text(size = 8, face = "bold"),
        legend.title = element_text(size = 8, face = "bold"))

if (feature == "volume") {
  p <- p + scale_y_continuous(limits = c(0,21000),
                             breaks = seq(0,21000, 4000))
} else if (feature == "thickness") {
  p <- p + scale_y_continuous(limits = c(0,3.5),
                             breaks = seq(0, 3.5, 0.25)) +
  coord_cartesian(ylim = c(2.5,3.5))

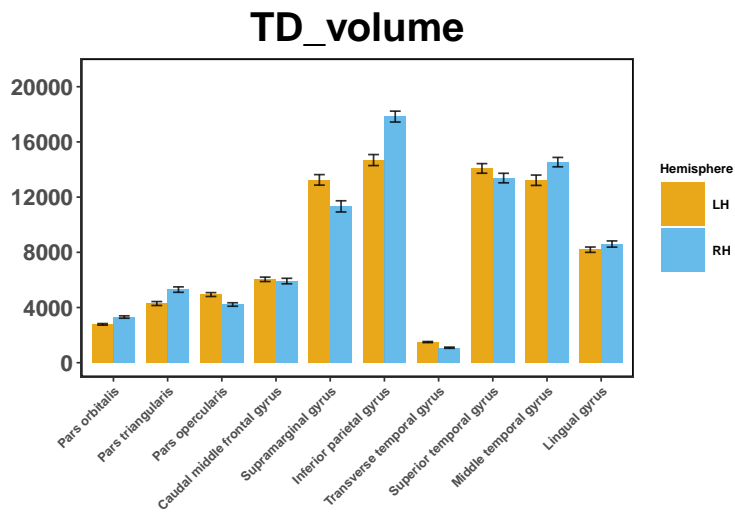
} else if (feature == "area") {
  p <- p + scale_y_continuous(limits = c(0,6000),
                             breaks = seq(0, 6000, 1000))
}

print(p)
# ggsave(paste0("Plot/Lat/", paste0(igroup, "_", feature), ".png"),
#        dpi=200, width=10, height=5)

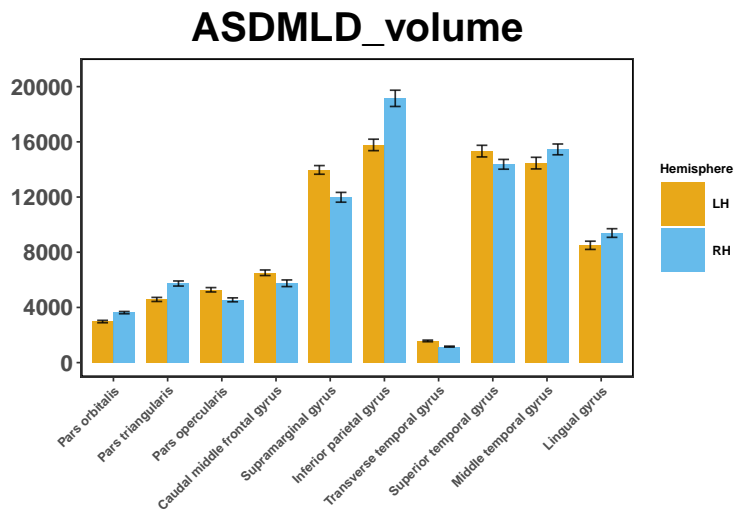
```

```
}
}
```

```
## `summarise()` has grouped output by 'ROI'. You can override using the `.groups`
## argument.
## `summarise()` has grouped output by 'ROI'. You can override using the `.groups`
## argument.
```

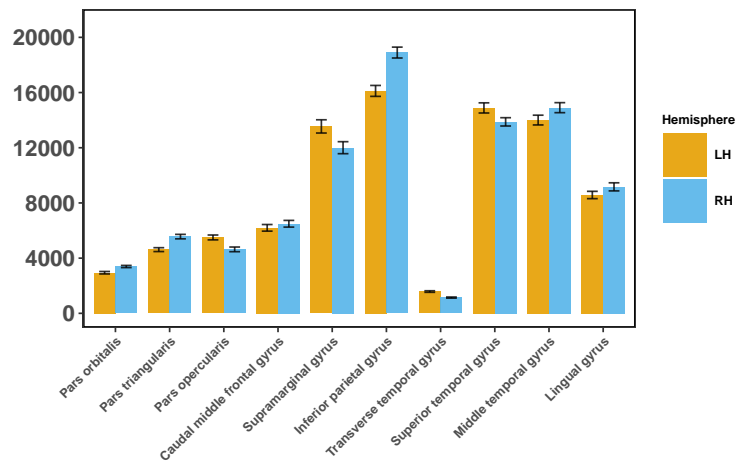


```
## `summarise()` has grouped output by 'ROI'. You can override using the `.groups`
## argument.
```



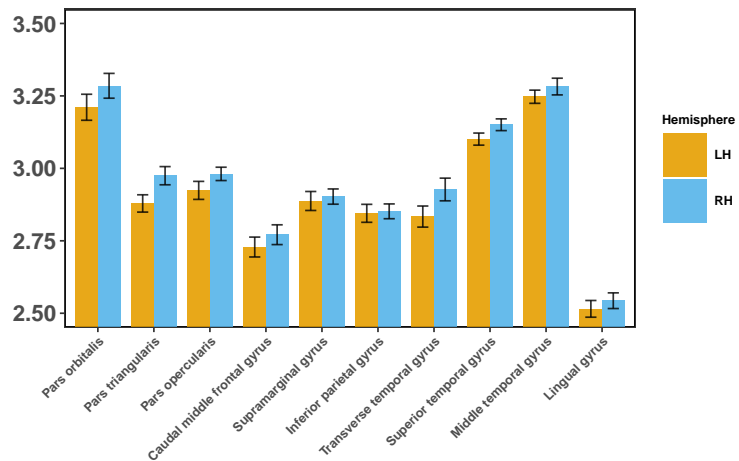
```
## `summarise()` has grouped output by 'ROI'. You can override using the `.groups`
## argument.
```

ASDSLD_volume

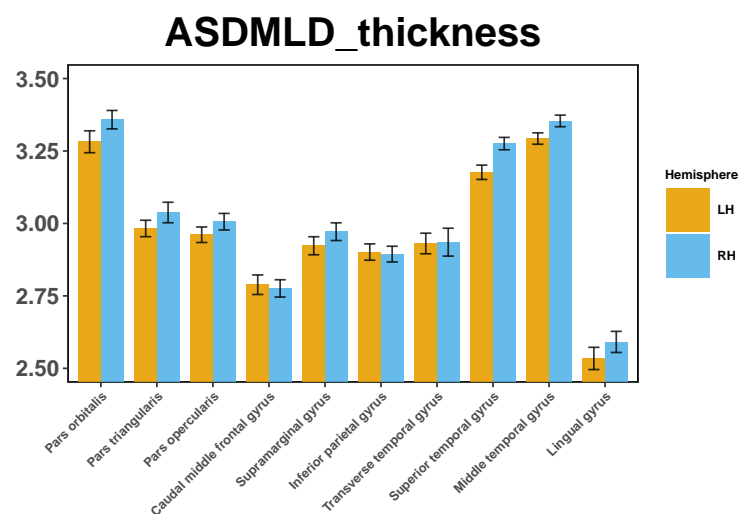


`summarise()` has grouped output by 'ROI'. You can override using the `.groups`
argument.

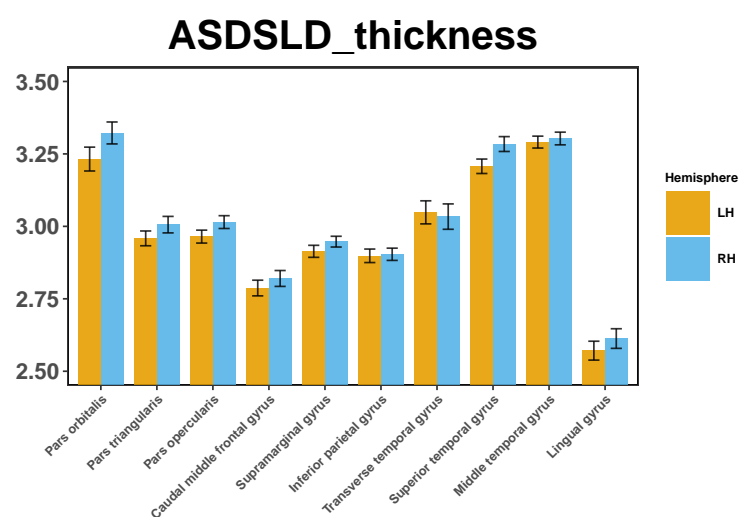
TD_thickness



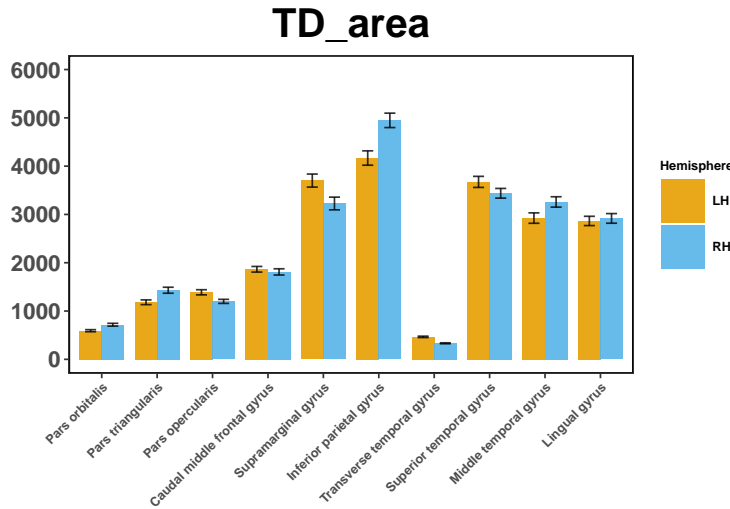
`summarise()` has grouped output by 'ROI'. You can override using the `.groups`
argument.



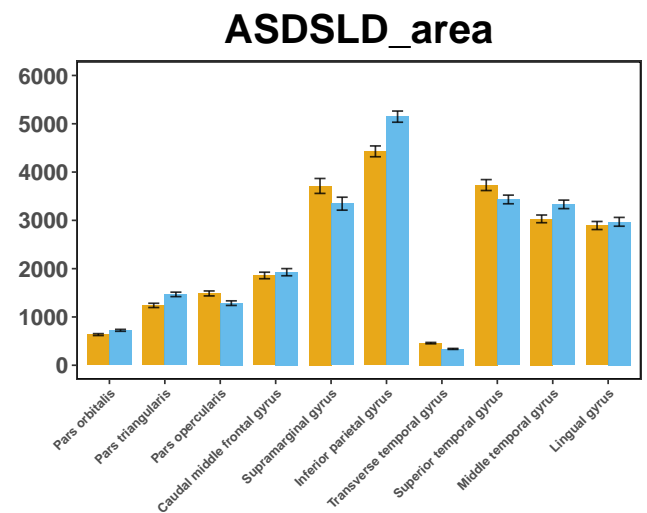
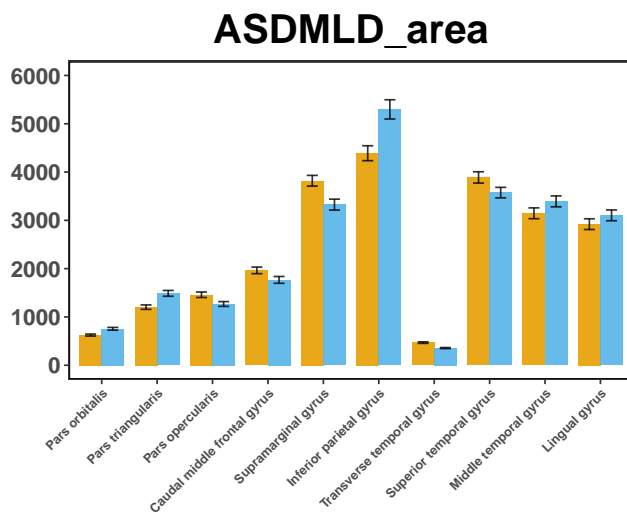
`summarise()` has grouped output by 'ROI'. You can override using the `.groups`
argument.



`summarise()` has grouped output by 'ROI'. You can override using the `.groups`
argument.



```
## `summarise()` has grouped output by 'ROI'. You can override using the `.groups`
## argument.
```



```
# print(p)
```

Group differences in cortical volume/thickness/surface

```
wb <- createWorkbook()
for (feature in c("volume", "thickness", "area")) {

  datafile_feature <- read.xlsx("./Table/Data/datafile_features.xlsx", sheet=feature)
  datafile_feature$eTIV_z <- scale(datafile_feature$eTIV)

  datafile_TDvsASDMLD <- datafile_feature[datafile_feature$subgroup != "ASDSLD",]
  datafile_TDvsASDSLD <- datafile_feature[datafile_feature$subgroup != "ASDMLD",]
```

```

datafile_ASD <- datafile_feature[datafile_feature$subgroup != "TD",]

i <- 0

bet_group_results <- data.frame(LR = character(), roi = character(),
                                diff1 = character(), Fvalue1=numeric(),
                                pvalue1=numeric(),pvalue.adj1=numeric(),
                                diff2 = character(), Fvalue2=numeric(),
                                pvalue2=numeric(),pvalue.adj2=numeric(),
                                diff3 = character(), Fvalue3=numeric(),
                                pvalue3=numeric(),pvalue.adj3=numeric())

for (LR in c("lh", "rh")) {
  for (iregion in ROIs) {

    i <- i + 1

    iroi <- paste0(LR,"_",iregion, "_", feature)

    model_1 <- lm(as.formula(paste0(iroi, "~subgroup+Age+Gender+eTIV_z")),
                  data = datafile_TDvsASDMLD)
    model_2 <- lm(as.formula(paste0(iroi, "~subgroup+Age+Gender+eTIV_z")),
                  data = datafile_TDvsASDSLDD)
    model_3 <- lm(as.formula(paste0(iroi, "~subgroup+Age+Gender+eTIV_z")),
                  data = datafile_ASD)

    model_result_1 <- anova(model_1)
    model_result_2 <- anova(model_2)
    model_result_3 <- anova(model_3)

    bet_group_results[i, 1:2] <- c(LR, paste0(iregion,"_",feature))
    bet_group_results[i, c(3,7,11)] <- c("TDvsASDMLD",
                                          "TDvsASDSLDD",
                                          "ASDMLDvsASDSLDD")

    bet_group_results[i, c(4:5,8:9,12:13)] <- cbind(round(c(model_result_1$`F value`[1],
                                                            model_result_1$`Pr(>F)`[1]),3),
                                                    round(c(model_result_2$`F value`[1],
                                                            model_result_2$`Pr(>F)`[1]),3),
                                                    round(c(model_result_3$`F value`[1],
                                                            model_result_3$`Pr(>F)`[1]),3)
                                                    )

  } # end for 10 regions

} # end for 2 hemispheres

# adjust p value
colnames(bet_group_results[,c(6,10,14)])

bet_group_results[bet_group_results$LR == "lh",][,c(6,10,14)] <- round(cbind(

```

```

p.adjust(bet_group_results$pvalue1[bet_group_results$LR == "lh"],method="fdr"),
p.adjust(bet_group_results$pvalue2[bet_group_results$LR == "lh"],method="fdr"),
p.adjust(bet_group_results$pvalue3[bet_group_results$LR == "lh"],method="fdr")
),3)

bet_group_results[bet_group_results$LR == "rh"],[,c(6,10,14)] <- round(cbind(
p.adjust(bet_group_results$pvalue1[bet_group_results$LR == "rh"],method="fdr"),
p.adjust(bet_group_results$pvalue2[bet_group_results$LR == "rh"],method="fdr"),
p.adjust(bet_group_results$pvalue3[bet_group_results$LR == "rh"],method="fdr")
),3)

#View(bet_group_results)
addWorksheet(wb,feature)
writeData(wb,feature,bet_group_results)

}
# saveWorkbook(wb,"./Table/betwgroup_results.xlsx")

knitr::kable(filter(bet_group_results, pvalue1 < 0.05 | pvalue2 < 0.05 | pvalue3 < 0.05))

```

LR	roi	diff1	Fvalue	pvalue	pvalue.adj	diff2	Fvalue	pvalue	pvalue.adj	diff3	Fvalue	pvalue	pvalue.adj
lh	parietal	TDvsASDMLD	0.042	0.105		TDvsASDSL	0.027	0.135		ASDMLDvsASDSL	0.562	0.771	
lh	inferiorparietal	TDvsASDMLD	0.041	0.105		TDvsASDSL	0.020	0.135		ASDMLDvsASDSL	0.579	0.771	
lh	superiortemporal	TDvsASDMLD	0.016	0.080		TDvsASDSL	0.540	0.900		ASDMLDvsASDSL	0.512	0.373	
lh	middletemporal	TDvsASDMLD	0.002	0.020		TDvsASDSL	0.150	0.375		ASDMLDvsASDSL	0.510	0.373	
rh	caudalmiddlefrontal	TDvsASDMLD	0.489	0.489		TDvsASDSL	0.093	0.413		ASDMLDvsASDSL	0.513	0.223	
rh	inferiorparietal	TDvsASDMLD	0.021	0.143		TDvsASDSL	0.124	0.413		ASDMLDvsASDSL	0.513	0.570	
rh	transversetemporal	TDvsASDMLD	0.029	0.143		TDvsASDSL	0.576	0.736		ASDMLDvsASDSL	0.517	0.223	
rh	middletemporal	TDvsASDMLD	0.043	0.143		TDvsASDSL	0.322	0.712		ASDMLDvsASDSL	0.519	0.570	

Correlation analysis (for each group, Language)

```

# compute correlations between feature and language scores in each subgroup
wb <- createWorkbook()
for (feature in c("volume","thickness","area")) {
  datafile_feature <- read.xlsx("./Table/Data/datafile_features.xlsx",sheet=feature)

  datafile_feature$eTIV_z <- scale(datafile_feature$eTIV)

  corr <- data.frame(group=character(), lateral=character(), roi = character(),
    partialR = numeric(), beta_value=numeric(),p_value=numeric(),
    adjusted_p_value=numeric())

  i <- 0
  for (igroup in c("TD","ASDMLD","ASDSL")){
    for (LR in c("lh","rh")){
      for (iregion in paste0(ROIs,"_", feature)){
        i<- i+1

```

```

data <- datafile_feature[datafile_feature$subgroup==igroup,]

fl <- as.formula(paste(paste0(LR, "_",iregion), "~ Gesell_Lang + Age + Gender + eTIV_z"))

model_Langcorr <- lm(fl, data=data)

model_result <- summary(model_Langcorr)

# partial R correlation
partial_correlation <- pcor.test(data[, paste0(LR, "_",iregion)],
                                data[, "Gesell_Lang"],
                                data[, c("Age", "Gender", "eTIV_z")],
                                method = "pearson")
pr <- round(partial_correlation$estimate,3)

corr[i, 1:3] <- c(igroup,LR,iregion)
corr[i, 4] <- pr
corr[i, 5:6] <-c(round(model_result$coefficients[2,1],3),
                 round(model_result$coefficients[2,4],3))

}
}
}

i <- 1
for (igroup in c("TD","ASDMLD","ASDSLD")){
  s <- 20*(i-1)+1
  e <- 20*i
  corr[c(s:e),7] <- round(c(
    p.adjust(corr$p_value[corr$group==igroup & corr$lateral=="lh"],method="fdr"),
    p.adjust(corr$p_value[corr$group==igroup & corr$lateral=="rh"],method="fdr")),3)

  i <- i+1
}

#View(corr)
addWorksheet(wb,feature)
writeData(wb,feature,corr)
}
# saveWorkbook(wb,"./Table/corr_language_results.xlsx")

# check correlation results
feature <- "volume" # "thickness" "area"
corr_volume <- read_xlsx("./Table/corr_language_results.xlsx",sheet = feature)
#View(corr_volume)
knitr::kable(filter(corr_volume, p_value < 0.05))

```

group	lateral	roi	partialR	β _value	p_value	adjusted_p_value
TD	rh	superiortemporal_volume	-0.345	-94.121	0.046	0.285
ASDMLD	lh	parsopercularis_volume	-0.493	-51.582	0.005	0.050
ASDMLD	rh	inferiorparietal_volume	0.396	134.116	0.028	0.280

```
feature <- "thickness"
corr_thickness <- read_xlsx("./Table/corr_language_results.xlsx",sheet = feature)
#View(corr_thickness)
knitr::kable(filter(corr_thickness, p_value < 0.05))
```

group	lateral	roi	partialR	β _value	p_value	adjusted_p_value
TD	rh	transversetemporal_thickness	-0.414	-0.017	0.015	0.15

```
feature <- "area"
corr_area <- read_xlsx("./Table/corr_language_results.xlsx",sheet = feature)
#View(corr_area)
knitr::kable(filter(corr_area, p_value < 0.05))
```

group	lateral	roi	partialR	β _value	p_value	adjusted_p_value
TD	rh	parsorbitalis_area	0.418	8.713	0.014	0.14
ASDMLD	lh	parsopercularis_area	-0.461	-14.923	0.009	0.09

Sup: Correlation analysis (with group differences)

```
colnames(data)[c(6:10)]
```

```
## [1] "Gesell_Adpt"      "Gesell_GrMot"      "Gesell_FineMot"    "Gesell_Lang"
## [5] "Gesell_Social"
```

```
# Beh <- c("Gesell_Adpt", "Gesell_GrMot", "Gesell_FineMot", "Gesell_Social", "Gesell_Lang")
Beh <- c("Gesell_Lang")
all_corr <- data.frame()

for (feature in c("volume", "thickness", "area")) {

  datafile_feature <- read.xlsx("./Table/Data/datafile_features.xlsx",sheet=feature)
  i <- 0
  corr <- data.frame()
  for (LR in c("lh","rh")){
    for (bb in Beh){
      pvalues1 <- numeric()
      pvalues2 <- numeric()
      pvalues3 <- numeric()
      for (ifeature in paste0(ROIs,"_", feature)){
```

```

    i <- i+1

    data <- datafile_feature

    data$eTIV_z <- scale(data$eTIV)

    fl <- as.formula(paste(paste0(LR, "_", ifeature), "~",
                          bb, "* subgroup + Age + Gender + eTIV_z"))

    model <- lm(fl, data=data)

    model_result <- anova(model)

    p_value_beh <- round(model_result[1,5],3)
    p_value_group <- round(model_result[2,5],3)
    p_value_int <- round(model_result[6,5],3)

    pvalues1 <- c(pvalues1, p_value_beh)
    pvalues2 <- c(pvalues2, p_value_group)
    pvalues3 <- c(pvalues3, p_value_int)

    rr <- strsplit(ifeature, "_")[[1]][1]
    ff <- strsplit(ifeature, "_")[[1]][2]

    corr[i, 1:4] <- c(bb, LR, rr, ff)
    corr[i, 5:7] <- c(p_value_beh, p_value_group, p_value_int)

  }
  # adjust p values for each 10 regions
  adjusted.p_value1 <- p.adjust(pvalues1, method = "fdr")
  adjusted.p_value2 <- p.adjust(pvalues2, method = "fdr")
  adjusted.p_value3 <- p.adjust(pvalues3, method = "fdr")
  corr[(i-9):i, 8] <- round(adjusted.p_value1, 3)
  corr[(i-9):i, 9] <- round(adjusted.p_value2, 3)
  corr[(i-9):i, 10] <- round(adjusted.p_value3, 3)
}
}
all_corr <- rbind(all_corr, corr)
}

colnames(all_corr) <- c("behavior", "lateral", "roi", "feature",
                      "p_value_Beh", "p_value_group", "p_value_int",
                      "adj.p_value_Beh", "adj.p_value_group", "adj.p_value_int")

write.xlsx(all_corr, "./corr_beh_groupdiff.xlsx")
# View(all_corr)
knitr::kable(all_corr[all_corr$p_value_int < 0.05,])

```

	behavior	lateral	roi	feature	p_value	Beh_value	group_value	adj.p_value	Beh_value	adj.p_value	int
16	Gesell_Lang	anhg	inferiorparietal	volume	0.044	0.178	0.045	0.088	0.297	0.247	
46	Gesell_Lang	anhg	inferiorparietalea	area	0.061	0.016	0.014	0.288	0.080	0.140	
51	Gesell_Lang	anhg	parsorbitalis	area	0.966	0.012	0.016	0.966	0.120	0.160	

Scatter plots for significant correlation results

```
# define variables
roi <- c("pars_orbitalis", "pars_triangularis", "pars_opercularis",
        "caudal_middle_frontal_gyrus", "supramarginal_gyrus", "inferior_parietal_gyrus",
        "transverse_temporal_gyrus", "superior_temporal_gyrus", "middle_temporal_gyrus",
        "lingual_gyrus")

hem <- c("Left", "Right")

# loop for plots
for (feature in c("volume", "thickness", "area")) {

  datafile_feature <- read.xlsx("./Table/Data/datafile_features.xlsx", sheet = feature)

  corr_new <- read.xlsx("./Table/corr_language_results.xlsx", sheet = feature)

  nn <- which(corr_new$p_value < 0.05)

  for (i in nn) {

    data <- datafile_feature[datafile_feature$subgroup == corr_new$group[i],]

    data$eTIV_z <- scale(data$eTIV)

    # regression model
    fl <- as.formula(paste0(paste0(corr_new$lateral[i], "_", corr_new$roi[i]),
                            "~ Gesell_Lang + Age + Gender + eTIV_z"))

    model_Langcorr <- lm(fl, data=data)

    # set up title for plots
    y.title <- paste0(hem[which(corr_new$lateral[i] == c("lh", "rh"))], " ",
                      roi[grep(corr_new$roi[i], paste0(ROIs, "_", feature))], " ")

    x_limits <- if(corr_new$group[i] == "ASDMLD") {
      c(44, max(data$Gesell_Lang))
    } else if (corr_new$group[i] == "ASDSLID") {
      c(20, max(data$Gesell_Lang))
    } else if (corr_new$group[i] == "TD"){
      c(75, max(data$Gesell_Lang))
    }
    breaks <- if(corr_new$group[i] == "ASDMLD") {
      seq(45, 70, by = 5)
    } else if (corr_new$group[i] == "ASDSLID") {
```



```

    seq(25, 45, by = 5)
  } else if (corr_new$group[i] == "TD"){
    seq(75, 100, by = 5)
  }

# plot
p <- ggplot(data, aes_string(x="Gesell_Lang", y=paste0(corr_new$lateral[i],
    "_",corr_new$roi[i])))) +

  geom_point(size=4) +
  geom_smooth(method = "lm", fullrange = T,
    mapping=aes(y=predict(model_Langcorr,data)),
    col = "red",lwd = 1.8) +
  labs(x="Language scores", y=y.title,
    title=corr_new$group[i]) +
  scale_x_continuous(limits = x_limits,breaks=breaks) +
  scale_y_continuous() +
  theme_classic()+
  # coord_cartesian(ylim = c(min(data$value), max(data$value)*1.1))+
  theme(axis.text=element_text(size=16, face = "bold"),
    axis.title.x=element_text(size=18,face = "bold"),
    axis.title.y=element_text(size=18,face = "bold"),
    plot.title = element_text( size = 25,face = "bold",hjust = 0.5),
    panel.background = element_rect(colour = "black", size=1))

print(p)

#ggsave(paste0("Plot/Corr/corr_plots_", corr_new$group[i],".",corr_new$roi[i],
#   ".png"), dpi=300, width=6, height=4)

}

}

```

```

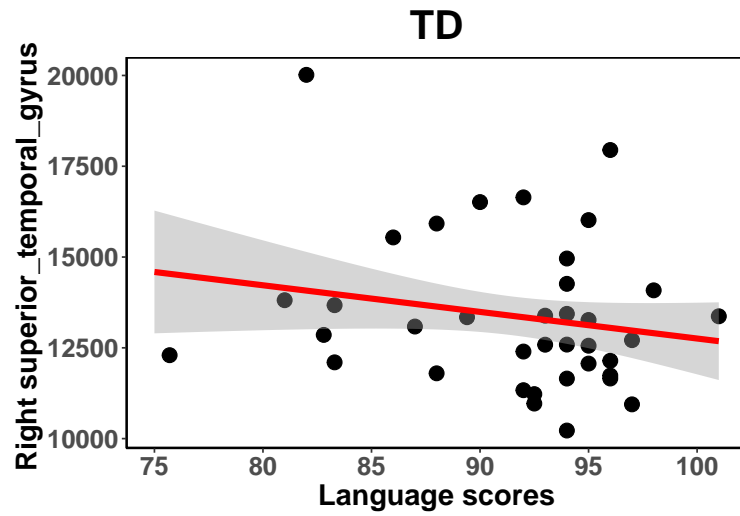
## Warning: `aes_string()` was deprecated in ggplot2 3.0.0.
## i Please use tidy evaluation ideoms with `aes()`
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.

## Warning: Using `size` aesthetic for lines was deprecated in ggplot2 3.4.0.
## i Please use `linewidth` instead.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.

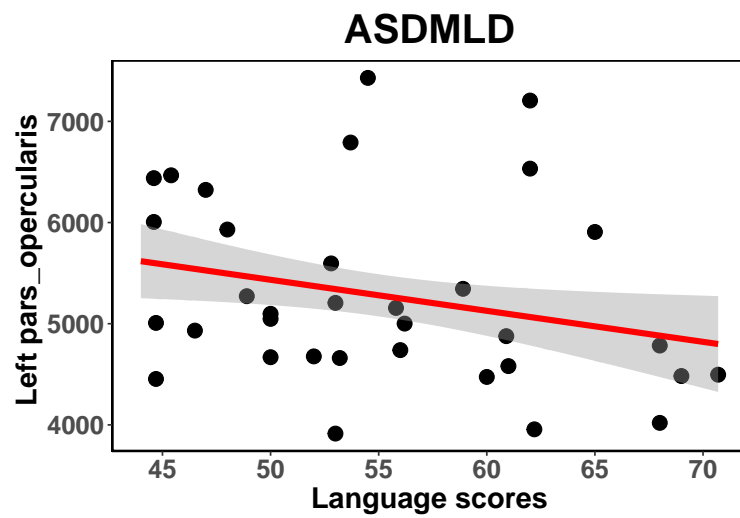
## Warning: The `size` argument of `element_rect()` is deprecated as of ggplot2 3.4.0.
## i Please use the `linewidth` argument instead.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.

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

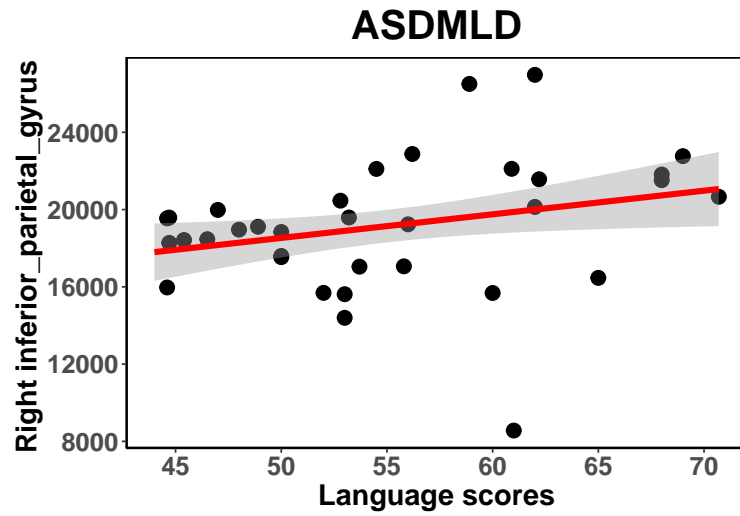
```



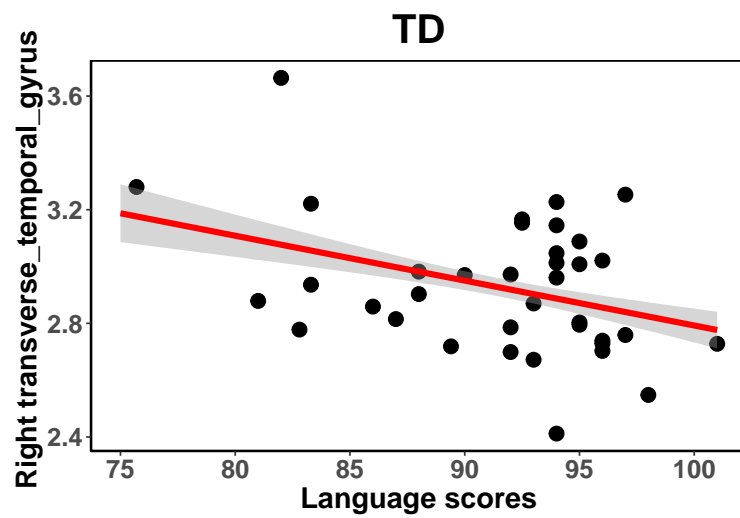
```
## `geom_smooth()` using formula = 'y ~ x'
```



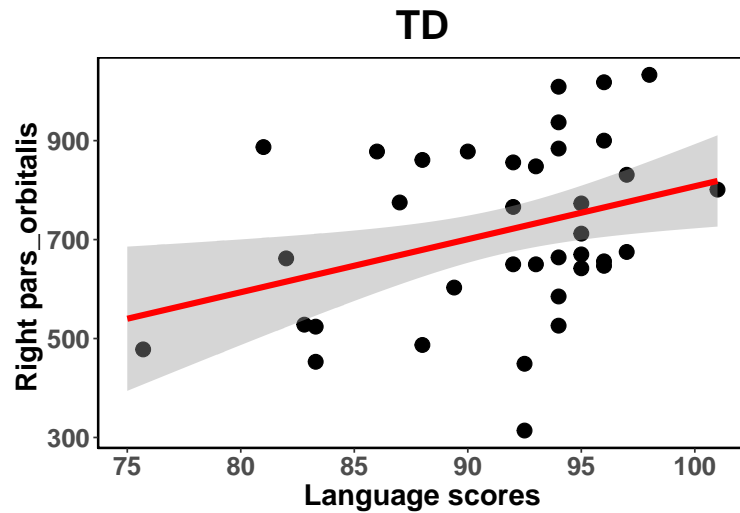
```
## `geom_smooth()` using formula = 'y ~ x'
```



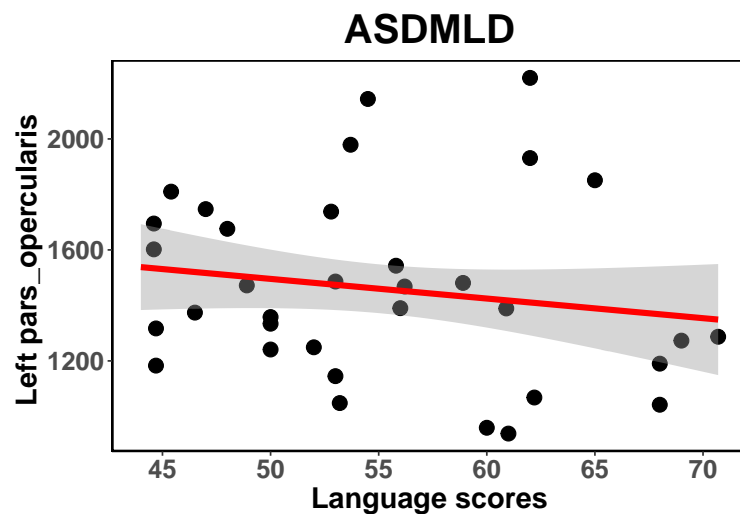
```
## `geom_smooth()` using formula = 'y ~ x'
```



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



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



Violin plot for ROIs showing significant correlations with language scores

```
# define variables
roi <- c("pars orbitalis","pars triangularis","pars opercularis",
        "caudal middle frontal gyrus","supramarginal gyrus","inferior parietal gyrus",
        "transverse temporal gyrus","superior temporal gyrus","middle temporal gyrus",
        "lingual gyrus")

hem <- c("Left", "Right")

# loop for plots
for (feature in c("volume", "thickness","area")) {
```

```

datafile_feature <- read.xlsx("./Table/Data/datafile_features.xlsx",sheet = feature)

corr_new <- readxl::read_excel("./Table/corr_language_results.xlsx",sheet=feature)

nn <- which(corr_new$p_value < 0.05)

for (n in nn) {

  ROI <- paste0(corr_new$lateral[n], "_", corr_new$roi[n])
  datafile_feature$subgroup <- factor(datafile_feature$subgroup,
                                     levels = c("TD", "ASDMLD",
                                                  "ASDSLD"))

  p <- ggplot(datafile_feature, aes_string(x="subgroup", y=ROI, fill="subgroup")) +
    geom_violin(alpha=0.9, width=0.7, trim = TRUE, linewidth=1) + #
    geom_boxplot(notch = FALSE, outlier.size = -1, color="white",
                 lwd=0.9,width=0.15) + #
    stat_summary(fun = "mean", geom = "point", shape = 4, size = 3,
                 color = "black") + #
    scale_y_continuous() +
    labs(title=ROI)+
    coord_cartesian(ylim = c(min(datafile_feature[,ROI])*0.9,
                              max(datafile_feature[,ROI])*1.25)) +
    scale_x_discrete(limits = c("TD", "ASDMLD", "ASDSLD")) +
    theme_bw() + #
    theme(panel.grid.major = element_blank(), #
          panel.grid.minor = element_blank(), #
          axis.text.x=element_text(size=16,face = "bold",color="black",
                                    margin=margin(t=18)),
          axis.text.y=element_text(size=16, face = "bold"),
          axis.title.x=element_blank(),
          axis.title.y=element_blank(),
          plot.title = element_text( size = 25,face = "bold",hjust = 0.5),
          panel.background = element_rect(colour = "black", linewidth=1),
          legend.position="none") +

    scale_fill_manual(values = c("TD" = "#ea9c9d", "ASDMLD" = "#93cc82",
                                  "ASDsevere" = "#4d97cd"))

  #ggsave(paste0("Plot/Bet/violin_subgroup_", ROI, ".png"), dpi=200,
  #        width=6, height=4)
  print(p)

}
}

```

