Hippocampal volume and rest-activity rhythms

Megan McMahon

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This analysis uses data from our NIA study. Here we are looking at hippocampal volume derived from the Freesurfer fsaverage5 parcellation in relation to aspects of rest-activity rhythms in both younger and older adults.

We use an an adjusted HC volume as documented in Brehmer et al. (2020) (https://doi.org/10.1016/j.neuroimage.2019.116475)

```
dataDir <- '~/Box/CogNeuroLab/Aging Decision Making R01/data/'
df <- readr::read_csv(paste0(dataDir, 'dataset_2020-10-10.csv'))
```

```
## Warning: Missing column names filled in: 'X1' [1]
```

```
##
## ── Column specification ─────────────────────────────────────────
## cols(
##    .default = col_logical(),
##    X1 = col_double(),
##    record_id = col_double(),
##    files = col_character(),
##    cc_fa = col_double(),
##    ccbody_fa = col_double(),
##    splenium_fa = col_double(),
##    genu_fa = col_double(),
##    coronaradiata_fa = col_double(),
##    postthalamicradiation_fa = col_double(),
##    suplongfasciculus_fa = col_double(),
##    externalcapsule_fa = col_double(),
##    global_fa = col_double(),
##    IS = col_double(),
##    IV = col_double(),
##    RA = col_double(),
##    L5 = col_double(),
##    L5_starttime = col_time(format = ""),
##    M10 = col_double(),
##    M10_starttime = col_time(format = ""),
##    cc_vol = col_double()
##    # ... with 370 more columns
## )
## ℹ Use `spec()` for the full column specifications.
```

```
fsvol <- readr::read_delim('/Volumes/schnyer/Aging_DecMem/Scan_Data/BIDS/derivatives/
freesurfer/aseg_vol_table.txt', delim = '\t')
```

```
##
## ── Column specification ─────────────────────────────────────────
## cols(
##    .default = col_double(),
##    `Measure:volume` = col_character()
## )
## ℹ Use `spec()` for the full column specifications.
```

```
fsvol$record_id <- substr(fsvol$`Measure:volume`, 5, 10)
fsvol$record_id
```

```
##     [1] "30004" "30008" "30009" "30012" "30015" "30019" "30020" "30023" "30040"
##    [10] "30057" "30064" "30066" "30069" "30074" "30085" "30088" "30090" "30091"
##    [19] "30095" "30096" "30105" "30116" "30118" "30119" "30128" "30181" "30217"
##    [28] "30227" "30236" "30242" "30255" "30274" "30283" "30295" "30330" "30346"
##    [37] "30376" "30395" "30400" "30403" "30407" "30412" "30417" "30426" "30432"
##    [46] "30433" "30466" "30469" "30476" "30478" "30568" "30570" "30581" "30584"
##    [55] "30588" "40160" "40170" "40175" "40288" "40351" "40490" "40496" "40500"
##    [64] "40512" "40515" "40516" "40519" "40520" "40522" "40524" "40547" "40550"
##    [73] "40564" "40601" "40608" "40615" "40619" "40623" "40624" "40629" "40638"
##    [82] "40649" "40650" "40655" "40658" "40664" "40665" "40668" "40672" "40685"
##    [91] "40694" "40720" "40728" "40730" "40738" "40743" "40750" "40758" "40767"
##   [100] "40768" "40769" "40773" "40775" "40777" "40778" "40779" "40782" "40784"
##   [109] "40796" "40803" "40811" "40855" "40859" "40861" "40876" "40878" "40930"
```

```
df1 <- merge(df, fsvol, by = 'record_id', all = TRUE)
```

```
colnames(fsvol)
```

```
##  [1] "Measure:volume"              "Left-Lateral-Ventricle"
##  [3] "Left-Inf-Lat-Vent"           "Left-Cerebellum-White-Matter"
##  [5] "Left-Cerebellum-Cortex"      "Left-Thalamus-Proper"
##  [7] "Left-Caudate"                "Left-Putamen"
##  [9] "Left-Pallidum"               "3rd-Ventricle"
## [11] "4th-Ventricle"               "Brain-Stem"
## [13] "Left-Hippocampus"            "Left-Amygdala"
## [15] "CSF"                         "Left-Accumbens-area"
## [17] "Left-VentralDC"              "Left-vessel"
## [19] "Left-choroid-plexus"         "Right-Lateral-Ventricle"
## [21] "Right-Inf-Lat-Vent"          "Right-Cerebellum-White-Matter"
## [23] "Right-Cerebellum-Cortex"     "Right-Thalamus-Proper"
## [25] "Right-Caudate"               "Right-Putamen"
## [27] "Right-Pallidum"              "Right-Hippocampus"
## [29] "Right-Amygdala"              "Right-Accumbens-area"
## [31] "Right-VentralDC"             "Right-vessel"
## [33] "Right-choroid-plexus"        "5th-Ventricle"
## [35] "WM-hypointensities"          "Left-WM-hypointensities"
## [37] "Right-WM-hypointensities"    "non-WM-hypointensities"
## [39] "Left-non-WM-hypointensities" "Right-non-WM-hypointensities"
## [41] "Optic-Chiasm"                "CC_Posterior"
## [43] "CC_Mid_Posterior"            "CC_Central"
## [45] "CC_Mid_Anterior"             "CC_Anterior"
## [47] "BrainSegVol"                 "BrainSegVolNotVent"
## [49] "BrainSegVolNotVentSurf"      "lhCortexVol"
## [51] "rhCortexVol"                 "CortexVol"
## [53] "lhCerebralWhiteMatterVol"    "rhCerebralWhiteMatterVol"
## [55] "CerebralWhiteMatterVol"      "SubCortGrayVol"
## [57] "TotalGrayVol"                "SupraTentorialVol"
## [59] "SupraTentorialVolNotVent"    "SupraTentorialVolNotVentVox"
## [61] "MaskVol"                     "BrainSegVol-to-eTIV"
## [63] "MaskVol-to-eTIV"             "lhSurfaceHoles"
## [65] "rhSurfaceHoles"              "SurfaceHoles"
## [67] "EstimatedTotalIntraCranialVol" "record_id"
```

Total HC volume

```
df1$hc_vol <- df1$`Left-Hippocampus` + df1$`Right-Hippocampus`
df1$thalamus_vol <- df1$`Left-Thalamus-Proper` + df1$`Right-Thalamus-Proper`
df1$caudate_vol <- df1$`Left-Caudate` + df1$`Right-Caudate`
df1$putamen_vol <- df1$`Left-Putamen` + df1$`Right-Putamen`
```
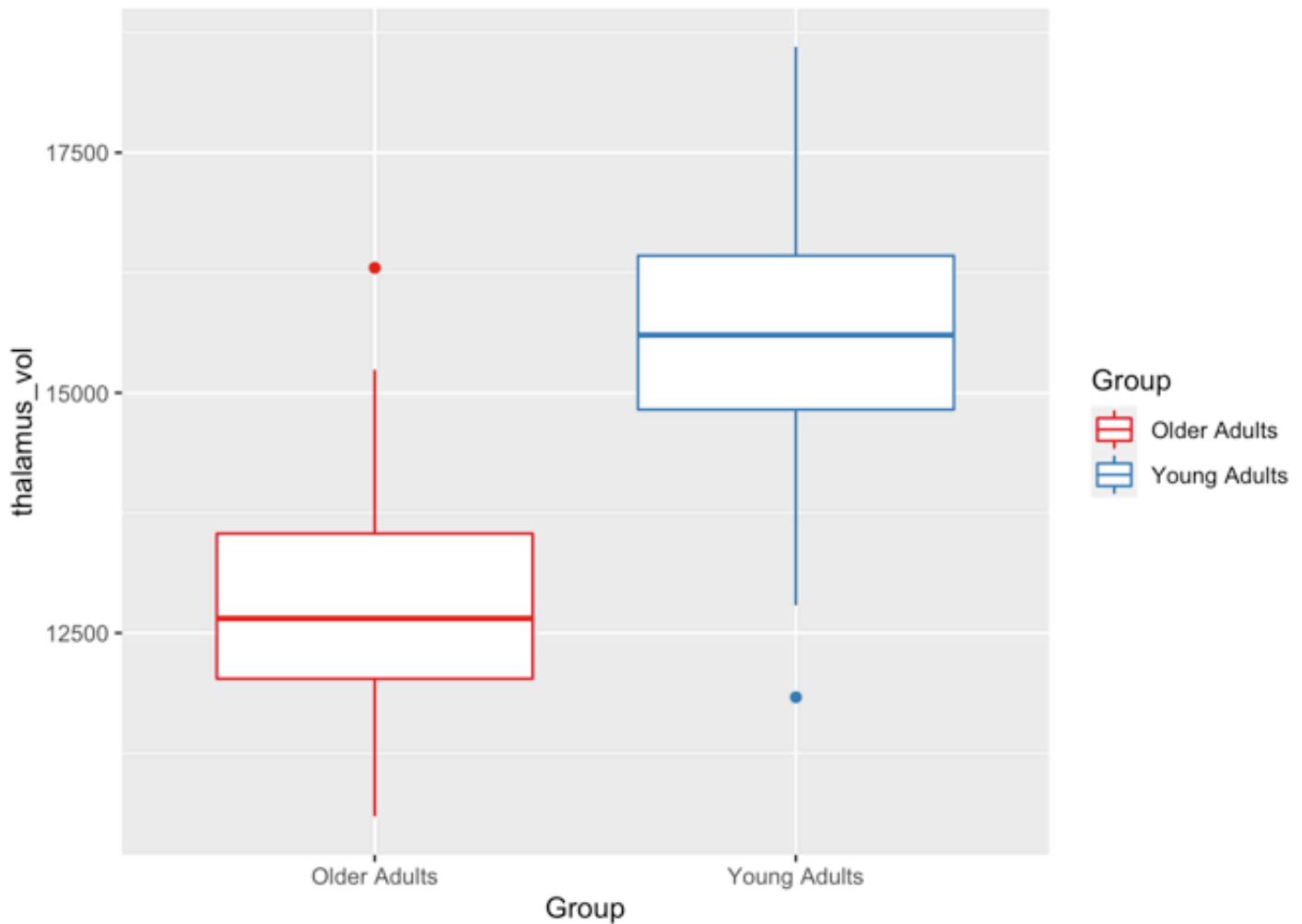
```
df1 %>%
  drop_na(Group) %>%
  ggplot(aes(x = `Group`, y = `hc_vol`, group = `Group`, color = `Group`))  +
  geom_boxplot() +
  scale_color_brewer(palette='Set1')
```

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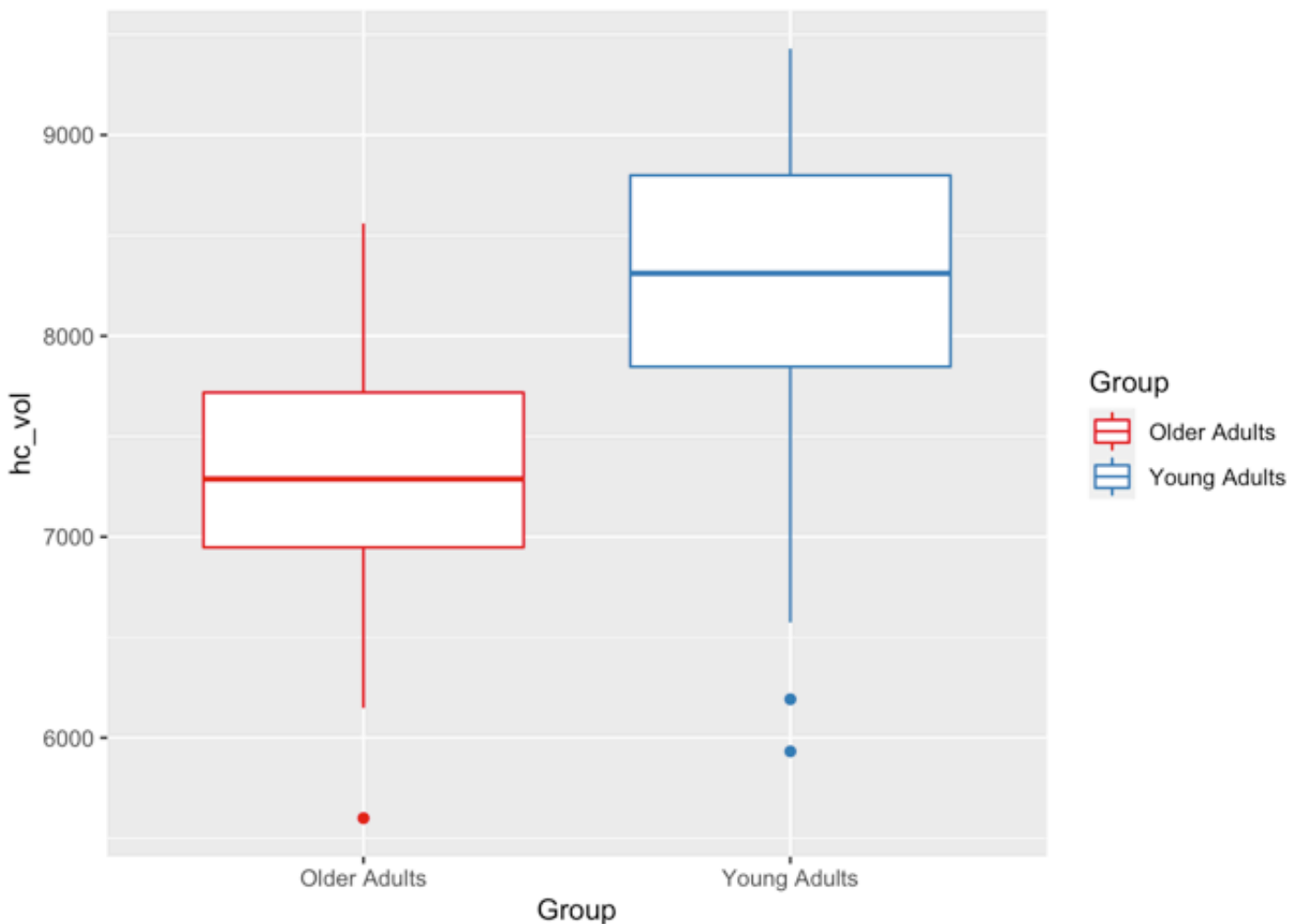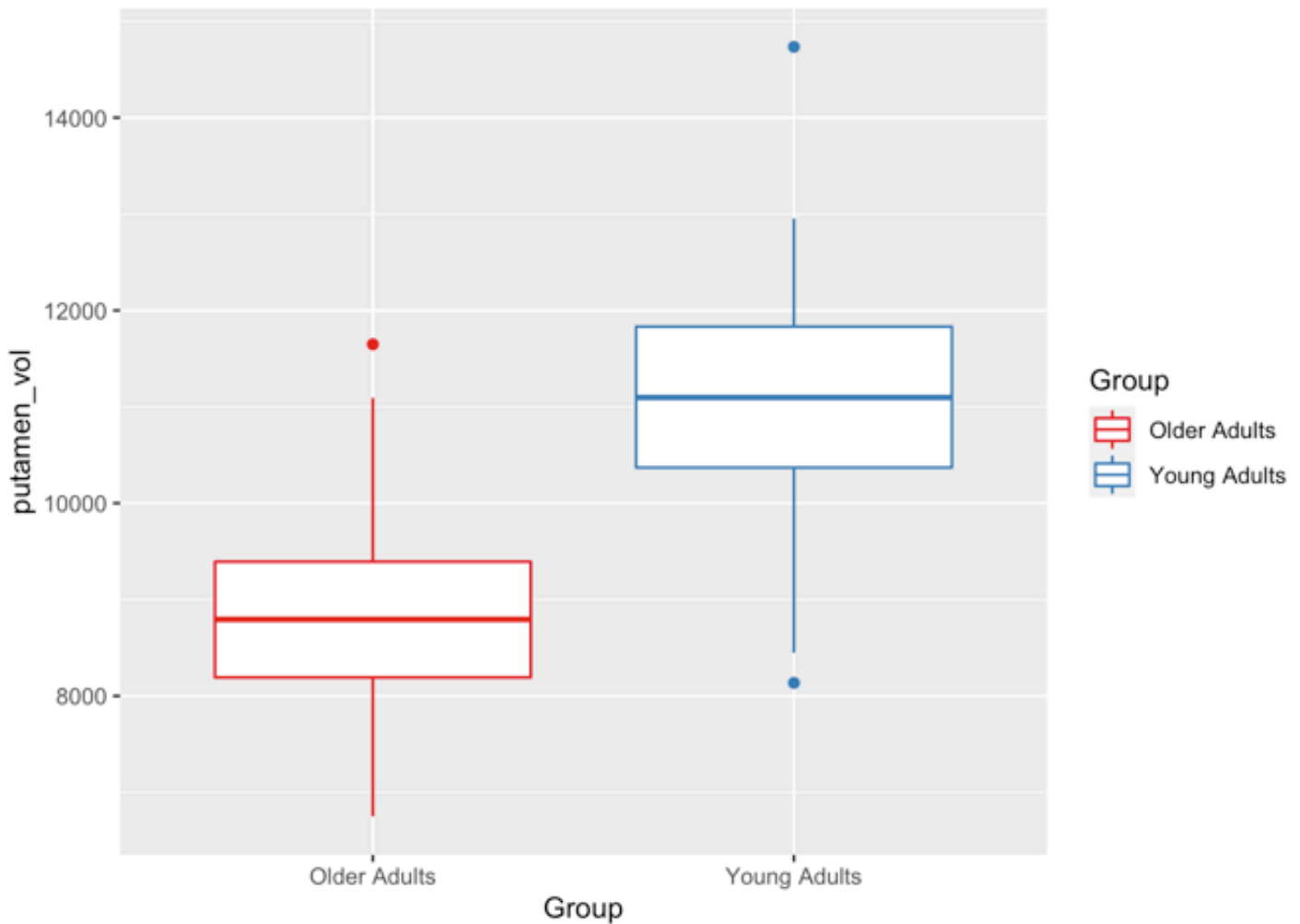


```
df1 %>%
  drop_na(Group) %>%
  ggplot(aes(x = `Group`, y = `thalamus_vol`, group = `Group`, color = `Group`))  +
  geom_boxplot() +
  scale_color_brewer(palette='Set1')
```

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

```
df1 %>%
  drop_na(Group) %>%
  ggplot(aes(x = `Group`, y = `putamen_vol`, group = `Group`, color = `Group`))  +
  geom_boxplot() +
  scale_color_brewer(palette='Set1')
```

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

```
df1 %>%
  drop_na(Group) %>%
  ggplot(aes(x = `Group`, y = `caudate_vol`, group = `Group`, color = `Group`))  +
  geom_boxplot() +
  scale_color_brewer(palette='Set1')
```

```
## Warning: Removed 2 rows containing non-finite values (stat_boxplot).
```
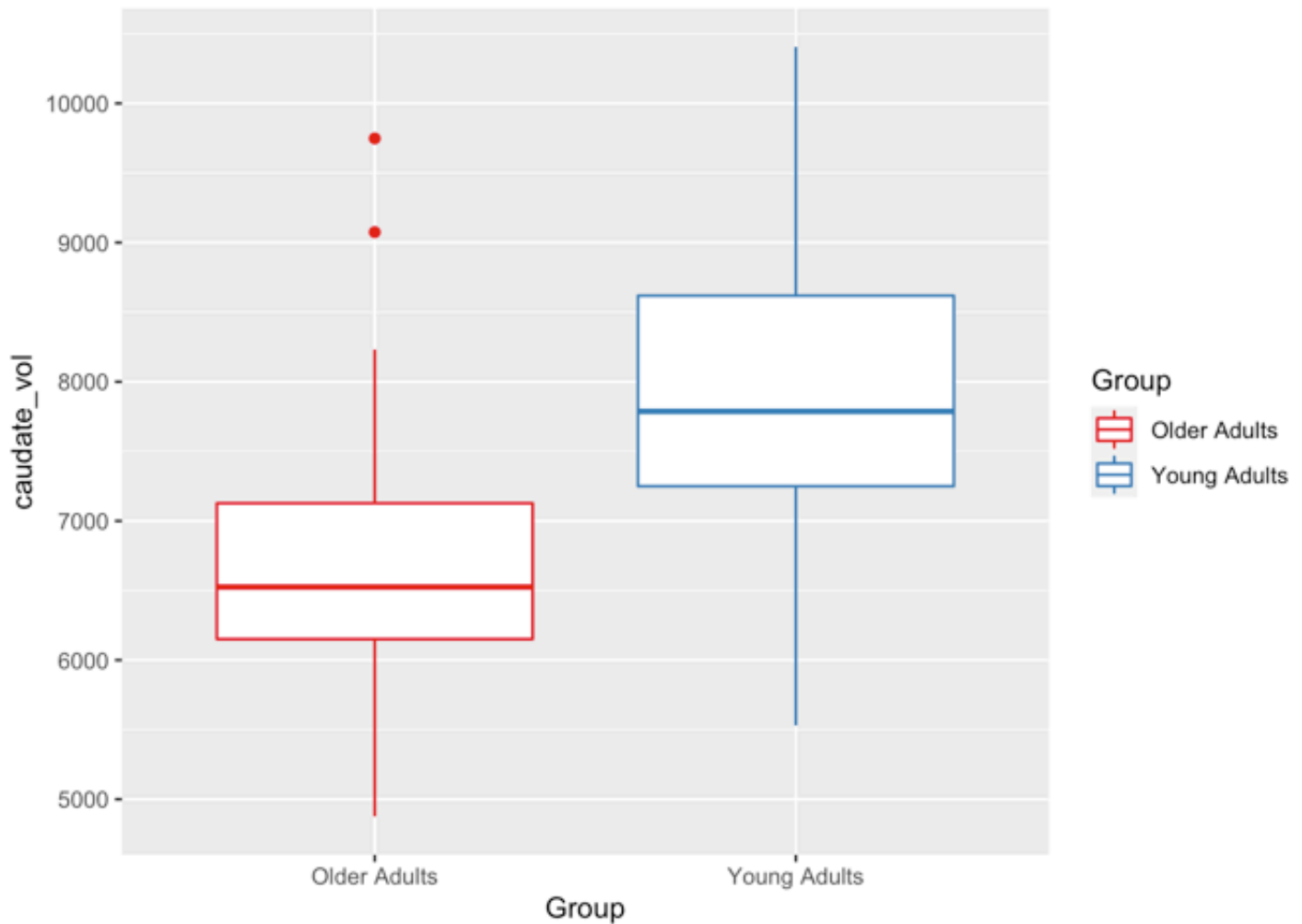
Adjusted HC volume

Adjusted HC volume = raw HC volume – b X (ICV–average ICV), where b is the slope of regression of the raw HC volume on ICV.

```
hc_icv_reg <- lm(EstimatedTotalIntraCranialVol ~ hc_vol, data = df1)
hc_b <- as.numeric(hc_icv_reg$coefficients['hc_vol'])
df1$hc_vol_adj <- df1$hc_vol - hc_b * (df1$EstimatedTotalIntraCranialVol - mean(df1$E
stimatedTotalIntraCranialVol, na.rm = TRUE))

thalamus_icv_reg <- lm(EstimatedTotalIntraCranialVol ~ thalamus_vol, data = df1)
thalamus_b <- as.numeric(thalamus_icv_reg$coefficients['thalamus_vol'])
df1$thalamus_vol_adj <- df1$thalamus_vol - thalamus_b * (df1$EstimatedTotalIntraCrani
alVol - mean(df1$EstimatedTotalIntraCranialVol, na.rm = TRUE))

caudate_icv_reg <- lm(EstimatedTotalIntraCranialVol ~ caudate_vol, data = df1)
caudate_b <- as.numeric(caudate_icv_reg$coefficients['caudate_vol'])
df1$caudate_vol_adj <- df1$caudate_vol - caudate_b * (df1$EstimatedTotalIntraCranialV
ol - mean(df1$EstimatedTotalIntraCranialVol, na.rm = TRUE))

putamen_icv_reg <- lm(EstimatedTotalIntraCranialVol ~ putamen_vol, data = df1)
putamen_b <- as.numeric(putamen_icv_reg$coefficients['putamen_vol'])
df1$putamen_vol_adj <- df1$putamen_vol - putamen_b * (df1$EstimatedTotalIntraCranialV
ol - mean(df1$EstimatedTotalIntraCranialVol, na.rm = TRUE))
```
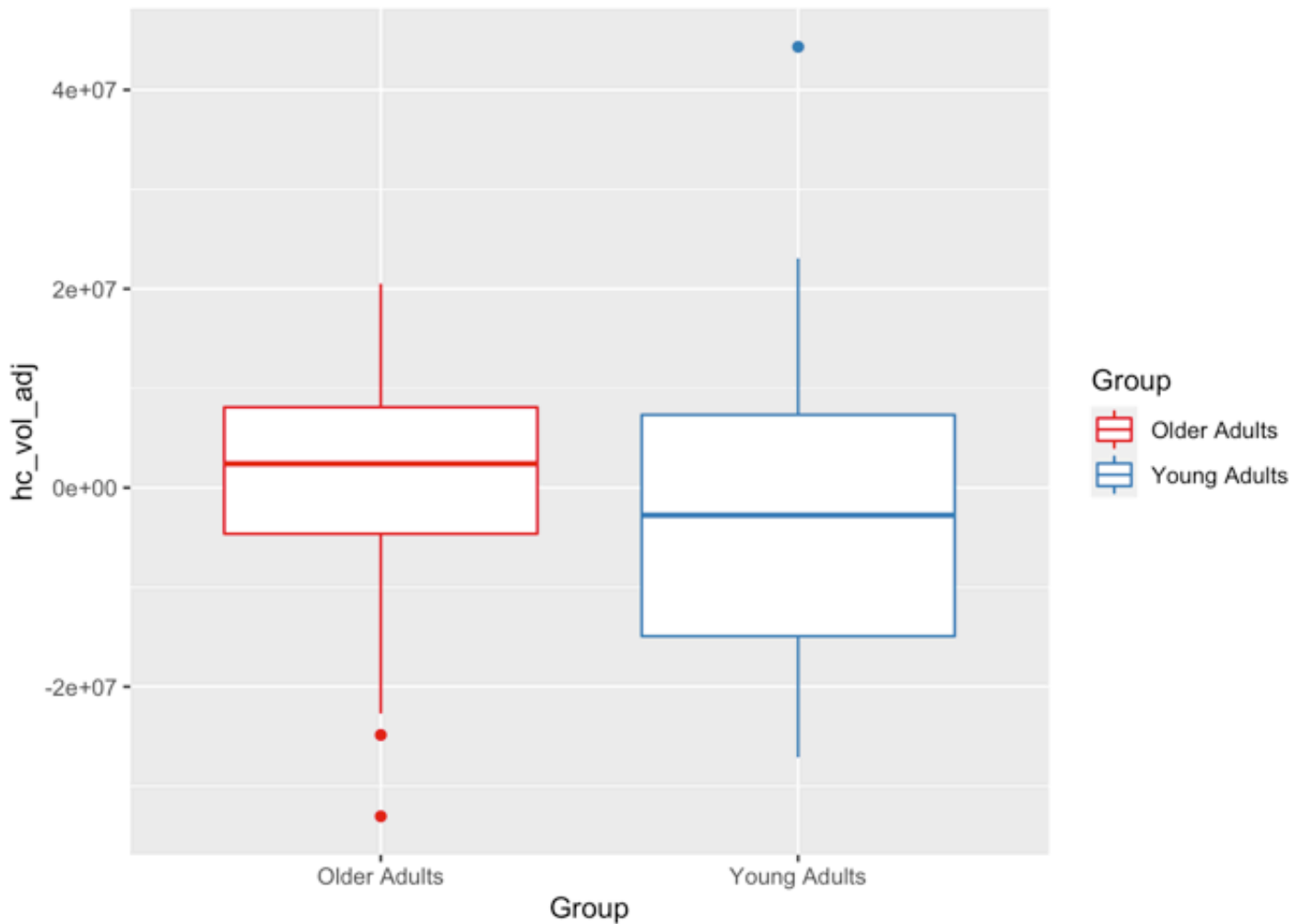
```
df1 %>%
  drop_na(Group) %>%
  ggplot(aes(x = `Group`, y = `hc_vol_adj`, group = `Group`, color = `Group`))  +
  geom_boxplot() +
  scale_color_brewer(palette='Set1')
```
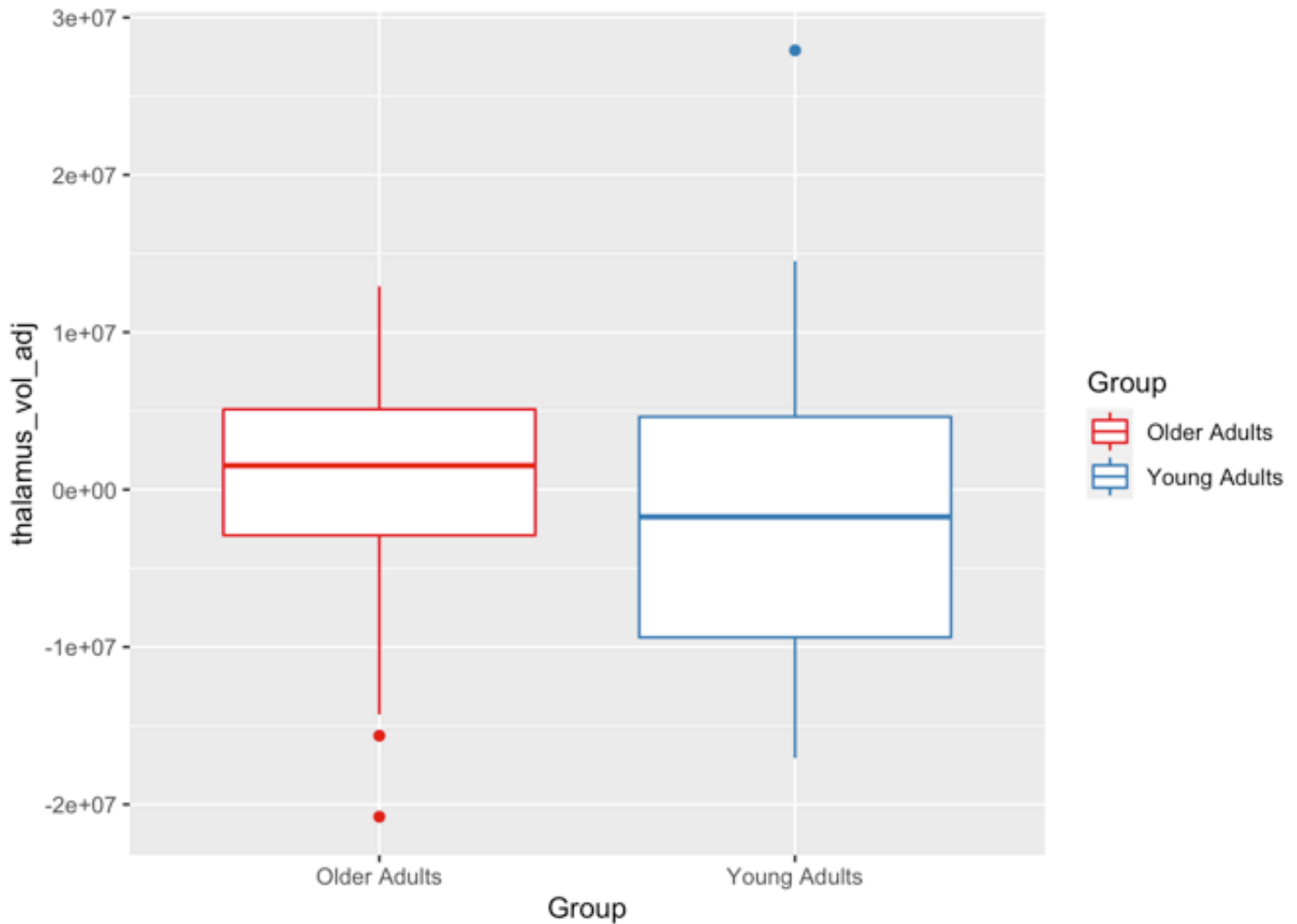
```
## Warning: Removed 2 rows containing non-finite values (stat_boxplot).
```
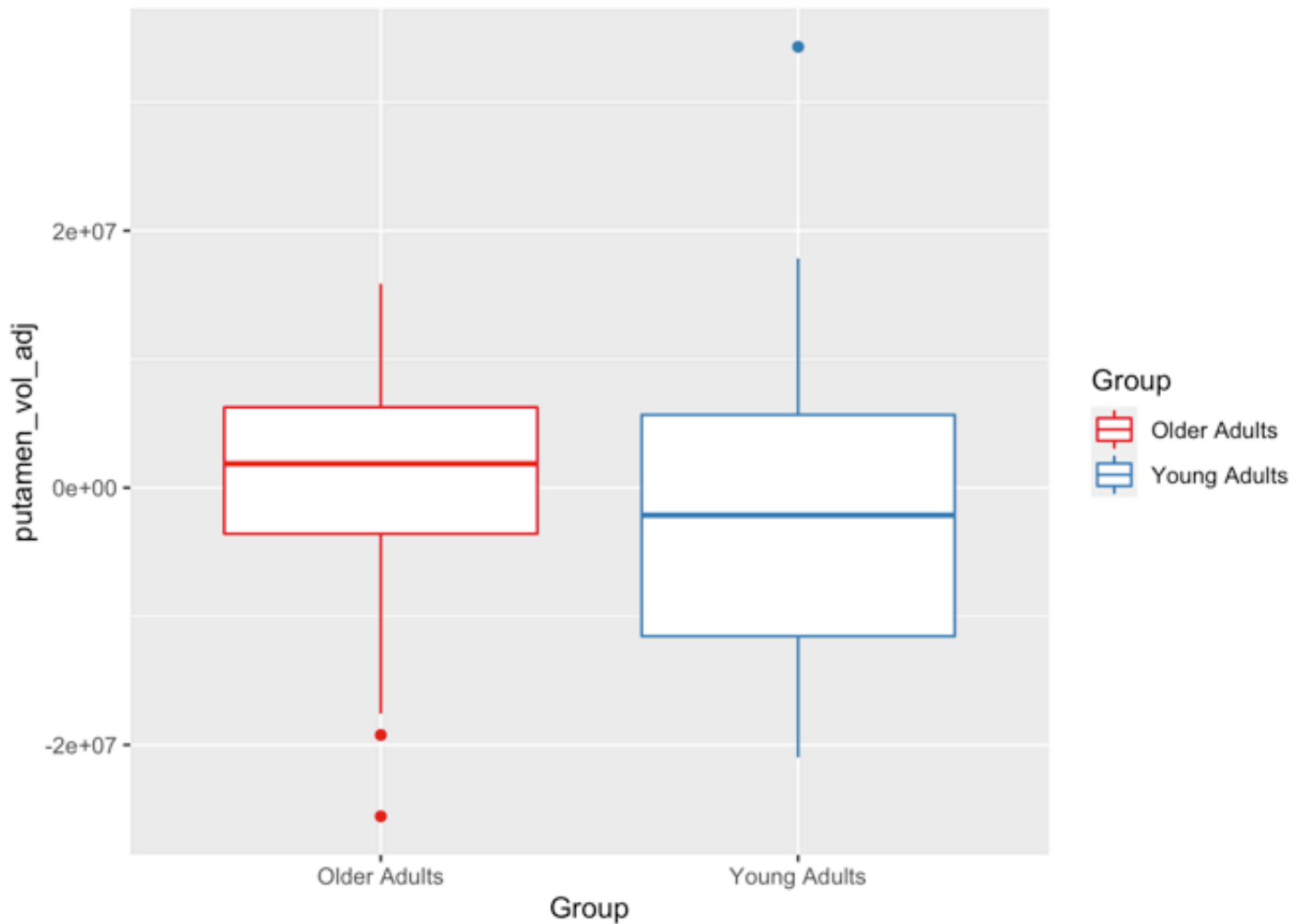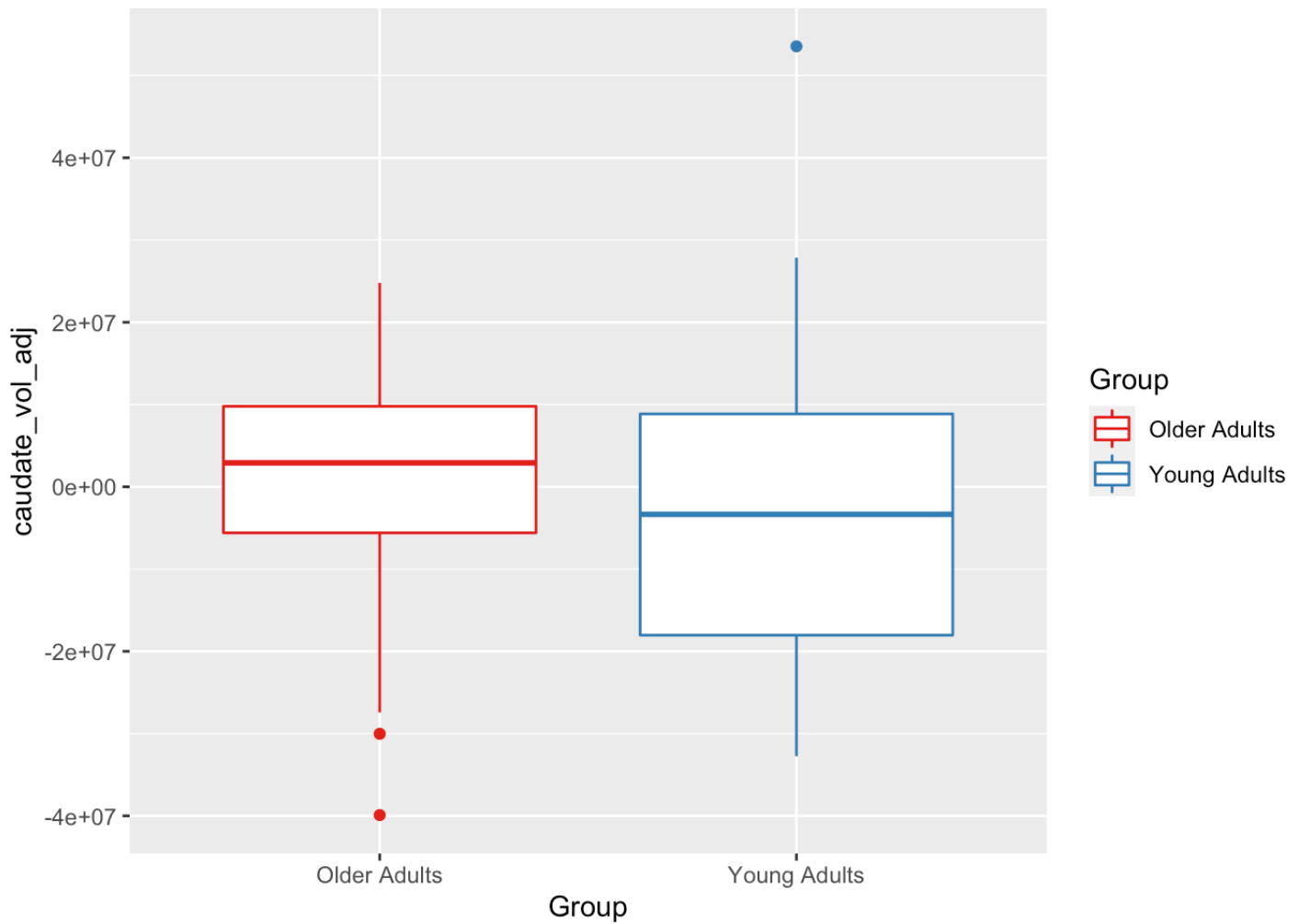
```
df1 %>%
  drop_na(Group) %>%
  ggplot(aes(x = `Group`, y = `thalamus_vol_adj`, group = `Group`, color = `Group`))
+
  geom_boxplot() +
  scale_color_brewer(palette='Set1')
```

```
## Warning: Removed 2 rows containing non-finite values (stat_boxplot).
```
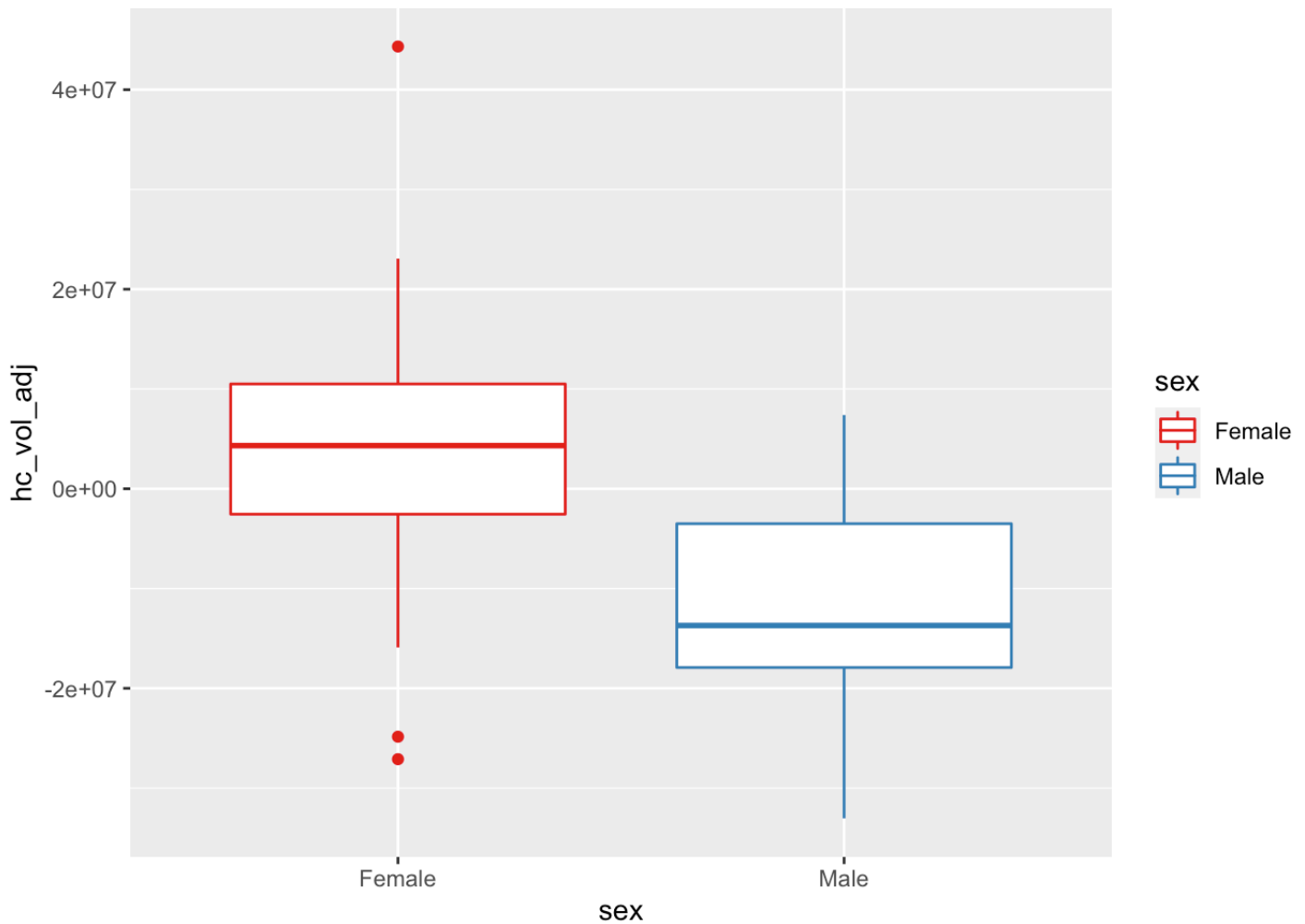
```
df1 %>%
  drop_na(Group) %>%
  ggplot(aes(x = `Group`, y = `putamen_vol_adj`, group = `Group`, color = `Group`))
+
  geom_boxplot() +
  scale_color_brewer(palette='Set1')
```

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

```
df1 %>%
  drop_na(Group) %>%
  ggplot(aes(x = `Group`, y = `caudate_vol_adj`, group = `Group`, color = `Group`))
+
  geom_boxplot() +
  scale_color_brewer(palette='Set1')
```

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

```
df1 %>%
  drop_na(Group) %>%
  ggplot() +
  geom_boxplot(aes(x = `sex`, y = `hc_vol_adj`, group = `sex`, color = `sex`))  +
  scale_color_brewer(palette='Set1')
```
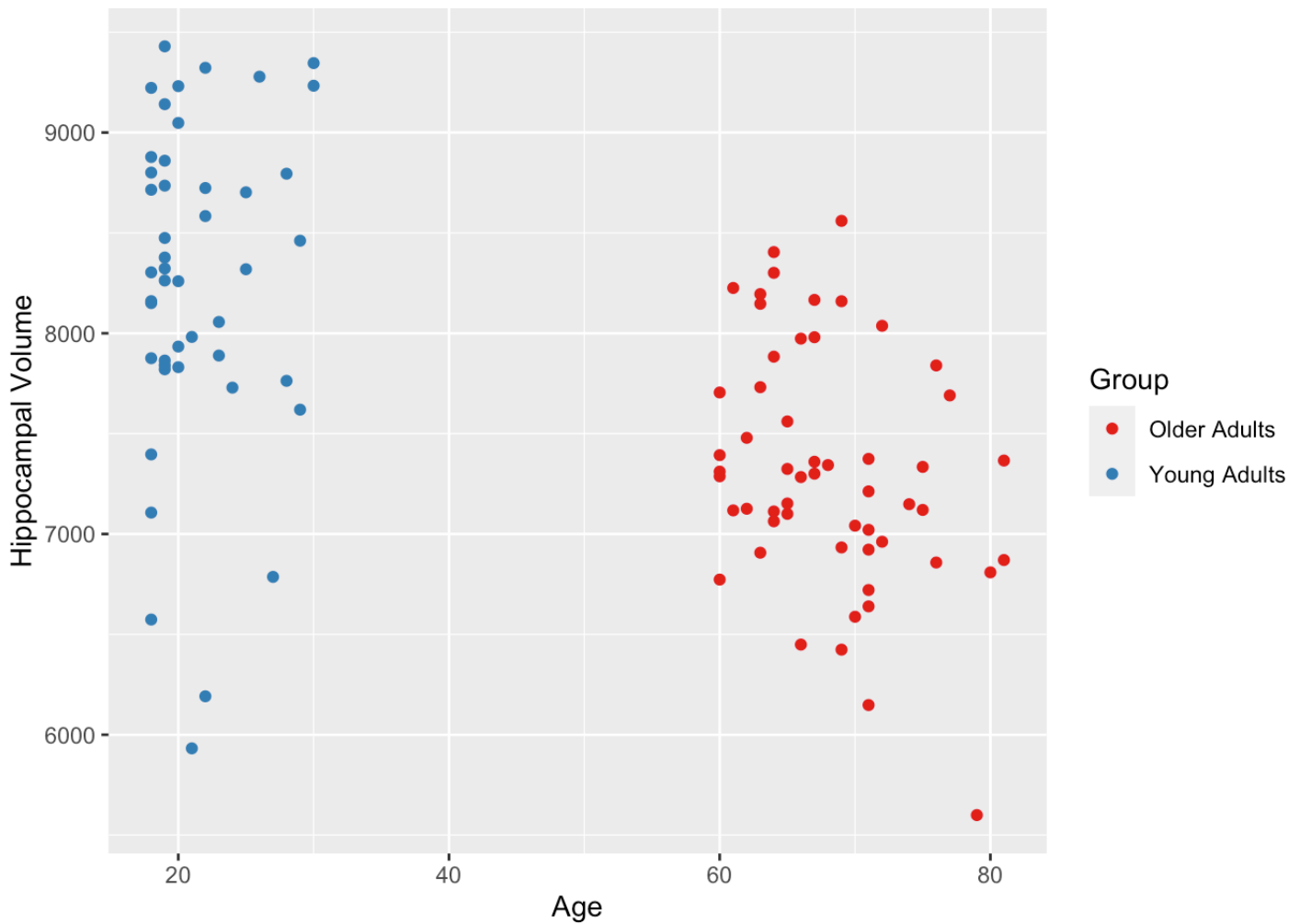
```
## Warning: Removed 2 rows containing non-finite values (stat_boxplot).
```
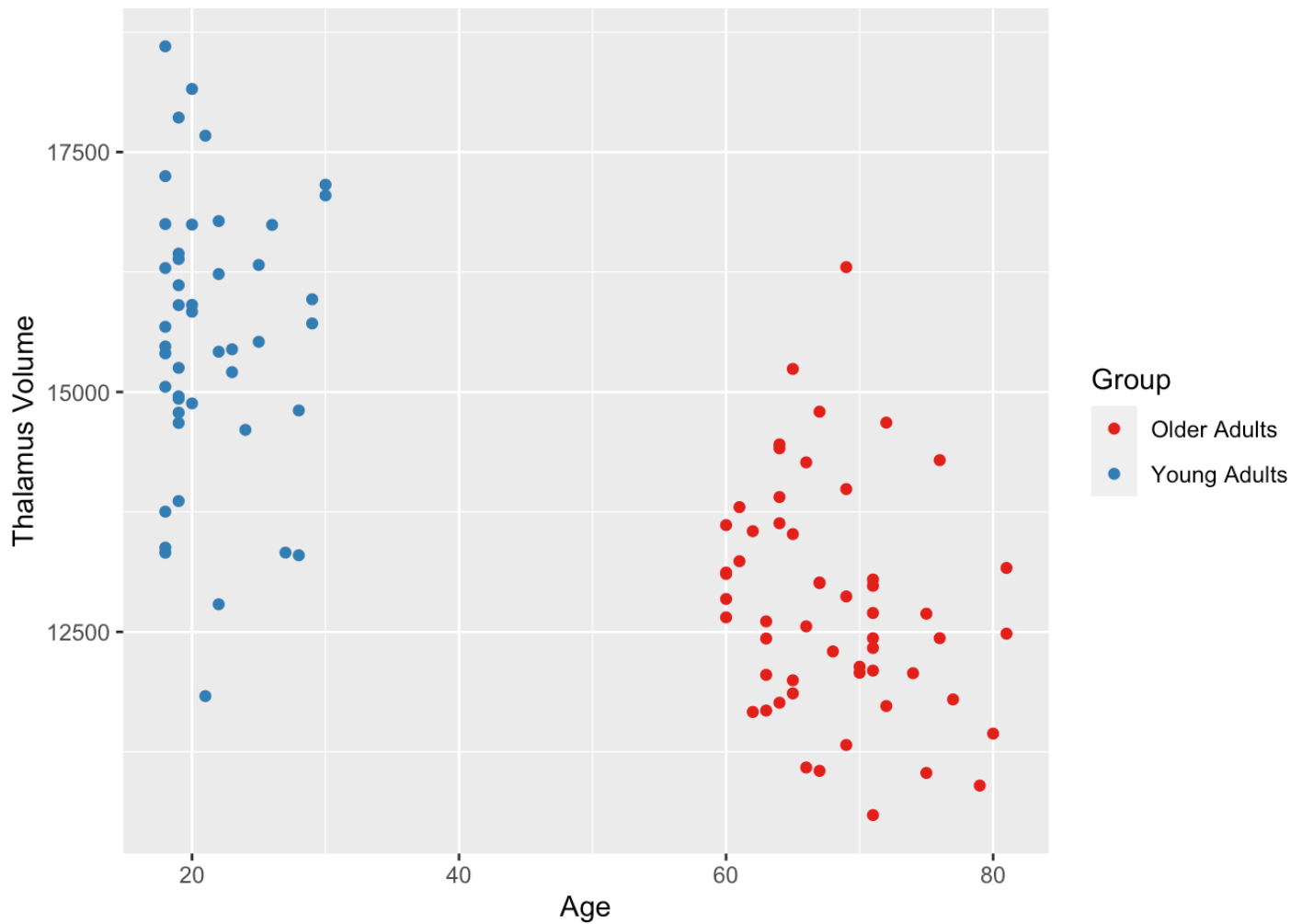
HC volume and age

```
df1 %>%
  drop_na(Group) %>%
  ggplot(aes(x = `age`, y = `hc_vol`, color = `Group`, group = `Group`)) +
  geom_point() +
  scale_color_brewer(palette='Set1') +
  xlab('Age') + ylab('Hippocampal Volume')
```

```
## Warning: Removed 2 rows containing missing values (geom_point).
```
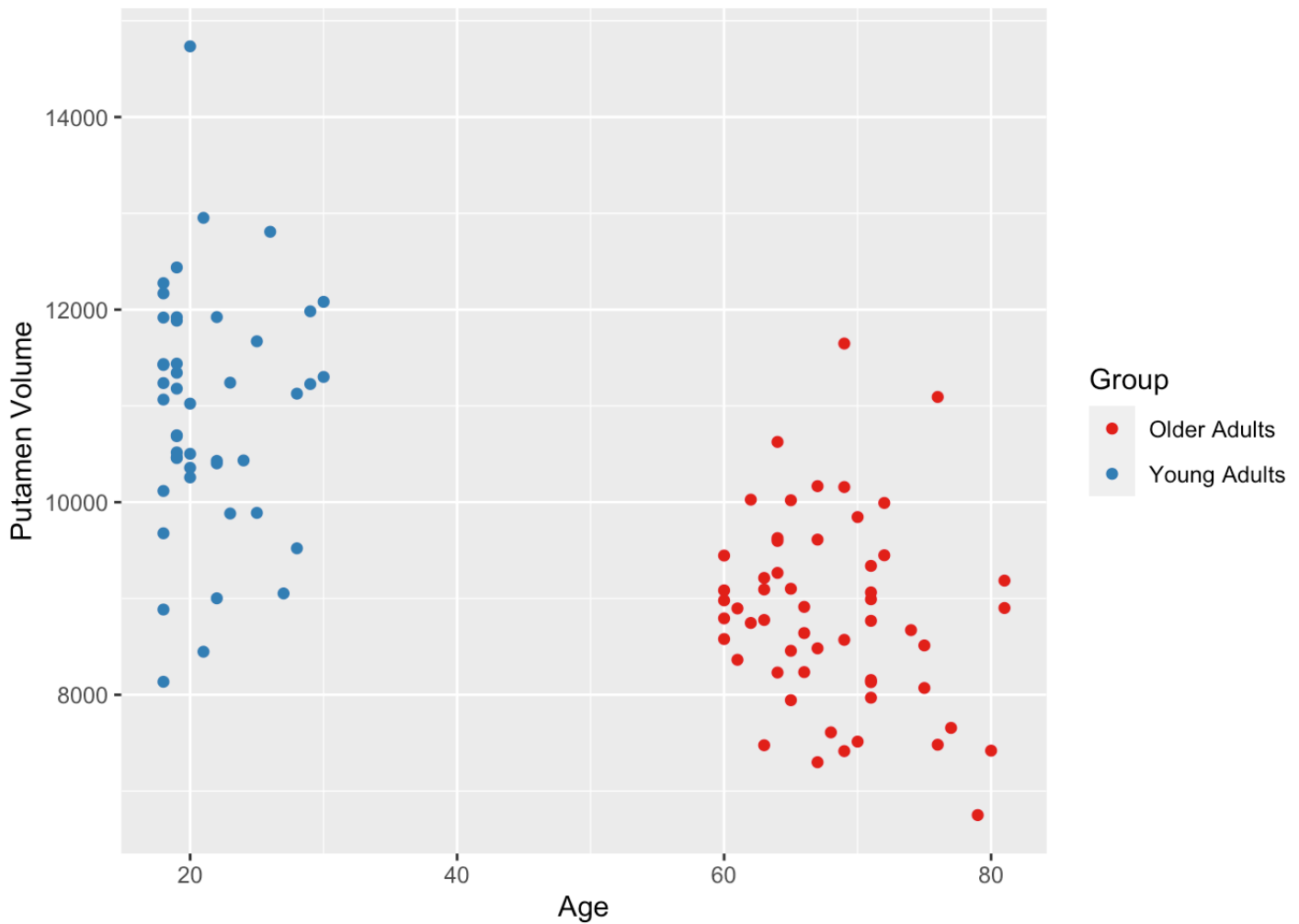
```
df1 %>%
  drop_na(Group) %>%
  ggplot(aes(x = `age`, y = `thalamus_vol`, color = `Group`, group = `Group`)) +
  geom_point() +
  scale_color_brewer(palette='Set1') +
  xlab('Age') + ylab('Thalamus Volume')
```

```
## Warning: Removed 2 rows containing missing values (geom_point).
```
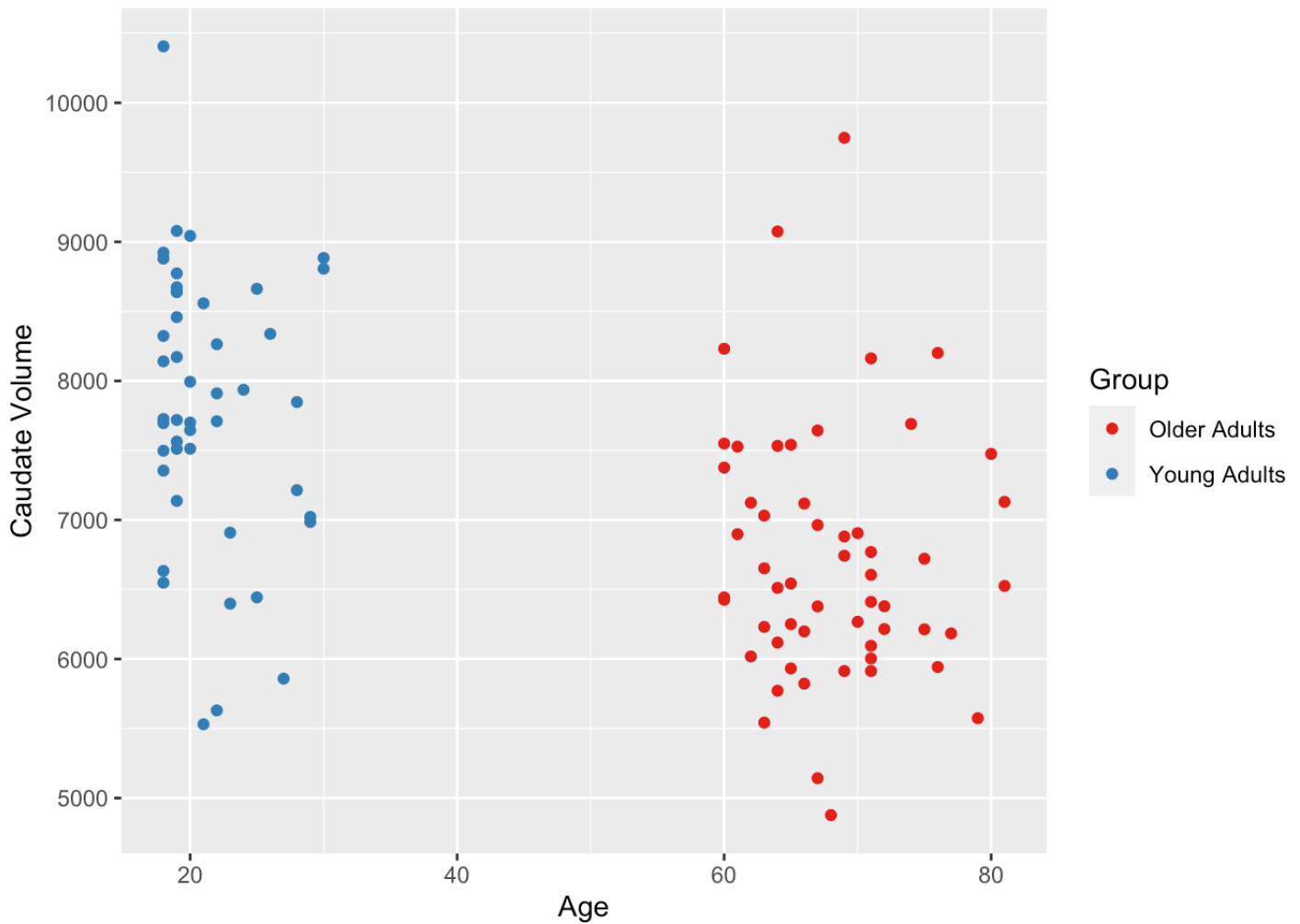
```
df1 %>%
  drop_na(Group) %>%
  ggplot(aes(x = `age`, y = `putamen_vol`, color = `Group`, group = `Group`)) +
  geom_point() +
  scale_color_brewer(palette='Set1') +
  xlab('Age') + ylab('Putamen Volume')
```

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

```
df1 %>%
  drop_na(Group) %>%
  ggplot(aes(x = `age`, y = `caudate_vol`, color = `Group`, group = `Group`)) +
  geom_point() +
  scale_color_brewer(palette='Set1') +
  xlab('Age') + ylab('Caudate Volume')
```

```
## Warning: Removed 2 rows containing missing values (geom_point).
```
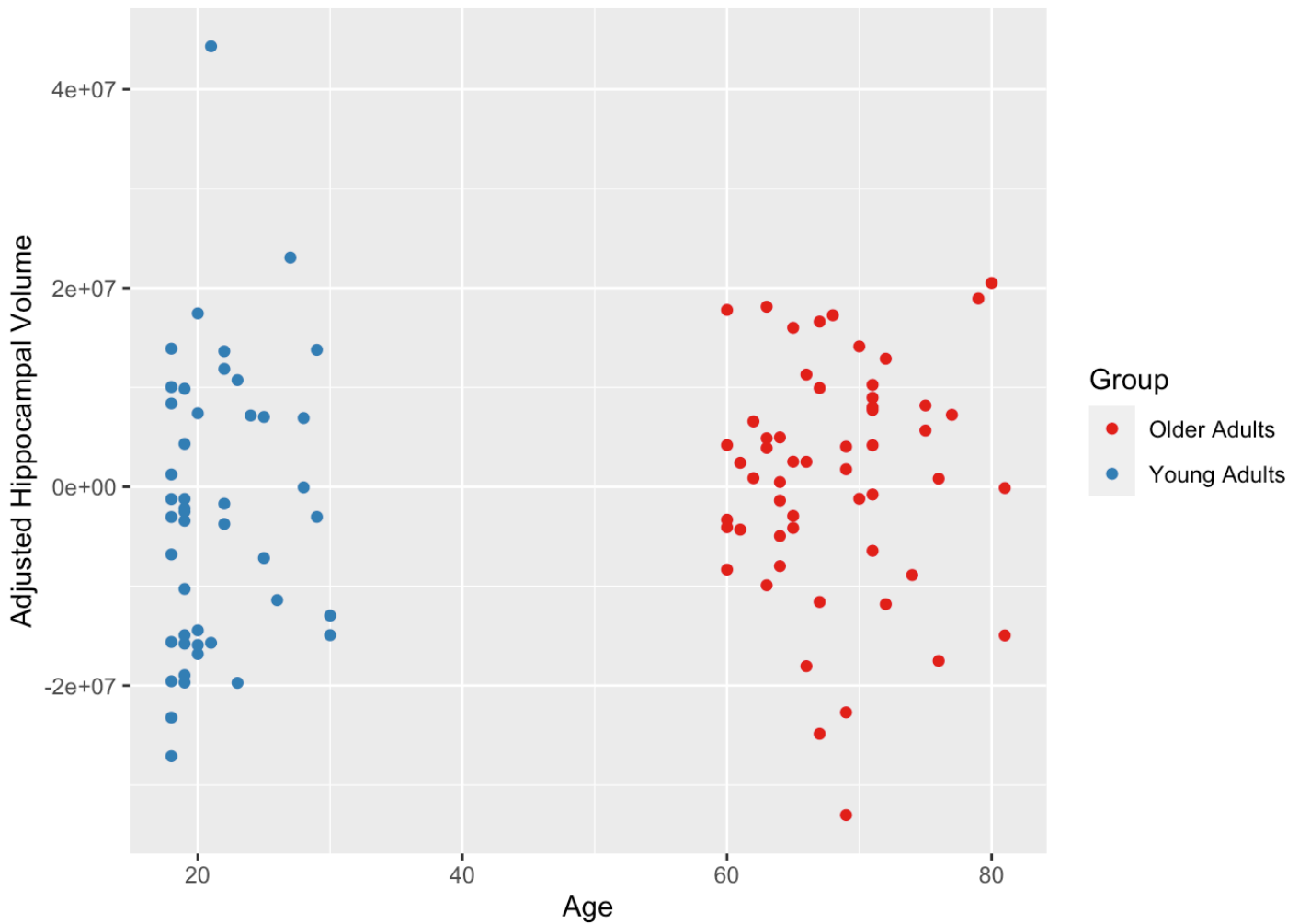
```
df1 %>%
  drop_na(Group) %>%
  ggplot(aes(x = `age`, y = `hc_vol_adj`, color = `Group`, group = `Group`)) +
  geom_point() +
  scale_color_brewer(palette='Set1') +
  xlab('Age') + ylab('Adjusted Hippocampal Volume')
```

```
## Warning: Removed 2 rows containing missing values (geom_point).
```
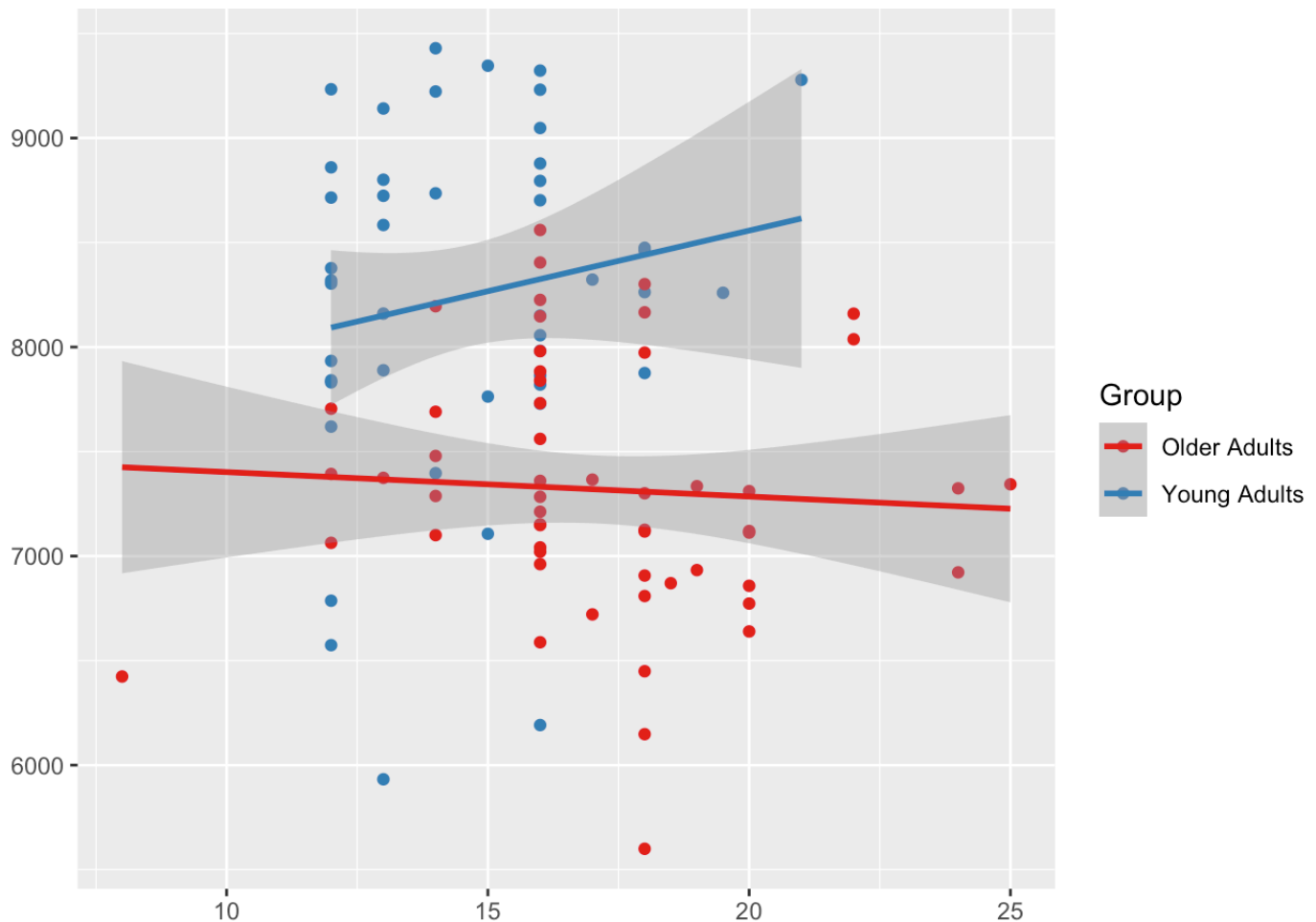
```
df1 %>%
  drop_na(Group) %>%
  ggplot(aes(x = `years_educ`, y = `hc_vol`, color = `Group`, group = `Group`)) +
  geom_point() +
  stat_smooth(method='lm') +
  scale_color_brewer(palette='Set1') +
  xlab('') + ylab('')
```

```
## `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).
```
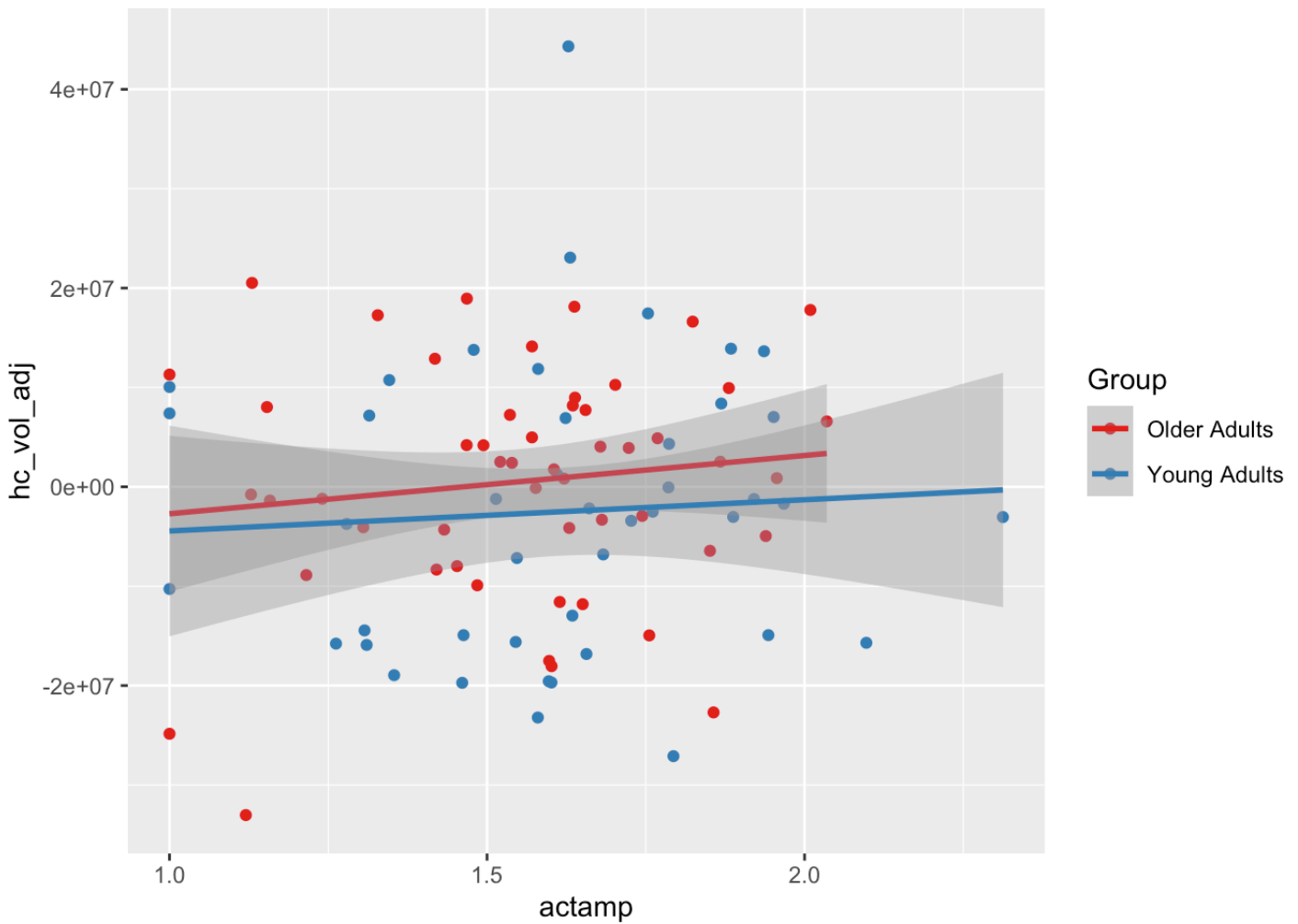
Rest-activity rhythms vs. HC volume

```
df1 %>%
  drop_na(Group) %>%
  filter(actamp < 3) %>%
  ggplot(aes(x = `actamp`, y = `hc_vol_adj`, group = `Group`, color = `Group`)) +
  geom_point() +
  geom_smooth(method = 'lm') +
  scale_color_brewer(palette='Set1')
```

```
## `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).
```

```
df1 %>%
  drop_na(Group) %>%
  filter(actamp < 3) %>%
  ggplot(aes(x = `actamp`, y = `thalamus_vol_adj`, group = `Group`, color = `Group`))
+
  geom_point() +
  geom_smooth(method = 'lm') +
  scale_color_brewer(palette='Set1')
```

```
## `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).
```

```
df1 %>%
  drop_na(Group) %>%
  filter(actamp < 3) %>%
  ggplot(aes(x = `actamp`, y = `putamen_vol_adj`, group = `Group`, color = `Group`))
+
  geom_point() +
  geom_smooth(method = 'lm') +
  scale_color_brewer(palette='Set1')
```
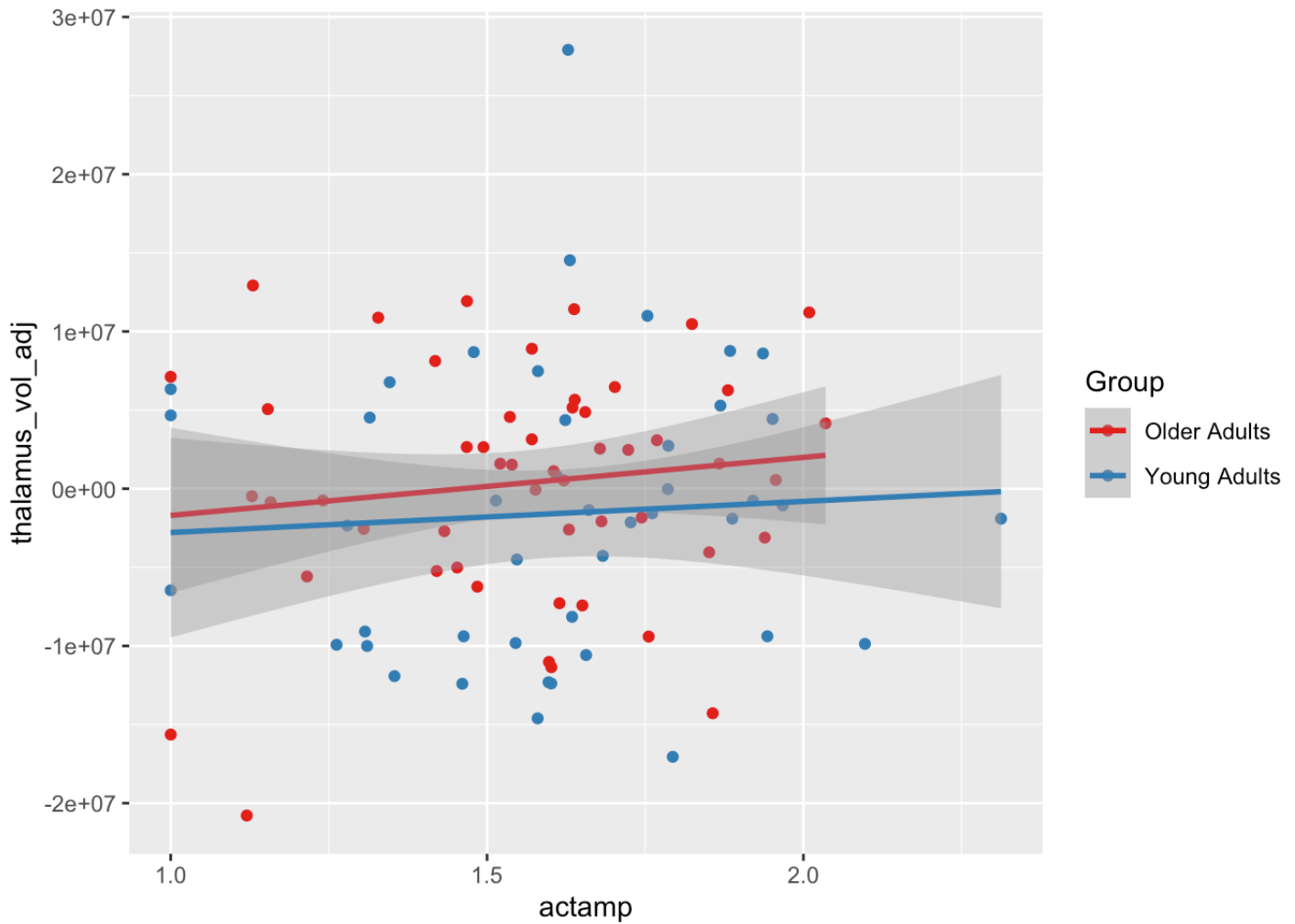
```
## `geom_smooth()` using formula 'y ~ x'
```

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

## Warning: Removed 2 rows containing missing values (geom_point).
```
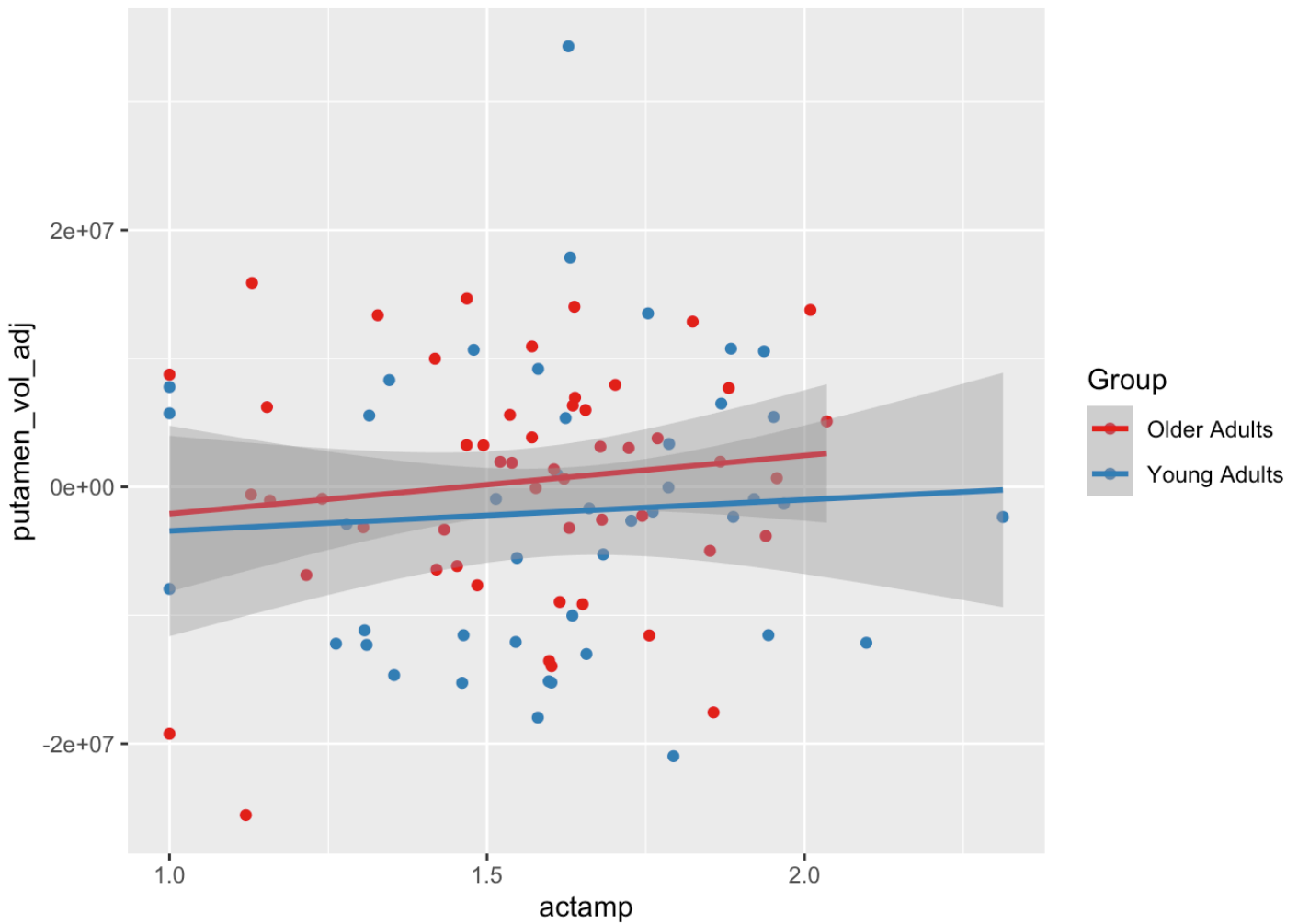
```
df1 %>%
  drop_na(Group) %>%
  filter(actamp < 3) %>%
  ggplot(aes(x = `actamp`, y = `caudate_vol_adj`, group = `Group`, color = `Group`))
+
  geom_point() +
  geom_smooth(method = 'lm') +
  scale_color_brewer(palette='Set1')
```

```
## `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).
```

```
df1$actquot <- df1$actamp / df1$actmesor

df1 %>%
  drop_na(Group) %>%
  filter(actamp < 3) %>%
  ggplot(aes(x = `actquot`, y = `hc_vol_adj`, group = `Group`, color = `Group`))  +
  geom_point() +
  geom_smooth(method = 'lm') +
  scale_color_brewer(palette='Set1')
```

```
## `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).
```
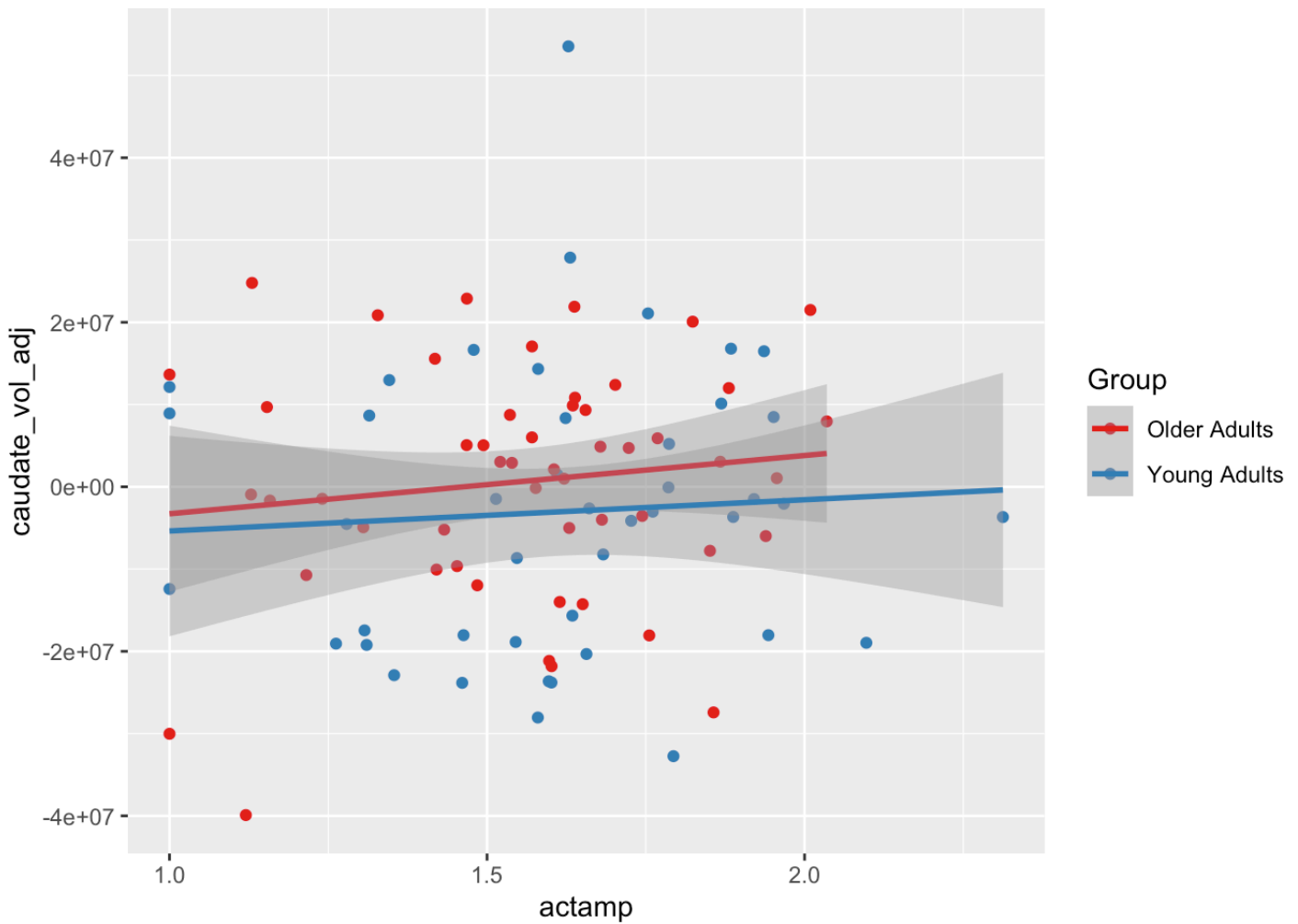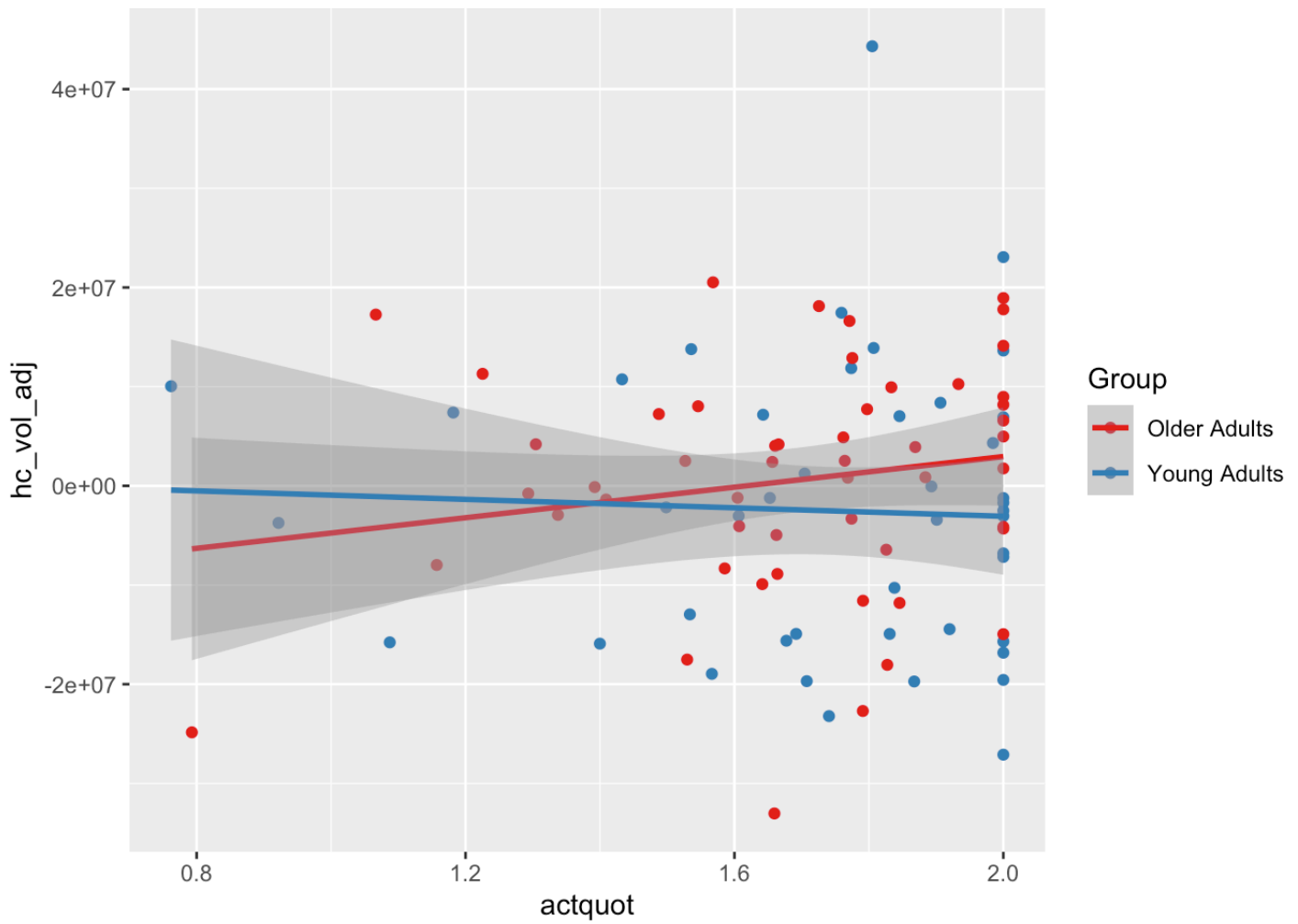
```
summary(lm(hc_vol_adj ~ actquot*Group, data = df1))
```

```
##
## Call:
## lm(formula = hc_vol_adj ~ actquot * Group, data = df1)
##
## Residuals:
##        Min        1Q    Median        3Q       Max
## -33617379  -9501835   1085781   8366718  46978000
##
## Coefficients:
##                            Estimate Std. Error t value Pr(>|t|)
## (Intercept)               -12950133   11455305  -1.130    0.261
## actquot                     8156054    6693129   1.219    0.226
## GroupYoung Adults          14150013   16351587   0.865    0.389
## actquot:GroupYoung Adults -10290755    9411982  -1.093    0.277
##
## Residual standard error: 13060000 on 93 degrees of freedom
##   (22 observations deleted due to missingness)
## Multiple R-squared:  0.03295,    Adjusted R-squared:  0.001756
## F-statistic: 1.056 on 3 and 93 DF,  p-value: 0.3716
```

```
summary(lm(hc_vol_adj ~ actquot + Group, data = df1))
```

```
##
## Call:
## lm(formula = hc_vol_adj ~ actquot + Group, data = df1)
##
## Residuals:
##        Min        1Q    Median        3Q       Max
## -33778518  -9639900     35616   8680319  46637902
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       -4153192    8162627  -0.509    0.612
## actquot            2951980    4710574   0.627    0.532
## GroupYoung Adults -3487895    2675179  -1.304    0.195
##
## Residual standard error: 13070000 on 94 degrees of freedom
##   (22 observations deleted due to missingness)
## Multiple R-squared:  0.02052,    Adjusted R-squared:  -0.0003197
## F-statistic: 0.9847 on 2 and 94 DF,  p-value: 0.3774
```

```
df1 %>%
  drop_na(Group) %>%
  filter(actamp < 3) %>%
  ggplot(aes(x = `fact`, y = `hc_vol_adj`, group = `Group`, color = `Group`))  +
  geom_point() +
  geom_smooth(method = 'lm') +
  scale_color_brewer(palette='Set1')
```

```
## `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).
```
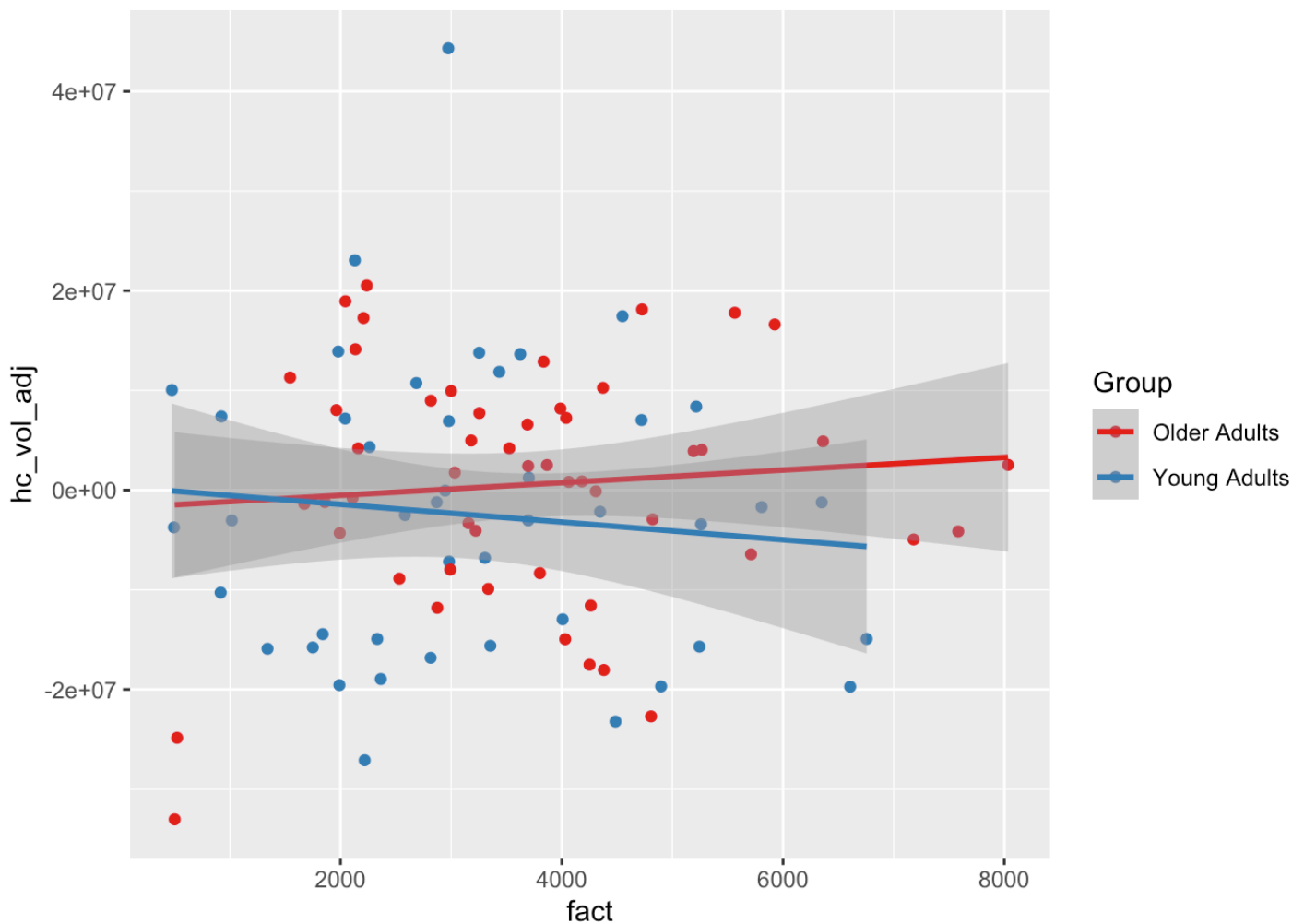
```
df1 %>%
  drop_na(Group) %>%
  filter(actamp < 3) %>%
  ggplot(aes(x = `IS`, y = `hc_vol_adj`, group = `Group`, color = `Group`))  +
  geom_point() +
  geom_smooth(method = 'lm') +
  scale_color_brewer(palette='Set1')
```

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

```
## Warning: Removed 12 rows containing non-finite values (stat_smooth).
```

```
## Warning: Removed 12 rows containing missing values (geom_point).
```

```
df1 %>%
  drop_na(Group) %>%
  filter(actamp < 3) %>%
  ggplot(aes(x = `IS`, y = `thalamus_vol_adj`, group = `Group`, color = `Group`)) +
  geom_point() +
  geom_smooth(method = 'lm') +
  scale_color_brewer(palette='Set1')
```

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

```
## Warning: Removed 12 rows containing non-finite values (stat_smooth).

## Warning: Removed 12 rows containing missing values (geom_point).
```

```
df1 %>%
   drop_na(Group) %>%
   filter(actamp < 3) %>%
   ggplot(aes(x = `IS`, y = `putamen_vol_adj`, group = `Group`, color = `Group`))  +
   geom_point() +
   geom_smooth(method = 'lm') +
   scale_color_brewer(palette='Set1')
```
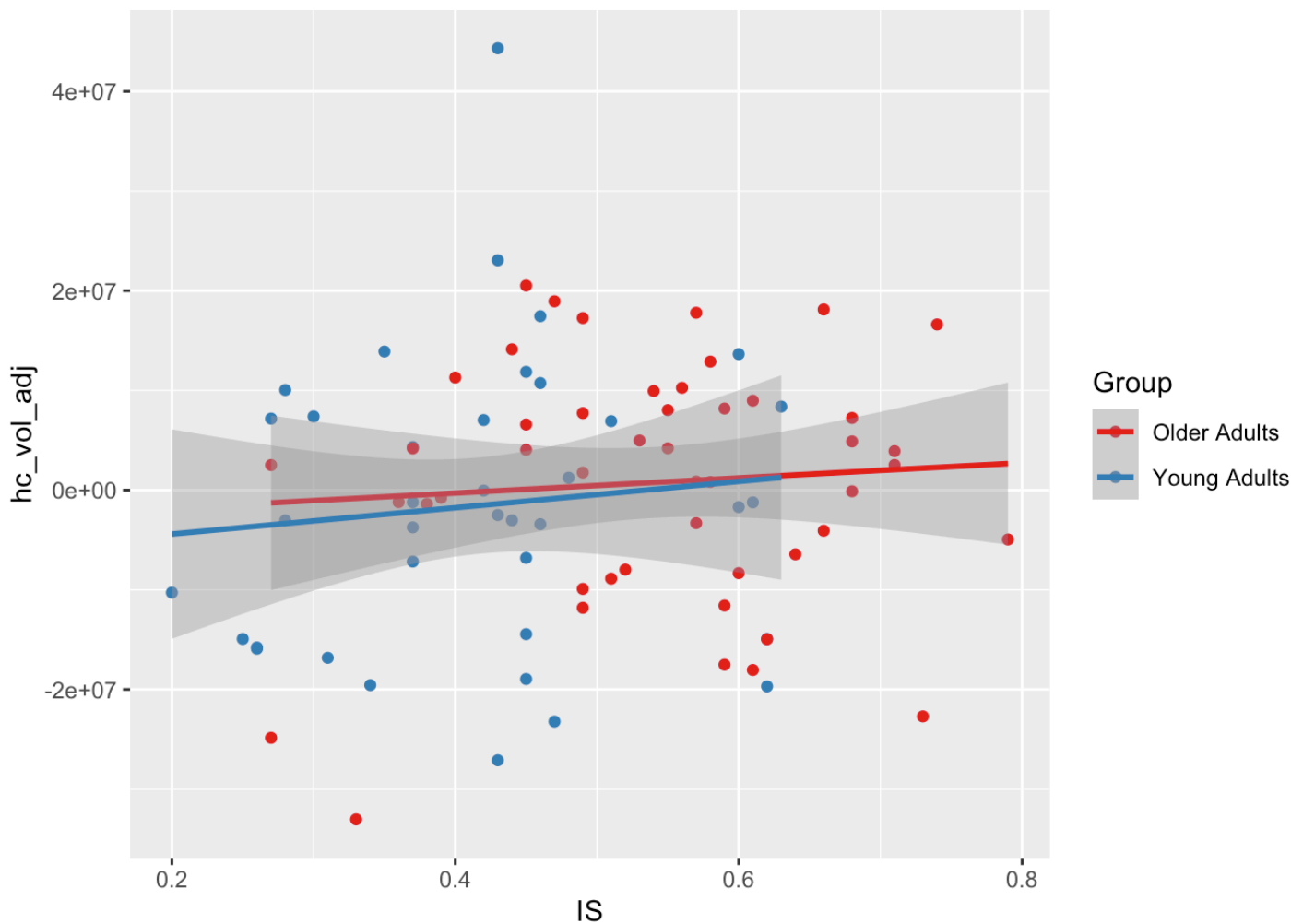
```
## `geom_smooth()` using formula 'y ~ x'
```

```
## Warning: Removed 12 rows containing non-finite values (stat_smooth).

## Warning: Removed 12 rows containing missing values (geom_point).
```
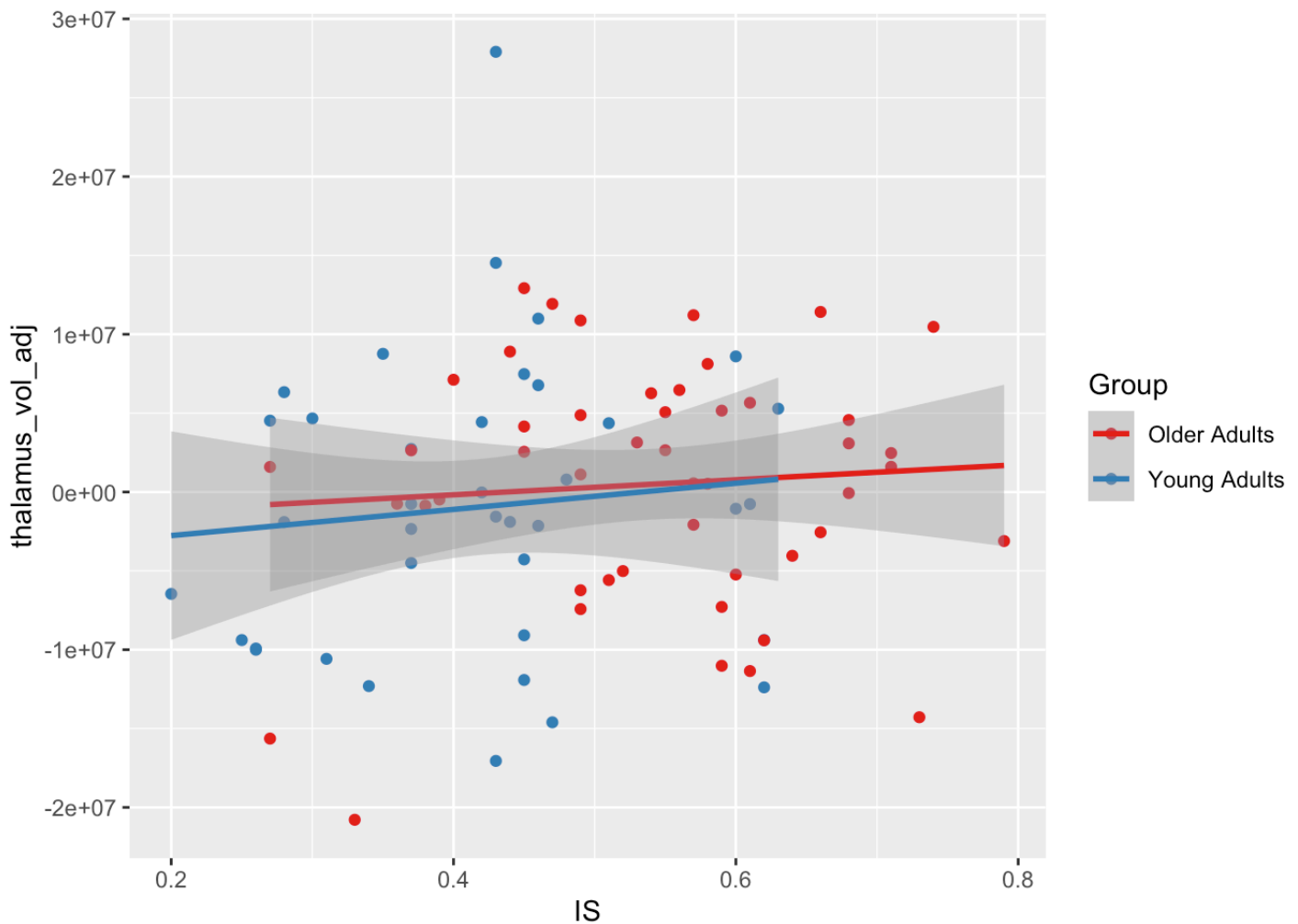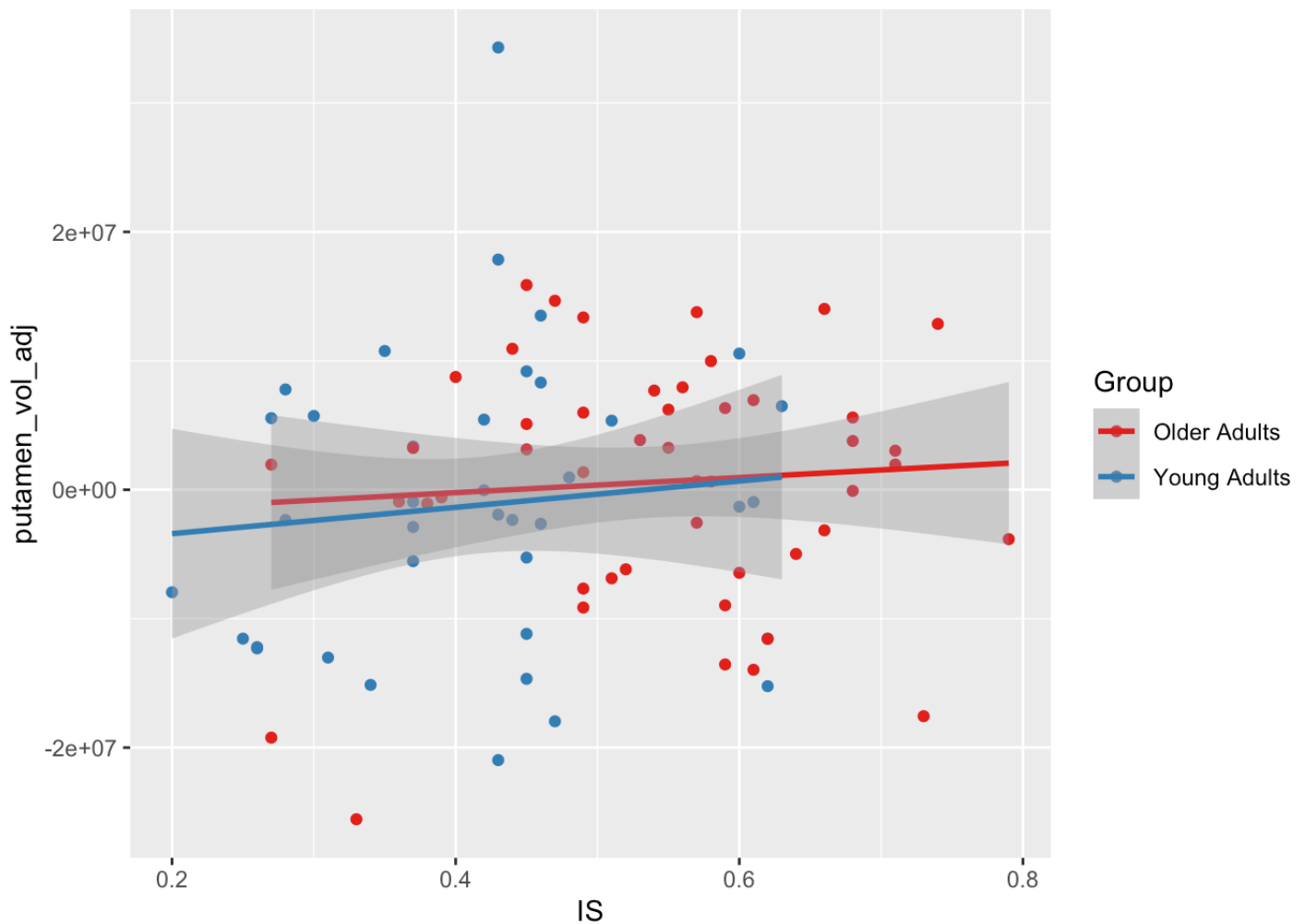
```
df1 %>%
  drop_na(Group) %>%
  filter(actamp < 3) %>%
  ggplot(aes(x = `IS`, y = `caudate_vol_adj`, group = `Group`, color = `Group`))  +
  geom_point() +
  geom_smooth(method = 'lm') +
  scale_color_brewer(palette='Set1')
```

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

```
## Warning: Removed 12 rows containing non-finite values (stat_smooth).

## Warning: Removed 12 rows containing missing values (geom_point).
```

```
df1 %>%
  drop_na(Group) %>%
  filter(actamp < 3) %>%
  ggplot(aes(x = `actupmesor`, y = `hc_vol_adj`, group = `Group`, color = `Group`))
+
  geom_point() +
  geom_smooth(method = 'lm') +
  scale_color_brewer(palette='Set1')
```

```
## `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).
```
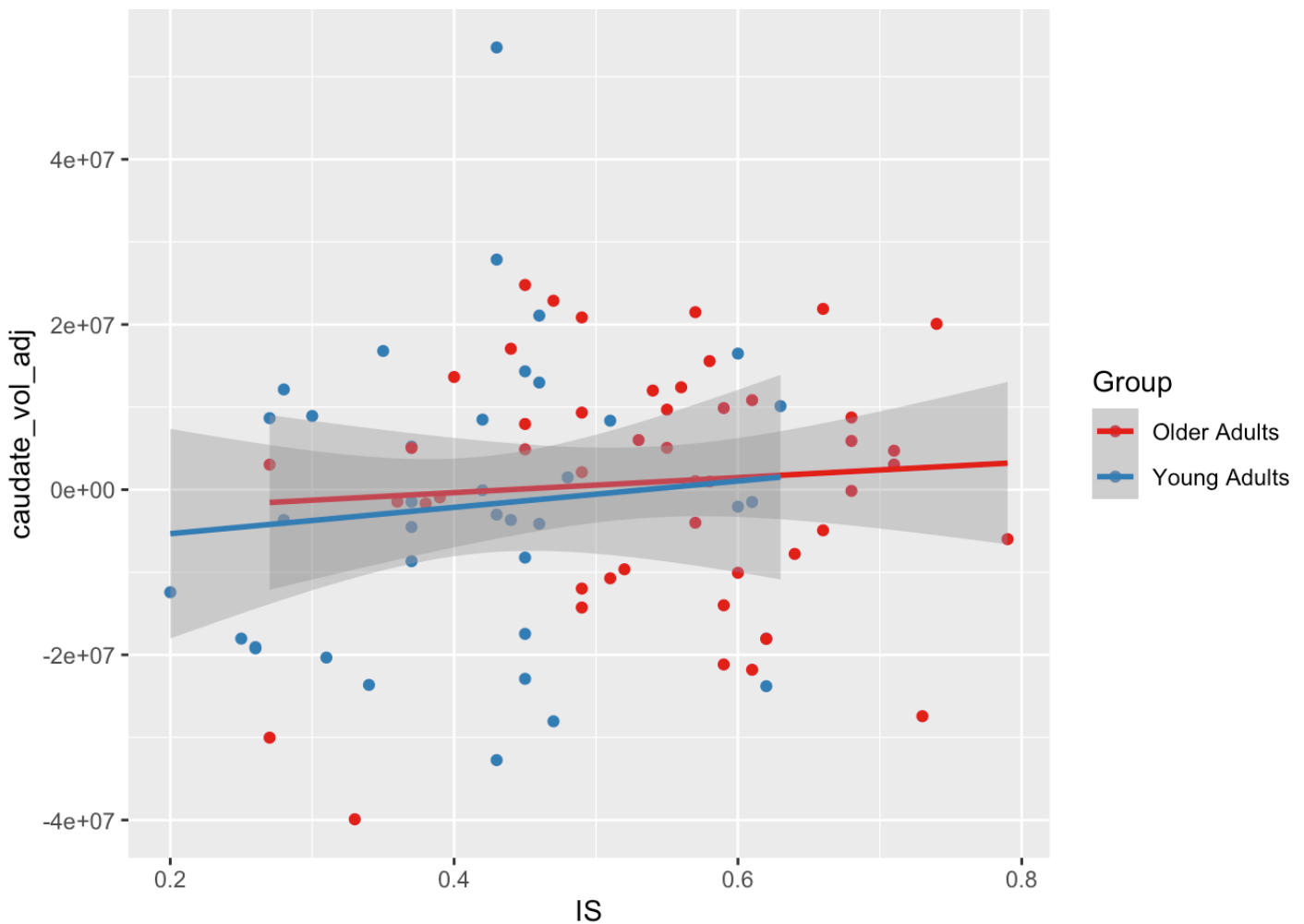
```
df1 %>%
  drop_na(Group) %>%
  filter(actamp < 3) %>%
  ggplot(aes(x = `actupmesor`, y = `thalamus_vol_adj`, group = `Group`, color = `Grou
p`))  +
  geom_point() +
  geom_smooth(method = 'lm') +
  scale_color_brewer(palette='Set1')
```

```
## `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).
```
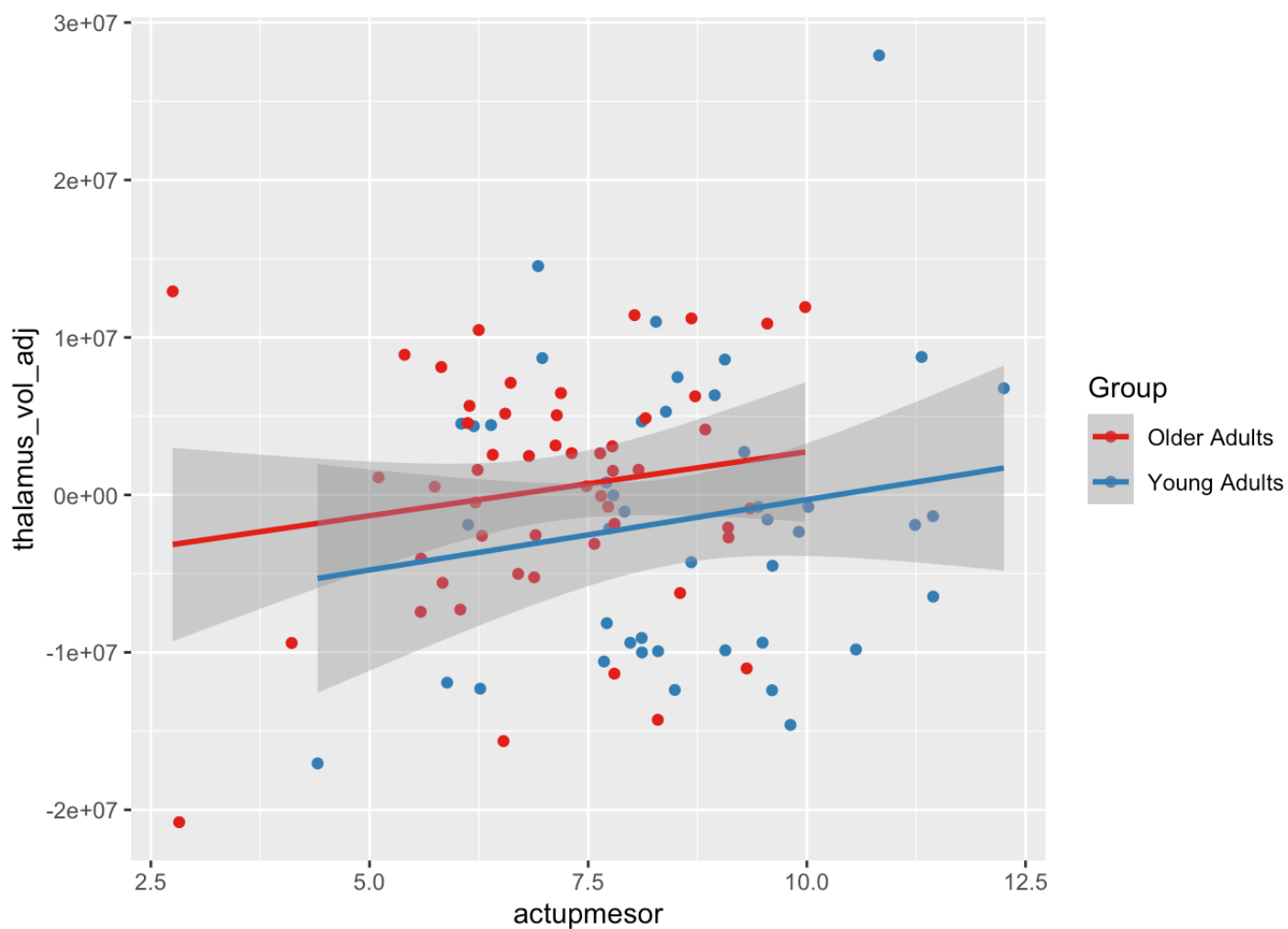
```
df1 %>%
  drop_na(Group) %>%
  filter(actamp < 3) %>%
  ggplot(aes(x = `actupmesor`, y = `caudate_vol_adj`, group = `Group`, color = `Group
`)) +
  geom_point() +
  geom_smooth(method = 'lm') +
  scale_color_brewer(palette='Set1')
```

```
## `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).
```
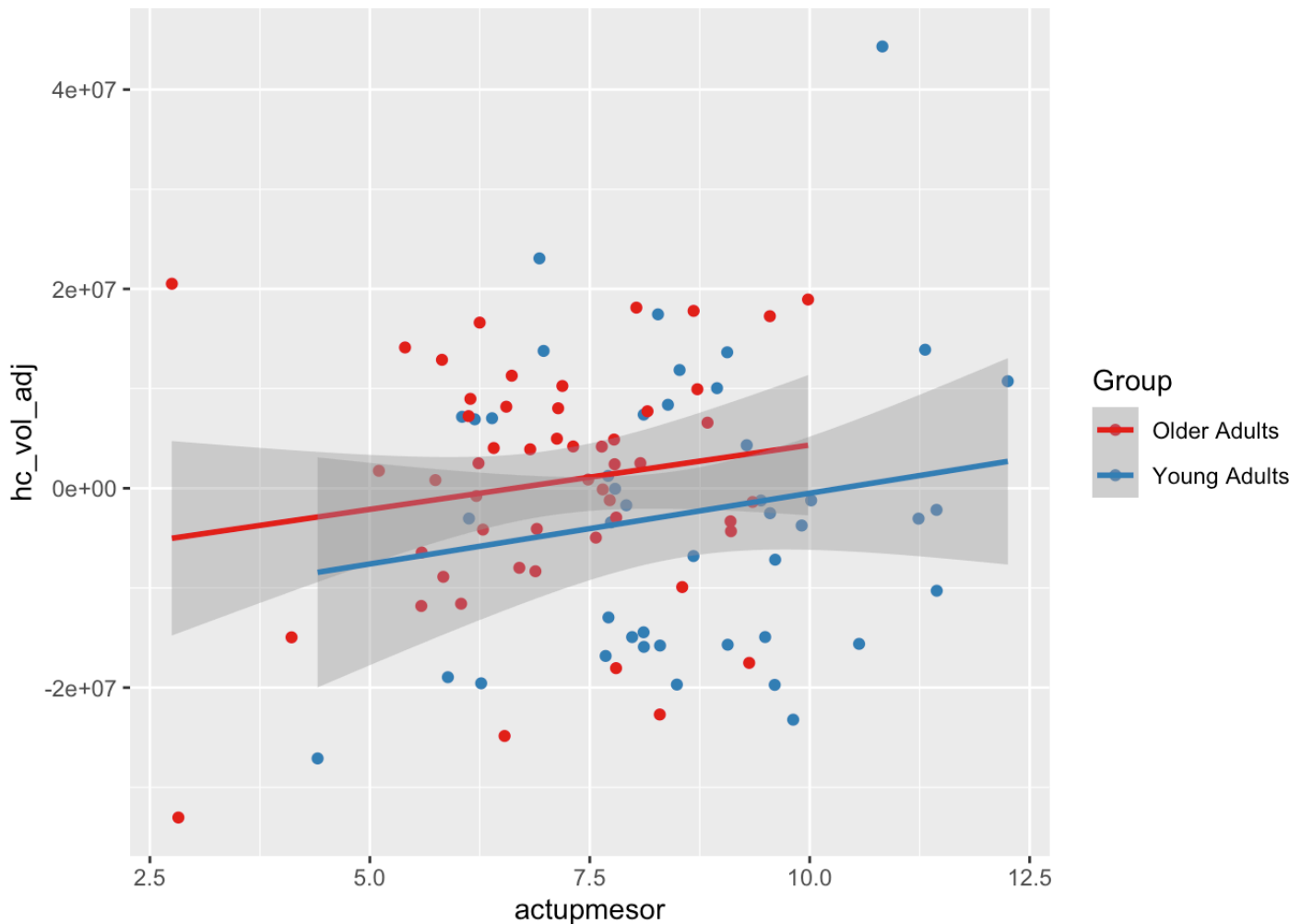
```
df1 %>%
  drop_na(Group) %>%
  filter(actamp < 3) %>%
  ggplot(aes(x = `actupmesor`, y = `putamen_vol_adj`, group = `Group`, color = `Group
`)) +
  geom_point() +
  geom_smooth(method = 'lm') +
  scale_color_brewer(palette='Set1')
```

```
## `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).
```
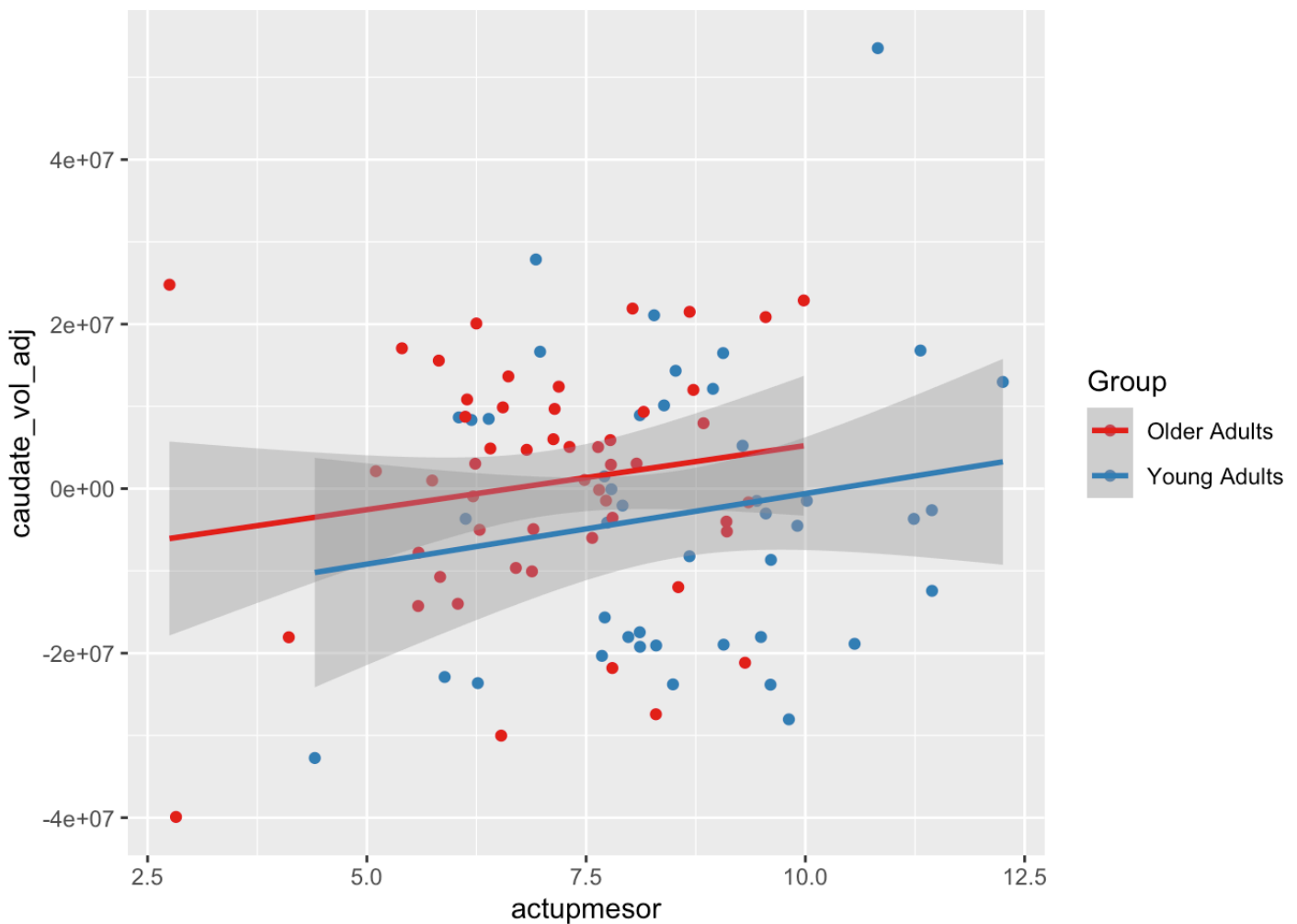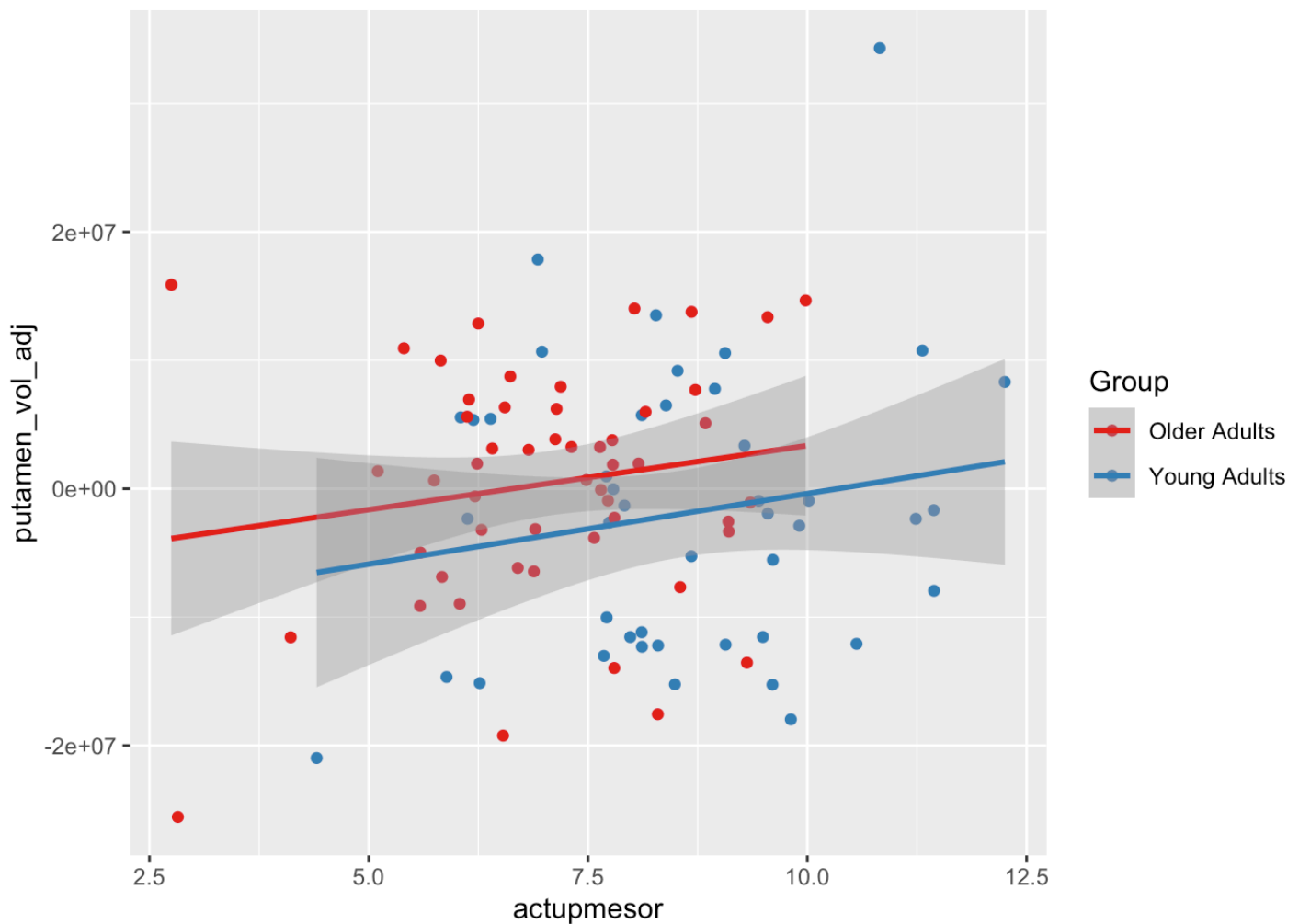


```
summary(lm(thalamus_vol_adj ~ actupmesor*Group, data = df1))
```

```
##
## Call:
## lm(formula = thalamus_vol_adj ~ actupmesor * Group, data = df1)
##
## Residuals:
##       Min        1Q    Median        3Q       Max
## -17002878  -5802003    174665   5247313  27477524
##
## Coefficients:
##                              Estimate Std. Error t value Pr(>|t|)
## (Intercept)                  -6579547    4747754  -1.386    0.169
## actupmesor                     990839     642712   1.542    0.127
## GroupYoung Adults            -2657221    7871395  -0.338    0.736
## actupmesor:GroupYoung Adults   -97468     963304  -0.101    0.920
##
## Residual standard error: 8119000 on 93 degrees of freedom
##   (22 observations deleted due to missingness)
## Multiple R-squared:  0.05625,    Adjusted R-squared:  0.0258
## F-statistic: 1.848 on 3 and 93 DF,  p-value: 0.144
```

```
summary(lm(thalamus_vol_adj ~ actupmesor + Group, data = df1))
```

```
##
## Call:
## lm(formula = thalamus_vol_adj ~ actupmesor + Group, data = df1)
##
## Residuals:
##       Min        1Q    Median        3Q       Max
## -17191904  -5754984    213491   5220003  27356171
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       -6268008    3594878  -1.744   0.0845 .
## actupmesor          947451     476218   1.990   0.0495 *
## GroupYoung Adults -3432864    1777279  -1.932   0.0564 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 8077000 on 94 degrees of freedom
##   (22 observations deleted due to missingness)
## Multiple R-squared:  0.05614,    Adjusted R-squared:  0.03606
## F-statistic: 2.796 on 2 and 94 DF,  p-value: 0.06616
```

```
df1 %>%
  drop_na(Group) %>%
  filter(RA > 0.4) %>%
  ggplot(aes(x = `RA`, y = `hc_vol_adj`, group = `Group`, color = `Group`))  +
  geom_point() +
  geom_smooth(method = 'lm') +
  scale_color_brewer(palette='Set1')
```

```
## `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).
```



```
summary(lm(hc_vol_adj ~ RA*Group, data = df1))
```
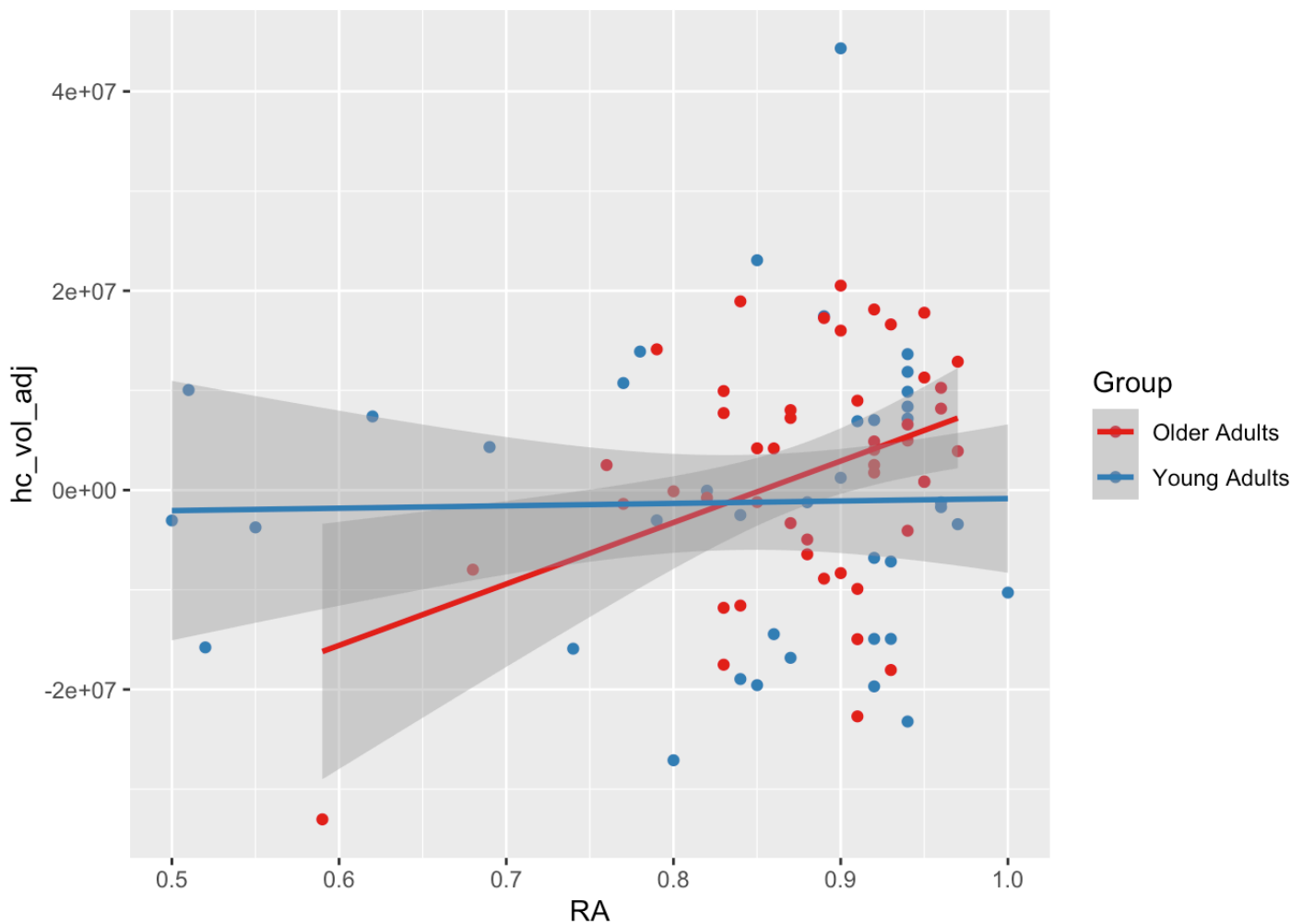
```
##
## Call:
## lm(formula = hc_vol_adj ~ RA * Group, data = df1)
##
## Residuals:
##       Min       1Q    Median        3Q       Max
## -26173471  -9337240    403594   8091913  45415209
##
## Coefficients:
##                          Estimate Std. Error t value Pr(>|t|)
## (Intercept)            -49938845   15871202  -3.147  0.00229 **
## RA                      58693113   18136831   3.236  0.00173 **
## GroupYoung Adults       46673756   20451672   2.282  0.02501 *
## RA:GroupYoung Adults   -56276680   23644469  -2.380  0.01957 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 12650000 on 84 degrees of freedom
##   (31 observations deleted due to missingness)
## Multiple R-squared:  0.1179, Adjusted R-squared:  0.08643
## F-statistic: 3.744 on 3 and 84 DF,  p-value: 0.01408
```

```
summary(lm(hc_vol_adj ~ RA*Group, data = filter(df1, RA > 0.4)))
```

```
##
## Call:
## lm(formula = hc_vol_adj ~ RA * Group, data = filter(df1, RA >
##     0.4))
##
## Residuals:
##       Min        1Q    Median        3Q       Max
## -26230752  -9441344    -78761   8195724  45415209
##
## Coefficients:
##                        Estimate Std. Error t value Pr(>|t|)
## (Intercept)          -52561249   21945522  -2.395   0.0189 *
## RA                    61637823   24874135   2.478   0.0152 *
## GroupYoung Adults     49296161   25493623   1.934   0.0566 .
## RA:GroupYoung Adults -59221390   29180923  -2.029   0.0456 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 12730000 on 83 degrees of freedom
##    (2 observations deleted due to missingness)
## Multiple R-squared:  0.08039,    Adjusted R-squared:  0.04715
## F-statistic: 2.419 on 3 and 83 DF,  p-value: 0.07198
```

```
summary(lm(hc_vol_adj ~ RA + age, data = filter(df1, Group == 'Older Adults')))
```

```
##
## Call:
## lm(formula = hc_vol_adj ~ RA + age, data = filter(df1, Group ==
##     "Older Adults"))
##
## Residuals:
##        Min        1Q    Median        3Q       Max
## -26248694  -6212114   1367706   5698632  18487618
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept) -57317753   23849834  -2.403  0.02034 *
## RA           59037132   15647286   3.773  0.00046 ***
## age            103494     274115   0.378  0.70750
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 10900000 on 46 degrees of freedom
##   (8 observations deleted due to missingness)
## Multiple R-squared:  0.2366, Adjusted R-squared:  0.2035
## F-statistic:  7.13 on 2 and 46 DF,  p-value: 0.002008
```

```
summary(lm(hc_vol_adj ~ RA + age, data = filter(df1, Group == 'Young Adults')))
```

```
##
## Call:
## lm(formula = hc_vol_adj ~ RA + age, data = filter(df1, Group ==
##     "Young Adults"))
##
## Residuals:
##        Min        1Q    Median        3Q       Max
## -23324752 -12138040    445111   9733646  45585701
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept) -18738110   19221532  -0.975    0.336
## RA            -781417   17633849  -0.044    0.965
## age            865743     683564   1.267    0.213
##
## Residual standard error: 14560000 on 36 degrees of freedom
##   (7 observations deleted due to missingness)
## Multiple R-squared:  0.04314,    Adjusted R-squared:  -0.01001
## F-statistic: 0.8116 on 2 and 36 DF,  p-value: 0.4521
```
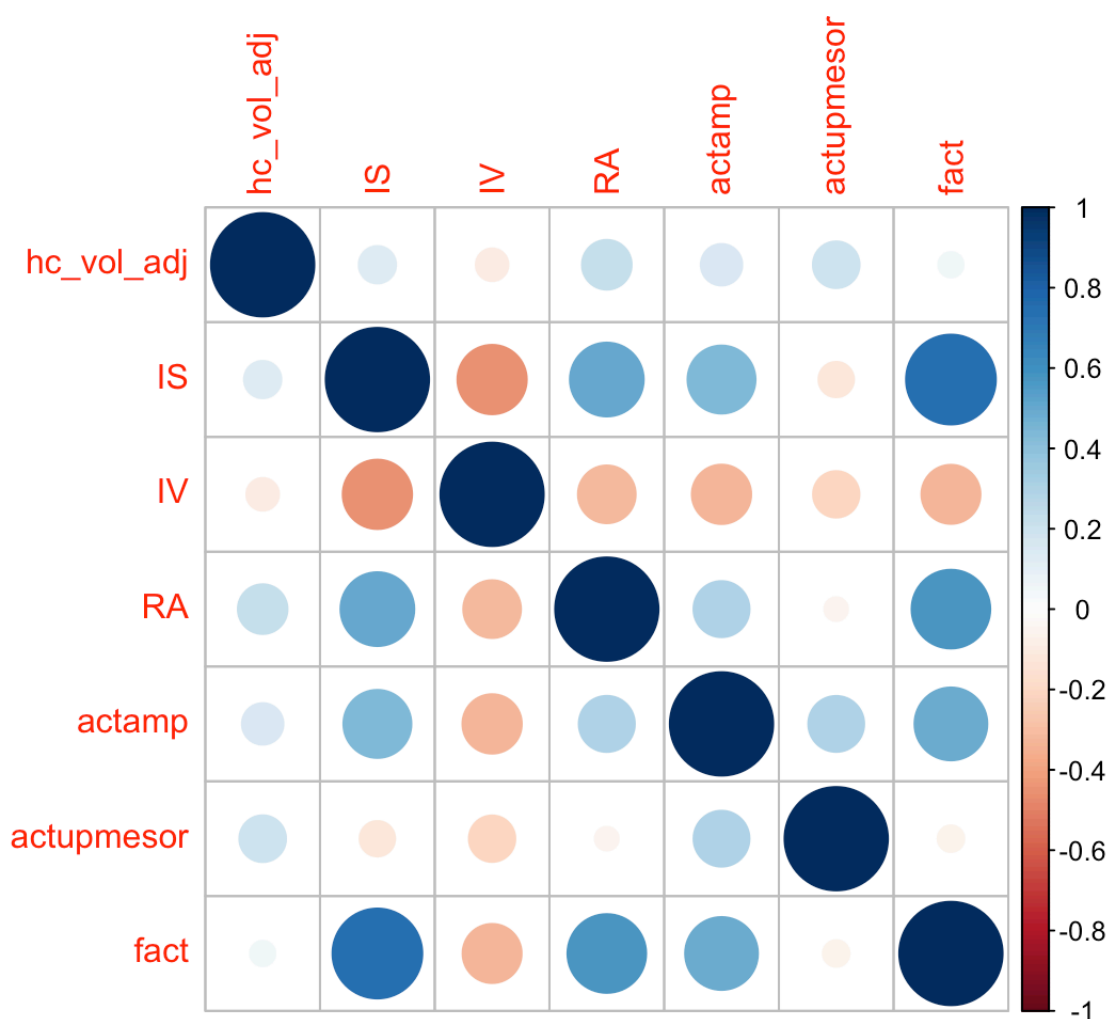
Correlation plots

```
library(corrplot)
```

```
## corrplot 0.84 loaded
```

```
cordf <- select(df1, hc_vol_adj, IS:RA, actamp, actupmesor, fact)
cordf1 <- dplyr::mutate_all(cordf, function(x) as.numeric(as.character(x)))
cordf1 <- cordf1[complete.cases(cordf1),]

cordft <- cor(cordf1, use = 'all.obs')
corrplot(cordft)
```

```
cordf <- df1 %>%
    filter(Group == 'Older Adults') %>%
    select(hc_vol_adj, IS:RA, actamp, actupmesor, fact)

cordf1 <- dplyr::mutate_all(cordf, function(x) as.numeric(as.character(x)))
cordf1 <- cordf1[complete.cases(cordf1),]

cordft <- cor(cordf, use = 'complete.obs')
corrplot(cordft)
```
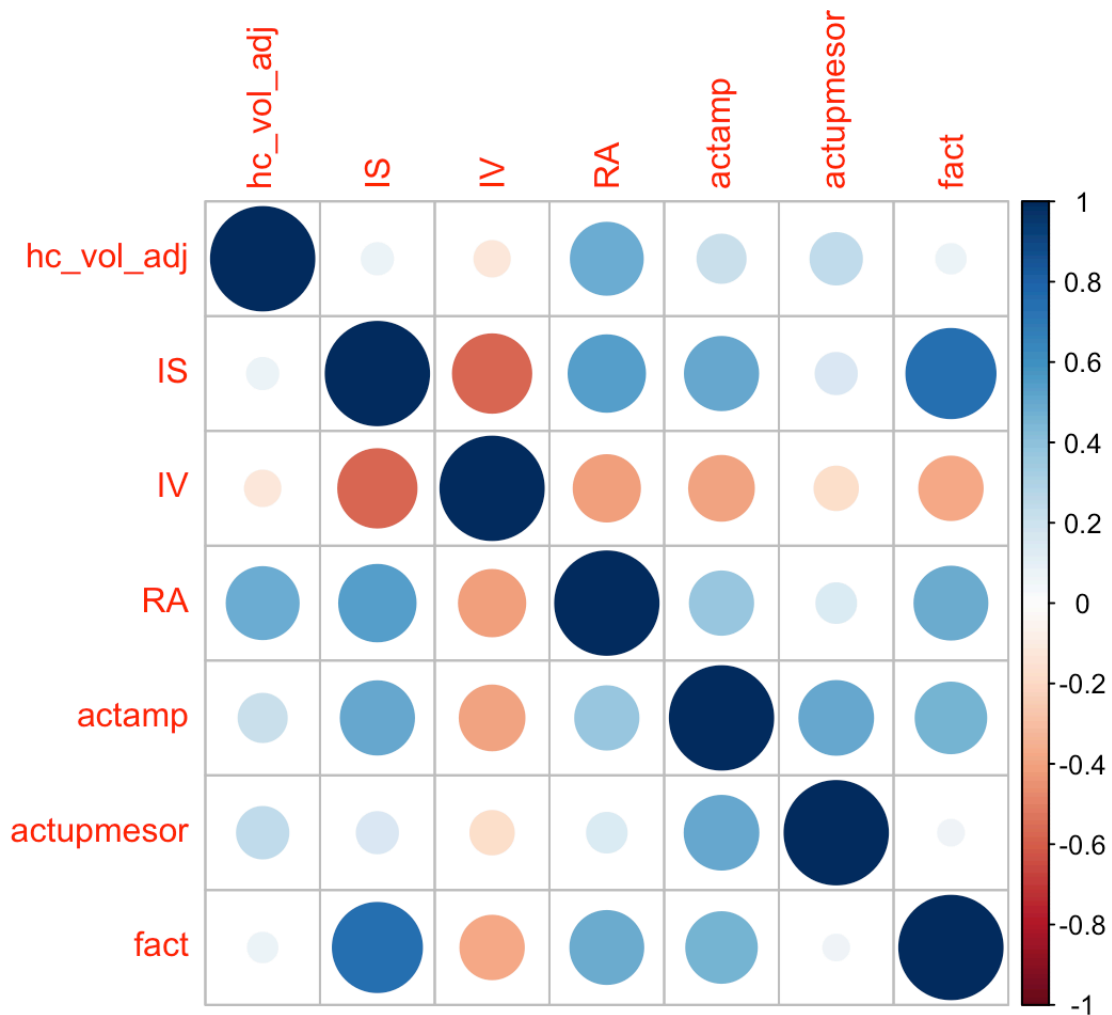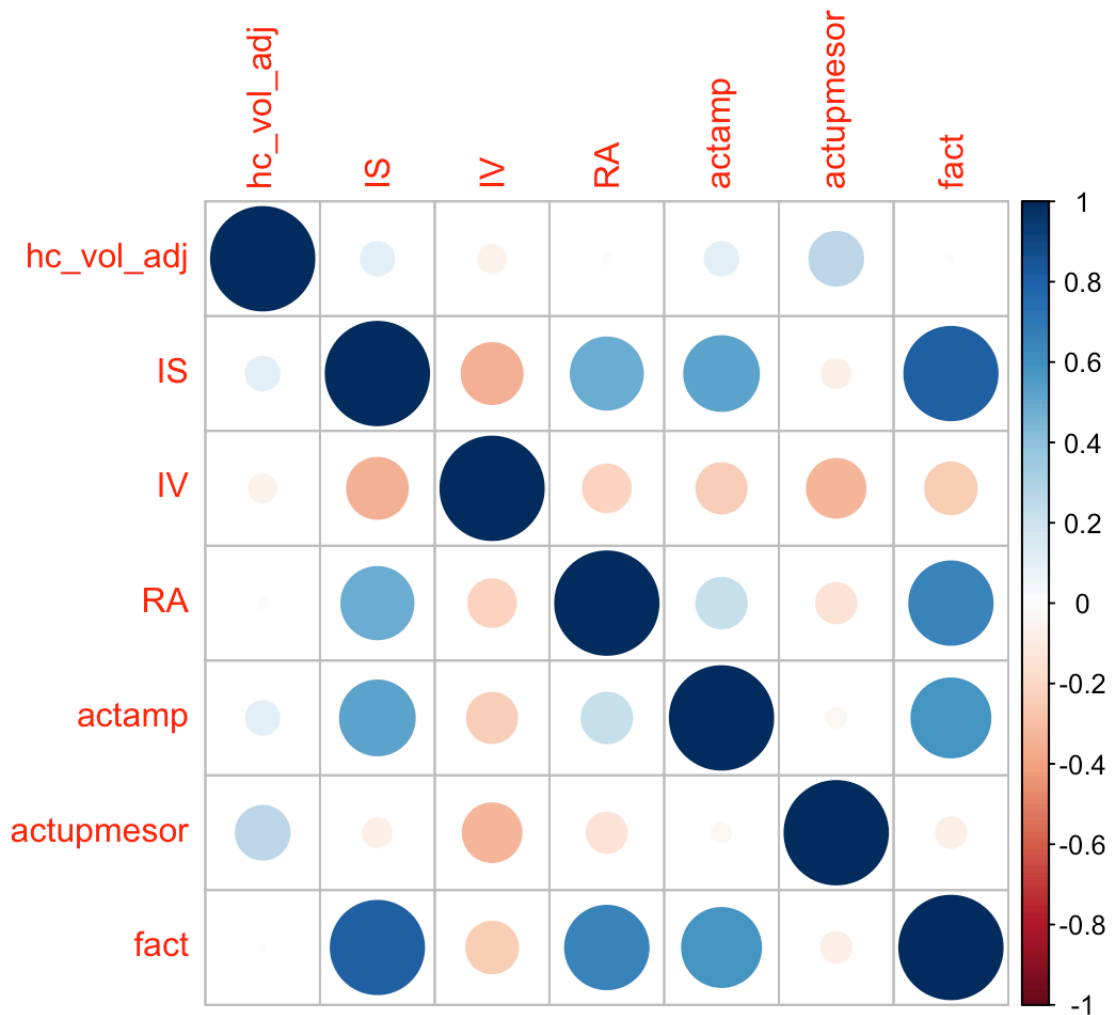
```
cordf <- df1 %>%
    filter(Group == 'Young Adults') %>%
    select(hc_vol_adj, IS:RA, actamp, actupmesor, fact)

cordf1 <- dplyr::mutate_all(cordf, function(x) as.numeric(as.character(x)))
cordf1 <- cordf1[complete.cases(cordf1),]

cordft <- cor(cordf, use = 'complete.obs')
corrplot(cordft)
```

```
library(corrr)

fsvol %>%
  merge(select(df, record_id, cvlt_zscore, cvlt_ldelay_recall, cvlt_sdelay_recall, cv
lt_listb, cvlt_recognition_hits, cvlt_recognition_fp), by='record_id') %>%
  select(-record_id, -`Measure:volume`) %>%
  corrr::correlate() %>%
  focus(cvlt_zscore, cvlt_ldelay_recall, cvlt_sdelay_recall, cvlt_listb, cvlt_recogni
tion_hits, cvlt_recognition_fp) %>%
  arrange(desc(cvlt_ldelay_recall))
```

```
## Warning in stats::cor(x = x, y = y, use = use, method = method): the standard
## deviation is zero
```

```
##
## Correlation method: 'pearson'
## Missing treated using: 'pairwise.complete.obs'
```

```
## # A tibble: 66 x 7
##    term             cvlt_zscore cvlt_ldelay_reca… cvlt_sdelay_reca… cvlt_listb
##    <chr>                  <dbl>             <dbl>             <dbl>      <dbl>
##  1 Right-Accumbens-a…    0.191             0.309             0.300    0.00796
##  2 Right-vessel         0.0858             0.273             0.247     -0.289
##  3 CC_Mid_Anterior       0.184             0.211             0.183      0.232
##  4 Left-Amygdala         0.212             0.184             0.109     0.0786
##  5 CC_Posterior          0.218             0.183             0.151      0.244
##  6 Right-Cerebellum-…    0.235             0.175            0.0913    -0.0850
##  7 Right-Hippocampus     0.126             0.160            0.0582      0.175
##  8 CC_Anterior           0.145             0.151             0.131      0.120
##  9 Left-Cerebellum-C…    0.167             0.138            0.0726    -0.0545
## 10 CC_Central            0.144             0.133             0.131      0.229
## # … with 56 more rows, and 2 more variables: cvlt_recognition_hits <dbl>,
## #   cvlt_recognition_fp <dbl>
```

```
df1$sex
```

```
##   [1] "Female" "Female" "Female" "Male"   "Male"   "Female" "Female" "Male"
##   [9] "Female" "Female" "Male"   "Female" "Male"   "Female" "Female" "Male"
##  [17] "Female" "Female" "Male"   "Female" NA       "Female" "Male"   "Male"
##  [25] "Male"   "Male"   "Male"   NA       "Female" "Female" "Female" "Male"
##  [33] NA       "Female" NA       "Female" "Female" "Male"   "Male"   "Female"
##  [41] NA       "Female" NA       "Female" "Female" NA       "Female" "Male"
##  [49] NA       "Male"   "Female" NA       "Female" "Female" "Male"   "Female"
##  [57] "Female" "Female" "Female" "Female" "Female" "Male"   NA       "Female"
##  [65] NA       NA       "Female" "Female" "Female" "Female" "Female" "Female"
##  [73] "Female" "Female" "Female" "Female" "Male"   "Female" "Female" "Female"
##  [81] "Female" "Female" "Male"   "Female" "Male"   "Female" "Female" "Female"
##  [89] "Female" "Female" "Female" "Female" "Female" "Female" "Female" NA
##  [97] "Female" "Female" "Female" "Male"   "Female" "Female" "Male"   "Female"
## [105] "Male"   "Female" "Female" "Male"   "Female" "Female" "Female" "Male"
## [113] "Male"   NA       NA       "Male"   "Female" "Male"   NA
```