

Reanalysis of 06-Wile

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Reference

Wile et al. (2017). Serotonin and dopamine transporter PET changes in the premotor phase of LRRK2 parkinsonism: cross-sectional studies. *Lancet Neurology*, 16(5), 351–359. [https://doi.org/10.1016/S1474-4422\(17\)30056-X](https://doi.org/10.1016/S1474-4422(17)30056-X)

Notes from reading methods section

- Dependant variable: 11C-DASB in cortex (first of many ANCOVAs reported)
- Independent variable: Group
 - Healthy controls (n=9)
 - LRRK2 w/o PD (n=9)
 - LRRK2 w PD (n=7)
 - sporadic PD (n=13)
- Covariate: age
- age was not estimable for LRRK2 without manifest Parkinson's disease
- Design: 4-way ANCOVA with group as IV and age as covariate

Loading data

Data is loaded, reshaped if necessary, and factors are specified.

```
PATH = file.path(path.expand("~/"), "Data", "ancova") # ancova project folder
data = read_excel(file.path(PATH, "dataPrimaryStudies", "06-Wile", "06-Wile.xlsx"))

# group variable is dummy coded, key for AncovaVariable file
# 0 = healthy control, 1 = LRRK2 premanifest, 2 = LRRK2 affected, 3 = sporadic PD
data$Group.factor = NA
data$Group.factor[data$Group == 0] = "healthy control"
data$Group.factor[data$Group == 1] = "LRRK2 premanifest"
data$Group.factor[data$Group == 2] = "LRRK2 affected"
data$Group.factor[data$Group == 3] = "sporadic PD"
data$Group.factor = factor(data$Group.factor,
                           levels = c("healthy control", "LRRK2 premanifest",
                                       "LRRK2 affected", "sporadic PD"))
```

Descriptives

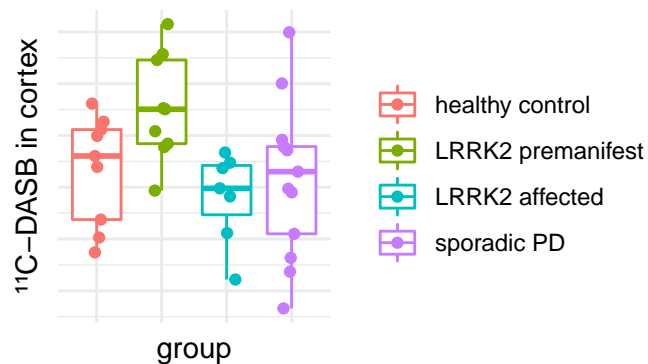
Number of samples and mean (SD) in levels of the independent variables. See Table 3 in publication.

```
idx = c(1, 3, 2, 4) # sorting as in publication
tab1 = array(NA, dim=c(4,3))
tab1[,1] = levels(data$Group.factor)
tab1[,2] = summary(data$Group.factor)
tab1[,3] = tapply(data$Cortex, data$Group.factor,
                  function(x) sprintf("%.2f (%.2f)", mean(x), sd(x)))
colnames(tab1) = c("group", "n", "mean (SD)")
print(tab1)
```

```
##      group      n    mean (SD)
## [1,] "healthy control"  "9"  "0.43 (0.10)"
## [2,] "LRRK2 premanifest" "9"  "0.55 (0.10)"
## [3,] "LRRK2 affected"   "7"  "0.38 (0.09)"
## [4,] "sporadic PD"      "13" "0.42 (0.15)"
```

Figure 2 in Publication

```
ggplot(data, aes(y=Cortex, x=Group.factor, color=Group.factor)) +
  geom_boxplot() +
  geom_point(position = position_jitter(width = 0.15, height = 0)) +
  theme_minimal() +
  theme(axis.text = element_blank(), legend.title = element_blank()) +
  xlab("group") + ylab("'11C-DASB in cortex")
```



ANCOVA

```
fit = aov(Cortex ~ Group.factor + `Age at PET`, data = data)

# Type I SS are appropriate for balanced (equal n per group)
# Type II SS are used by SAS and SPSS and appropriate for unbalanced designs
# result = summary(fit) # Type I
result = Anova(fit, type=3) # Type III
print(result)

## Anova Table (Type III tests)
##
## Response: Cortex
```

```
##              Sum Sq Df F value    Pr(>F)
## (Intercept)  0.30582  1 21.1500 5.984e-05 ***
## Group.factor 0.12125  3  2.7951  0.0555 .
## `Age at PET` 0.00073  1  0.0502  0.8241
## Residuals    0.47717 33
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# For Type I SS
# stats.reanalysis = data.frame(Fvalue = sprintf("%.2f",result[[1]]$`F value`[1]),
#                                df1 = result[[1]]$Df[1],
#                                df2 = result[[1]]$Df[2],
#                                pvalue = formatPval(result[[1]]$`Pr(>F)`[1]))

# For Type III SS
stats.rep.IV = data.frame(Fvalue = sprintf("%.2f",result$`F value`[2]),
                          df1 = result$Df[2],
                          df2 = result$Df[4],
                          pvalue = formatPval(result$`Pr(>F)`[2]))

stats.rep.CV = data.frame(Fvalue = sprintf("%.2f",result$`F value`[3]),
                          df1 = result$Df[3],
                          df2 = result$Df[4],
                          pvalue = formatPval(result$`Pr(>F)`[3]))
```

Comparing ANCOVA in original study with reanalysis

Independant variable

```
tab.IV = rbind(stats.orig.IV, stats.rep.IV)
rownames(tab.IV) = c("original Study", "reanalysis")
print(t(tab.IV))
```

```
##          original Study reanalysis
## Fvalue NA              "2.80"
## df1    NA              " 3"
## df2    NA              "33"
## pvalue "0.026"         "0.056"
```

Covariate

```
tab.CV = rbind(stats.orig.CV, stats.rep.CV)
rownames(tab.CV) = c("original Study", "reanalysis")
print(t(tab.CV))
```

```
##          original Study reanalysis
## Fvalue NA              "0.05"
## df1    NA              " 1"
## df2    NA              "33"
## pvalue NA              "0.82"
```