FMPH221 Project Report Code

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Functions

```r
# used to scale data to 0 to 1 [later important for log transformation]
normalize <- function(x) {
    (x - min(x)) / (max(x) - min(x))
}
```

Data and key

```r
neuromaps_df <- read.csv("../data/neuromaps-mni152_y-siips_res-basc444.csv")
neuromaps_df <- apply(neuromaps_df, 2, normalize) |> as.data.frame()
neuromaps_key <- read.csv("../data/neuromaps-key.csv")
```

Log transforming the skewed variables

Chosen by a visual inspection of each histogram

```r
logcols <- c(
    "aghourian2017.feobv",
    "bedard2019.feobv",
    "gallezot2010.p943",
    "jaworska2020.fallypride",
    "sandiego2015.flb457",
    "sasaki2012.fepe2i",
    "tuominen.feobv"
)
neuromaps_df[logcols] <- log(neuromaps_df[logcols] + 1)
```

Principal Component Analyses to reduce collinearity and dimensionality

Many of the predictors are measuring the same thing, at least at the resolution we're working with

```r
neuromaps_pca <- data.frame(siips = neuromaps_df$siips)

for (group in unique(neuromaps_key$description)) {
    colnames <- neuromaps_key[neuromaps_key$description == group, "colname"]
    if (length(colnames) > 1) { # first PC
        pcs <- prcomp(neuromaps_df[, colnames])
        neuromaps_pca[, paste0(group, ".pc1")] <- pcs$x[, 1]
    } else { # leave as is
        neuromaps_pca[group] <- neuromaps_df[, colnames]
    }
}
```

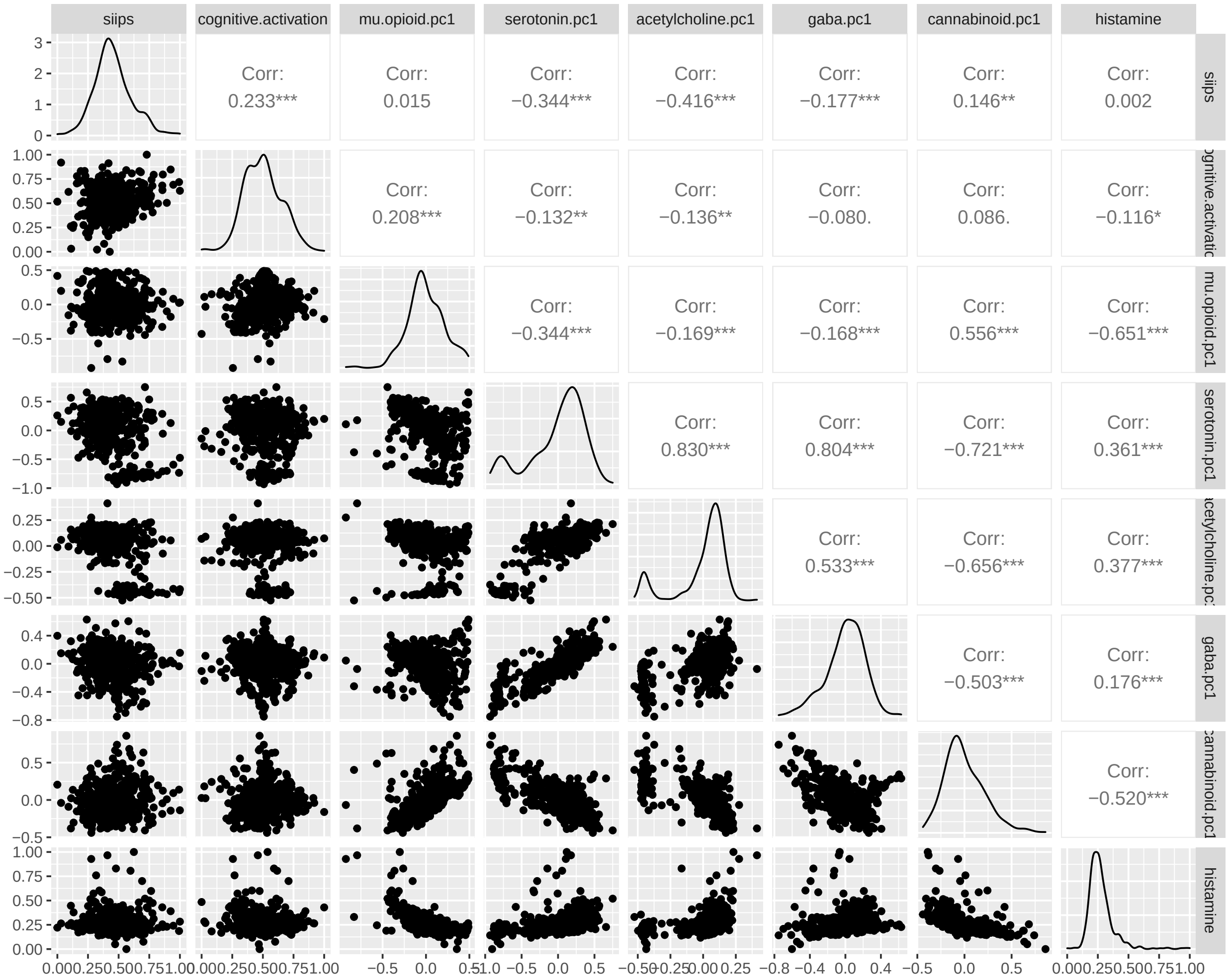
Variable selection

Using in-sample criteria to maximize adjusted R^2

```
xs <- as.matrix(neuromaps_pca[, -1])
all_subsets <- leaps(xs, neuromaps_pca$siips, method = "adjr2")
col_idx <- all_subsets$which[which.max(all_subsets$adjr2), ]
neuromaps_subset <- data.frame(siips = neuromaps_pca$siips, xs[, col_idx])
```

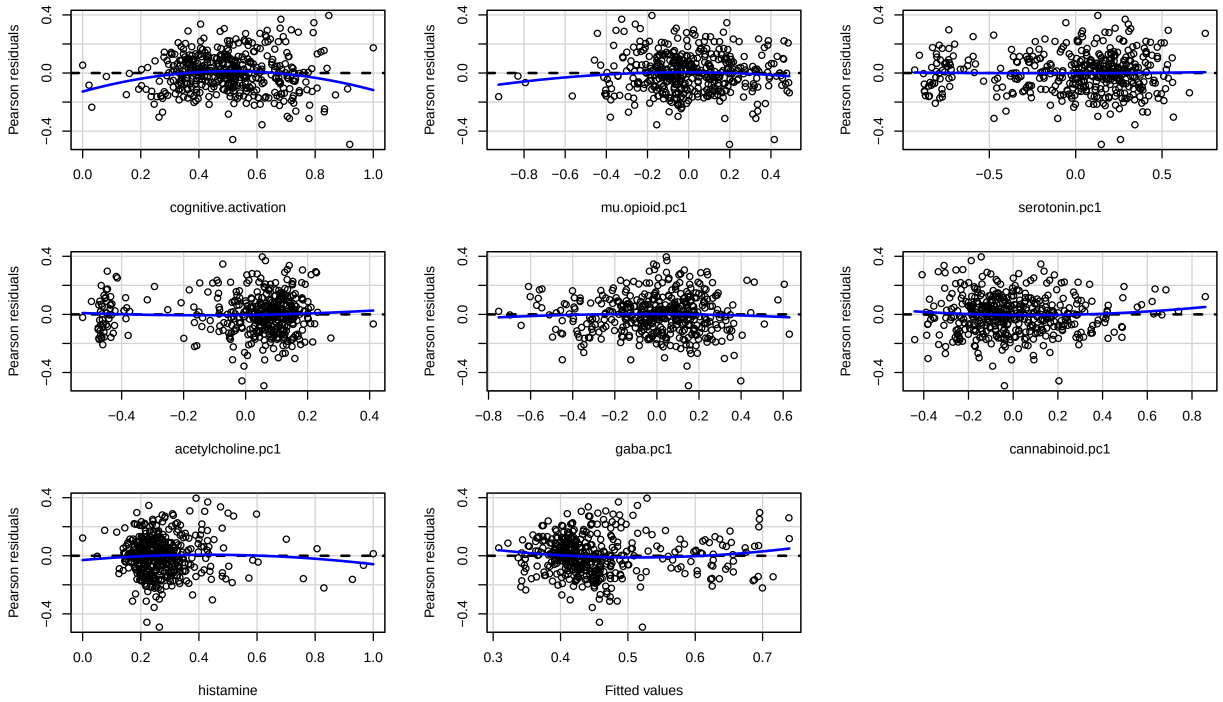
Pairs Plot

```
ggpairs(neuromaps_subset)
```



Naive model

```
ols1 <- lm(siips ~ ., data = neuromaps_subset)
residualPlots(ols1) #  nonlinearity
```



```
##                      Test stat Pr(>|Test stat|)
## cognitive.activation   -3.0341         0.002557 **
## mu.opioid.pc1          -1.6227         0.105369
## serotonin.pc1           0.2382         0.811865
## acetylcholine.pc1       0.7013         0.483506
## gaba.pc1               -0.6238         0.533089
## cannabinoid.pc1         1.0840         0.278982
## histamine              -1.1978         0.231653
## Tukey test              1.9282         0.053836 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
vif(ols1) # collinearity
```

```
## cognitive.activation        mu.opioid.pc1        serotonin.pc1
##             1.088422             2.838364            10.478633
##    acetylcholine.pc1             gaba.pc1      cannabinoid.pc1
##             5.358733             3.783645             3.015873
##            histamine
##             2.103284
```

```
ncvTest(ols1) # heteroscedasticity
```

```
## Non-constant Variance Score Test
## Variance formula: ~ fitted.values
## Chisquare = 8.132561, Df = 1, p = 0.0043477
```

Addressing nonlinearity: quadratic terms

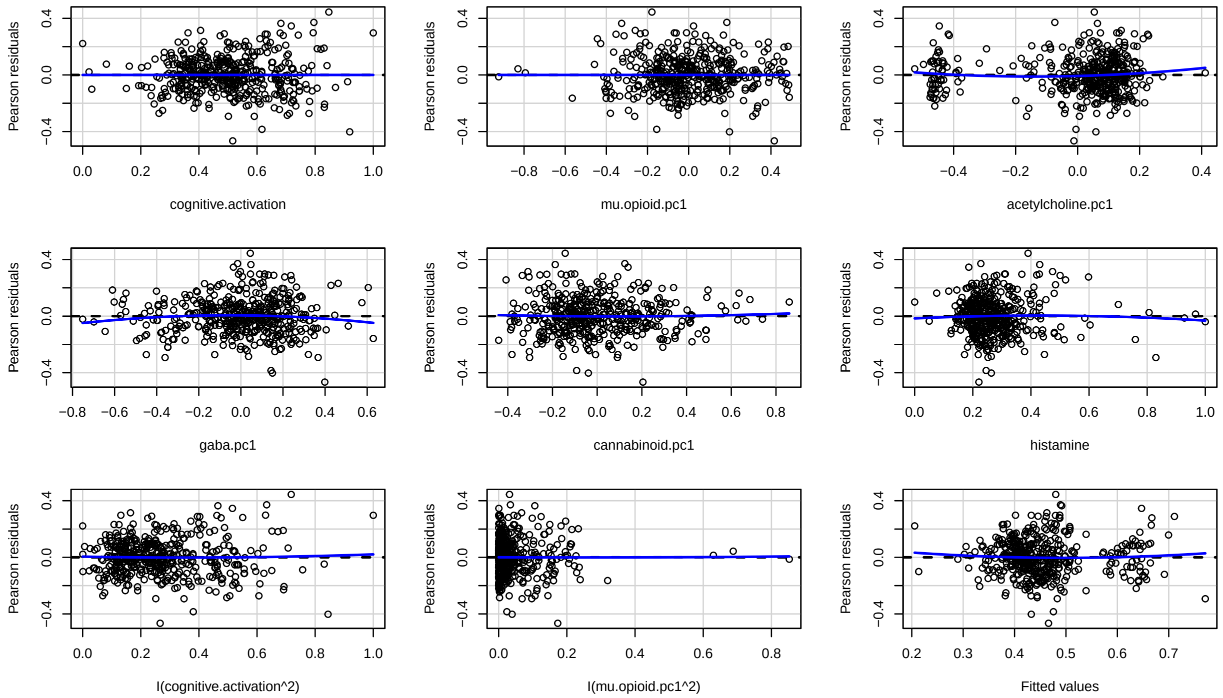
Addressing collinearity: removing serotonin

```
ols2 <- update(ols1, ~ . - serotonin.pc1 + I(cognitive.activation^2) + I(mu.opioid.pc1^2))

anova(ols1, ols2) # confirm ols2 is a better model
```

```
## Analysis of Variance Table
##
## Model 1: siips ~ cognitive.activation + mu.opioid.pc1 + serotonin.pc1 +
##     acetylcholine.pc1 + gaba.pc1 + cannabinoid.pc1 + histamine
## Model 2: siips ~ cognitive.activation + mu.opioid.pc1 + acetylcholine.pc1 +
##     gaba.pc1 + cannabinoid.pc1 + histamine + I(cognitive.activation^2) +
##     I(mu.opioid.pc1^2)
##   Res.Df    RSS Df Sum of Sq      F   Pr(>F)
## 1    436 7.6417
## 2    435 7.4994  1   0.14233 8.2556 0.004261 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
residualPlots(ols2) # fixes nonlinearities
```



```
##                           Test stat Pr(>|Test stat|)
## cognitive.activation         1.3599           0.1746
## mu.opioid.pc1               -0.0589           0.9531
## acetylcholine.pc1            1.3049           0.1926
## gaba.pc1                    -1.5065           0.1327
## cannabinoid.pc1              0.4015           0.6883
## histamine                   -0.6729           0.5013
## I(cognitive.activation^2)    0.6000           0.5488
```

```
## I(mu.opioid.pc1^2)           0.0850           0.9323
## Tukey test                   0.8646           0.3873
```

```
ncvTest(ols2) # heteroscedasticity still an issue
```

```
## Non-constant Variance Score Test
## Variance formula: ~ fitted.values
## Chisquare = 8.027564, Df = 1, p = 0.0046071
```

Check to see if errors are autocorrelated

```
durbinWatsonTest(ols2) # GLS model doesn't seem nessessary
```

```
##  lag Autocorrelation D-W Statistic p-value
##    1      0.04565254      1.908337   0.354
##  Alternative hypothesis: rho != 0
```

Bootstrap to re-estimate standard errors and t-values, under heteroscedasity

```
n_bootstraps <- 1000
n_samples <- nrow(neuromaps_subset)
ols_coefs <- ols2$coefficients
boot_coefs <- matrix(0, n_bootstraps, length(ols_coefs))

for (i in 1:n_bootstraps) {
    idx <- sample(1:n_samples, replace = TRUE)
    m <- update(ols2, ~., data = neuromaps_subset[idx, ])
    boot_coefs[i, ] <- m$coefficients
}

stderr <- apply(boot_coefs, 2, sd)
ci <- apply(boot_coefs, 2, quantile, probs = c(0.025, 0.975))
tvals <- ols_coefs / stderr
pvals <- 2 * pt(-abs(tvals), df = nrow(neuromaps_subset) - length(ols_coefs))
```

Compiling bootstrap results

```
boot_summary <- data.frame(
    "Estimate" = ols_coefs,
    "Std Error" = stderr,
    "t value" = tvals,
    "p value" = pvals
)
```

Compare summary tables

```
summary(ols2)$coefficients |> round(3) # OLS model
```

```
##                            Estimate Std. Error t value Pr(>|t|)
## (Intercept)                   0.119      0.056   2.136    0.033
## cognitive.activation          0.795      0.196   4.057    0.000
## mu.opioid.pc1                 0.093      0.046   2.031    0.043
## acetylcholine.pc1            -0.469      0.051  -9.110    0.000
## gaba.pc1                      0.045      0.035   1.276    0.203
```

```
## cannabinoid.pc1            -0.090      0.058  -1.540    0.124
## histamine                   0.420      0.089   4.709    0.000
## I(cognitive.activation^2)  -0.616      0.186  -3.311    0.001
## I(mu.opioid.pc1^2)         -0.205      0.099  -2.084    0.038
```

```
boot_summary |> round(3) # nonparametric bootstrap
```

```
##                           Estimate Std.Error t.value p.value
## (Intercept)                  0.119     0.064   1.845   0.066
## cognitive.activation         0.795     0.255   3.112   0.002
## mu.opioid.pc1                0.093     0.046   2.003   0.046
## acetylcholine.pc1           -0.469     0.055  -8.508   0.000
## gaba.pc1                     0.045     0.039   1.165   0.245
## cannabinoid.pc1             -0.090     0.053  -1.700   0.090
## histamine                    0.420     0.090   4.647   0.000
## I(cognitive.activation^2)   -0.616     0.266  -2.317   0.021
## I(mu.opioid.pc1^2)          -0.205     0.085  -2.429   0.016
```

Compare confidence intervals

```
ci_df <- confint(ols2) |> cbind(t(ci))
colnames(ci_df) <- c("ols-2.5%", "ols-97.5%", "boot-2.5%", "boot-97.5%")
ci_df |> round(3)
```

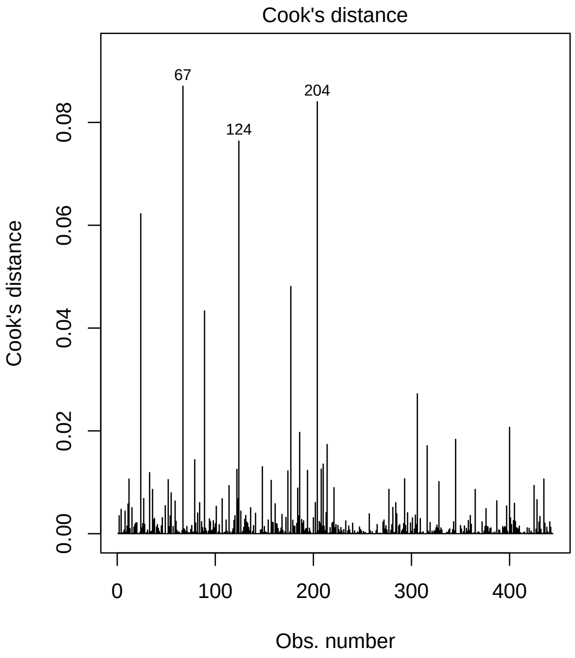
```
##                           ols-2.5% ols-97.5% boot-2.5% boot-97.5%
## (Intercept)                  0.010     0.228    -0.025      0.235
## cognitive.activation         0.410     1.180     0.355      1.367
## mu.opioid.pc1                0.003     0.183     0.003      0.188
## acetylcholine.pc1           -0.570    -0.367    -0.567     -0.358
## gaba.pc1                    -0.024     0.115    -0.032      0.121
## cannabinoid.pc1             -0.204     0.025    -0.196      0.008
## histamine                    0.244     0.595     0.254      0.612
## I(cognitive.activation^2)   -0.982    -0.250    -1.204     -0.170
## I(mu.opioid.pc1^2)          -0.399    -0.012    -0.374     -0.053
```

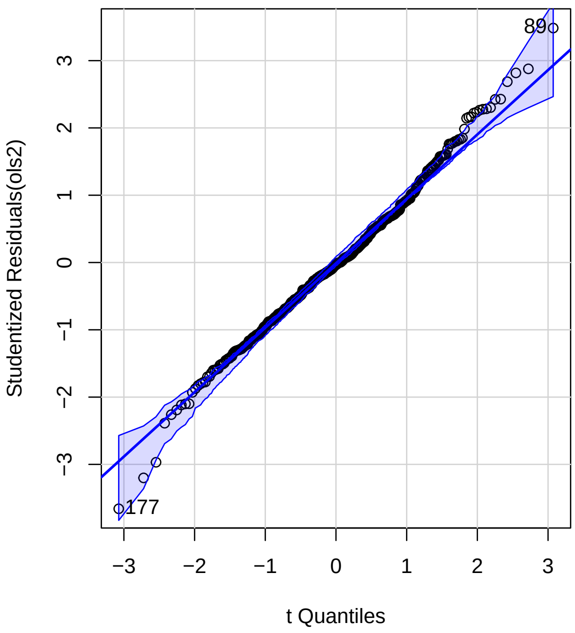
Check for outliers and normality of residuals

```
outlierTest(ols2)
```

```
## No Studentized residuals with Bonferroni p < 0.05
## Largest |rstudent|:
##      rstudent unadjusted p-value Bonferroni p
## 177 -3.659496         0.00028381      0.12601
```

```
par(mfrow = c(1, 2))
plot(ols2, 4) # influence
qqPlot(ols2) # normality
```


Cook's distance
Cook's distance
0.00
0.02
0.04
0.06
0.08
67
124
204
0
100
200
300
400
Obs. number


Studentized Residuals(ols2)
−3
−2
−1
0
1
2
3
89
177
−3
−2
−1
0
1
2
3
t Quantiles

```
## [1]  89 177
```