

# Depression & Cognitive Impairment

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March 12, 2019

## Load data

```
setwd('.')
data1 <- read.csv('...csv', sep = ',', header = TRUE)

library(VIM)
library(Hmisc)
library(ggplot2)
library(reshape2)
library(tableone)
library(Matching)
library(ipw)
library(survey)
library(MatchIt)
library(CCA)
library(vegan)
```

## Data processing

The data contains no extreme values. 9 variables out of 41 have 1 or 2 missing values, which don't have correlations with each other, hence we assume the missingness is MAR. Therefore median imputations could be used for the NAs, or we simply delete the observations with NAs. Most of the variables are positively correlated with the correlation coefficient close to zero. In the heatmap, negative correlations are blue, positive ones are red.

```
# descriptive analysis
```

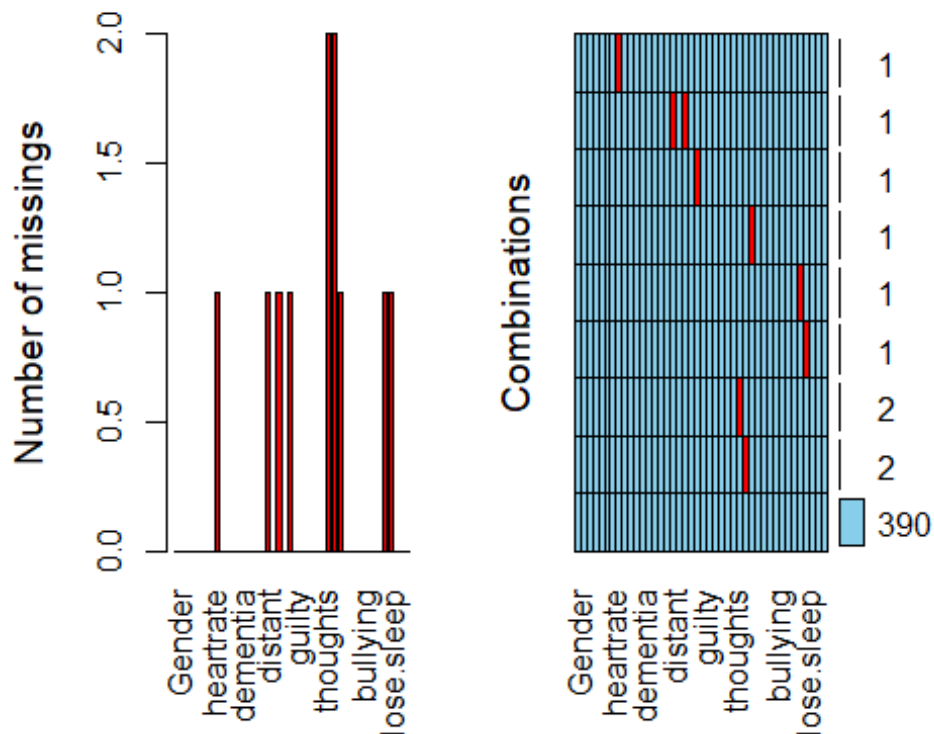
```
summary(data1)
```

```
##      Gender      anxiety_1      anxiety_2      restless.agitated.te
##      nse
##  Min.      :1.000  Min.      :1.000  Min.      :1.00  Min.      :1.000
##  1st Qu.:1.000  1st Qu.:2.000  1st Qu.:1.00  1st Qu.:2.000
##  Median :1.000  Median :2.000  Median :2.00  Median :2.000
```

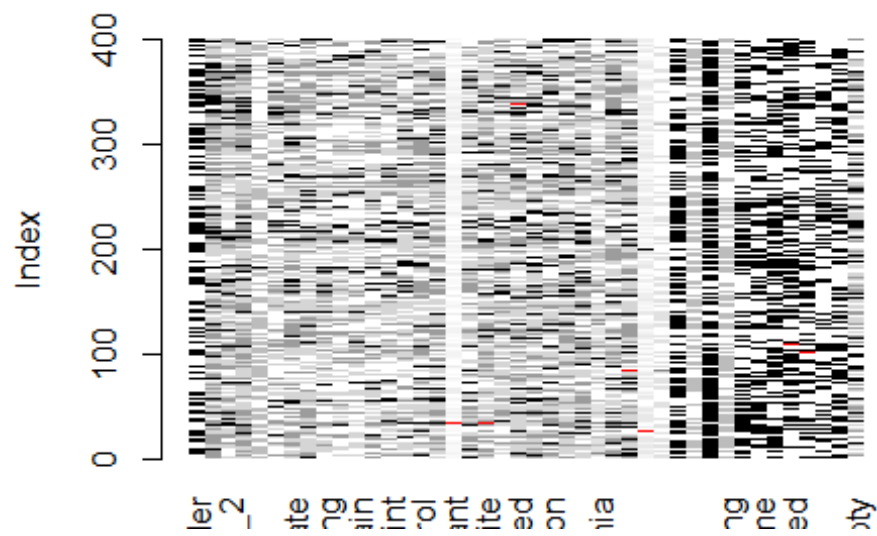
```
## Mean      :1.492    Mean      :2.455    Mean      :2.16    Mean      :2.397
## 3rd Qu.:2.000    3rd Qu.:3.000    3rd Qu.:3.00    3rd Qu.:3.000
## Max.      :2.000    Max.      :4.000    Max.      :4.00    Max.      :4.000

## Max.      :4.00    Max.      :4.000    Max.      :4.00    Max.      :4.000
##
## distant      body.weight      appetite      slow.down
## Min.      : 1.000    Min.      :1.000    Min.      :1.00    Min.      :1.000
## 1st Qu.: 1.000    1st Qu.:1.000    1st Qu.:1.00    1st Qu.:1.000
## Median : 2.000    Median :2.000    Median :2.00    Median :2.000
## Mean      : 2.175    Mean      :2.103    Mean      :2.15    Mean      :2.095
## 3rd Qu.: 3.000    3rd Qu.:3.000    3rd Qu.:3.00    3rd Qu.:3.000
## Max.      :21.000    Max.      :4.000    Max.      :4.00    Max.      :4.000
## NA's      :1              NA's      :1
```

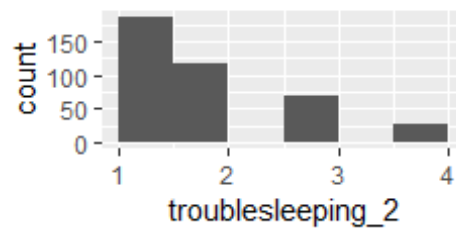
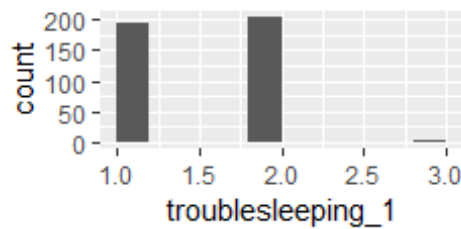
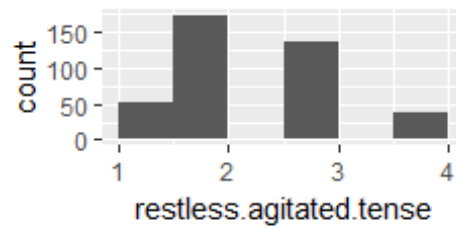
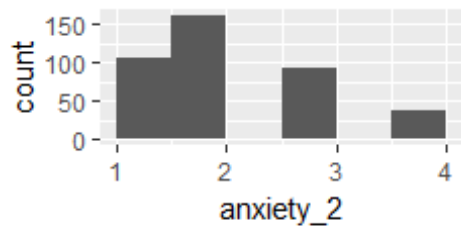
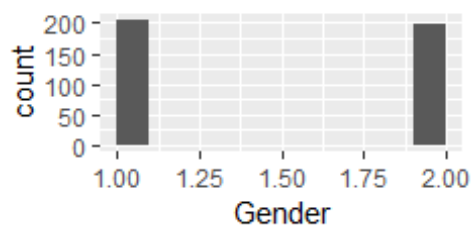
```
aggr(data1, prop = FALSE, numbers = TRUE)
```



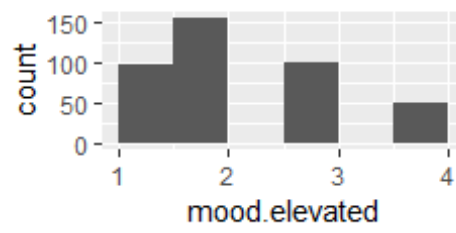
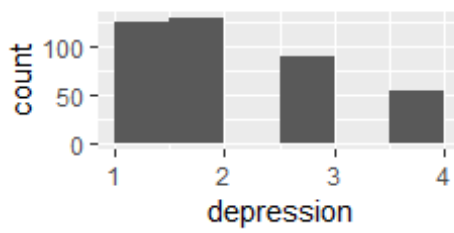
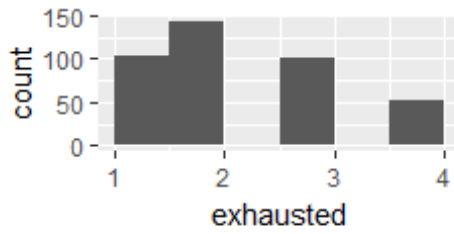
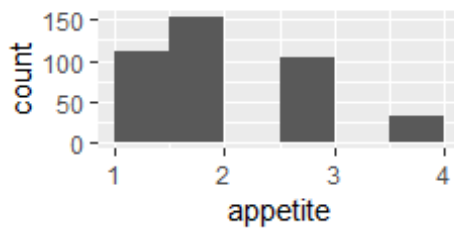
```
matrixplot(data1)
visualize(data1, vnam = TRUE)
```



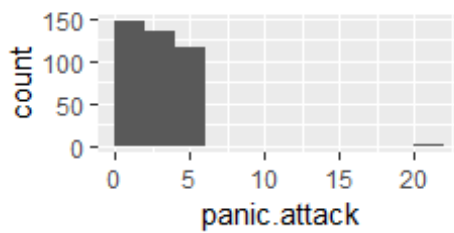
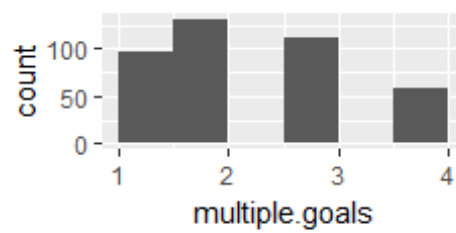
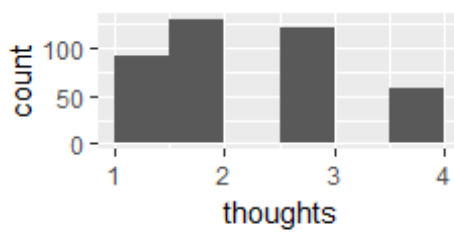
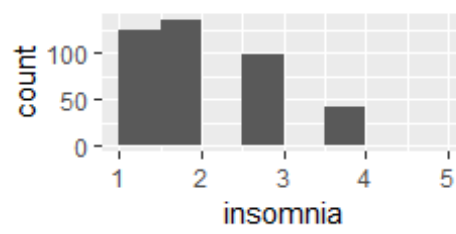
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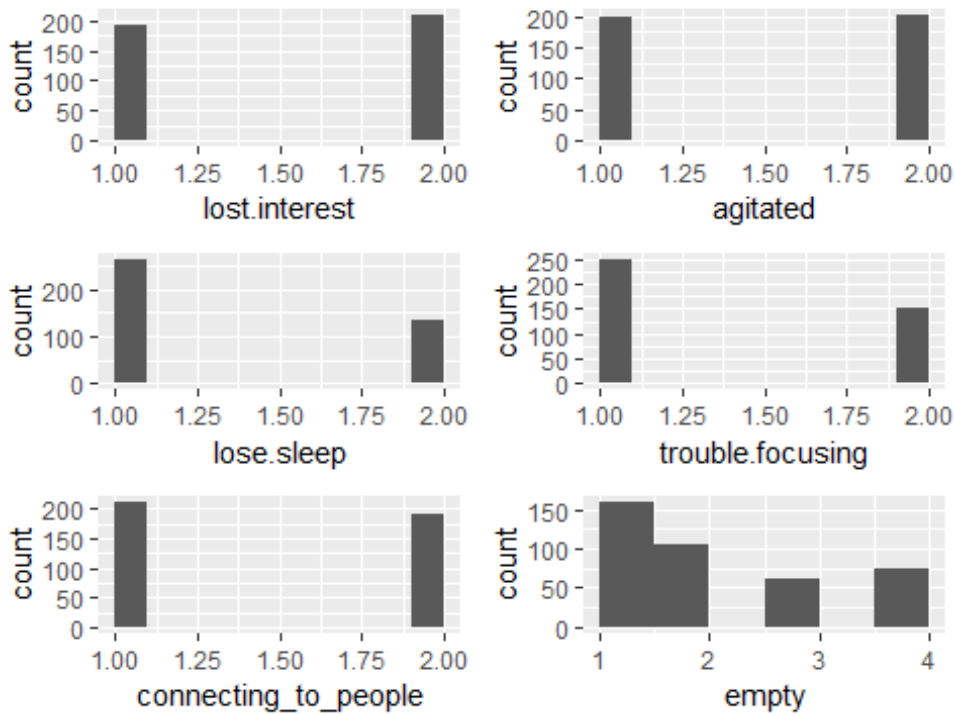
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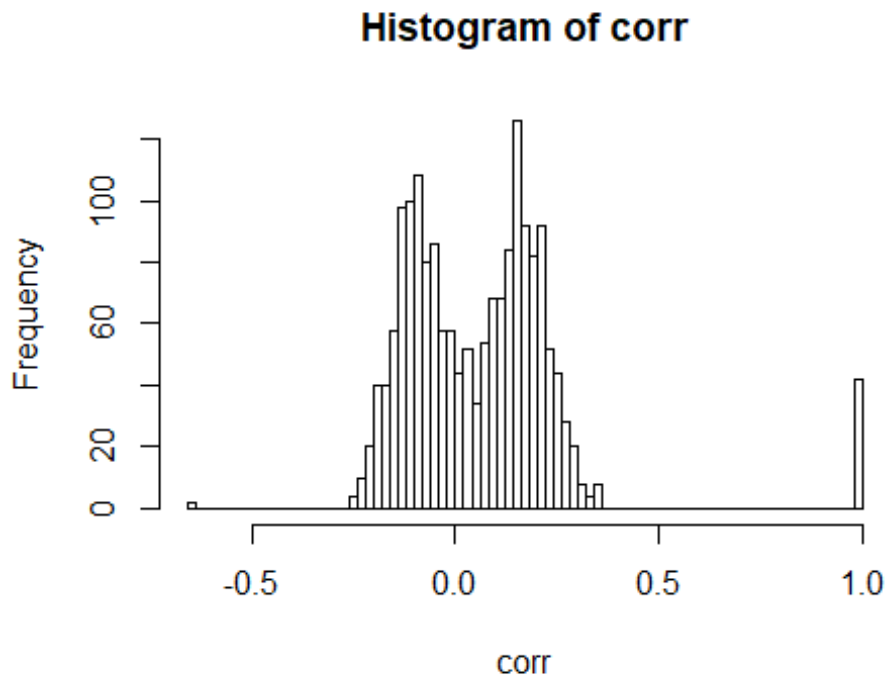


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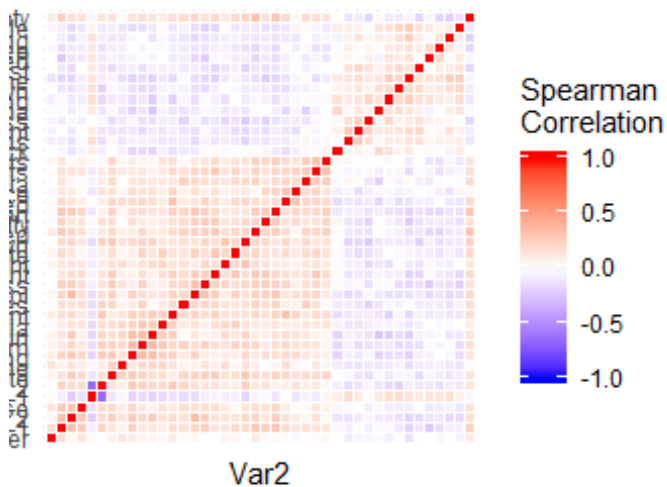
```
# missing data imputation
for(i in 1:length(data1)){
  data1[,i] <- impute(data1[,i], median)
  data1[,i] <- as.numeric(data1[,i])
}
matrixplot(data1)
```

```
# correlation
corr <- round(cor(data1, method = 'spearman'),2)
hist(corr, breaks = 100)
```



```
heatMap <- function(data, color_limit, color_name){
  corr <- melt(data)
  ggplot(corr, aes(Var2, Var1, fill = value)) +
    geom_tile(color = "white") +
    scale_fill_gradient2(low = "blue", high = "red", mid = "white", midpo
int = 0, limit = color_limit, space = "Lab", name = color_name) +
    theme_minimal() +
    theme(axis.text.x = element_blank()) +
    coord_fixed()
}

heatMap(corr, color_limit = c(-1,1), color_name = "Spearman\nCorrelatio
n")
```



```
# classify questions
confounding <- data1[,c(1,7,8,9,11,20,28,31)]
depression <- data1[,c(2,3,4,5,6,15,16,17,18,19,21,22,23,29,30,32,33,34,
35,36,37,39,41,42)]
cognitive <- data1[,c(10,12,13,14,24,25,26,27,38,40)]
```

## Incidence of cooccurrence

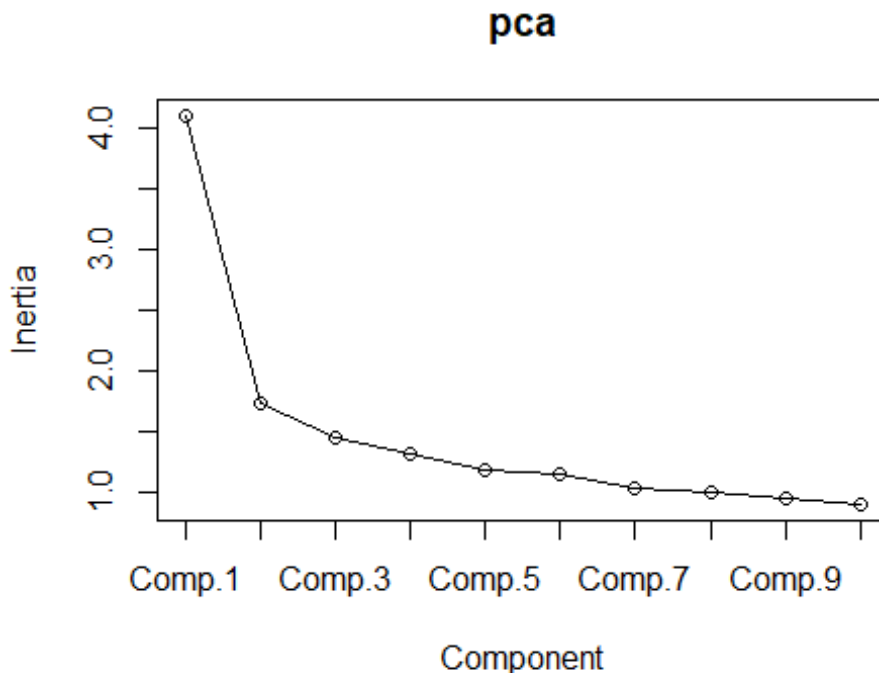
kmeans has a drawback that we cannot explain why a subject is classified into one group instead of another. Pca has a problem that no principle component can be extracted. Hence maybe we will use anomaly detection to find the subjects with a risk of getting depression or cognitive impairment, and then calculate the possibility of cooccurrence conditioned on two cases respectively. It seems the occurrence of depression and cognitive impairment is more common in the cognitive impaired group than in the depressed group.

```
fit <- kmeans(depression, 5)
fit
## 5      1.591304    1.382609                1.626087 1.713043
##
## Clustering vector:
##  [1] 1 4 2 2 4 5 5 2 5 5 2 5 4 2 5 5 1 5 5 2 2 3 5 1 3 2 3 1 2 5 1
## 3 3 2 2
##
## Within cluster sum of squares by cluster:
```

```
## [1] 922.6707 993.6351 1215.5930 902.7442 1586.8696
## (between_SS / total_SS = 25.1 %)
##
## Available components:
##
## [1] "cluster"      "centers"      "totss"        "withinss"
## [5] "tot.withinss" "betweenss"    "size"         "iter"
## [9] "ifault"

pca <- princomp(depression, cor = TRUE)
summary(pca, loading = TRUE)

## Importance of components:
##
##              Comp.1      Comp.2      Comp.3      Comp.4
## Standard deviation 2.0242141 1.31127048 1.19966537 1.14153119
## Proportion of Variance 0.1707268 0.07164293 0.05996654 0.05429556
## Cumulative Proportion 0.1707268 0.24236971 0.30233625 0.35663181
##
##              Comp.5      Comp.6      Comp.7      Comp.8
## Standard deviation 1.08436590 1.06640697 1.01096203 0.9982408
## Proportion of Variance 0.04899372 0.04738433 0.04258518 0.0415202
## Cumulative Proportion 0.40562554 0.45300986 0.49559504 0.5371152
##
##              Comp.9      Comp.10      Comp.11      Comp.12
## Standard deviation 0.9982408 0.9982408 0.9982408 0.9982408
## Proportion of Variance 0.0415202 0.0415202 0.0415202 0.0415202
## Cumulative Proportion 0.5371152 0.5786354 0.6201556 0.6616758
##
reepplot(pca, type = 'lines')
```



```
findAtRisk <- function(data, quantil){
  for (i in 1:length(data)) {
    data[,i] <- ifelse(data[,i] == max(data[,i]),1,0)
  }
}
```



```

    }
    risk_score <- rowMeans(data)
    at_risk <- which(risk_score > quantile(risk_score, quantil))
    return(at_risk)
}

coOccurence <- function(data1, data2, quantil){
  #the possibility of data2 conditioned on data1
  breaks <- length(quantil)
  cooccur_matrix <- matrix(data = NA, nrow = breaks, ncol = breaks)
  for(i in 1:breaks){
    for(j in 1:breaks){
      array1 <- findAtRisk(data1, quantil[i])
      array2 <- findAtRisk(data2, quantil[j])
      cooccur_incidence <- intersect(array1, array2)
      cooccur_matrix[i,j] <- length(cooccur_incidence)/length(array1)
    }
  }
  row.names(cooccur_matrix) <- as.character(quantil)
  colnames(cooccur_matrix) <- as.character(quantil)
  return(cooccur_matrix)
}

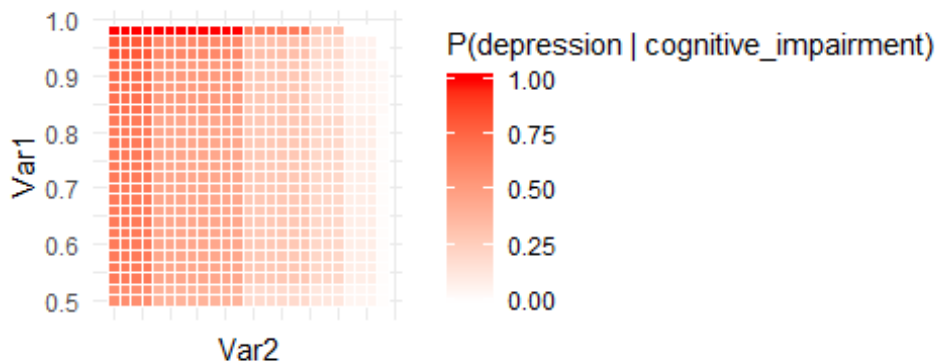
quantil <- seq(0.5, 0.99, 0.02)
dep2cog <- coOccurence(depression, cognitive, quantil)
cog2dep <- coOccurence(cognitive, depression, quantil)

par(mfrow = c(1,2))
heatMap(dep2cog, color_limit = c(0,1), color_name = "P(cognitive_impairment | depression)")

```



```
heatMap(cog2dep, color_limit = c(0,1), color_name = "P(depression | cog  
nitive_impairment)")
```



##

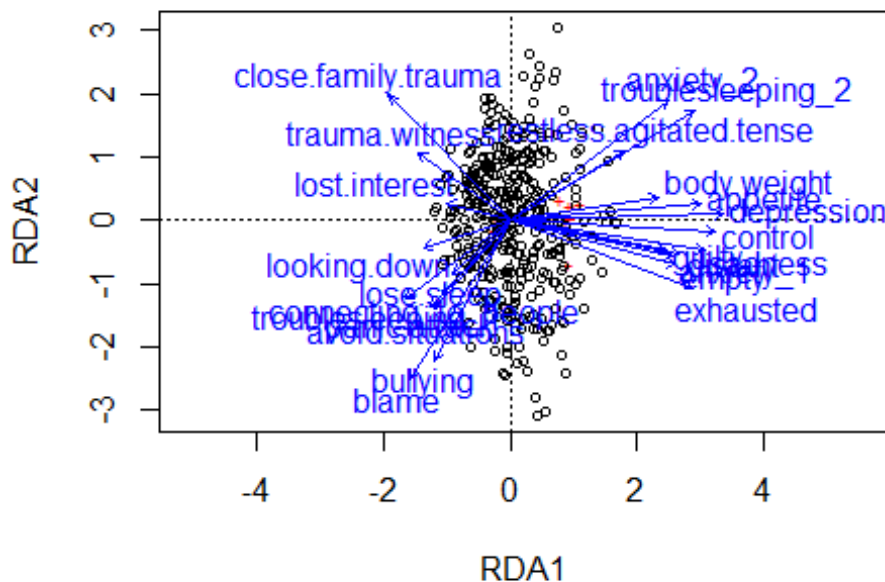
## Redundancy Analysis

```
decorana(cognitive)
```

```
##
## Call:
## decorana(veg = cognitive)
##
## Detrended correspondence analysis with 26 segments.
## Rescaling of axes with 4 iterations.
##
##              DCA1    DCA2    DCA3    DCA4
## Eigenvalues    0.02527 0.02309 0.02020 0.01732
## Decorana values 0.02528 0.02261 0.01947 0.01604
## Axis lengths   0.79095 0.74932 0.70305 0.68282

sp0 <- rda(cognitive ~., depression)
sp0

## 1.3569 0.8961 0.8519 0.7090 0.6611 0.6407 0.5585 0.4889 0.2098 0.182
6
plot(sp0)
```



## Causal Inference

Next we use IPSW to compare the score of cognitive impairment in people who feel depressed and who don't. The 95% confidence interval of depression's effect on cognition does not contain 0, which means the relationship between depression and cognitive impairment is statistically significant. However, cognition does not have a significant correlation to depression after adjusting for confoundings.

```
causalEffect <- function(treat_data, confounding, outcome_data, quantil)
{
  print(paste('Effect of', deparse(substitute(treat_data)), 'on', deparse(substitute(outcome_data))))

  treated <- findAtRisk(treat_data, quantil)
  treat <- rep(0, length(data1[,1]))
  treat[treated] <- 1

  outcome <- rowMeans(outcome_data)

  xvars <- colnames(confounding)

  data3 <- cbind(confounding,treat)

  # Propensity score matching
  psmodel <- glm(treat ~ ., family = binomial(link = 'logit'), data = d
```

```

ata3)
  ps <- predict(psmmodel, type = 'response')
  weight <- ifelse(data3$treat == 1, 1/(ps), 1/(1-ps))
  weighteddata <- svydesign(ids = ~1, data = data3, weights = ~ weight)

  weightedtable <- svyCreateTableOne(vars = xvars, strata = 'treat', da
ta = weighteddata, test = FALSE)
  print(weightedtable, smd = TRUE)

  # 95% C.I. for causal effect
  weightmodel <- ipwpoint(exposure = treat, family = 'binomial', link =
'logit',
                        denominator = ~ ., data = data3, trunc = .0
1)
  summary(weightmodel$weights.trunc)

  ipwplot(weights = weightmodel$weights.trunc, logscale = FALSE, main =
'weights', xlim = c(0,22))
  data3$wt <- weightmodel$weights.trunc

  data3 <- cbind(outcome, data3)
  msm <- (svyglm(outcome ~ treat, design = svydesign(~1, weights = ~ wt,
data = data3)))
  print(coef(msm))
  print(confint(msm))
}

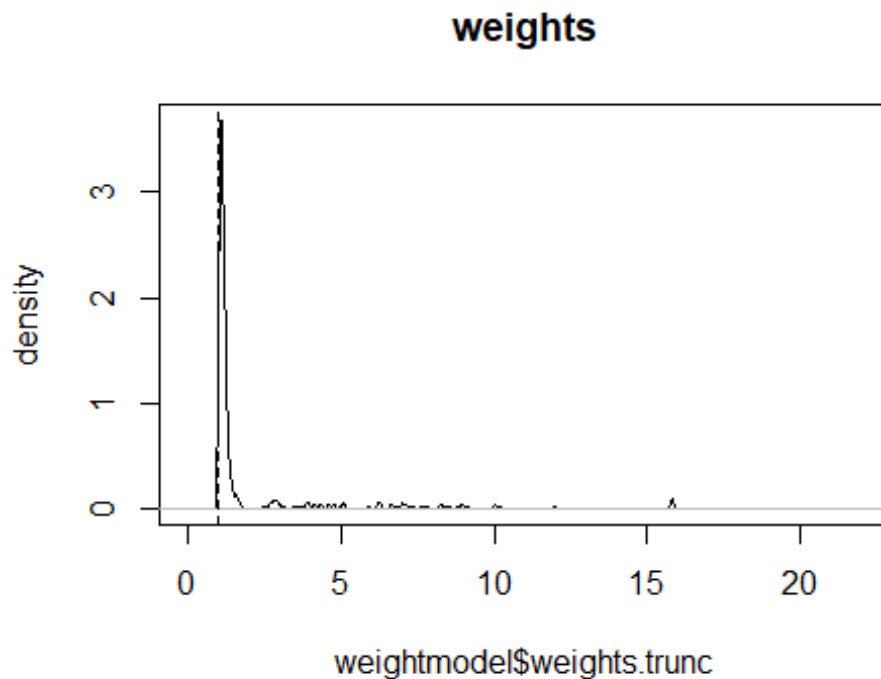
```

```
causalEffect(depression, confounding, cognitive, 0.8)
```

```

## [1] "Effect of depression on cognitive"
##
##              Stratified by treat
##              0              1              SMD
##  n              399.62          417.31
##  Gender (mean (sd))          1.49 (0.50)          1.46 (0.50)          0.068
##  te (mean (sd))              2.17 (0.95)          2.05 (1.00)          0.116
##  ng (mean (sd))              2.11 (0.94)          1.99 (0.80)          0.138
##  ng (mean (sd))              1.91 (0.98)          1.89 (0.91)          0.026
##  chest.pain (mean (sd))      1.83 (0.97)          1.75 (0.91)          0.082
##  n (mean (sd))              2.09 (0.90)          1.99 (1.05)          0.108
##  mu (mean (sd))              2.33 (0.99)          2.23 (1.04)          0.096
##  tt (mean (sd))              1.59 (0.49)          1.52 (0.50)          0.145

```

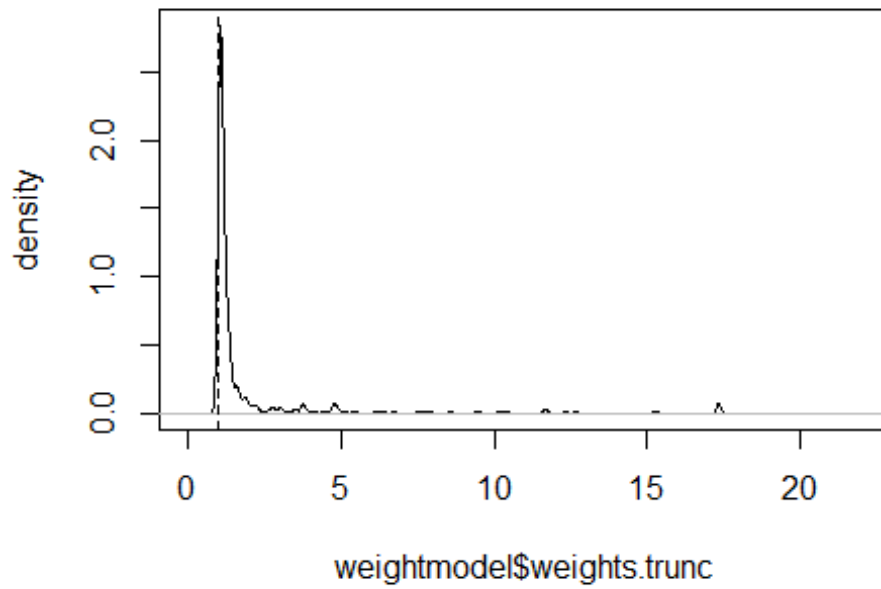


```
## (Intercept)      treat
##  1.9355813    0.1558179
##                2.5 %   97.5 %
## (Intercept) 1.89302534 1.9781373
## treat      0.03161911 0.2800167
```

**causalEffect**(cognitive, confounding, depression, 0.8)

```
## [1] "Effect of cognitive on depression"
##                                     Stratified by treat
##                                     0           1           SMD
##  n                                398.05      433.03
##  Gender (mean (sd))                1.49 (0.50)  1.56 (0.50)  0.132
##  te (mean (sd))                    2.16 (0.93)  2.07 (1.05)  0.097
##  ng (mean (sd))                    2.10 (0.91)  2.08 (1.05)  0.022
##  ng (mean (sd))                    1.90 (0.95)  1.82 (0.96)  0.086
##  cn (mean (sd))                    1.83 (0.96)  1.85 (1.00)  0.029
##  sn (mean (sd))                    2.10 (0.88)  2.14 (1.13)  0.039
##  ls (mean (sd))                    2.32 (0.96)  2.14 (1.16)  0.163
##  tt (mean (sd))                    1.59 (0.49)  1.54 (0.50)  0.093
```

## weights



```
## (Intercept)      treat
## 1.93062460  0.04887152
##              2.5 %    97.5 %
## (Intercept) 1.90344194 1.9578073
## treat      -0.03214008 0.1298831
```