

# marcorr2.R

ella

Wed Mar 14 01:37:33 2018

```
# testing march 2018 data for low variance adjustment
options(warn=-1)
library(tidyverse)

## -- Attaching packages ----- tidyverse 1.2.1 --

## v ggplot2 2.2.1.9000      v purrr   0.2.4
## v tibble  1.4.2          v dplyr   0.7.4
## v tidyr   0.8.0          v stringr 1.2.0
## v readr   1.1.1          v forcats 0.2.0

## -- Conflicts ----- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()     masks stats::lag()

march2018<-rio::import("marchtest.sas7bdat")
source("pcor.R")

# in these tests we will only use bmi group 3

# set up the dummy variables and only take bmi group 3
bmig3<-filter(march2018,bmi_grp==2) %>%
  mutate(raceg1=if_else(race_grp==1,1,0),
         raceg2=if_else(race_grp==2,1,0)) #if_else accounts for missing values

# unadjusted correlation
cor(bmig3$age,bmig3$`_1_2_DIPALMITOYLGLYCEROL`,method="spearman")

## [1] -0.05036589

# Partial correlation from residuals -----
age = bmig3$age
metab = bmig3$`_1_2_DIPALMITOYLGLYCEROL`
race = as.factor(bmig3$race_grp)
group1 = bmig3$raceg1
group2 = bmig3$raceg2
group0 = bmig3$raceg0

testdf<-data.frame(age,metab,group1)

# conduct normal linear least-squares regression with y as target and z as predictor
regress.age = lm(age~race)

# extract residuals from this regression
residuals.age = residuals(regress.age)

# conduct normal linear least-squares regression with x as target and z as predictor
```

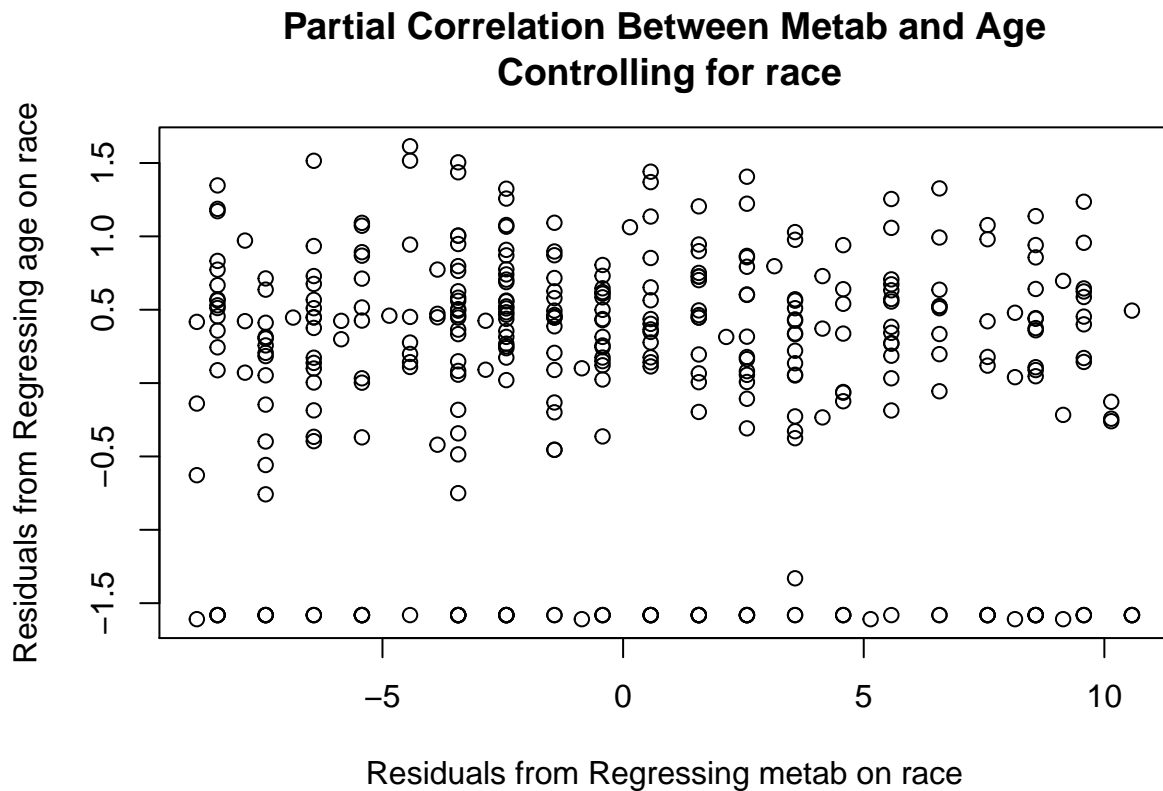
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regress.metab = lm(metab~group1)

# extract residuals from this regression
residuals.metab = residuals(regress.metab)

plot(residuals.age, residuals.metab, xlab = 'Residuals from Regressing metab on race', ylab = 'Residuals from Regressing age on race')

```



```

# sample size
n = length(age)

# use Spearman correlation coefficient to calculate the partial correlation

# regular cor function for spearman correlation of residuals not the same calculation in sas glm and reg
parcor = cor(residuals.age, residuals.metab, method = 'spearman', use="pairwise.complete.obs")
print(parcor)

## [1] -0.04972032

# also try Harrel's rcorr - this gives us exactly the same as SAS via glm and reg
rc<-Hmisc::rcorr(residuals.age, residuals.metab, type = 'spearman')

print(rc$r)

##           x           y
## x  1.00000000 -0.04964792
## y -0.04964792  1.00000000

```

```

print(rc$P)

##           x           y
## x           NA 0.3409181
## y 0.3409181           NA

# another partial correlation from ggm - does not match sas
ggm::pcor(c("age","metab","group1"),var(testdf))

## [1] -0.06530587

# ppcor package test -----
ppcor::pcor.test(bmig3$age,bmig3$`_1_2_DIPALMITOYLGLYCEROL`,c(bmig3$raceg1),method="spearman")

##      estimate  p.value  statistic  n gp  Method
## 1 -0.05021309 0.3361017 -0.9631595 370 1 spearman

# ppcor partial correlation - this one matches SAS proc corr partial correlation!
ppcor::pcor(testdf,method="spearman")

## $estimate
##           age           metab           group1
## age  1.000000000 -0.05021309  0.005551692
## metab -0.050213094  1.00000000  -0.024630871
## group1 0.005551692 -0.02463087  1.000000000
##
## $p.value
##           age           metab           group1
## age  0.0000000 0.3361017 0.9153574
## metab 0.3361017 0.0000000 0.6372053
## group1 0.9153574 0.6372053 0.0000000
##
## $statistic
##           age           metab           group1
## age  0.0000000 -0.9631595  0.1063568
## metab -0.9631595  0.0000000 -0.4720028
## group1 0.1063568 -0.4720028  0.0000000
##
## $n
## [1] 370
##
## $gp
## [1] 1
##
## $method
## [1] "spearman"

# RVAideMemoire package
print(RVAideMemoire::pcor(age,metab,list(group1),use="pairwise.complete.obs",method="spearman"))

## [1] -0.04972032

# psych package using hmisc
unadjrcor<-Hmisc::rcorr(as.matrix(testdf),type="spearman")
psychrcor<-psych::partial.r(as.matrix(unadjrcor$r),c(1,2),c(3))
print(format(psychrcor,digits=8))

##           age           metab

```

```
## age " 1.000000000" "-0.050213096"  
## metab "-0.050213096" " 1.000000000"
```

```
print(format(psych::corr.p(psychcor,n=nrow(testdf)-2)$p,digits=8)) # p-value
```

```
## age metab  
## age "0.00000000" "0.33676177"  
## metab "0.33676177" "0.00000000"
```

```
# psych package using cor
```

```
psychcor<-psych::partial.r(cor(testdf,method="spearman"),c(1,2),c(3))  
print(format(psychcor,digits=8))
```

```
## age metab  
## age " 1.000000000" "-0.050213094"  
## metab "-0.050213094" " 1.000000000"
```

```
print(format(psych::corr.p(psychcor,n=nrow(testdf)-2)$p,digits=8))
```

```
## age metab  
## age "0.00000000" "0.33676179"  
## metab "0.33676179" "0.00000000"
```