# marcorr.R

*ella*

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```
# 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
```

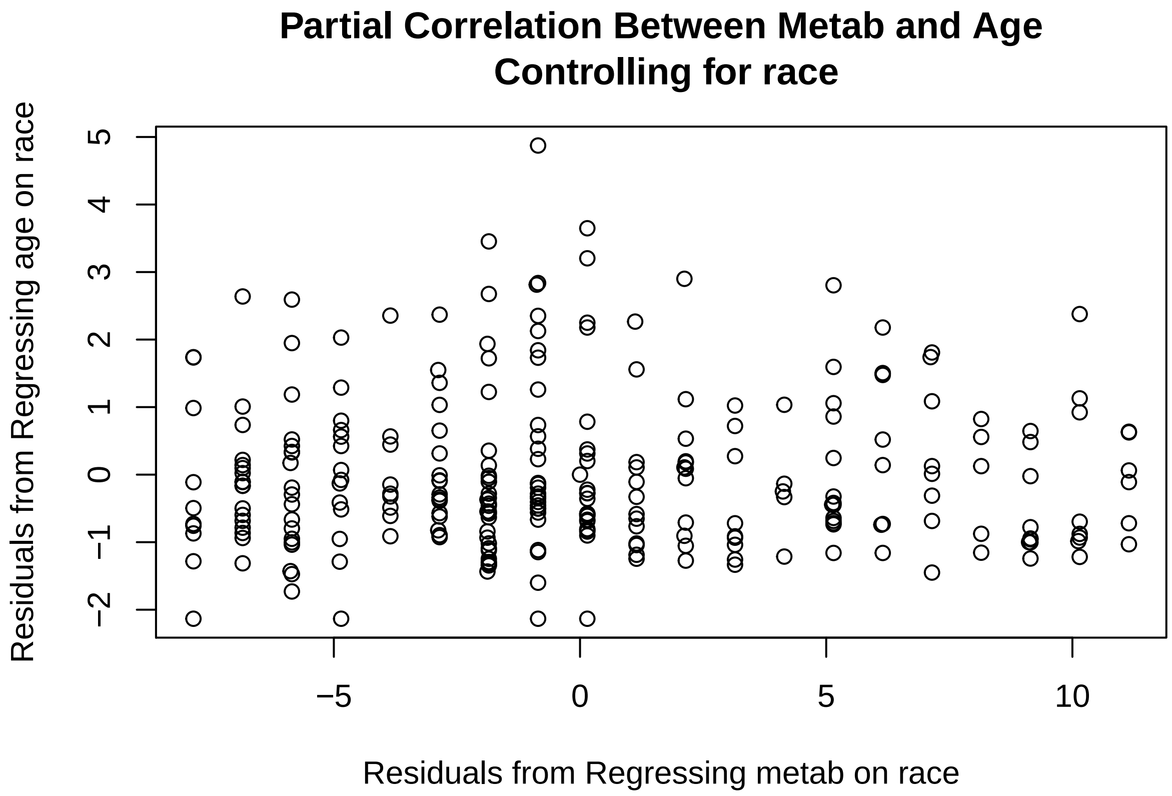
```
## -- Conflicts ------------------------------------- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
```

```
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==3) %>%
  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_PROPANEDIOL`,method="spearman")
```

```
## [1] -0.01785744
```

```
# Partial correlation from residuals ---------------------------
age = bmig3$age
metab = bmig3$`_1_2_PROPANEDIOL`
race = as.factor(bmig3$race_grp)
group1 = bmig3$raceg1
group2 = bmig3$raceg2

testdf<-data.frame(age,metab,group1,group2)

# 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
regress.metab = lm(metab~group1+group2)
```

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

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



```
# 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 re
parcor = cor(residuals.age, residuals.metab, method = 'spearman',use="pairwise.complete.obs")
print(parcor)
```

```
## [1] -0.004991148
```

```
# 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  1.000000000 -0.004893797
## y -0.004893797  1.000000000
```

```
print(rc$P)
```

```
##          x        y
## x       NA 0.936324
## y 0.936324       NA
```

```
# another partial correlation from ggm - does not match sas
ggm::pcor(c("age","metab","group1","group2"),var(testdf))
```

```
## [1] 0.004670885
```

```
# ppcor package test ----------------
ppcor::pcor.test(bmig3$age,bmig3$`_1_2_PROPANEDIOL`,c(bmig3$raceg1,bmig3$raceg0),method="spearman")
```

```
##      estimate   p.value  statistic   n gp   Method
## 1 -0.01845269 0.7636454 -0.3010055 269  1 spearman
```

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

```
## $estimate
##                 age        metab       group1      group2
## age     1.000000000 -0.009476199 -0.117404116 -0.10267663
## metab  -0.009476199  1.000000000 -0.003520196  0.08581556
## group1 -0.117404116 -0.003520196  1.000000000 -0.03108686
## group2 -0.102676633  0.085815559 -0.031086858  1.00000000
##
## $p.value
##               age     metab     group1     group2
## age    0.00000000 0.8775156 0.05536131 0.09407042
## metab  0.87751563 0.0000000 0.95434543 0.16204118
## group1 0.05536131 0.9543454 0.00000000 0.61306555
## group2 0.09407042 0.1620412 0.61306555 0.00000000
##
## $statistic
##               age       metab      group1     group2
## age     0.0000000 -0.15426827 -1.92451002 -1.6803354
## metab  -0.1542683  0.00000000 -0.05730499  1.4021486
## group1 -1.9245100 -0.05730499  0.00000000 -0.5063021
## group2 -1.6803354  1.40214855 -0.50630209  0.0000000
##
## $n
## [1] 269
##
## $gp
## [1] 2
##
## $method
## [1] "spearman"
```

```
# RVAideMemoire package
print(RVAideMemoire::pcor(age,metab,list(group1,group2),use="pairwise.complete.obs",method="spearman"))
```

```
## [1] -0.004991148
```

```
# psych package using hmisc
unadjrcor<-Hmisc::rcorr(as.matrix(testdf),type="spearman")
psychrcor<-psych::partial.r(as.matrix(unadjrcor$r),c(1,2),c(3,4))
print(format(psychrcor,digits=8))
```

```
##       age             metab
## age   " 1.0000000000" "-0.0094762005"
## metab "-0.0094762005" " 1.0000000000"
```

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

```
##       age          metab
## age   "0.00000000" "0.87751562"
## metab "0.87751562" "0.00000000"
```

```
# psych package using cor
psychcor<-psych::partial.r(cor(testdf,method="spearman"),c(1,2),c(3,4))
print(format(psychcor,digits=8))
```

```
##       age             metab
## age   " 1.0000000000" "-0.0094761992"
## metab "-0.0094761992" " 1.0000000000"
```

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

```
##       age          metab
## age   "0.00000000" "0.87751563"
## metab "0.87751563" "0.00000000"
```