Statistical Inferences II (Confidence Interval)

Lucie Lu

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Permutation Confidence Invertals

In the previous section, I have obtained the p-value by repeatedly calculating the test statistic from a large number of permutations of the data. On its surface, the permutation confidence interval in this section is simply the set of all values of the parameter for which the null hypothesis is not rejected. To obtain a confidence interval, I tried to use some p-values to test a numer of different hypotheses to create a collection of non-rejected hypotheses. This is how we calculate the confidence interval from the permutation tests.

My null hypotheses in this hypothesis testing are addictive treatment effects. I used two methods to calculate the confidence intervals: one with the *uniroot* function to find two tails of confidence limits where the p-value from the *lm* or *lmrob* function of the certain hypothesis is less than 5%, which is the conventional benchmark of leading to the rejection of that hypothesis. The confidence interval calculated from this method agrees with the default confidence interval in the *lm* function. The assumption of this method is a central limit theorem (CLT) and independent identically distributed random samples (iid).

The second test sets the significance level 0.05, and specify the confidence coefficient 0.95 to reflect the true coverage probability. I created null hypotheses as a constant addictive effect and compute an interval estimate where the right and left end points' p values are approximately equal to 0.05. Within the two-sided confidence intervals, the estimates' p-values are larger than 0.05. I show part of the procedure in this method in table "Searching for non-rejected intervals under permutation for *lm* and *lmrob* models."

From the table we can see this second method (see the results in the "permuted lm confidence interval" and "permuted *lmrob* confidence interval") produces confidence intervals that do not accord with the first method. At this moment, I cannot figure out why the confidence intervals in the second method have no overlap with the ones in the first method.

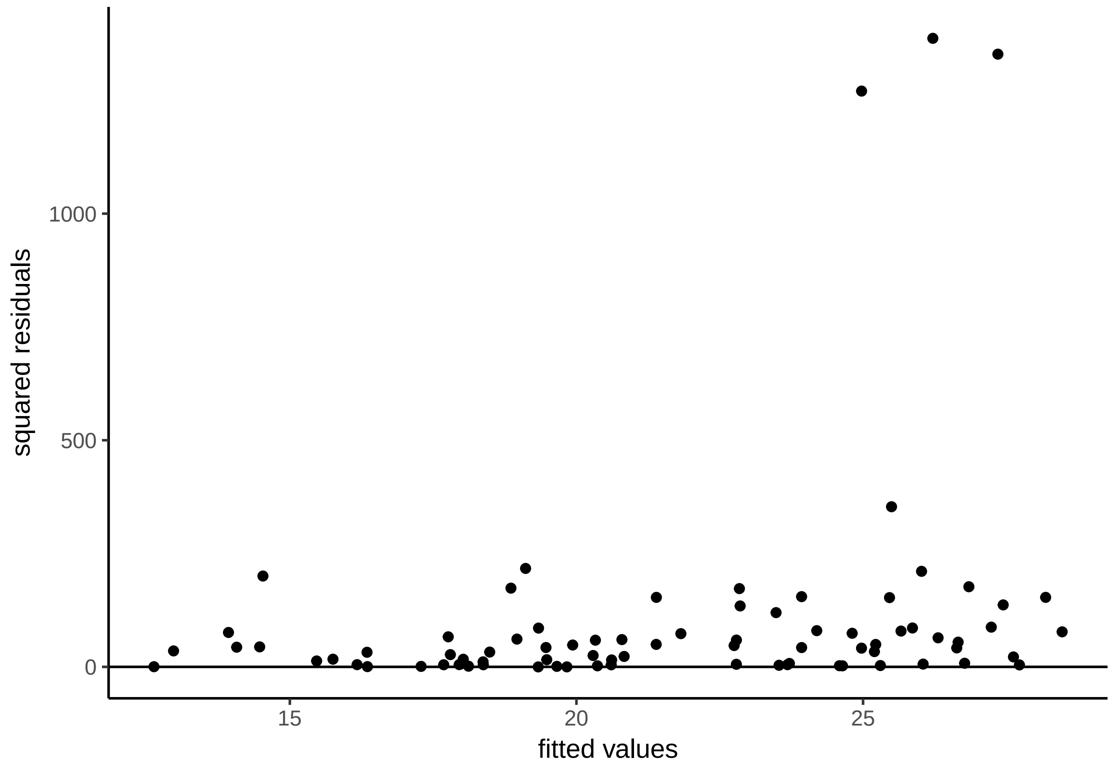
	1	2	3	4	5	6	7	8	9	10	11	12	13
additive treatment effect	-10.00	-9.00	-8.00	-7.00	-6.00	-5.00	-4.00	-3.00	-2.00	-1.00	0.00	1.00	2.00
p-values for lm	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.10	0.21	0.43	0.66	0.98
p-values for lmrob	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.06	0.17	0.50

	2.5 %	97.5 %
standard lm confidence interval	-7.51	3.52
uniroot lm confidence interval	-8.07	2.40
permuted lm confidence interval	-1.00	7.00
standard lmrob confidence interval	-6.50	-0.12
uniroot lmrob confidence interval	-6.50	-0.12
permuted lmrob confidence interval	0.00	6.00

Statistical Inference and Assessment Strategies II

When I have a relatively large sample (N=81), the central limit theory and asymptotic theory can help me not to actually conduct a permutation test to do the hypothesis testing. The hypothetical experimental pool is fairly large. A second method that works well in my dataset is to use mathematical formulas for standard errors that relax the IID assumption and resist highly influential points in a variety of ways (like the "HC" standard errors and the "Robust Cluster" standard errors). What matters is to correct the OLS standard errors. In this section, I will use a simple univariate regression model to demonstrate the process of using a variety of ways to calculate the robust standard errors from the *lm* model.

In my dataset, I worry about the assumption of IID because I suspect the random variables are not independent and identically distributed because I do not know how the observational data are generated. There is an a priori reason to suspect that there is heteroscedasticity in my data, given that this problem is common in cross-sectional data. Heteroscedasticity occurs when the variance of the errors varies across observations (Long & Ervin, 2000, p. 217). In simple words, when the variance of errors is not constant, one of the important assumptions of a linear model, homoscedasticity is violated. In the presence of heteroscedasticity, ordinary least squares estimates are still consistent, but the tests of significance are generally inappropriate because the standard errors obtained from the classic variance covariance matrix are no longer consistent. We will then perform an invalid statistical inference if we do not correct for the possible presence of heteroskedasticity. Figure 2 reveals that we might have a heteroskedasticity problem.



I simplify my regression without controlling for covariates as the following at this moment: $Tariff_{i,t} = \beta_0 + \beta_1 * Democarcy_{i,t-1} + \varepsilon_i$. The standard errors drawn from the OLS canned function will be biased if there is a presence of heteroskedasticity of unknown form in my dataset. Note that the assumption the variance of the error term for each x is constant (Homoskedasticity) is not necessary to show that OLS estimators are unbiased. Heteroscedasticity occurs when the variance of the errors varies across observations (Long & Ervin, 2000, p.217). In simple words, when the variance of errors is not constant, one of the important assumptions of a linear model, homoscedasticity is violated. In the presence of heteroscedasticity, ordinary least squares estimates are still consistent, but the tests of significance are generally inappropriate because the standard errors obtained from the classic variance covariance matrix are no longer consistent. We will then perform an invalid statistical inference if we do not correct for the possible presence of heteroskedasticity. Figure 2 reveals that we might have a heteroskedasticity problem.

Here, I use a avariety of approaches to correct OLS standard errors, by hands and by using packages. The table shows that the results are similar.

To apply the heteroskedasticity consistent covariance matrix (HCCME), I simplify my regression without controlling for covariates as the following at this moment: $tradepolicy_{i,t} = \beta_0 + \beta_1 * DEMOCRACY_{i,t-1} + \varepsilon_i$.

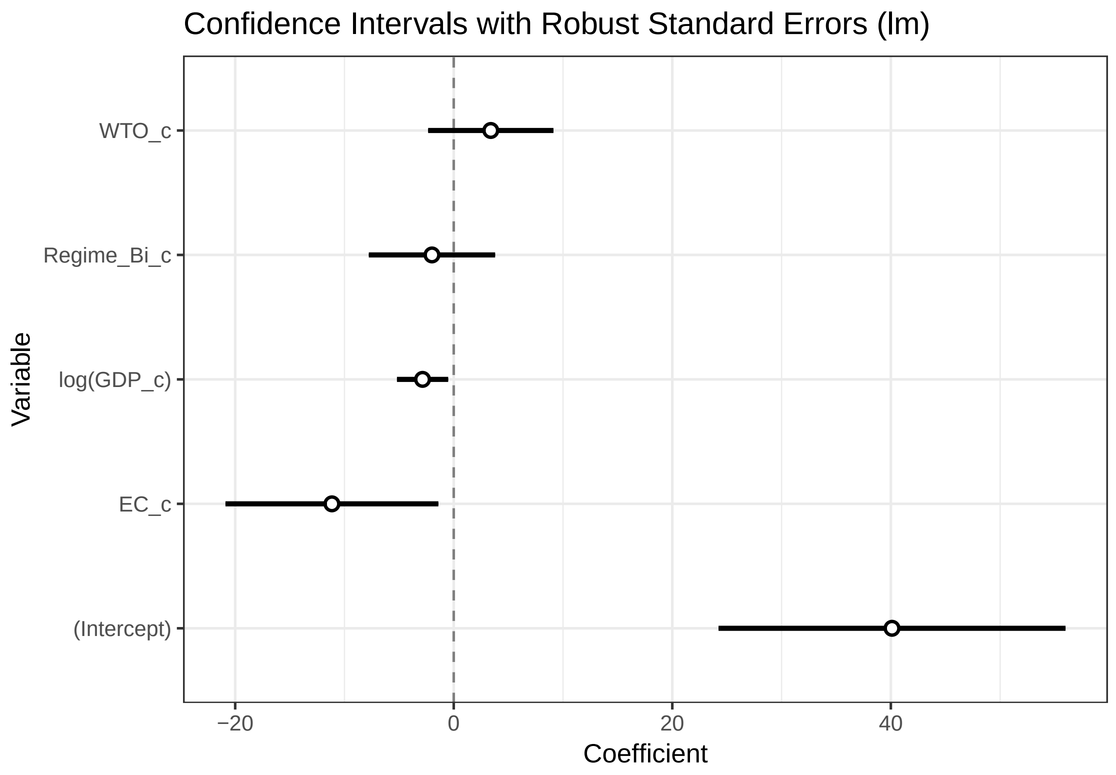
I calculated the unclusterd HC0, HC1, HC2, and HC3 robust standard errors by heteroskedasticity consistent covariance matrix (HCCME) (also known as White robust errors) and by using a “sandwich” R-statistic package. The results are the same, so I know the results computed by the programming packages are reliable in a more complicated model. According to (Long & Ervin, 2000), HC0 is the most commonly used, but HC3-based test is more reliable when the sample size is smaller than 250. I also use the "wild bootstrap" simulation method to cross-check the results. The "HC" standard errors taking into account the Heteroscedasticity in fact smaller than the default standard errors from the OLS.

The clustered versions of standard errors from different methods are also very close to the unclustered versions. After controlling for clustering, I note that the using different methods including covariance matrix and wild bootstrap, the clustered standard errors and unclustered standard errors turn out to be very similar. It is possibly due to the fact that I have collapsed the data in different periods for the given countries, so that the correlated model errors in different time periods within the country level have been removed. In other words, the variances over time within-country are no longer present in the dataset. The number of clustering at the country level may still exist, but the standard errors controlling for the unknown form of cluster error correlation do not deviate much from the unclusterd robust standard errors. The previous tables show the comparions of the standard errors calculted by different methods.

	Variance–covariance matrix	Sandwich package
Standard OLS	2.68	2.68
HC0	2.53	2.53
HC1	2.57	2.57
HC2	2.58	2.58
HC3	2.62	2.62

	Robust Standard Errors
Clustered HC0	2.53
Clustered HC1	2.57
Clustered HC2	2.58
Clustered HC3	2.62
Clustered SEs from Variance-Covariance matrix	2.57
Wild Bootstrap	2.64
Clustered Wild Bootstrap	2.49

Confidence Intervals computed by Robust Standard Errors



I plotted the confidence intervals computed by the clustered robust standard errors in the complete *lm* model with covariates. I assume the standard errors obtained from the clustered function I wrote are accurate because they have corrected for the possible problems of clustering on the state level and the heteroskedasty in the data structure. I also verified the results from the clustered function are not misleading because they tend to agree with the other methods. Because I do not know the structure of heteroskedasticity, it is safe to use the clustered robust standard errors. I also compute the confidence interval with the White HC3 and the clustered standard errors. They are the same (results are not shown).

In the first plot entitled "Confidence Intervals with Robust Standard Errors (lm)", we can see the confidence interval for the targeted estimator includes zero. It means that I cannot reject the null hypothesis that the treatment effect (the effects of democracies on tariff rates) equals to zero. In addition, although the confidence intervals of log(GDP) and economic crisis do not include zero, they are pretty close to it. Also, the robust standard error for economic crisis is quite large, and hence the confidence interval is wide, which suggests the certainty of this estimate is also large.

The second plot shows the confidence intervals calculated from the default *lmrobust* function. For all the estimators, the confidence intervals are very close to zero. I cannot reject the possibility that there is no treatment effect. Democratic developing countries on average over time may not have lower tariff rates than non-democratic developing countries.

Coverage Probability of the Confidence Interval

I also use a simulation method for estimating the coverage probability of the confidence interval calculated from the robust standard error I calculated. Because I have a relatively large sample, I compute the 95% confidence interval as an asymptotic one: $\hat{\beta} plusorminus 1.96 * se$. After I obtained the confidence interval, I need to check its coverage probability.

Here I explain how I proceed to calculate the coverage probability of the confidence interval. Under simulation, I had 1000 samples drawn from the same population (of a sample size from original dataset without replacement). I then use the standard error to compute the confidence interval for each sample. I then computed the proportion of samples for which the *true* mean of the 'population' fall into the confidence interval in each of the 1000 iterations. In such a large repeated sample, I want to check if the confidence intervals include the true population parameter 95 percent of the time.

Unfortunately, the confidence interval fails to meet its desired object. 100% of the estimated confidence intervals contain the true population mean. This confidence interval is too wide, including the True parameter more than it should. I will risk accepting a null hypothesis when it is false. In other words, my hypothesis testing is underpowered: I may fail to reject a null hypothesis when it is false.

It suggests my standard errors are not accurate, or my hypothesis testing fails to achieve its purpose. Or, this result may suggest that my method of calculating the coverage probability is not correct.

```r
## To make the pdf file do
## render("exploration4.Rmd",output_format=pdf_document())

require(knitr)
opts_chunk$set(
  tidy=FALSE,     # display code as typed
  size="small",    # slightly smaller font for code
  echo=TRUE,
  results='markup',
  strip.white=TRUE,
  fig.path='figs/fig',
  cache=FALSE,
  highlight=TRUE,
  width.cutoff=132,
  size='footnotesize',
  out.width='.9\\textwidth',
  message=FALSE,
  comment=NA)

##First, just setup the R environment for today:
if(!file.exists('figs')) dir.create('figs')

options(SweaveHooks=list(fig=function(){
               par(mar=c(3.5, 3, 1.1, 0),
                   pty="s",
                   mgp=c(1.5,0.5,0),
                   oma=c(0,0,0,0))},
             echo=function(){options(continue=" ") ##Don't show "+" prompts,
             options(prompt=" ")
             }),
    digits=4,
    scipen=8,
    width=132
    )
options(error=function(){options(prompt="> ",continue="+ ");NULL})


#To prepare the environment
library(readstata13)
library(dplyr)
library(ggplot2)
#install.packages("ggrepel")
library(ggrepel)
library(stargazer)

#install.packages("devtools")
library(devtools)

library(foreign)
#install.packages("gplots")
library(gplots)

library(lmtest)
library(sandwich)

library(tidyverse)

library(MASS)
library(robustbase)

#install.packages("rmngb")
library(rmngb)
library(here)

#devtools::install_github("ropenscilabs/gramr")
library("gramr")
#write_good_ip()

library(xtable)

getwd()
set_here(path=".", verbose=T)
here()

list.files(path=".")
load("mydata_5collapseyear.rda")

OLS_5_0Bs <- lm(Tariff_c ~ Regime_Bi_c, data=mydata_5)
summary(OLS_5_0Bs)$coefficient[2,1] #-4.29

OLS_5_5Bs <- lm(Tariff_c ~ Regime_Bi_c + log(GDP_c) + EC_c + WTO_c, data=mydata_5)
summary(OLS_5_5Bs)$coefficient[2,1] #-2.84

############


#z is the experiment, shuffle the mydata4$Regime_l1_Bi variable to create a pretend experiment

set.seed(2018)

mydata_5test <- mydata_5

#rm(mydata_5test$a)
#mydata_5test %>% select(-a)
mydata_5test$Z <- sample(rep(c(0,1), each = 1, len = 81))



#'A confidence interval is a collection of not-rejected hypotheses.'
#Under lm:
OLS_5_5Bs <- lm(Tariff_c ~ Regime_Bi_c + log(GDP_c) + EC_c + WTO_c, data=mydata_5)

#Under lm assumption:
confint(OLS_5_5Bs, parm="Regime_Bi_c")
cicanned_lm <- round(confint(OLS_5_5Bs, parm="Regime_Bi_c"),2)
```

```
#############
mytest2ForUniRoot_test<-function(x,y=mydata_5$Tariff_c,z=mydata_5$Regime_Bi_c){
             newy<-y-(z*x)
             .05-summary(lm(newy~ z + GDP_c + EC_c + WTO_c, data=mydata_5))$coef["z","Pr(>|t|)"]
}

#mytest2ForUniRoot_test(20)
#mytest2ForUniRoot(-20)
upperlim<-uniroot(mytest2ForUniRoot_test,interval=c(0,20),extendInt="no")
lowerlim<-uniroot(mytest2ForUniRoot_test,interval=c(-20,0),extendInt="no")
ciroot_lm <- round(c(lowerlim$root,upperlim$root),2)


#This is another way to find the confidence interval using uniroot. The function here is still about ea


### The root means the solution that makes a function equal to 0, and uniroot command is telling R to fi
###"extendInt=No" is telling R not extend search if a different sign cannot be found. In other words, re

cicanned_lm
ciroot_lm

#'A confidence interval is a collection of not-rejected hypotheses.'
#Under lmrob:
lmrob_5Bs <- lmrob(Tariff_c ~ Regime_Bi_c + GDP_c + EC_c + WTO_c, data=mydata_5)

confint(lmrob_5Bs, parm="Regime_Bi_c")

cicanned_lmrob <- round (confint(lmrob_5Bs, parm="Regime_Bi_c"), 2)

##############

mytest3ForUniRoot_test<-function(x,y=mydata_5$Tariff_c,z=mydata_5$Regime_Bi_c){
             newy<-y-(z*x)
             .05-summary(lmrob(newy~ z + GDP_c + EC_c + WTO_c, data=mydata_5))$coef["z","Pr(>|t|)"]
}

#mytest3ForUniRoot_test(20)
#mytest3ForUniRoot_test(-20)
###First, the root means the solution that makes
#a function equal to 0, and uniroot command is telling R
#to find only one solution. Second, the upperlim and lowerlim
#represent the two-tail test. Both upperlim and lowerlim
#tell R to search only one root from the interval 0 to 20 or -20 to 0.
### "extendInt=No" is telling R not extend search if a different sign cannot be found. In other words, i


upperlim<-uniroot(mytest3ForUniRoot_test,interval=c(0,20),extendInt="yes")
lowerlim<-uniroot(mytest3ForUniRoot_test,interval=c(-20,-0.9),extendInt="yes")
ciroot_lmrob <- round(c(lowerlim$root,upperlim$root),2)

cicanned_lmrob
ciroot_lmrob
```

```
## Confidence interval: choose alpha=.05
set.seed(2349854)

OLS_5_5Bs <- lm(Tariff_c ~ Regime_Bi_c + log(GDP_c) + EC_c + WTO_c, data=mydata_5)
simlmtest_lm5Bs <- summary(OLS_5_5Bs)$coef[2,1]
simlmtest_lm5Bs #-2.386


#Imagine we re-run the "experiment"
newExp_lm<-function(y){
  ## A function to randomly assign treatment effect
shuffledz <- sample(mydata_5test$Z)
newlmtest <- coef(lm(y ~ shuffledz+ GDP_c + EC_c + WTO_c, data=mydata_5test))[["shuffledz"]]
  return(newlmtest)
}

myTestStat4_lm<-function(x,newz=shuffledz,y=mydata_5test$Tariff_c){
  shuffledz <- sample(mydata_5test$Z)
  newy<-y-(newz*x)
    coef(lm(newy~ newz + GDP_c + EC_c + WTO_c, data=mydata_5test))[["newz"]]
}

MyFisherTest4_lm <- function(x,thez){
  ## return a p-value
  randDistH0<-replicate(1000,myTestStat4_lm(x=x))
  pTwoSided <- 2*min(c(mean(randDistH0>=simlmtest_lm5Bs),
              mean(randDistH0<=simlmtest_lm5Bs)))
  return(pTwoSided)
}
#######
######

library(foreach)
res1<-foreach(h=seq(-10, 10, 1),.combine='c') %dopar% {message("."); MyFisherTest4_lm(x=h, thez=mydata_
#Now I can use foreach to execute the function repeatedly, passing it the values -10 through 5, and ret


printCIres1lm <- rbind(seq(-10, 10, 1),res1)
printCIres1lm

#CI for lm by using using permutation here is [-1, 7].

lmrob_5Bs <- lmrob(Tariff_c ~ Regime_Bi_c + GDP_c + EC_c + WTO_c, data=mydata_5, control = lmrob.contro

simlmrobtest_5Bs <- summary(lmrob_5Bs)$coef[2,1]
simlmrobtest_5Bs #-3.31

## Confidence interval: choose alpha=.05
set.seed(2349854)
#Imagine we re-run the "experiment"

newExp_lmrob<-function(y){
  ## A function to randomly assign treatment effect
```

```
shuffledz <- sample(mydata_5test$Z)
newlmtest <- coef(lmrob(y ~ shuffledz + GDP_c + EC_c + WTO_c, data=mydata_5test))[["shuffledz"]]
  return(newlmtest)
}

myTestStat4_lmrob<-function(x,newz=shuffledz,y=mydata_5test$Tariff_c){
  shuffledz <- sample(mydata_5test$Z)
  newy<-y-(newz*x)
    coef(lmrob(newy ~ newz + GDP_c + EC_c + WTO_c, data=mydata_5test))[["newz"]]
    #return(coef)
}


MyFisherTest4_lmrob <- function(x,thez){
  ## return a p-value
  randDistH0<-replicate(1000,myTestStat4_lmrob(x=0))
  pTwoSided <- 2*min(c(mean(randDistH0>=simlmrobtest_5Bs),
              mean(randDistH0<=simlmrobtest_5Bs)))
  return(pTwoSided)
}


MyFisherTest4_lmrob <- function(x,thez){
  ## return a p-value
  randDistH0<-replicate(1000,myTestStat4_lmrob(x=x))
  pTwoSided <- 2*min(c(mean(randDistH0>=simlmrobtest_5Bs),
              mean(randDistH0<=simlmrobtest_5Bs)))
  return(pTwoSided)
}
#######
######
library(foreach)
res1_lmrob<-foreach(h=seq(-10,10,1),.combine='c') %dopar% {message("."); MyFisherTest4_lmrob(x=h, thez=


printCIres1lmrob <- rbind(seq(-10,10,1),res1_lmrob)
printCIres1lmrob

#CI here is [0,3].

ci_permute <- round(as.matrix(rbind(printCIres1lm, res1_lmrob)),2)
#ci_permute
rownames(ci_permute) <- c("additive treatment effect", "p-values for lm", "p-values for lmrob")
xtable(ci_permute)


print(xtable::xtable(ci_permute, caption = "Searching for non-rejected intervals under permuation for l
      html.table.attributes="border=1", width = "\\textwidth", caption.placement = "top"), comment=F, f

ci_permute_lm <- c(-1, 7)
ci_permute_lmrob <- c(0, 6)

collect_ci_test <- as.matrix(rbind(cicanned_lm, ciroot_lm, ci_permute_lm, cicanned_lmrob,ciroot_lmrob, 
```

```r
rownames(collect_ci_test) <- c("standard lm confidence interval", "uniroot lm confidence interval", "pe

collect_ci_test


print(xtable::xtable(collect_ci_test, caption = "Collections of Confudence Intervals under pumutation f
      html.table.attributes="border=1"), comment=F, floating = F)

OLS_5_5Bs <- lm(Tariff_c ~ Regime_Bi_c + log(GDP_c) + EC_c + WTO_c, data=mydata_5)

library(ggplot2)

ggplot(data=NULL, aes(OLS_5_5Bs$fitted.values, OLS_5_5Bs$residuals^2))+
  geom_point()+
  geom_hline(yintercept = 0)+
  theme_classic()+
  xlab("fitted values")+
  ylab("squared residuals")


#OLS_5_5Bs <- lm(Tariff_c ~ Regime_Bi_c + log(GDP_c) + EC_c + WTO_c, data=mydata_5)

OLS_5_0Bs <- lm(Tariff_c ~ Regime_Bi_c, data=mydata_5)
summary(OLS_5_0Bs)

#X <- model.matrix(~Regime_l1, data=mydata4_small)#use the discrete polity score
#nrow(X) #3246 observations

X_m5 <- model.matrix(~Regime_Bi_c, data=mydata_5test)#make a model matrix
dim(X_m5) #81

y_m5<- mydata_5test$Tariff_c
N <- length(y_m5) #81

b_m5<- solve(t(X_m5) %*% X_m5) %*% t(X_m5) %*% y_m5 #coefficient Regime: NA because there are missing v
b_m5 #-4.287

ehat_m5<-y_m5 - (X_m5 %*% b_m5)
names(ehat_m5)<-row.names(mydata_5test)
sigma2_m5<-sum(ehat_m5^2)/(nrow(mydata_5test)-length(b_m5))
#sum(ehat^2) is the sum of residuals sqaures; sigam^2 is the variance of the random errors, which equal

vcovb_m5<- sigma2_m5 * solve(t(X_m5) %*% X_m5)
vcovb_m5
#This is covariance matrix for the estimated coefficients.

seb_m5<-sqrt(diag(vcovb_m5))
seb_m5
#This is the standard errors for estimated coefficients.

cbind(b_m5,seb_m5)
#This is the matrix of coefficients and standard errors
```

```
#Performs the (formal) Breusch-Pagan test against heteroskedasticity.
bptest(Tariff_c ~ Regime_Bi_c, data=mydata_5)
#The Breusch-Pagan test fits a linear regression model to the residuals of a linear regression model.
#The residuals should not be well explained by the predictors. My null hypothesis here is variance of e
#The p-value is 0.8, which means that we do not reject against the null hypothesis of homoscedasticity.
OLS_5_OBs <- lm(Tariff_c ~ Regime_Bi_c, data=mydata_5)
summary(OLS_5_OBs)

#We use Long & Ervin (2000) and the code, along with the sandwich package to calculate HC0... etc.
H_m5 <- diag(X_m5 %*% solve(t(X_m5) %*% X_m5) %*% t(X_m5)) #This is leverage, Leverage tells us how muc

#install.packages("sandwich")
library(sandwich)

##OLS standard Errors
## We need an N x N matrix in the middle of this next calculation
vcovIID_m5 <- (solve(crossprod(X_m5)) %*% t(X_m5)) %*% (sigma2_m5 * diag(1,N,N))%*% (X_m5%*%solve(cross
#vcov(OLS_4_0) by default function
sebIID_m5  <- sqrt(diag(vcovIID_m5))

sebIID_m5 #this is the same as the coeff from the canned regression under the assumption of homoscedast

sandseb_m5<- sqrt(diag(vcovHC(OLS_5_OBs, type = "const")))
sandseb_m5 #sebIID_m5 == sandseb_m5


## Make a block diagonal sigma/middle matrix
thesigmaHC0_m5<-diag(as.vector(ehat_m5)^2,nrow=length(ehat_m5),ncol=length(ehat_m5))
dimnames(thesigmaHC0_m5)<-list(names(ehat_m5),names(ehat_m5))

##HC0
vcovHC0_m5 <- (solve(crossprod(X_m5)) %*% t(X_m5)) %*% (thesigmaHC0_m5) %*% ( X_m5 %*% solve(crossprod(

sebHC0_m5<-sqrt(diag(vcovHC0_m5))
sandsebHC0_m5 <- sqrt(diag(vcovHC(OLS_5_OBs, type = "HC0")))

sebHC0_m5
sandsebHC0_m5

##HC1
vcovHC1_m5 <- (N/(N-2))*vcovHC0_m5 ## 2 coeff: beta1, intercept

sebHC1_m5 <-sqrt(diag(vcovHC1_m5))
sandsebHC1_m5 <- sqrt(diag(vcovHC(OLS_5_OBs, type = "HC1")))

sebHC1_m5
sandsebHC1_m5

##HC2
thesigmaHC2_m5<-diag(as.vector(ehat_m5)^2/(1-H_m5),nrow=length(ehat_m5),ncol=length(ehat_m5))
dimnames(thesigmaHC2_m5)<-list(names(ehat_m5),names(ehat_m5))

vcovHC2_m5 <- (solve(crossprod(X_m5)) %*% t(X_m5)) %*% (thesigmaHC2_m5) %*% ( X_m5 %*% solve(crossprod(
##car::hccm(OLS_4_0,type="hc2")

sebHC2_m5 <- sqrt(diag(vcovHC2_m5))
sandsebHC2_m5 <- sqrt(diag(vcovHC(OLS_5_OBs, type = "HC2")))

sebHC2_m5
sandsebHC2_m5

#HC3 Long & Ervin prefer HC3 write that HC3 divides ehat^2 by (1-h)^2 further inflates ehat^2 which adj
thesigmaHC3_m5<-diag(as.vector(ehat_m5)^2/(1-H_m5)^2,nrow=length(ehat_m5),ncol=length(ehat_m5))
dimnames(thesigmaHC3_m5)<-list(names(ehat_m5),names(ehat_m5))

vcovHC3_m5 <- (solve(crossprod(X_m5)) %*% t(X_m5)) %*% (thesigmaHC3_m5) %*% ( X_m5 %*% solve(crossprod(

#car::hccm(OLS_4_0,type="hc3")
#These are also called White-corrected or White-Huber covariance matrices.

sebHC3_m5 <- sqrt(diag(vcovHC3_m5))
sandsebHC3_m5 <- sqrt(diag(vcovHC(OLS_5_OBs, type = "HC3")))

sebHC3_m5
sandsebHC3_m5

#options(digits=4)
#Without considering clustering
SEOLS_m5 <- c(sandseb_m5[2], summary(OLS_5_OBs)$coef[2,2])
SEhc0_m5 <- c(sebHC0_m5[2], sandsebHC0_m5[2])
SEhc1_m5 <- c(sebHC1_m5[2], sandsebHC1_m5[2])
SEhc2_m5 <- c(sebHC2_m5[2], sandsebHC2_m5[2])
SEhc3_m5 <- c(sebHC3_m5[2], sandsebHC3_m5[2])

SEcol1<- rbind(SEOLS_m5, SEhc0_m5, SEhc1_m5, SEhc2_m5, SEhc3_m5)
SEcol1
cname_SEcol1 <- c("Variance-covariance matrix", "Sandwich package")
rname_sEcol1 <- c("Standard OLS", "HC0", "HC1", "HC2", "HC3")
rownames(SEcol1) <- rname_sEcol1
colnames(SEcol1) <- cname_SEcol1

SEcol1
xtable(SEcol1)

print(xtable::xtable(SEcol1, caption = "Calculating Standard Errors under Heteroskedasticity",type = "la
      html.table.attributes="border=1"),comment=F, floating = F)


library(multiwayvcov)

#Clustering in consideration
## For comparison, produce White HC0 VCOV the hard way
vcov_hc0_cm5 <- cluster.vcov(OLS_5_OBs, 1:nrow(mydata_5test), df_correction = FALSE)
coeftest(OLS_5_OBs, vcov_hc0_cm5)
## Produce White HC1 VCOV the hard way
vcov_hc1_cm5 <- cluster.vcov(OLS_5_OBs, 1:nrow(mydata_5test), df_correction = TRUE)
```

```r
coeftest(OLS_5_OBs, vcov_hc1_cm5)
## Produce White HC2 VCOV the hard way
vcov_hc2_cm5 <- cluster.vcov(OLS_5_OBs, 1:nrow(mydata_5test), df_correction = FALSE, leverage = 2)
coeftest(OLS_5_OBs, vcov_hc2_cm5)
## Produce White HC3 VCOV the hard way
vcov_hc3_cm5 <- cluster.vcov(OLS_5_OBs, 1:nrow(mydata_5test), df_correction = FALSE, leverage = 3)
coeftest(OLS_5_OBs, vcov_hc3_cm5)


mydata_5test$CountryF <- as.factor(mydata_5test$Country)

##Comments: there are not many differences between clustered and non-clustered HC0, HC1, HC2, and HC3.

##Consider clustering with cluster.cov
# Cluster by country
vcov_cm5_c <- cluster.vcov(OLS_5_OBs, mydata_5test$CountryF)
coeftest(OLS_5_OBs, vcov_cm5_c)


######try cluster functions

robustse_test <- function(model, cluster){
 require(sandwich)
 require(lmtest)
 M <- length(unique(cluster))
 N <- length(cluster)
 K <- model$rank
 dfc <- (M/(M - 1)) * ((N - 1)/(N - K))
 uj <- apply(estfun(model), 2, function(x) tapply(x, cluster, sum));
 rcse.cov <- dfc * sandwich(model, meat = crossprod(uj)/N)
 rcse.se <- coeftest(model, rcse.cov)
 return(list(rcse.cov, rcse.se))
}

vcov <- robustse_test(OLS_5_OBs, mydata_5test$CountryF)[[1]]
coefs <- robustse_test(OLS_5_OBs, mydata_5test$CountryF)[[2]]

OLS_5_5Bs <- lm(Tariff_c ~ Regime_Bi_c + log(GDP_c) + EC_c + WTO_c, data=mydata_5)
summary(OLS_5_5Bs)

robustse_test <- function(model, cluster){
 require(sandwich)
 require(lmtest)
 M <- length(unique(cluster))
 N <- length(cluster)
 K <- model$rank
 dfc <- (M/(M - 1)) * ((N - 1)/(N - K))
 uj <- apply(estfun(model), 2, function(x) tapply(x, cluster, sum));
 rcse.cov <- dfc * sandwich(model, meat = crossprod(uj)/N)
 rcse.se <- coeftest(model, rcse.cov)
 return(list(rcse.cov, rcse.se))
}
```

```r
vcov_5_5Bs <- robustse_test(OLS_5_5Bs, mydata_5test$CountryF)[[1]]
coefs_5_5Bs <- robustse_test(OLS_5_5Bs, mydata_5test$CountryF)[[2]]

vcov_5_5Bs
coefs_5_5Bs

#summary(OLS_5_5Bs)
# Wild Bootstrap.
#https://cran.r-project.org/web/packages/multiwayvcov/multiwayvcov.pdf


set.seed(19900814)
#install.packages("multiwayvcov")
library(multiwayvcov)
library(lmtest)

OLS_5_0Bs <- lm(Tariff_c ~ Regime_Bi_c, data=mydata_5)
summary(OLS_5_0Bs)

# Wild Bootstrap
vcovWB_m5 <- cluster.boot(OLS_5_0Bs, cluster=1:nrow(mydata_5test),boot_type="wild")
coeftest(OLS_5_0Bs,vcovWB_m5)

# Clustered Wild Bootstrap
##Cluster by country
vcovWBC_m5_c <- cluster.boot(OLS_5_0Bs,cluster=mydata_5test$CountryF,boot_type="wild")
coeftest(OLS_5_0Bs,vcovWBC_m5_c) # Wild Bootstrap with Clustering by country

#When considering clustering


#robust covariance matrix vcovHC
SE_c_hc0 <- sqrt(vcov_hc0_cm5)[2,2]
SE_c_hc1 <- sqrt(vcov_hc1_cm5)[2,2]
SE_c_hc2 <- sqrt(vcov_hc2_cm5)[2,2]
SE_c_hc3 <- sqrt(vcov_hc3_cm5)[2,2]
SE_c_func <- robustse_test(OLS_5_0Bs, mydata_5test$CountryF)[[2]][2,2]
SE_w <- sqrt((vcovWB_m5)[2,2])
SE_c_w <- sqrt((vcovWBC_m5_c)[2,2])


SEcol2<- rbind(SE_c_hc0, SE_c_hc1, SE_c_hc2, SE_c_hc3, SE_c_func, SE_w, SE_c_w)
cname_SEcol2 <- c("Robust Standard Errors")
rname_sEcol2 <- c("Clustered HC0", "Clustered HC1", "Clustered HC2", "Clustered HC3", "Clustered SEs fr
rownames(SEcol2) <- rname_sEcol2
colnames(SEcol2) <- cname_SEcol2

SEcol2
xtable(SEcol2)
print(xtable::xtable(SEcol2, caption = "Calculating Robust Standard Errors consider Clustering",type =
      html.table.attributes="border=1"), comment=F, floating = F)

#try clustered function by country
```

```
coefci(OLS_5_0Bs, parm = NULL, level = 0.95, vcov. = vcov_cm5_c,
       df = (nrow(mydata_5test)-length(b_m5)))

#try clustered HC1
coefci(OLS_5_0Bs, parm = NULL, level = 0.95, vcov. = vcov_hc1_cm5,
       df = (nrow(mydata_5test)-length(b_m5)))

#They are the same

## Produce White HC1 VCOV confidence interval the hard way
vcov_hc1_cm5_5Bs <- cluster.vcov(OLS_5_5Bs, 1:nrow(mydata_5test), df_correction = TRUE)
coeftest(OLS_5_5Bs, vcov_hc1_cm5_5Bs)

coefci(OLS_5_5Bs, parm = NULL, level = 0.95, vcov. = vcov_hc1_cm5_5Bs,
       df = (nrow(mydata_5test)-length(b_m5)))


#CI with Clustering Function
coeftest(OLS_5_5Bs, vcov_5_5Bs)

coefci(OLS_5_5Bs, parm = NULL, level = 0.95, vcov. = vcov_5_5Bs,
       df = (nrow(mydata_5test)-length(b_m5)))


b <- coeftest(OLS_5_5Bs, vcov_5_5Bs)

#rownames(b)

#rownames <- c("Intercept", "Democracy", "GDP", "Economic Crisis", "WTO")

model1Frame <- data.frame(Variable = rownames(b),
                          Coefficient = (b)[,1],
                          SE = (b)[,2])
interval <- -qnorm((1-0.95)/2)

zp1 <- ggplot(model1Frame)
zp1 <- zp1 + geom_hline(yintercept = 0, colour = gray(1/2), lty = 2)
zp1 <- zp1 + geom_linerange(aes(x = Variable, ymin = Coefficient - SE*interval, ymax = Coefficient + SE
                             lwd = 1, position = position_dodge(width = 1/2))
zp1 <- zp1 + geom_pointrange(aes(x = Variable, y = Coefficient, ymin = Coefficient - SE*interval,
                                 ymax = Coefficient + SE*interval),
                              lwd = 1/2, position = position_dodge(width = 1/2),
                              shape = 21, fill = "WHITE")
zp1 <- zp1 + coord_flip() + theme_bw()
zp1 <- zp1 + ggtitle("Confidence Intervals with Robust Standard Errors (lm)")
print(zp1)




lmrob_5Bs <- lmrob(Tariff_c ~ Regime_Bi_c + log(GDP_c) + EC_c + WTO_c, data=mydata_5)
```

```
model2Frame <- data.frame(Variable = rownames(summary(lmrob_5Bs)$coef),
            Coefficient = summary(lmrob_5Bs)$coef[, 1],
            SE = summary(lmrob_5Bs)$coef[, 2])
interval <- -qnorm((1-0.95)/2)

zp2 <- ggplot(model2Frame)
zp2 <- zp2 + geom_hline(yintercept = 0, colour = gray(1/2), lty = 2)
zp2 <- zp2 + geom_linerange(aes(x = Variable, ymin = Coefficient - SE*interval, ymax = Coefficient + SE
                            lwd = 1, position = position_dodge(width = 1/2))
zp2 <- zp2 + geom_pointrange(aes(x = Variable, y = Coefficient, ymin = Coefficient - SE*interval,
                                 ymax = Coefficient + SE*interval),
                             lwd = 1/2, position = position_dodge(width = 1/2),
                             shape = 21, fill = "WHITE")
zp2 <- zp2 + coord_flip() + theme_bw()
zp2 <- zp2 + ggtitle("Confidence Intervals with Robust Standard Errors (lmrob)")
print(zp2)

OLS_5_5Bs <- lm(Tariff_c ~ Regime_Bi_c + log(GDP_c) + EC_c + WTO_c, data=mydata_5)
#summary(OLS_5_5Bs)

#nsamps<-1000
#sampfits<-data.frame(t(replicate(nsamps,coef(lm(milworry~age3,data=sample_n(chile90[,c("age3","milworr

#quantile(sampfits[,"age355ymas"],c(.025,.975))

library(dplyr)
set.seed (20892380)

beta.obs.boot <- numeric (10000)

#origin.fit <- fitted(origin)
#origin.resid <- resid(origin)
for (i in 1: 10000){
  this.ind <- sample (81, 81, replace = T)
  beta.obs.boot[i] <- coef(lm(mydata_5$Tariff_c[this.ind] ~ mydata_5$Regime_Bi_c [this.ind] + mydata_5$
}

plot(density(beta.obs.boot), lwd=3, col = "steelblue")
#v=as.numeric(coef(OLS_3_5Bs)[2])
abline(v=as.numeric(coef(OLS_5_5Bs)[2]), lwd=3, col= "gold")

#bootstrap quantile interval
quantile(beta.obs.boot,c(.025,.975))
CI_lm_m1 <- round(quantile(beta.obs.boot,c(.025,.975)), 2)
CI_lm_m1
set.seed (20892380)
nsamps<-10000
resample_original<-data.frame(t
                              (replicate(nsamps,
      coef(lm(Tariff_c ~ Regime_Bi_c + mydata_5$GDP_c + mydata_5$EC_c + mydata_5$WTO_c,
              data=sample_n(mydata_5[,c("Regime_Bi_c","Tariff_c")],size=81,replace=T))))))

  plot(density(resample_original$Regime_Bi_c), main = "Distribution of the test statistic using bootstr
```

```r
  abline(v=as.numeric(coef(OLS_5_5Bs)[2]), lwd=3, col= "gold")

  quantile(resample_original[,"Regime_Bi_c"],c(.025,.975))
  round( quantile(resample_original[,"Regime_Bi_c"],c(.025,.975)),2)
  #Confidence interval [-9.13, 1.28]

set.seed (20892380)
nsamps<-10000
resample_original<-data.frame(t
                              (replicate(nsamps,
      coef(lm(Tariff_c ~ Regime_Bi_c + mydata_5$GDP_c + mydata_5$EC_c + mydata_5$WTO_c,
              data=sample_n(mydata_5[,c("Regime_Bi_c","Tariff_c")],size=81,replace=F))))))

  plot(density(resample_original$Regime_Bi_c), main = "Distribution of the test statistic using bootstra
  abline(v=as.numeric(coef(OLS_5_5Bs)[2]), lwd=3, col= "gold")

  quantile(resample_original[,"Regime_Bi_c"],c(.025,.975))
  #coverage interval
   round(quantile(resample_original[,"Regime_Bi_c"],c(.025,.975)),2)


CP <- NULL
res_t <- matrix (, nrow = 1000, ncol = 100)
for (j in 1:100){
resample_original<-data.frame(t
                              (replicate(1000,
      coef(lm(Tariff_c ~ Regime_Bi_c + mydata_5$GDP_c + mydata_5$EC_c + mydata_5$WTO_c,
              data=sample_n(mydata_5[,c("Regime_Bi_c","Tariff_c")],size=81,replace=F))))))

res_t[,j] <- resample_original$Regime_Bi_c

t <- mean(res_t[,j])
## Coverage probabilities.
n  <- 81
SE <- SEOLS_m5[1]
## Simulate a data set.
#X <- resample_original[,2]

## Construct the CI.
M <- apply(res_t,2,mean)
C <- 1.96*SE

## Check for coverage.
ci <- ((M-C < 0) & ( M+C > 0))
ci

# or that it is
#ci <- (M-C)<=0 # if the coefficient is positive
#ci <- (M+C)>=0 # if the coefficient is negative
# Then do
CP[j] <- mean(ci)
}
```

```r
CP[j]

cat("\\newpage")
```