Package ‘clusterSEs’

April 5, 2021

Title Calculate Cluster-Robust p-Values and Confidence Intervals

Version 2.6.5

Description Calculate p-values and confidence intervals using cluster-adjusted
t-statistics (based on Ibragimov and Muller (2010) <DOI:10.1198/jbes.2009.08046>, pairs clus-
ter bootstrapped t-statistics, and wild cluster bootstrapped t-statistics (the latter two tech-
niques based on Cameron, Gelbach, and Miller (2008) <DOI:10.1162/rest.90.3.414>). Proce-
dures are included for use with GLM, ivreg, plm (pooling or fixed effects), and mlogit models.

Depends R (>= 3.3.0), AER, Formula, plm, stats

Imports sandwich, lmtest, mlogit (>= 1.1-0), utils, dfidx

License GPL (>= 2)

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cluster.bs.glm  Pairs Cluster Bootstrapped p-Values For GLM

Description

This software estimates p-values using pairs cluster bootstrapped t-statistics for GLM models (Cameron, Gelbach, and Miller 2008). The data set is repeatedly re-sampled by cluster, a model is estimated, and inference is based on the sampling distribution of the pivotal (t) statistic.

Usage

```r
cluster.bs.glm(
  mod,
  dat,
  cluster,
  ci.level = 0.95,
  boot.reps = 1000,
  stratify = FALSE,
  cluster.se = TRUE,
  report = TRUE,
  prog.bar = TRUE,
  output.replicates = FALSE,
  seed = NULL
)
```

Arguments

- **mod**: A model estimated using `glm`.
- **dat**: The data set used to estimate `mod`.
- **cluster**: A formula of the clustering variable.
- **ci.level**: What confidence level should CIs reflect?
- **boot.reps**: The number of bootstrap samples to draw.
- **stratify**: Sample clusters only (= FALSE) or clusters and observations by cluster (= TRUE).
- **cluster.se**: Use clustered standard errors (= TRUE) or ordinary SEs (= FALSE) for bootstrap replicates.
- **report**: Should a table of results be printed to the console?
- **prog.bar**: Show a progress bar of the bootstrap (= TRUE) or not (= FALSE).
- **output.replicates**: Should the cluster bootstrap coefficient replicates be output (= TRUE) or not (= FALSE)?
- **seed**: Random number seed for replicability (default is NULL).
**Value**

A list with the elements

- `p.values` A matrix of the estimated p-values.
- `ci` A matrix of confidence intervals.
- `replicates` Optional: A matrix of the coefficient estimates from each cluster bootstrap replicate.

**Note**


**Author(s)**

Justin Esarey

**References**


**Examples**

```r
## Not run:

# example one: predict whether respondent has a university degree
require(effects)
data(WVS)
logit.model <- glm(degree ~ religion + gender + age, data=WVS, family=binomial(link="logit"))
summary(logit.model)

# compute pairs cluster bootstrapped p-values
clust.bs.p <- cluster.bs.glm(logit.model, WVS, ~ country, report = T)

# example two: predict chicken weight
rm(list=ls())
data(ChickWeight)
dum <- model.matrix(~ ChickWeight$Diet)
```

ChickWeight$Diet2 <- as.numeric(dum[,2])
ChickWeight$Diet3 <- as.numeric(dum[,3])
ChickWeight$Diet4 <- as.numeric(dum[,4])

weight.mod2 <- glm(formula = weight~Diet2+Diet3+Diet4+log(Time+1), data=ChickWeight)

# compute pairs cluster bootstrapped p-values
clust.bs.w <- cluster.bs.glm(weight.mod2, ChickWeight, ~ Chick, report = T)

###################################################################
# example three: murder rate by U.S. state, with interaction term
###################################################################
rm(list=ls())
require(datasets)
state.x77.dat <- data.frame(state.x77)
state.x77.dat$Region <- state.region
state.x77.dat$IncomeXHS <- state.x77.dat$Income * state.x77.dat$HS.Grad
income.mod <- glm(Murder ~ Income + HS.Grad + IncomeXHS, data=state.x77.dat)

# compute pairs cluster bootstrapped p-values
clust.bs.inc <- cluster.bs.glm(income.mod, state.x77.dat, ~ Region,
                                report = T, output.replicates=T, boot.reps=10000)

# compute effect of income on murder rate, by percentage of HS graduates
# using conventional standard errors
HS.grad.vec <- seq(from=38, to=67, by=1)
me.income <- coefficients(income.mod)[2] + coefficients(income.mod)[4]*HS.grad.vec
plot(me.income ~ HS.grad.vec, type="l", ylim=c(-0.0125, 0.0125),
     xlab="% HS graduates", ylab="ME of income on murder rate")
se.income <- sqrt( vcov(income.mod)[2,2] + vcov(income.mod)[4,4]*(HS.grad.vec)^2 +
                   2*vcov(income.mod)[2,4]*HS.grad.vec )
se.income <- sqrt( vcov(income.mod)[2,2] + vcov(income.mod)[4,4]*(HS.grad.vec)^2 +
                   2*vcov(income.mod)[2,4]*HS.grad.vec )
ci.h <- me.income + qt(0.975, lower.tail=T, df=46) * se.income
ci.l <- me.income - qt(0.975, lower.tail=T, df=46) * se.income
lines(ci.h ~ HS.grad.vec, lty=2)
lines(ci.l ~ HS.grad.vec, lty=2)

# use pairs cluster bootstrap to compute CIs, including bootstrap bias-correction factor
# including bootstrap bias correction factor
# cluster on Region

# marginal effect replicates =
me.boot <- matrix(data = clust.bs.inc$replicates[,2], nrow=10000, ncol=30, byrow=F) +
           as.matrix(clust.bs.inc$replicates[,4]) %*% t(HS.grad.vec)

# compute bias-corrected MEs
me.income.bias.cor <- 2*me.income - apply(X=me.boot, FUN=mean, MARGIN=2)

# adjust bootstrap replicates for bias
me.boot.bias.cor <- me.boot + matrix(data = 2*(me.income -
               apply(X=me.boot, FUN=mean, MARGIN=2)),
               ncol=30, nrow=10000, byrow=T)

# compute pairs cluster bootstrap 95% CIs, including bias correction
me.boot.plot <- apply(X = me.boot.bias.cor, FUN=quantile, MARGIN=2, probs=c(0.025, 0.975))
# plot bootstrap bias-corrected marginal effects
lines(me.income.bias.cor ~ HS.grad.vec, lwd=2)
# plot 95% CIs
# a little lowess smoothing applied to compensate for discontinuities
# arising from shifting between replicates
lines(lowess(me.boot.plot[1,] ~ HS.grad.vec), lwd=2, lty=2)
lines(lowess(me.boot.plot[2,] ~ HS.grad.vec), lwd=2, lty=2)

# finishing touches to plot
legend(lty=c(1,2,1,2), lwd=c(1,1,2,2), "topleft",
      legend=c("Model Marginal Effect", "Conventional 95% CI",
                "BS Bias-Corrected Marginal Effect", "Cluster Bootstrap 95% CI"))

## End(Not run)

---

### cluster.bs.ivreg

**Pairs Cluster Bootstrapped p-Values For Regression With Instrumental Variables**

**Description**

This software estimates p-values using pairs cluster bootstrapped t-statistics for instrumental variables regression models (Cameron, Gelbach, and Miller 2008). The data set is repeatedly resampled by cluster, a model is estimated, and inference is based on the sampling distribution of the pivotal (t) statistic.

**Usage**

```r
cluster.bs.ivreg(
  mod, 
  dat, 
  cluster, 
  ci.level = 0.95, 
  boot.reps = 1000, 
  stratify = FALSE, 
  cluster.se = TRUE, 
  report = TRUE, 
  prog.bar = TRUE, 
  output.replicates = FALSE, 
  seed = NULL
)
```

**Arguments**

- `mod` A model estimated using ivreg.
- `dat` The data set used to estimate `mod`.
- `cluster` A formula of the clustering variable.
What confidence level should CIs reflect?

The number of bootstrap samples to draw.

Sample clusters only (= FALSE) or clusters and observations by cluster (= TRUE).

Use clustered standard errors (= TRUE) or ordinary SEs (= FALSE) for bootstrap replicates.

Should a table of results be printed to the console?

Show a progress bar of the bootstrap (= TRUE) or not (= FALSE).

Should the cluster bootstrap coefficient replicates be output (= TRUE) or not (= FALSE)?

Random number seed for replicability (default is NULL).

A list with the elements

A matrix of the estimated p-values.

A matrix of confidence intervals.

Optional: A matrix of the coefficient estimates from each cluster bootstrap replicate.


Justin Esarey


```r
## Not run:

# example one: predict cigarette consumption
```
require(AER)
data("CigarettesSW", package = "AER")
CigarettesSW$rprice <- with(CigarettesSW, price/cpi)
CigarettesSW$rincome <- with(CigarettesSW, income/population/cpi)
CigarettesSW$tcoeff <- with(CigarettesSW, (taxs - tax)/cpi)
fm <- ivreg(log(packs) ~ log(rprice) + log(rincome) |
          log(rincome) + tcoeff + I(tax/cpi), data = CigarettesSW)

# compute pairs cluster bootstrapped p-values
cluster.bs.c <- cluster.bs.ivreg(fm, dat = CigarettesSW, cluster = ~state, report = T)

require(plm)
require(AER)
data(EmplUK)
EmplUK$lag.wage <- lag(EmplUK$wage)
emp.iv <- ivreg(emp ~ wage + log(capital+1) | output + lag.wage + log(capital+1), data = EmplUK)

# compute cluster-adjusted p-values
cluster.bs.e <- cluster.bs.ivreg(mod = emp.iv, dat = EmplUK, cluster = ~firm)

## End(Not run)

---

cluster.bs.mlogit  Pairs Cluster Bootstrapped p-Values For mlogit

### Description

This software estimates p-values using pairs cluster bootstrapped t-statistics for multinomial logit models (Cameron, Gelbach, and Miller 2008). The data set is repeatedly re-sampled by cluster, a model is estimated, and inference is based on the sampling distribution of the pivotal (t) statistic.

### Usage

```r
cluster.bs.mlogit(
  mod,
  dat,
  cluster,
  ci.level = 0.95,
  boot.reps = 1000,
  cluster.se = TRUE,
  report = TRUE,
  prog.bar = TRUE,
  output.replicates = FALSE,
)```
seed = NULL
)

Arguments

mod  
A model estimated using \texttt{mlogit}.

dat  
The data set used to estimate \texttt{mod}.

cluster  
A formula of the clustering variable.

ci.level  
What confidence level should CIs reflect?

boot.reps  
The number of bootstrap samples to draw.

cluster.se  
Use clustered standard errors (= TRUE) or ordinary SEs (= FALSE) for bootstrap replicates.

report  
Should a table of results be printed to the console?

prog.bar  
Show a progress bar of the bootstrap (= TRUE) or not (= FALSE).

output.replicates  
Should the cluster bootstrap coefficient replicates be output (= TRUE) or not (= FALSE)?

seed  
Random number seed for replicability (default is NULL).

Value

A list with the elements

\texttt{p.values}  
A matrix of the estimated p-values.

\texttt{ci}  
A matrix of confidence intervals.

Note


Author(s)

Justin Esarey

References


Examples

## Not run:

# example one: train ticket selection
require(mlogit)
data("Train", package="mlogit")
Train$choiceid <- 1:nrow(Train)

Tr <- dfidx(Train, shape = "wide", varying = 4:11, sep = ",",
choice = "choice", idx = list(c("choiceid", "id")),
idnames = c(NA, "alt"))
Tr$price <- Tr$price/100 * 2.20371
Tr$time <- Tr$time/60

ml.Train <- mlogit(choice ~ price + time + change + comfort | -1, Tr)

# compute pairs cluster bootstrapped p-values
# note: few reps to speed up example
cluster.bs.tr <- cluster.bs.mlogit(ml.Train, Tr, ~ id, boot.reps=100)

# example two: predict type of heating system installed in house
require(mlogit)
data("Heating", package = "mlogit")
H <- Heating
H$region <- as.numeric(H$region)
H.ml <- dfidx(H, shape="wide", choice="depvar", varying=c(3:12),
idx = list(c("idcase", "region")))

m <- mlogit(depvar~ic+oc, H.ml)

# compute pairs cluster bootstrapped p-values
cluster.bs.h <- cluster.bs.mlogit(m, H.ml, ~ region, boot.reps=1000)

## End(Not run)

---

**cluster.bs.plm**  
**Pairs Cluster Bootstrapped p-Values For PLM**

**Description**

This software estimates p-values using pairs cluster bootstrapped t-statistics for fixed effects panel linear models (Cameron, Gelbach, and Miller 2008). The data set is repeatedly re-sampled by cluster, a model is estimated, and inference is based on the sampling distribution of the pivotal (t) statistic.
Usage

```
cluster.bs.plm(
  mod,
  dat,
  cluster = "group",
  ci.level = 0.95,
  boot.reps = 1000,
  cluster.se = TRUE,
  report = TRUE,
  prog.bar = TRUE,
  output.replicates = FALSE,
  seed = NULL
)
```

Arguments

- **mod**: A "within" model estimated using `plm`.
- **dat**: The data set used to estimate `mod`.
- **cluster**: Clustering dimension ("group", the default, or "time").
- **ci.level**: What confidence level should CIs reflect?
- **boot.reps**: The number of bootstrap samples to draw.
- **cluster.se**: Use clustered standard errors (= TRUE) or ordinary SEs (= FALSE) for bootstrap replicates.
- **report**: Should a table of results be printed to the console?
- **prog.bar**: Show a progress bar of the bootstrap (= TRUE) or not (= FALSE).
- **output.replicates**: Should the cluster bootstrap coefficient replicates be output (= TRUE) or not (= FALSE)?
- **seed**: Random number seed for replicability (default is NULL).

Value

A list with the elements

- **p.values**: A matrix of the estimated p-values.
- **ci**: A matrix of confidence intervals.

Author(s)

Justin Esarey

References

Examples

```
# Not run:

# predict employment levels, cluster on group
require(plm)
data(EmplUK)

emp.1 <- plm(emp ~ wage + log(capital+1), data = EmplUK,
model = "within", index=c("firm", "year"))
cluster.bs.plm(mod=emp.1, dat=EmplUK, cluster="group", ci.level = 0.95,
boot.reps = 1000, cluster.se = TRUE, report = TRUE,
prog.bar = TRUE)

# cluster on time
cluster.bs.plm(mod=emp.1, dat=EmplUK, cluster="time", ci.level = 0.95,
boot.reps = 1000, cluster.se = TRUE, report = TRUE,
prog.bar = TRUE)
```

```
## End(Not run)
```

---

cluster.im.glm

*Cluster-Adjusted Confidence Intervals And p-Values For GLM*

**Description**

Computes p-values and confidence intervals for GLM models based on cluster-specific model estimation (Ibragimov and Muller 2010). A separate model is estimated in each cluster, and then p-values and confidence intervals are computed based on a t/normal distribution of the cluster-specific estimates.

**Usage**

```r
cluster.im.glm(
  mod, 
  dat, 
  cluster, 
  ci.level = 0.95, 
  report = TRUE, 
  drop = FALSE, 
  truncate = FALSE, 
  return.vcv = FALSE 
)
```
Arguments

mod A model estimated using glm.
dat The data set used to estimate mod.
cluster A formula of the clustering variable.
ci.level What confidence level should CIs reflect?
report Should a table of results be printed to the console?
drop Should clusters within which a model cannot be estimated be dropped?
truncate Should outlying cluster-specific beta estimates be excluded?
return.vcv Should a VCV matrix and the means of cluster-specific coefficient estimates be returned?

Value

A list with the elements

p.values A matrix of the estimated p-values.
ci A matrix of confidence intervals.
vcv.hat Optional: A cluster-level variance-covariance matrix for coefficient estimates.
beta.bar Optional: A vector of means for cluster-specific coefficient estimates.

Note

Confidence intervals are centered on the cluster averaged estimate, which can diverge from original model estimates under several circumstances (e.g., if clusters have different numbers of observations). Consequently, confidence intervals may not be centered on original model estimates. If drop = TRUE, any cluster for which all coefficients cannot be estimated will be automatically dropped from the analysis. If truncate = TRUE, any cluster for which any coefficient is more than 6 times the interquartile range from the cross-cluster mean will also be dropped as an outlier.

Author(s)

Justin Esarey

References


### Examples

```r
## Not run:

# example one: predict whether respondent has a university degree
# example two: linear model of whether respondent has a university degree
# with interaction between gender and age + country FEs

# compute cluster-adjusted p-values
clust.im.p <- cluster.im.glm(logit.model, WVS, ~ country, report = T)

# example two: linear model of whether respondent has a university degree
# with interaction between gender and age + country FEs

WVS$degree.n <- as.numeric(WVS$degree)
WVS$gender.n <- as.numeric(WVS$gender)
WVS$genderXage <- WVS$gender.n * WVS$age
lin.model <- glm(degree.n ~ gender.n + age + genderXage + religion + as.factor(country), data=WVS)

# compute marginal effect of male gender on probability of obtaining a university degree
# using conventional standard errors
age.vec <- seq(from=18, to=90, by=1)
me.age <- coefficients(lin.model)[2] + coefficients(lin.model)[4]*age.vec
plot(me.age ~ age.vec, type="l", ylim=c(-0.1, 0.1), xlab="age", ylab="ME of male gender on Pr(university degree)"

se.age <- sqrt( vcov(lin.model)[2,2] + vcov(lin.model)[4,4]*(age.vec)^2 +
                2*vcov(lin.model)[2,4]*age.vec)

# center the CIs on the ME using average of cluster-level estimates
# important: divide by sqrt(G) to convert SE of cluster-level estimates into SE of the mean, where G = number of clusters
G <- length(unique(WVS$country))
ci.h.im <- me.age.im + qt(0.975, lower.tail=T, df=(G-1)) * se.age.im/sqrt(G)
ci.l.im <- me.age.im - qt(0.975, lower.tail=T, df=(G-1)) * se.age.im/sqrt(G)
```
cluster.im.ivreg

Cluster-Adjusted Confidence Intervals And p-Values For GLM

Description

Computes p-values and confidence intervals for GLM models based on cluster-specific model estimation (Ibragimov and Muller 2010). A separate model is estimated in each cluster, and then p-values and confidence intervals are computed based on a t/normal distribution of the cluster-specific estimates.

Usage

cluster.im.ivreg(
  mod,
  dat,
  cluster,
  ci.level = 0.95,
  report = TRUE,
  drop = FALSE,
  return.vcv = FALSE
)

Arguments

mod A model estimated using ivreg.
dat The data set used to estimate mod.
cluster A formula of the clustering variable.
ci.level What confidence level should CIs reflect?
report Should a table of results be printed to the console?
drop Should clusters within which a model cannot be estimated be dropped?
return.vcv Should a VCV matrix and the means of cluster-specific coefficient estimates be returned?
**Value**

A list with the elements

- **p.values** A matrix of the estimated p-values.
- **ci** A matrix of confidence intervals.

**Note**

Confidence intervals are centered on the cluster averaged estimate, which can diverge from original model estimates under several circumstances (e.g., if clusters have different numbers of observations). Consequently, confidence intervals may not be centered on original model estimates. If drop = TRUE, any cluster for which all coefficients cannot be estimated will be automatically dropped from the analysis.

**Author(s)**

Justin Esarey

**References**


**Examples**

```r
## Not run:
# example: pooled IV analysis of employment
require(plm)
require(AER)
data(EmplUK)
EmplUK$lag.wage <- lag(EmplUK$wage)
emp.iv <- ivreg(emp ~ wage + log(capital+1) | output + lag.wage + log(capital+1), data = EmplUK)

# compute cluster-adjusted p-values
cluster.im.e <- cluster.im.ivreg(mod=emp.iv, dat=EmplUK, cluster = ~firm)

## End(Not run)
```
cluster.im.mlogit  
Cluster-Adjusted Confidence Intervals And p-Values For mlogit

Description

Computes p-values and confidence intervals for multinomial logit models based on cluster-specific model estimation (Ibragimov and Muller 2010). A separate model is estimated in each cluster, and then p-values and confidence intervals are computed based on a t/normal distribution of the cluster-specific estimates.

Usage

cluster.im.mlogit(
  mod,  
  dat,  
  cluster,  
  ci.level = 0.95,  
  report = TRUE,  
  truncate = FALSE,  
  return.vcv = FALSE
)

Arguments

mod  
A model estimated using mlogit.

dat  
The data set used to estimate mod.

cluster  
A formula of the clustering variable.

ci.level  
What confidence level should CIs reflect?

report  
Should a table of results be printed to the console?

truncate  
Should outlying cluster-specific beta estimates be excluded?

return.vcv  
Should a VCV matrix and the means of cluster-specific coefficient estimates be returned?

Value

A list with the elements

p.values  
A matrix of the estimated p-values.

ci  
A matrix of confidence intervals.
Note

Confidence intervals are centered on the cluster averaged estimate, which can diverge from original model estimates under several circumstances (e.g., if clusters have different numbers of observations). Consequently, confidence intervals may not be centered on original model estimates. Any cluster for which all coefficients cannot be estimated will be automatically dropped from the analysis. If truncate = TRUE, any cluster for which any coefficient is more than 6 times the interquartile range from the cross-cluster mean will also be dropped as an outlier.

Author(s)

Justin Esarey

References


Examples

```r
# example: predict type of heating system installed in house
require(mlogit)
data("Heating", package = "mlogit")
H <- Heating
H$region <- as.numeric(H$region)
H.ml <- dfidx(H, shape="wide", choice="depvar", varying=c(3:12),
idx = list(c("idcase", "region")))
m <- mlogit(depvar~ic+oc, H.ml)

# compute cluster-adjusted p-values
cluster.im.h <- cluster.im.mlogit(m, H.ml, ~ region)
```

## End(Not run)

Description

This software estimates p-values using wild cluster bootstrapped t-statistics for linear family GLM models (Cameron, Gelbach, and Miller 2008). Residuals are repeatedly re-sampled by cluster to form a pseudo-dependent variable, a model is estimated for each re-sampled data set, and inference is based on the sampling distribution of the pivotal (t) statistic. Users may choose whether to
impose the null hypothesis for independent variables; the null is never imposed for the intercept or any model that includes factor variables, interactions, or polynomials (although manually specified versions of these can circumvent the restriction). Confidence intervals are only reported when the null hypothesis is not imposed.

Usage

```r
cluster.wild.glm(
  mod,
  dat,
  cluster,
  ci.level = 0.95,
  impose.null = TRUE,
  boot.reps = 1000,
  report = TRUE,
  prog.bar = TRUE,
  output.replicates = FALSE,
  seed = NULL
)
```

Arguments

- `mod`: A linear (identity link) model estimated using `glm`.
- `dat`: The data set used to estimate `mod`.
- `cluster`: A formula of the clustering variable.
- `ci.level`: What confidence level should CIs reflect? (Note: only reported when `impose.null` == FALSE).
- `impose.null`: Should we impose the null Ho?
- `boot.reps`: The number of bootstrap samples to draw.
- `report`: Should a table of results be printed to the console?
- `prog.bar`: Show a progress bar of the bootstrap (= TRUE) or not (= FALSE).
- `output.replicates`: Should the cluster bootstrap coefficient replicates be output (= TRUE) or not (= FALSE)? Only available when `impose.null` = FALSE.
- `seed`: Random number seed for replicability (default is NULL).

Value

A list with the elements

- `p.values`: A matrix of the estimated p-values.
- `ci`: A matrix of confidence intervals (if null not imposed).

Note

Author(s)
Justin Esarey

References

Examples
```r
## Not run:
#########################################
# example one: predict chicken weight
#########################################
# predict chick weight using diet, do not impose the null hypothesis
# because of factor variable "Diet"
data(ChickWeight)
weight.mod <- glm(formula = weight~Diet,data=ChickWeight)
cluster.wd.w.1 <- cluster.wild.glm(weight.mod, dat = ChickWeight, cluster = ~Chick, boot.reps = 1000)

# impose null
dum <- model.matrix(~ ChickWeight$Diet)
ChickWeight$Diet2 <- as.numeric(dum[,2])
ChickWeight$Diet3 <- as.numeric(dum[,3])
ChickWeight$Diet4 <- as.numeric(dum[,4])

weight.mod2 <- glm(formula = weight~Diet2+Diet3+Diet4,data=ChickWeight)
cluster.wd.w.2 <- cluster.wild.glm(weight.mod2, dat = ChickWeight, cluster = ~Chick, boot.reps = 1000)

########################################################################
# example two: linear model of whether respondent has a university degree
# with interaction between gender and age + country FEs
########################################################################
require(effects)
data(WVS)
WVS$degree.n <- as.numeric(WVS$degree)
WVS$gender.n <- as.numeric(WVS$gender)
WVS$genderXage <- WVS$gender.n * WVS$age
lin.model <- glm(degree.n ~ gender.n + age + genderXage + religion, data=WVS)

# compute marginal effect of male gender on probability of obtaining a university degree
# using conventional standard errors
age.vec <- seq(from=18, to=90, by=1)
```
me.age <- coefficients(lin.model)[2] + coefficients(lin.model)[4]*age.vec
plot(me.age ~ age.vec, type="l", ylim=c(-0.1, 0.1), xlab="age", ylab="ME of male gender on Pr(university degree)"
se.age <- sqrt( vcov(lin.model)[2,2] + vcov(lin.model)[4,4]*(age.vec)^2 + 2*vcov(lin.model)[2,4]*age.vec)
ci.h <- me.age + qt(0.975, lower.tail=T, df=lin.model$df.residual) * se.age
ci.l <- me.age - qt(0.975, lower.tail=T, df=lin.model$df.residual) * se.age
lines(ci.h ~ age.vec, lty=2)
lines(ci.l ~ age.vec, lty=2)

# cluster on country, compute CIs for marginal effect of gender on degree attainment
clust.wild.result <- cluster.wild.glm(lin.model, WVS, ~ country, impose.null = F, report = T, output.replicates=T)
replicates <- clust.wild.result$replicates
me.boot <- matrix(data=NA, nrow=dim(replicates)[1], ncol=length(age.vec))
for(i in 1:dim(replicates)[1]){
  me.boot[i,] <- replicates[i,"gender.n"] + replicates[i,"genderXage"]*age.vec
}
ci.wild <- apply(FUN=quantile, X=me.boot, MARGIN=2, probs=c(0.025, 0.975))

# a little lowess smoothing applied to compensate for discontinuities
# arising from shifting between replicates
lines(lowess(ci.wild[,1] ~ age.vec), lty=3)
lines(lowess(ci.wild[,2] ~ age.vec), lty=3)

# finishing touches to plot
legend(lty=c(1,2,3), "topleft", legend=c("Model Marginal Effect", "Conventional 95% CI", "Wild BS 95% CI"))

## End(Not run)

---

**cluster.wild.ivreg**

Wild Cluster Bootstrapped p-Values For For Regression With Instrumental Variables

**Description**

This software estimates p-values using wild cluster bootstrapped t-statistics for instrumental variables regression models (Cameron, Gelbach, and Miller 2008). Residuals are repeatedly re-sampled by cluster to form a pseudo-dependent variable, a model is estimated for each re-sampled data set, and inference is based on the sampling distribution of the pivotal (t) statistic. Users may choose whether to impose the null hypothesis for independent variables; the null is never imposed for the intercept or any model that includes factor variables, interactions, or polynomials (although manually specified versions of these can circumvent the restriction). Confidence intervals are only reported when the null hypothesis is *not* imposed.
cluster.wild.ivreg

Usage

cluster.wild.ivreg(
  mod,
  dat,
  cluster,
  ci.level = 0.95,
  impose.null = TRUE,
  boot.reps = 1000,
  report = TRUE,
  prog.bar = TRUE,
  output.replicates = FALSE,
  seed = NULL
)

Arguments

  mod  A linear (identity link) model estimated using ivreg.
  dat  The data set used to estimate mod.
  cluster A formula of the clustering variable.
  ci.level What confidence level should CIs reflect? (Note: only reported when impose.null == FALSE).
  impose.null Should we impose the null Ho?
  boot.reps The number of bootstrap samples to draw.
  report Should a table of results be printed to the console?
  prog.bar Show a progress bar of the bootstrap (= TRUE) or not (= FALSE).
  output.replicates Should the cluster bootstrap coefficient replicates be output (= TRUE) or not (= FALSE)? Only available when impose.null = FALSE.
  seed Random number seed for replicability (default is NULL).

Value

  A list with the elements

  p.values  A matrix of the estimated p-values.
  ci  A matrix of confidence intervals (if null not imposed).

Note


Author(s)

  Justin Esarey
References


Examples

```r
## Not run:

#############################################
# example one: predict cigarette consumption
#############################################
require(AER)
data("CigarettesSW", package = "AER")
CigarettesSW$rprice <- with(CigarettesSW, price/cpi)
CigarettesSW$rincome <- with(CigarettesSW, income/population/cpi)
CigarettesSW$tdiff <- with(CigarettesSW, (taxs - tax)/cpi)
fm <- ivreg(log(packs) ~ log(rprice) + log(rincome) | log(rincome) + tdiff + I(tax/cpi), data = CigarettesSW)
# compute cluster-adjusted p-values
cluster.wd.c <- cluster.wild.ivreg(fm, dat=CigarettesSW, cluster = ~state, report = T)

#################################################
# example two: pooled IV analysis of employment
#################################################
require(plm)
require(AER)
data(EmplUK)
EmplUK$lag.wage <- lag(EmplUK$wage)
emp.iv <- ivreg(emp ~ wage + log(capital+1) | output + lag.wage + log(capital+1), data = EmplUK)
# compute cluster-adjusted p-values
cluster.wd.e <- cluster.wild.ivreg(mod=emp.iv, dat=EmplUK, cluster = ~firm)

## End(Not run)
```

cluster.wild.plm

Wild Cluster Bootstrapped p-Values For PLM

Description

This software estimates p-values using wild cluster bootstrapped t-statistics for fixed effects panel linear models (Cameron, Gelbach, and Miller 2008). Residuals are repeatedly re-sampled by cluster to form a pseudo-dependent variable, a model is estimated for each re-sampled data set, and
inference is based on the sampling distribution of the pivotal (t) statistic. The null is never imposed for PLM models.

Usage

```
cluster.wild.plm(
    mod,  
    dat,  
    cluster,  
    ci.level = 0.95,  
    boot.reps = 1000,  
    report = TRUE,  
    prog.bar = TRUE,  
    output.replicates = FALSE,  
    seed = NULL
)
```

Arguments

- **mod**: A "within" model estimated using `plm`.
- **dat**: The data set used to estimate `mod`.
- **cluster**: Clustering dimension ("group", the default, or "time").
- **ci.level**: What confidence level should CIs reflect? (Note: only reported when `impose.null` == FALSE).
- **boot.reps**: The number of bootstrap samples to draw.
- **report**: Should a table of results be printed to the console?
- **prog.bar**: Show a progress bar of the bootstrap (= TRUE) or not (= FALSE).
- **output.replicates**: Should the cluster bootstrap coefficient replicates be output (= TRUE) or not (= FALSE)?
- **seed**: Random number seed for replicability (default is NULL).

Value

A list with the elements

- **p.values**: A matrix of the estimated p-values.
- **ci**: A matrix of confidence intervals (if null not imposed).

Author(s)

Justin Esarey
References


Examples

```r
## Not run:

# predict employment levels, cluster on group
require(plm)
data(EmplUK)

emp.1 <- plm(emp ~ wage + log(capital+1), data = EmplUK, model = "within",
    index=c("firm", "year"))
cluster.wild.plm(mod=emp.1, dat=EmplUK, cluster="group", ci.level = 0.95,
    boot.reps = 1000, report = TRUE, prog.bar = TRUE)

# cluster on time
cluster.wild.plm(mod=emp.1, dat=EmplUK, cluster="time", ci.level = 0.95,
    boot.reps = 1000, report = TRUE, prog.bar = TRUE)

## End(Not run)
```
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