Package ‘plm’

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Description

plm is a package for R which intends to make the estimation of linear panel models straightforward. plm provides functions to estimate a wide variety of models and to make (robust) inference.
Details

For a gentle and comprehensive introduction to the package, please see the package’s vignette.

The main functions to estimate models are:

- `plm`: panel data estimators using `lm` on transformed data, `-pgmm` generalized method of moments (GMM) estimation for panel data,
- `pvcm` variable coefficients models
- `pmg` mean groups (MG), demeaned MG and common correlated effects (CCEMG) estimators.

Next to the model estimation functions, the package offers several functions for statistical tests related to panel data/models.

Multiple functions for (robust) variance–covariance matrices are at hand as well.

The package also provides data sets to demonstrate functions and to replicate some text book/paper results. Use `data(package="plm")` to view a list of available data sets in the package.

Examples

data("Produc", package = "plm")
zz <- plm(log(gsp) ~ log(pcap) + log(pc) + log(emp) + unemp,
data = Produc, index = c("state","year"))
summary(zz)

# replicates some results from Baltagi (2013), table 3.1
data("Grunfeld", package = "plm")
p <- plm(inv ~ value + capital,
data = Grunfeld, model="pooling")
wi <- plm(inv ~ value + capital,
data = Grunfeld, model="within", effect = "twoways")
swar <- plm(inv ~ value + capital,
data = Grunfeld, model="random", effect = "twoways")
amemiya <- plm(inv ~ value + capital,
data = Grunfeld, model = "random", random.method = "amemiya",
effect = "twoways")
walhus <- plm(inv ~ value + capital,
data = Grunfeld, model = "random", random.method = "walhus",
effect = "twoways")
Description

Angrist and Newey’s version of the Chamberlain test

Usage

```r
aneweytest(formula, data, subset, na.action, index = NULL, ...)
```

Arguments

- **formula**: a symbolic description for the model to be estimated,
- **data**: a `data.frame`,
- **subset**: see `lm()`,
- **na.action**: see `lm()`,
- **index**: the indexes,
- **...**: further arguments.

Details

Angrist and Newey’s test is based on the results of the artifactual regression of the within residuals on the covariates for all the periods.

Value

An object of class "htest".

Author(s)

Yves Croissant

References


See Also

`piest()` for Chamberlain’s test

Examples

```r
data("RiceFarms", package = "plm")
aneweytest(log(goutput) ~ log(seed) + log(totlabor) + log(size), RiceFarms, index = "id")
```
Cigar

Cigarette Consumption

Description

a panel of 46 observations from 1963 to 1992

Format

A data frame containing:

- state  state abbreviation
- year   the year
- price  price per pack of cigarettes
- pop    population
- pop16  population above the age of 16
- cpi    consumer price index (1983=100)
- ndi    per capita disposable income
- sales  cigarette sales in packs per capita
- pimin  minimum price in adjoining states per pack of cigarettes

Details

*total number of observations*: 1380

*observation*: regional

*country*: United States

Source

Online complements to Baltagi (2001):
http://www.wiley.com/legacy/wileychi/baltagi/

Online complements to Baltagi (2013):
http://bcs.wiley.com/he-bcs/Books?action=resource&bcsId=4338&itemId=1118672321&resourceId=13452

References


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cipstest

Cross-sectionally Augmented IPS Test for Unit Roots in Panel Models

**Description**

Cross-sectionally augmented Im, Pesaran and Shin (IPS) test for unit roots in panel models.

**Usage**

```r
cipstest(x, lags = 2, type = c("trend", "drift", "none"),
          model = c("cmg", "mg", "dmg"), truncated = FALSE, ...)
```

**Arguments**

- `x`: an object of class "pseries",
- `lags`: lag order for Dickey-Fuller augmentation,
- `type`: one of "trend", "drift", "none",
- `model`: one of "cmg", "mg", "dmg",
- `truncated`: logical specifying whether to calculate the truncated version of the test,
- `...`: further arguments passed to `critvals`.

**Details**

This cross-sectionally augmented version of the IPS unit root test (H0: the `pseries` has a unit root) is a so-called second-generation panel unit root test: it is in fact robust against cross-sectional dependence, provided that the default `type="cmg"` is calculated. Else one can obtain the standard (model="mg") or cross-sectionally demeaned (model="dmg") versions of the IPS test.

**Value**

An object of class "htest".

**Author(s)**

Giovanni Millo

**References**


1https://doi.org/10.1162/003465300558551
See Also

purtest()

Examples

data("Produc", package = "plm")
Produc <- pdata.frame(Produc, index=c("state", "year"))
## check whether the gross state product (gsp) is trend-stationary
cipstest(Produc$gsp, type = "trend")

cortab  

Cross–sectional correlation matrix

description

Computes the cross–sectional correlation matrix

Usage

cortab(x, grouping, groupnames = NULL, value = "statistic", ...)

Arguments

x  
an object of class pseries


grouping  
grouping variable,


groupnames  
a character vector of group names,

value  
to complete

...  
further arguments

Value

A matrix
Description

a panel of 90 observational units (counties) from 1981 to 1987

Format

A data frame containing:

- **county** county identifier
- **year** year from 1981 to 1987
- **crrmte** crimes committed per person
- **prbarr** 'probability' of arrest
- **prbconv** 'probability' of conviction
- **prbpris** 'probability' of prison sentence
- **avgsen** average sentence, days
- **polpc** police per capita
- **density** people per square mile
- **taxpc** tax revenue per capita
- **region** factor. One of 'other', 'west' or 'central'.
- **smsa** factor. (Also called "urban"). Does the individual reside in a SMSA (standard metropolitan statistical area)?
- **pctmin** percentage minority in 1980
- **wcon** weekly wage in construction
- **wtuc** weekly wage in transportation, utilities, communications
- **wtrd** weekly wage in wholesale and retail trade
- **wfr** weekly wage in finance, insurance and real estate
- **wser** weekly wage in service industry
- **wmfg** weekly wage in manufacturing
- **wfed** weekly wage in federal government
- **wsta** weekly wage in state government
- **wloc** weekly wage in local government
- **mix** offence mix: face-to-face/other
- **pctymle** percentage of young males (between ages 15 to 24)
- **lcrmte** log of crimes committed per person
- **lprbarr** log of 'probability' of arrest
- **lprbconv** log of 'probability' of conviction
\textbf{lprbpris} log of ‘probability’ of prison sentence
\textbf{lavgse}n log of average sentence, days
\textbf{lpolpc} log of police per capita
\textbf{ldensity} log of people per square mile
\textbf{ltaxpc} log of tax revenue per capita
\textbf{lpctmin} log of percentage minority in 1980
\textbf{lwcon} log of weekly wage in construction
\textbf{lwtruc} log of weekly wage in transportation, utilities, communications
\textbf{lwtrd} log of weekly wage in wholesale and retail trade
\textbf{lwfir} log of weekly wage in finance, insurance and real estate
\textbf{lwser} log of weekly wage in service industry
\textbf{lwmfg} log of weekly wage in manufacturing
\textbf{lwfed} log of weekly wage in federal government
\textbf{lwsta} log of weekly wage in state government
\textbf{lwloc} log of weekly wage in local government
\textbf{lmix} log of offence mix: face-to-face/other
\textbf{lpctymle} log of percentage of young males (between ages 15 to 24)

\textbf{Details}

\textit{total number of observations} : 630
\textit{observation} : regional
\textit{country} : United States

The variables l* (lcrmrte, lprbarr, ...) contain the pre-computed logarithms of the base variables as found in the original data set. Note that these values slightly differ from what R’s log() function yields for the base variables. In order to reproduce examples from the literature, the pre-computed logs need to be used, otherwise the results differ slightly.

\textbf{Source}

Journal of Applied Econometrics Data Archive (complements Baltagi (2006)):

Online complements to Baltagi (2001):
http://www.wiley.com/legacy/wileychi/baltagi/

Online complements to Baltagi (2013):
http://bcs.wiley.com/he-bcs/Books?action=resource&bcsId=4338&itemId=1118672321&resourceId=13452

References


detect.lindep  
*Functions to detect linear dependence*

Description

Little helper functions to aid users to detect linear dependent columns in a two-dimensional data structure, especially in a (transformed) model matrix - typically useful in interactive mode during model building phase.

Usage

detect.lindep(object, ...)  
## S3 method for class 'matrix'
detect.lindep(object, suppressPrint = FALSE, ...)

## S3 method for class 'data.frame'
detect.lindep(object, suppressPrint = FALSE, ...)

## S3 method for class 'plm'
detect.lindep(object, suppressPrint = FALSE, ...)

## S3 method for class 'plm'
alias(object, ...)

## S3 method for class 'pdata.frame'
alias(object, model = c("pooling", "within",  
"Between", "between", "mean", "random", "fd"), effect = c("individual",  
"time", "twoways"), ...)

Arguments

object  
for detect.lindep: an object which should be checked for linear dependence (of class "matrix", "data.frame", or "plm"); for alias: either an estimated model of class "plm" or a "pdata.frame". Usually, one wants to input a model matrix here or check an already estimated plm model,

...  
further arguments.
for `detect.lindep` only: logical indicating whether a message shall be printed; defaults to printing the message, i.e. to `suppressPrint = FALSE`,

model (see `plm`),
effect (see `plm`),

Details

Linear dependence of columns/variables is (usually) readily avoided when building one’s model. However, linear dependence is sometimes not obvious and harder to detect for less experienced applied statisticians. The so-called "dummy variable trap" is a common and probably the best-known fallacy of this kind (see e.g. Wooldridge (2016), sec. 7-2.). When building linear models with `lm` or `plm`'s pooling model, linear dependence in one’s model is easily detected, at times post hoc.

However, linear dependence might also occur after some transformations of the data, albeit it is not present in the untransformed data. The within transformation (also called fixed effect transformation) used in the "within" model can result in such linear dependence and this is harder to come to mind when building a model. See Examples for two examples of linear dependent columns after the within transformation: ex. 1) the transformed variables have the opposite sign of one another; ex. 2) the transformed variables are identical.

During `plm`'s model estimation, linear dependent columns and their corresponding coefficients in the resulting object are silently dropped, while the corresponding model frame and model matrix still contain the affected columns. The `plm` object contains an element `aliased` which indicates any such aliased coefficients by a named logical.

Both functions, `detect.lindep` and `alias`, help to detect linear dependence and accomplish almost the same: `detect.lindep` is a stand alone implementation while `alias` is a wrapper around `stats::alias.lm()`, extending the `alias` generic to classes "plm" and "pdata.frame". `alias` hinges on the availability of the package `MASS Two` on the system. Not all arguments of `alias.lm` are supported. Output of `alias` is more informative as it gives the linear combination of dependent columns (after data transformations, i.e. after (quasi-)demeaning) while `detect.lindep` only gives columns involved in the linear dependence in a simple format (thus being more suited for automatic post-processing of the information).

Value

For `detect.lindep`: A named numeric vector containing column numbers of the linear dependent columns in the object after data transformation, if any are present. `NULL` if no linear dependent columns are detected.

For `alias`: return value of `stats::alias.lm()` run on the (quasi-)demeaned model, i.e. the information outputted applies to the transformed model matrix, not the original data.

Note

function `detect.lindep` was called `detect_lin_de` initially but renamed for naming consistency later with a back-compatible solution.

2https://CRAN.R-project.org/package=MASS
Author(s)

Kevin Tappe

References


See Also

stats::alias(), stats::model.matrix() and especially plm's model.matrix() for (transformed) model matrices. plm's model.frame().

Examples

```r
### Example 1 ###
# prepare the data
data("Cigar", package = "plm")
Cigar[, "fact1"] <- c(0,1)
Cigar[, "fact2"] <- c(1,0)
Cigar.p <- pdata.frame(Cigar)

# setup a formula and a model frame
form <- price ~ 0 + cpi + fact1 + fact2
mf <- model.frame(Cigar.p, form)
# no linear dependence in the pooling model's model matrix
# (with intercept in the formula, there would be linear dependence)
detect.lindep(model.matrix(mf, model = "pooling"))
# linear dependence present in the FE transformed model matrix
modmat_FE <- model.matrix(mf, model = "within")
detect.lindep(modmat_FE)
mod_FE <- plm(form, data = Cigar.p, model = "within")
detect.lindep(mod_FE)
alias(mod_FE) # => fact1 == -1*fact2
plm(form, data = mf, model = "within")$aliased # "fact2" indicated as aliased

# look at the data: after FE transformation fact1 == -1*fact2
head(modmat_FE)
all.equal(modmat_FE[, "fact1"], -1*modmat_FE[, "fact2"])

### Example 2 ###
# Setup the data:
# Assume CEOs stay with the firms of the Grunfeld data
# for the firm's entire lifetime and assume some fictional
# data about CEO tenure and age in year 1935 (first observation
# in the data set) to be at 1 to 10 years and 38 to 55 years, respectively.
# => CEO tenure and CEO age increase by same value (+1 year per year).
data("Grunfeld", package = "plm")
set.seed(42)
# add fictional data
Grunfeld$CEOTenure <- c(replicate(10, seq(from=s<-sample(1:10, 1), to=s+19, by=1)))
```
Grunfeld$CEOage <- c(replicate(10, seq(from=s<-sample(38:65, 1), to=s+19, by=1)))

# look at the data
head(Grunfeld, 50)

form <- inv ~ value + capital + CEOtenure + CEOage
mf <- model.frame(pdata.frame(Grunfeld), form)
# no linear dependent columns in original data/pooling model
modmat_pool <- model.matrix(mf, model="pooling")
detect.lindep(modmat_pool)
mod_pool <- plm(form, data = Grunfeld, model = "pooling")
alias(mod_pool)

# CEOtenure and CEOage are linear dependent after FE transformation
# (demeaning per individual)
modmat_FE <- model.matrix(mf, model="within")
detect.lindep(modmat_FE)
mod_FE <- plm(form, data = Grunfeld, model = "within")
detect.lindep(mod_FE)
alias(mod_FE)

# look at the transformed data: after FE transformation CEOtenure == 1*CE0age
head(modmat_FE, 50)
all.equal(modmat_FE[, "CEOtenure"], modmat_FE[, "CEOage"])

---

**EmplUK**

*Employment and Wages in the United Kingdom*

**Description**

An unbalanced panel of 140 observations from 1976 to 1984

**Format**

A data frame containing:

- **firm** firm index
- **year** year
- **sector** the sector of activity
- **emp** employment
- **wage** wages
- **capital** capital
- **output** output
Details

total number of observations: 1031
observation: firms
country: United Kingdom

Source

ercomp
Estimation of the error components

Description
This function enables the estimation of the variance components of a panel model.

Usage

ercomp(object, ...)

## S3 method for class 'plm'
ercomp(object, ...)

## S3 method for class 'pdata.frame'
ercomp(object, effect = c("individual", "time", "twoways", "nested"), method = NULL, models = NULL, dfcor = NULL, index = NULL, ...)

## S3 method for class 'formula'
ercomp(object, data, effect = c("individual", "time", "twoways", "nested"), method = NULL, models = NULL, dfcor = NULL, index = NULL, ...)

## S3 method for class 'ercomp'
print(x, digits = max(3, getOption("digits") - 3), ...)

Arguments

object a formula or a plm object,
... further arguments.
effect the effects introduced in the model, see plm() for details,
method method of estimation for the variance components, see plm() for details,
models the models used to estimate the variance components (an alternative to the previous argument),
ercomp

dfcor  a numeric vector of length 2 indicating which degree of freedom should be used,
index  the indexes,
data  a data.frame,
x  an ercomp object,
digits  digits,

Value

An object of class "ercomp": a list containing

- `sigma2` a named numeric with estimates of the variance components,
- `theta` contains the parameter(s) used for the transformation of the variables: For a one-way model, a numeric corresponding to the selected effect (individual or time); for a two-ways model a list of length 3 with the parameters. In case of a balanced model, the numeric has length 1 while for an unbalanced model, the numerics’ length equal the number of observations.

Author(s)

Yves Croissant

References


See Also

plm() where the estimates of the variance components are used if a random effects model is estimated

Examples

data("Produc", package = "plm")
# an example of the formula method
ercomp(log(gsp) ~ log(pcap) + log(pc) + log(emp) + unemp, data = Produc, 
    method = "walhus", effect = "time")
# same with the plm method
z <- plm(log(gsp) ~ log(pcap) + log(pc) + log(emp) + unemp, 
    data = Produc, random.method = "walhus", 
    effect = "time", model = "random")
ercomp(z)  
# a two-ways model  
ercomp(log(gsp) ~ log(pcap) + log(pc) + log(emp) + unemp, data = Produc,  
method = "amemiya", effect = "twoways")

---

**fixef.plm**

**Extract the Fixed Effects**

**Description**

Function to extract the fixed effects from a `plm` object and associated summary method.

**Usage**

```r
## S3 method for class 'plm'
fixef(object, effect = NULL, type = c("level", "dfirst",  
"dmean"), vcov = NULL, ...)

## S3 method for class 'fixef'
print(x, digits = max(3, getOption("digits") - 2),  
width = getOption("width"), ...)

## S3 method for class 'fixef'
summary(object, ...)

## S3 method for class 'summary.fixef'
print(x, digits = max(3, getOption("digits") - 2),  
width = getOption("width"), ...)
```

**Arguments**

- **effect**: one of "individual" or "time", only relevant in case of two–ways effects models,
- **type**: one of "level", "dfirst", or "dmean",
- **vcov**: a variance–covariance matrix furnished by the user or a function to calculate one (see Examples),
- **...**: further arguments.
- **x, object**: an object of class "plm", an object of class "fixef" for the print and the summary method,
- **digits**: digits,
- **width**: the maximum length of the lines in the print output,
Details

Function `fixef` calculates the fixed effects and returns an object of class `c("fixef", "numeric")`. By setting the `type` argument, the fixed effects may be returned in levels ("level"), as deviations from the first value of the index ("dfirst"), or as deviations from the overall mean ("dmean"). If the argument `vcov` was specified, the standard errors (stored as attribute "se" in the return value) are the respective robust standard errors.

The associated `summary` method returns an extended object of class `c("summary.fixef", "matrix")` with more information (see sections Value and Examples).

References with formulae (except for the two-ways unbalanced case) are, e.g., Greene (2012), Ch. 11.4.4, p. 364, formulae (11-25); Wooldridge (2010), Ch. 10.5.3, pp. 308-309, formula (10.58).

Value

For function `fixef` an object of class `c("fixef", "numeric")` is returned:
It is a numeric vector containing the fixed effects with attribute `se` which contains the standard errors. There are two further attributes: attribute `type` contains the chosen type (the value of argument `type` as a character); attribute `df.residual` holds the residual degrees of freedom (integer) from the fixed effects model (plm object) on which `fixef` was run.

For function `summary.fixef` an object of class `c("summary.fixef", "matrix")` is returned:
It is a matrix with four columns in this order: the estimated fixed effects, their standard errors and associated t-values and p-values. The type of the fixed effects and the standard errors in the `summary.fixef` objects correspond to was requested in the `fixef` function by arguments `type` and `vcov`, respectively.

Author(s)

Yves Croissant

References


See Also

`within_intercept()` for the overall intercept of fixed effect models along its standard error, `plm()` for `plm` objects and within models (= fixed effects models) in general. See `ranef()` to extract the random effects from a random effects model.

Examples

data("Grunfeld", package = "plm")
gi <- plm(inv ~ value + capital, data = Grunfeld, model = "within")
fixef(gi)
summary(fixef(gi))
summary(fixef(gi))[, c("Estimate", "Pr>|t|")]
# only estimates and p-values
Gasoline

# relationship of type = "dmean" and "level" and overall intercept
fx_level <- fixef(gi, type = "level")
fx_dmean <- fixef(gi, type = "dmean")
overallint <- within_intercept(gi)
all.equal(overallint + fx_dmean, fx_level, check.attributes = FALSE) # TRUE

# extract time effects in a twoways effects model
gi_tw <- plm(inv ~ value + capital, data = Grunfeld,
model = "within", effect = "twoways")
fixef(gi_tw, effect = "time")

# with supplied variance-covariance matrix as matrix, function,
# and function with additional arguments
fx_level_robust1 <- fixef(gi, vcov = vcovHC(gi))
fx_level_robust2 <- fixef(gi, vcov = vcovHC)
fx_level_robust3 <- fixef(gi, vcov = function(x) vcovHC(x, method = "white2"))
summary(fx_level_robust1) # gives fixed effects, robust SEs, t- and p-values

# calc. fitted values of oneway within model:
fixefs <- fixef(gi)[index(gi, which = "id")]
fitted_by_hand <- fixefs + gi$coefficients["value"] * gi$model$value +
    gi$coefficients["capital"] * gi$model$capital

Gasoline

Gasoline Consumption

Description

A panel of 18 observations from 1960 to 1978

Format

A data frame containing:

- **country**  a factor with 18 levels
- **year** the year
- **lgaspcar** logarithm of motor gasoline consumption per car
- **lincomep** logarithm of real per-capita income
- **lrpmpg** logarithm of real motor gasoline price
- **lcarpcap** logarithm of the stock of cars per capita

Details

- total number of observations : 342
- observation : country
- country : OECD
Grunfeld

Source

Online complements to Baltagi (2001):
http://www.wiley.com/legacy/wileychi/baltagi/

Online complements to Baltagi (2013):
http://bcs.wiley.com/he-bcs/Books?action=resource&bcsId=4338&itemId=1118672321&resourceId=13452

References


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Grunfeld

*Grunfeld’s Investment Data*

Description

A balanced panel of 10 observational units (firms) from 1935 to 1954

Format

A data frame containing :

- **firm** observation
- **year** date
- **inv** gross Investment
- **value** value of the firm
- **capital** stock of plant and equipment

Details

*total number of observations* : 200
*observation* : production units
*country* : United States
Note

The Grunfeld data as provided in package `plm` is the same data as used in Baltagi (2001), see Examples below.

NB:
Various versions of the Grunfeld data circulate online. Also, various text books (and also varying among editions) and papers use different subsets of the original Grunfeld data, some of which contain errors in a few data points compared to the original data used by Grunfeld (1958) in his PhD thesis. See Kleiber/Zeileis (2010) and its accompanying website for a comparison of various Grunfeld data sets in use.

Source

Online complements to Baltagi (2001):
http://www.wiley.com/legacy/wileychi/baltagi/
http://www.wiley.com/legacy/wileychi/baltagi/supp/Grunfeld.fil

Online complements to Baltagi (2013):
http://bcs.wiley.com/he-bcs/Books?action=resource&bcsId=4338&itemId=1118672321&resourceId=13452

References


See Also

For the complete Grunfeld data (11 firms), see `AER::Grunfeld`, in the `AER` package.

Examples

```r
## Not run:
# Compare plm's Grunfeld data to Baltagi's (2001) Grunfeld data:
data("Grunfeld", package="plm")
Grunfeld_baltagi2001 <- read.csv("http://www.wiley.com/legacy/wileychi/
  baltagi/supp/Grunfeld.fil", sep="", header = FALSE)
library(compare)
compare::compare(Grunfeld, Grunfeld_baltagi2001, allowAll = T) # same data set
## End(Not run)
```
has.intercept  

Check for the presence of an intercept in a formula or in a fitted model

Description

The presence of an intercept is checked using the formula which is either provided as the argument of the function or extracted from a fitted model.

Usage

```r
has.intercept(object, ...)  
## Default S3 method:
has.intercept(object, ...)  
## S3 method for class 'formula'
has.intercept(object, ...)  
## S3 method for class 'Formula'
has.intercept(object, rhs = NULL, ...)  
## S3 method for class 'panelmodel'
has.intercept(object, ...)  
## S3 method for class 'plm'
has.intercept(object, part = "first", ...)  
```

Arguments

- `object`: a formula, a Formula or a fitted model (of class `plm` or `panelmodel`), further arguments.
- `rhs`, `part`: the index of the right hand sides part of the formula for which one wants to check the presence of an intercept (relevant for the Formula and the plm methods).

Value

- a boolean

Hedonic

Hedonic Prices of Census Tracts in the Boston Area

Description

A cross-section
**Format**

A dataframe containing:

- **mv** median value of owner–occupied homes
- **crim** crime rate
- **zn** proportion of 25,000 square feet residential lots
- **indus** proportion of no–retail business acres
- **chas** is the tract bounds the Charles River?
- **nox** annual average nitrogen oxide concentration in parts per hundred million
- **rm** average number of rooms
- **age** proportion of owner units built prior to 1940
- **dis** weighted distances to five employment centers in the Boston area
- **rad** index of accessibility to radial highways
- **tax** full value property tax rate ($/$10,000)
- **ptratio** pupil/teacher ratio
- **blacks** proportion of blacks in the population
- **lstat** proportion of population that is lower status
- **townid** town identifier

**Details**

- *number of observations*: 506
- *observation*: regional
- *country*: United States

**Source**

Online complements to Baltagi (2001):
http://www.wiley.com/legacy/wileychi/baltagi/

Online complements to Baltagi (2013):
http://bcs.wiley.com/he-bcs/Books?action=resource&bcsId=4338&itemId=1118672321&resourceId=13452

**References**

Description

This function extracts the information about the structure of the individual and time dimensions of panel data. Grouping information can also be extracted if the panel data were created with a grouping variable.

Usage

```r
## S3 method for class 'pindex'
index(x, which = NULL, ...)
## S3 method for class 'pdata.frame'
index(x, which = NULL, ...)
## S3 method for class 'pseries'
index(x, which = NULL, ...)
## S3 method for class 'panelmodel'
index(x, which = NULL, ...)
```

Arguments

- `x` an object of class "pindex", "pdata.frame", "pseries" or "panelmodel",
- `which` the index(es) to be extracted (see details),
- `...` further arguments.

Details

Panel data are stored in a "pdata.frame" which has an "index" attribute. Fitted models in "plm" have a "model" element which is also a "pdata.frame" and therefore also has an "index" attribute. Finally, each series, once extracted from a "pdata.frame", becomes of class "pseries", which also has this "index" attribute. "index" methods are available for all these objects. The argument "which" indicates which index should be extracted. If `which = NULL`, all indexes are extracted. "which" can also be a vector of length 1, 2, or 3 (3 only if the pdata frame was constructed with an additional group index) containing either characters (the names of the individual variable and/or of the time variable and/or the group variable or "id" and "time") and "group" or integers (1 for the individual index, 2 for the time index, and 3 for the group index (the latter only if the pdata frame was constructed with such)).

Value

A vector or an object of class `c("pindex","data.frame")` containing either one index, individual and time index, or (any combination of) individual, time and group indexes.
is.pbalanced

Author(s)
Yves Croissant

See Also
pdata.frame(), plm()

Examples

data("Grunfeld", package = "plm")
Gr <- pdata.frame(Grunfeld, index = c("firm", "year"))
m <- plm(inv ~ value + capital, data = Gr)
index(Gr, "firm")
index(Gr, "time")
index(Gr$inv, c(2, 1))
index(m, "id")

# with additional group index
data("Produc", package = "plm")
pProduc <- pdata.frame(Produc, index = c("state", "year", "region"))
index(pProduc, 3)
index(pProduc, "region")
index(pProduc, "group")

is.pbalanced  Check if data are balanced

Description
This function checks if the data are balanced, i.e. if each individual has the same time periods

Usage
is.pbalanced(x, ...)

## Default S3 method:
is.pbalanced(x, y, ...)

## S3 method for class 'data.frame'
is.pbalanced(x, index = NULL, ...)

## S3 method for class 'pdata.frame'
is.pbalanced(x, ...)

## S3 method for class 'pseries'
is.pbalanced(x, ...)
## S3 method for class 'panelmodel'
is.pbalanced(x, ...)

## S3 method for class 'pgmm'
is.pbalanced(x, ...)

### Arguments

- **x**: an object of class `pdata.frame`, `data.frame`, `pseries`, `panelmodel`, `pgmm`
- **...**: further arguments.
- **y**: to describe
- **index**: only relevant for `data.frame` interface; if `NULL`, the first two columns of the data.frame are assumed to be the index variables; if not `NULL`, both dimensions ('individual', 'time') need to be specified by `index` as character of length 2 for data frames, for further details see `pdata.frame()`.

### Details

Balanced data are data for which each individual has the same time periods. The returned values of the `is.pbalanced(object)` methods are identical to `pdim(object)$balanced`. `is.pbalanced` is provided as a short cut and is faster than `pdim(object)$balanced` because it avoids those computations performed by `pdim` which are unnecessary to determine the balancedness of the data.

### Value

A logical indicating whether the data associated with object `x` are balanced (TRUE) or not (FALSE).

### See Also

- `punbalancedness()` for two measures of unbalancedness,
- `make.pbalanced()` to make data balanced;
- `is.pconsecutive()` to check if data are consecutive;
- `make.pconsecutive()` to make data consecutive (and, optionally, also balanced).
- `pdim()` to check the dimensions of a `pdata.frame` (and other objects),
- `pvar()` to check for individual and time variation of a `pdata.frame` (and other objects),
- `pseries()`, `data.frame()`, `pdata.frame()`.

### Examples

```r
# take balanced data and make it unbalanced
# by deletion of 2nd row (2nd time period for first individual)
data("Grunfeld", package = "plm")
Grunfeld_missing_period <- Grunfeld[-2, ]
is.pbalanced(Grunfeld_missing_period) # check if balanced: FALSE
pdim(Grunfeld_missing_period)$balanced # same
```
# pdata.frame interface
pGrunfeld_missing_period <- pdata.frame(Grunfeld_missing_period)
is.pbalanced(Grunfeld_missing_period)

# pseries interface
is.pbalanced(pGrunfeld_missing_period$inv)

---

is.pconsecutive  Check if time periods are consecutive

Description

This function checks for each individual if its associated time periods are consecutive (no "gaps" in time dimension per individual)

Usage

is.pconsecutive(x, ...)

## Default S3 method:
is.pconsecutive(x, id, time, na.rm.tindex = FALSE, ...)

## S3 method for class 'data.frame'
is.pconsecutive(x, index = NULL,
               na.rm.tindex = FALSE, ...)

## S3 method for class 'pseries'
is.pconsecutive(x, na.rm.tindex = FALSE, ...)

## S3 method for class 'pdata.frame'
is.pconsecutive(x, na.rm.tindex = FALSE, ...)

## S3 method for class 'panelmodel'
is.pconsecutive(x, na.rm.tindex = FALSE, ...)

Arguments

x  usually, an object of class pdata.frame, data.frame, pseries, or an estimated panelmodel; for the default method x can also be an arbitrary vector or NULL, see Details.

...  further arguments.

id, time  only relevant for default method: vectors specifying the id and time dimensions, i.e. a sequence of individual and time identifiers, each as stacked time series,

na.rm.tindex  logical indicating whether any NA values in the time index are removed before consecutiveness is evaluated (defaults to FALSE).
is.pconsecutive

index only relevant for data.frame interface; if NULL, the first two columns of the data.frame are assumed to be the index variables; if not NULL, both dimensions ('individual', 'time') need to be specified by index for is.pconsecutive on data frames, for further details see pdata.frame().

Details

(p)data.frame, pseries and estimated panelmodel objects can be tested if their time periods are consecutive per individual. For evaluation of consecutiveness, the time dimension is interpreted to be numeric, and the data are tested for being a regularly spaced sequence with distance 1 between the time periods for each individual (for each individual the time dimension can be interpreted as sequence t, t+1, t+2, ... where t is an integer). As such, the "numerical content" of the time index variable is considered for consecutiveness, not the "physical position" of the various observations for an individuals in the (p)data.frame/pseries (it is not about "neighbouring" rows). If the object to be evaluated is a pseries or a pdata.frame, the time index is coerced from factor via as.character to numeric, i.e. the series as.numeric(as.character(index(<pseries/pdata.frame>))[[2]]) is evaluated for gaps.

The default method also works for argument x being an arbitrary vector (see Examples), provided one can supply arguments id and time, which need to ordered as stacked time series. As only id and time are really necessary for the default method to evaluate the consecutiveness, x = NULL is also possible. However, if the vector x is also supplied, additional input checking for equality of the lengths of x, id and time is performed, which is safer.

For the data.frame interface, the data is ordered in the appropriate way (stacked time series) before the consecutiveness is evaluated. For the pdata.frame and pseries interface, ordering is not performed because both data types are already ordered in the appropriate way when created.

Note: Only the presence of the time period itself in the object is tested, not if there are any other variables. NA values in individual index are not examined but silently dropped - In this case, it is not clear which individual is meant by id value NA, thus no statement about consecutiveness of time periods for those "NA-individuals" is possible.

Value

A named logical vector (names are those of the individuals). The i-th element of the returned vector corresponds to the i-th individual. The values of the i-th element can be:

list("TRUE") if the i-th individual has consecutive time periods,
list("FALSE") if the i-th individual has non-consecutive time periods,
list("NA") if there are any NA values in time index of the i-th the individual; see also argument na.rm.tindex to remove those.

Author(s)

Kevin Tappe
See Also

make.pconsecutive() to make data consecutive (and, as an option, balanced at the same time) and make.pbalanced() to make data balanced.
pdim() to check the dimensions of a 'pdata.frame' (and other objects), pvar() to check for individual and time variation of a 'pdata.frame' (and other objects), lag() for lagged (and leading) values of a 'pseries' object.

Examples

data("Grunfeld", package = "plm")
is.pconsecutive(Grunfeld)
is.pconsecutive(Grunfeld, index=c("firm", "year"))

# delete 2nd row (2nd time period for first individual)
# -> non consecutive
Grunfeld_missing_period <- Grunfeld[-2, ]
is.pconsecutive(Grunfeld_missing_period)
all(is.pconsecutive(Grunfeld_missing_period)) # FALSE

# delete rows 1 and 2 (1st and 2nd time period for first individual)
# -> consecutive
Grunfeld_missing_period_other <- Grunfeld[-c(1,2), ]
is.pconsecutive(Grunfeld_missing_period_other) # all TRUE

# delete year 1937 (3rd period) for _all_ individuals
Grunfeld_wo_1937 <- Grunfeld[Grunfeld$year != 1937, ]
is.pconsecutive(Grunfeld_wo_1937) # all FALSE

# pdata.frame interface
pGrunfeld <- pdata.frame(Grunfeld)
pGrunfeld_missing_period <- pdata.frame(Grunfeld_missing_period)
is.pconsecutive(pGrunfeld) # all TRUE
is.pconsecutive(pGrunfeld_missing_period) # first FALSE, others TRUE

# panelmodel interface (first, estimate some models)
mod_pGrunfeld <- plm(inv ~ value + capital, data = Grunfeld)
mod_pGrunfeld_missing_period <- plm(inv ~ value + capital, data = Grunfeld_missing_period)
is.pconsecutive(mod_pGrunfeld)
is.pconsecutive(mod_pGrunfeld_missing_period)
nobs(mod_pGrunfeld) # 200
nobs(mod_pGrunfeld_missing_period) # 199

# pseries interface
pinv <- pGrunfeld$inv
is.pseries <- pGrunfeld_missing_period$inv

is.pconsecutive(pinv)

is.pconsecutive(pinv_missing_period)

# default method for arbitrary vectors or NULL
inv <- Grunfeld$inv
inv_missing_period <- Grunfeld_missing_period$inv
is.pconsecutive(inv, id = Grunfeld$firm, time = Grunfeld$year)

is.pconsecutive(inv_missing_period, id = Grunfeld_missing_period$firm,
                 time = Grunfeld_missing_period$year)

# (not run) demonstrate mismatch lengths of x, id, time
# is.pconsecutive(x = inv_missing_period, id = Grunfeld$firm, time = Grunfeld$year)

# only id and time are needed for evaluation
is.pconsecutive(NULL, id = Grunfeld$firm, time = Grunfeld$year)

is.pseries

Check if an object is a pseries

Description

This function checks if an object qualifies as a pseries

Usage

is.pseries(object)

Arguments

object object to be checked for pseries features

Details

A "pseries" is a wrapper around a "basic class" (numeric, factor, logical, or character).

To qualify as a pseries, an object needs to have the following features:

- class contains "pseries" and there are at least two classes ("pseries" and the basic
class),
- have an appropriate index attribute (defines the panel structure),
- any of is.numeric, is.factor, is.logical, is.character, is.complex is
  TRUE.

Value

A logical indicating whether the object is a pseries (TRUE) or not (FALSE).
See Also

`pseries()` for some computations on pseries and some further links.

Examples

```r
# Create a pdata.frame and extract a series, which becomes a pseries
data("EmplUK", package = "plm")
Em <- pdata.frame(EmplUK)
z <- Em$output

class(z) # pseries as indicated by class
is.pseries(z) # and confirmed by check

# destroy index of pseries and re-check
attr(z, "index") <- NA
is.pseries(z) # now FALSE
```

---

### LaborSupply  

**Wages and Hours Worked**

**Description**

A panel of 532 observations from 1979 to 1988

**Format**

A data frame containing:

- `lnhr` log of annual hours worked
- `lnwg` log of hourly wage
- `kids` number of children
- `age` age
- `disab` bad health
- `id` id
- `year` year

**Details**

*number of observations*: 5320

**Source**

Online complements to Ziliak (1997).

References


---

**lag.plm**

**lag, lead, and diff for panel data**

Description

lag, lead, and diff functions for class pseries.

Usage

```r
lead(x, k = 1, ...)  
## S3 method for class 'pseries'
lag(x, k = 1, shift = c("time", "row"), ...)  
## S3 method for class 'pseries'
lead(x, k = 1, shift = c("time", "row"), ...)  
## S3 method for class 'pseries'
diff(x, lag = 1, shift = c("time", "row"), ...)  
```

Arguments

- **x** a pseries object,
- **k** an integer, the number of lags for the lag and lead methods (can also be negative). For the lag method, a positive (negative) k gives lagged (leading) values. For the lead method, a positive (negative) k gives leading (lagged) values, thus, `lag(x, k = -1)` yields the same as `lead(x, k = 1)`. If k is an integer with length > 1 (k = c(k1,k2,...)) a matrix with multiple lagged pseries is returned,
- `...` further arguments (currently none evaluated).
- **shift** character, either "time" (default) or "row" determining how the shifting in the lag/lead/diff functions is performed (see Details and Examples).
- **lag** the number of lags for the diff method, can also be of length > 1 (see argument k) (only non–negative values in argument lag are allowed for diff).

---

3https://doi.org/10.1017/CBO9780511811241
Details

This set of functions perform lagging, leading (lagging in the opposite direction), and differencing operations on `pseries` objects, i.e., they take the panel structure of the data into account by performing the operations per individual.

Argument `shift` controls the shifting of observations to be used by methods `lag`, `lead`, and `diff`:

#' - `shift = "time"` (default): Methods respect the numerical value in the time dimension of the index. The time dimension needs to be interpretable as a sequence \( t, t+1, t+2, \ldots \) where \( t \) is an integer (from a technical viewpoint, `as.numeric(as.character(index(your_pdata.frame)[[2]]))` needs to result in a meaningful integer).

• `shift = "row"`: Methods perform the shifting operation based solely on the "physical position" of the observations, i.e. neighbouring rows are shifted per individual. The value in the time index is not relevant in this case.

For consecutive time periods per individual, a switch of shifting behaviour results in no difference. Different return values will occur for non-consecutive time periods per individual ("holes in time"), see also Examples.

Value

• An object of class `pseries`, if the argument specifying the lag has length 1 (argument \( k \) in functions `lag` and `lead`, argument `lag` in function `diff`).

• A matrix containing the various series in its columns, if the argument specifying the lag has length > 1.

Note

The sign of \( k \) in `lag.pseries` results in inverse behaviour compared to `stats::lag()` and `zoo::lag.zoo()`.

Author(s)

Yves Croissant and Kevin Tappe

See Also

To check if the time periods are consecutive per individual, see `is.pconsecutive()`.

For further function for `pseries` objects: `between()`, `Between()`, `Within()`, `summary.pseries()`, `print.summary.pseries()`, `as.matrix.pseries()`.

Examples

```r
# First, create a pdata.frame
data("EmplUK", package = "plm")
Em <- pdata.frame(EmplUK)

# Then extract a series, which becomes additionally a pseries
```
### make.pbalanced

**Make data balanced**

**Description**

This function makes the data balanced, i.e. each individual has the same time periods, by filling in or dropping observations.

**Usage**

```r
make.pbalanced(x, balance.type = c("fill", "shared.times", 
  "shared.individuals"), ...)
```

```r
## S3 method for class 'pseries'
make.pbalanced(x, balance.type = c("fill", 
  "shared.times", "shared.individuals"), ...)
```

```r
## S3 method for class 'pdata.frame'
make.pbalanced(x, balance.type = c("fill", 
  "shared.times", "shared.individuals"), ...)
```
make.pbalanced

"shared.times", "shared.individuals"), ...)

## S3 method for class 'data.frame'
make.pbalanced(x, balance.type = c("fill",
    "shared.times", "shared.individuals"), index = NULL, ...)

Arguments

- **x**: an object of class pdata.frame, data.frame, or pseries;
- **balance.type**: character, one of "fill", "shared.times", or "shared.individuals", see Details,
- **index**: only relevant for data.frame interface; if NULL, the first two columns of the data.frame are assumed to be the index variables; if not NULL, both dimensions ('individual', 'time') need to be specified by index as character of length 2 for data frames, for further details see pdata.frame(),

Details

(p)data.frame and pseries objects are made balanced, meaning each individual has the same time periods. Depending on the value of balance.type, the balancing is done in different ways:

- **balance.type = "fill"** (default): The union of available time periods over all individuals is taken (w/o NA values). Missing time periods for an individual are identified and corresponding rows (elements for pseries) are inserted and filled with NA for the non-index variables (elements for a pseries). This means, only time periods present for at least one individual are inserted, if missing.
- **balance.type = "shared.times"**: The intersect of available time periods over all individuals is taken (w/o NA values). Thus, time periods not available for all individuals are discarded, i.e., only time periods shared by all individuals are left in the result).
- **balance.type = "shared.individuals"**: All available time periods are kept and those individuals are dropped for which not all time periods are available, i.e., only individuals shared by all time periods are left in the result (symmetric to "shared.times").

The data are not necessarily made consecutive (regular time series with distance 1), because balancedness does not imply consecutiveness. For making the data consecutive, use make.pconsecutive() (and, optionally, set argument balanced = TRUE to make consecutive and balanced, see also Examples for a comparison of the two functions.

Note: Rows of (p)data.frames (elements for pseries) with NA values in individual or time index are not examined but silently dropped before the data are made balanced. In this case, it cannot be inferred which individual or time period is meant by the missing value(s) (see also Examples). Especially, this means: NA values in the first/last position of the original time periods for an individual are dropped, which are usually meant to depict the beginning and ending of the time series for that individual. Thus, one might want to check if there are any NA values in the index variables before applying make.pbalanced, and especially check for NA values in the first and last position for each individual in original data and, if so, maybe set those to some meaningful begin/end value for the time series.
Value

An object of the same class as the input \( x \), i.e. a \( \text{pdata.frame} \), \( \text{data.frame} \) or a \( \text{pseries} \) which is made balanced based on the index variables. The returned data are sorted as a stacked time series.

Author(s)

Kevin Tappe

See Also

is.pbalanced() to check if data are balanced; is.pconsecutive() to check if data are consecutive; make.pconsecutive() to make data consecutive (and, optionally, also balanced). punbalancedness() for two measures of unbalancedness, pdim() to check the dimensions of a \( \text{pdata.frame} \) (and other objects), pvar() to check for individual and time variation of a \( \text{pdata.frame} \) (and other objects), lag() for lagging (and leading) values of a \( \text{pseries} \) object. pseries(), data.frame(), pdata.frame().

Examples

```r
# take data and make it unbalanced
# by deletion of 2nd row (2nd time period for first individual)
data("Grunfeld", package = "plm")
nrow(Grunfeld) # 200 rows
Grunfeld_missing_period <- Grunfeld[-2, ] # check if balanced: FALSE
make.pbalanced(Grunfeld_missing_period)$balanced # make it balanced (by filling)
nrow(make.pbalanced(Grunfeld_missing_period))
nrow(make.pbalanced(Grunfeld_missing_period, balance.type = "shared.times")) # (shared periods)

# more complex data:
# First, make data unbalanced (and non-consecutive)
# by deletion of 2nd time period (year 1936) for all individuals
# and more time periods for first individual only
Grunfeld_unbalanced <- Grunfeld[Grunfeld$year != 1936, ]
Grunfeld_unbalanced <- Grunfeld_unbalanced[-c(1, 4), ]
pdim(Grunfeld_unbalanced)$balanced # FALSE
all(is.pconsecutive(Grunfeld_unbalanced)) # FALSE

g_bal <- make.pbalanced(Grunfeld_unbalanced)
pdim(g_bal)$balanced # TRUE
unique(g_bal$year) # all years but 1936
nrow(g_bal) # 190 rows
head(g_bal) # 1st individual: years 1935, 1939 are NA

# NA in 1st, 3rd time period (years 1935, 1937) for first individual
Grunfeld_NA <- Grunfeld
Grunfeld_NA[c(1, 3), "year"] <- NA
g_bal_NA <- make.pbalanced(Grunfeld_NA)
head(g_bal_NA) # years 1935, 1937: NA for non-index vars
```

make.pconsecutive

Description

This function makes the data consecutive for each individual (no "gaps" in time dimension per individual) and, optionally, also balanced

Usage

make.pconsecutive(x, ...)

## S3 method for class 'data.frame'
make.pconsecutive(x, balanced = FALSE,
                  index = NULL, ...)

## S3 method for class 'pdata.frame'
make.pconsecutive(x, balanced = FALSE, ...)

## S3 method for class 'pseries'
make.pconsecutive(x, balanced = FALSE, ...)
Arguments

\( x \)  

an object of class \texttt{pdata.frame}, \texttt{data.frame}, or \texttt{pseries},

\( \ldots \)  
further arguments.

\texttt{balanced}  

logical, indicating whether the data should \textit{additionally} be made balanced (default: \texttt{FALSE}),

\texttt{index}  

only relevant for \texttt{data.frame} interface; if \texttt{NULL}, the first two columns of the \texttt{data.frame} are assumed to be the index variables; if not \texttt{NULL}, both dimensions (‘individual’, ‘time’) need to be specified by \texttt{index} as character of length 2 for \texttt{data frames}, for further details see \texttt{pdata.frame()},

Details

(p)data.frame and pseries objects are made consecutive, meaning their time periods are made consecutive per individual. For consecutiveness, the time dimension is interpreted to be numeric, and the data are extended to a regularly spaced sequence with distance 1 between the time periods for each individual (for each individual the time dimension become a sequence \( t, t+1, t+2, \ldots \) where \( t \) is an integer). Non-index variables are filled with \texttt{NA} for the inserted elements (rows for (p)data.frames, vector elements for pseries).

With argument \texttt{balanced = TRUE}, additionally to be made consecutive, the data also can be made a balanced panel/pseries. Note: This means consecutive AND balanced; balancedness does not imply consecutiveness. In the result, each individual will have the same time periods in their time dimension by taking the min and max of the time index variable over all individuals (w/o \texttt{NA} values) and inserting the missing time periods. Looking at the number of rows of the resulting (p)data.frame (elements for pseries), this results in \( \text{nrow(make.pconsecutive, balanced = FALSE)} \leq \text{nrow(make.pconsecutive, balanced = TRUE)} \). For making the data only balanced, i.e. not demanding consecutiveness at the same time, use \texttt{make.pbalanced()} (see Examples for a comparison).

Note: rows of (p)data.frames (elements for pseries) with \texttt{NA} values in individual or time index are not examined but silently dropped before the data are made consecutive. In this case, it is not clear which individual or time period is meant by the missing value(s). Especially, this means: If there are \texttt{NA} values in the first/last position of the original time periods for an individual, which usually depicts the beginning and ending of the time series for that individual, the beginning/end of the resulting time series is taken to be the min and max (w/o \texttt{NA} values) of the original time series for that individual, see also Examples. Thus, one might want to check if there are any \texttt{NA} values in the index variables before applying make.pconsecutive, and especially check for \texttt{NA} values in the first and last position for each individual in original data and, if so, maybe set those to some meaningful begin/end value for the time series.

Value

An object of the same class as the input \( x \), i.e. a pdata.frame, data.frame or a pseries which is made time–consecutive based on the index variables. The returned data are sorted as a stacked time series.

Author(s)

Kevin Tappe
See Also

is.pconsecutive() to check if data are consecutive; make.pbalanced() to make data only balanced (not consecutive).

punbalancedness() for two measures of unbalancedness, pdim() to check the dimensions of a ‘pdata.frame’ (and other objects), pvar() to check for individual and time variation of a ‘pdata.frame’ (and other objects), lag() for lagged (and leading) values of a ‘pseries’ object.
pseries(), data.frame(), pdata.frame().

Examples

# take data and make it non-consecutive
# by deletion of 2nd row (2nd time period for first individual)
data("Grunfeld", package = "plm")
nrow(Grunfeld)           # 200 rows
Grunfeld_missing_period <- Grunfeld[-2, ]
is.pconsecutive(Grunfeld_missing_period) # check for consecutiveness
make.pconsecutive(Grunfeld_missing_period) # make it consecutiveness

# argument balanced:
# First, make data non-consecutive and unbalanced
# by deletion of 2nd time period (year 1936) for all individuals
# and more time periods for first individual only
Grunfeld_unbalanced <- Grunfeld[Grunfeld$year != 1936, ]
Grunfeld_unbalanced <- Grunfeld_unbalanced[-c(1,4), ]
all(is.pconsecutive(Grunfeld_unbalanced)) # FALSE
pdim(Grunfeld_unbalanced)$balanced # FALSE

g_consec_bal <- make.pconsecutive(Grunfeld_unbalanced, balanced = TRUE)
all(is.pconsecutive(g_consec_bal)) # TRUE
pdim(g_consec_bal)$balanced # TRUE
nrow(g_consec_bal)           # 200 rows
head(g_consec_bal)           # 1st individual: years 1935, 1936, 1939 are NA

# make consecutive
# default: balanced = FALSE

# NA in 1st, 3rd time period (years 1935, 1937) for first individual
Grunfeld_NA <- Grunfeld
Grunfeld_NA[c(1, 3), "year"] <- NA
g_NA <- make.pconsecutive(Grunfeld_NA)
head(g_NA) # 1936 is begin for 1st individual, 1937: NA for non-index vars
nrow(g_NA) # 199, year 1935 from original data is dropped

# pdata.frame interface
pGrunfeld_missing_period <- pdata.frame(Grunfeld_missing_period)
Males

Wages and Education of Young Males

Description
A panel of 545 observations from 1980 to 1987

Format
A data frame containing:

- nr identifier
- year year
- school years of schooling
- exper years of experience (computed as age-6-school)
- union wage set by collective bargaining?
- ethn a factor with levels black, hisp, other
- married married?
- health health problem?
- wage log of hourly wage
- industry a factor with 12 levels
- occupation a factor with 9 levels
- residence a factor with levels rural area, north east, northern central, south

Details

- total number of observations: 4360
- observation: individuals
- country: United States
model.frame.pdata.frame

## S3 method for class 'pdata.frame'
model.frame(formula, data = NULL, ...,
            lhs = NULL, rhs = NULL, dot = "previous")

## S3 method for class 'pdata.frame'
formula(x, ...)

## S3 method for class 'plm'
model.matrix(object, ...)

## S3 method for class 'pdata.frame'
model.matrix(object, model = c("pooling", "within",
                            "Between", "Sum", "between", "mean", "random", "fd"),
            effect = c("individual", "time", "twoways", "nested"), rhs = 1,
            theta = NULL, cstcovar.rm = NULL, ...)

### Arguments

- **data**
  - a formula, see Details,
  - further arguments.
- **...**
- **lhs**
  - inherited from package Formula::Formula() (see there),
- **rhs**
  - inherited from package Formula::Formula() (see there),
- **dot**
  - inherited from package Formula::Formula() (see there),
- **x**
  - a model.frame

### Description

Methods to create model frame and model matrix for panel data.

### Usage

```r
## S3 method for class 'pdata.frame'
model.frame(formula, data = NULL, ...,
            lhs = NULL, rhs = NULL, dot = "previous")

## S3 method for class 'pdata.frame'
formula(x, ...)

## S3 method for class 'plm'
model.matrix(object, ...)

## S3 method for class 'pdata.frame'
model.matrix(object, model = c("pooling", "within",
                            "Between", "Sum", "between", "mean", "random", "fd"),
            effect = c("individual", "time", "twoways", "nested"), rhs = 1,
            theta = NULL, cstcovar.rm = NULL, ...)
```

### References


Source

object, formula
an object of class "pdata.frame" or an estimated model object of class "plm",
model one of "pooling", "within", "Sum", "Between", "between", "random", "fd" and "ht",
effect the effects introduced in the model, one of "individual", "time", "twoways" or "nested",
theta the parameter for the transformation if model = "random",
cstcovar.rm remove the constant columns, one of "none", "intercept", "covariates", "all".

Details
The lhs and rhs arguments are inherited from Formula, see there for more details.
The model.frame methods return a pdata.frame object suitable as an input to plm's model.matrix.
The model.matrix methods builds a model matrix with transformations performed as specified by the model and effect arguments (and theta if model = "random" is requested), in this case the supplied data argument should be a model frame created by plm's model.frame method. If not, it is tried to construct the model frame from the data. Constructing the model frame first ensures proper NA handling, see Examples.

Value
The model.frame methods return a pdata.frame.
The model.matrix methods return a matrix.

Author(s)
Yves Croissant

See Also
pmodel.response() for (transformed) response variable.
Formula::Formula() from package Formula, especially for the lhs and rhs arguments.

Examples
# First, make a pdata.frame
data("Grunfeld", package = "plm")
pGrunfeld <- pdata.frame(Grunfeld)

# then make a model frame from a pFormula and a pdata.frame
#pform <- pFormula(inv ~ value + capital)
#mf <- model.frame(pform, data = pGrunfeld)
form <- inv ~ value
mf <- model.frame(pGrunfeld, form)

# then construct the (transformed) model matrix (design matrix)
# from formula and model frame
#modmat <- model.matrix(pform, data = mf, model = "within")
modmat <- model.matrix(mf, model = "within")

## retrieve model frame and model matrix from an estimated plm object
#fe_model <- plm(pform, data = pGrunfeld, model = "within")
fe_model <- plm(form, data = pGrunfeld, model = "within")
model.frame(fe_model)
model.matrix(fe_model)

# same as constructed before
all.equal(mf, model.frame(fe_model), check.attributes = FALSE) # TRUE
all.equal(modmat, model.matrix(fe_model), check.attributes = FALSE) # TRUE

---

**mtest**

*Arellano–Bond test of Serial Correlation*

**Description**

Test of serial correlation for models estimated by GMM

**Usage**

mtest(object, order = 1, vcov = NULL)

**Arguments**

- **object**: an object of class "pgmm",
- **order**: the order of the serial correlation (1 or 2),
- **vcov**: a matrix of covariance for the coefficients or a function to compute it.

**Details**

The Arellano–Bond test is a test of correlation based on the residuals of the estimation. By default, the computation is done with the standard covariance matrix of the coefficients. A robust estimator of this covariance matrix can be supplied with the `vcov` argument.

**Value**

An object of class "htest".

**Author(s)**

Yves Croissant

**References**

(Arellano and Bond 1991)
See Also

pgmm()

Examples

data("EmplUK", package = "plm")
ar <- pgmm(log(emp) ~ lag(log(emp), 1:2) + lag(log(wage), 0:1) +
    lag(log(capital), 0:2) + lag(log(output), 0:2) | lag(log(emp), 2:99),
data = EmplUK, effect = "twoways", model = "twosteps")
mtest(ar, order = 1)
mtest(ar, order = 2, vcov = vcovHC)

Description

This function extracts the total number of 'observations' from a fitted panel model.

Usage

## S3 method for class 'panelmodel'
nobs(object, ...)
## S3 method for class 'pgmm'
nobs(object, ...)

Arguments

object     a panelmodel object for which the number of total observations is to be extracted.
...
 further arguments.

Details

The number of observations is usually the length of the residuals vector. Thus, nobs gives the
number of observations actually used by the estimation procedure. It is not necessarily the number
of observations of the model frame (number of rows in the model frame), because sometimes the
model frame is further reduced by the estimation procedure. This is e.g. the case for first-difference
models estimated by plm(...(), model = "fd") where the model frame does not yet contain
the differences (see also Examples).

Value

A single number, normally an integer.
Parity

See Also

pdim()

Examples

```r
# estimate a panelmodel
data("Produc", package = "plm")
z <- plm(log(gsp) ~ log(pcap) + log(pc) + log(emp) + unemp, data = Produc,
     model = "random", subset = gsp > 5000)

nobs(z) # total observations used in estimation
pdim(z)$nT$N # same information
pdim(z) # more information about the dimensions (no. of individuals and time periods)

# illustrate difference between nobs and pdim for first-difference model
data("Grunfeld", package = "plm")
fdmod <- plm(inv ~ value + capital, data = Grunfeld, model = "fd")
nobs(fdmod) # 190
pdim(fdmod)$nT$N # 200
```

Parity

Purchasing Power Parity and other parity relationships

Description

A panel of 104 quarterly observations from 1973Q1 to 1998Q4

Format

A data frame containing:

- **country**: country codes: a factor with 17 levels
- **time**: the quarter index, 1973Q1-1998Q4
- **ls**: log spot exchange rate vs. USD
- **lp**: log price level
- **is**: short term interest rate
- **il**: long term interest rate
- **ld**: log price differential vs. USA
- **uis**: U.S. short term interest rate
- **uil**: U.S. long term interest rate
Details

total number of observations: 1768
observation: country
country: OECD

Source


References


pbgtest

Breusch–Godfrey Test for Panel Models

Description

Test of serial correlation for (the idiosyncratic component of) the errors in panel models.

Usage

pbgtest(x, ...)

## S3 method for class 'panelmodel'
pbgtest(x, order = NULL, type = c("Chisq", "F"), ...

## S3 method for class 'formula'
pbgtest(x, order = NULL, type = c("Chisq", "F"), data, model = c("pooling", "random", "within"), ...)

Arguments

x

an object of class "panelmodel" or of class "formula",

... further arguments (see lmtest::bgtest()).

order

an integer indicating the order of serial correlation to be tested for. NULL (default) uses the minimum number of observations over the time dimension (see also section Details below).

type

type of test statistic to be calculated; either "Chisq" (default) for the Chi-squared test statistic or "F" for the F test statistic,
data only relevant for formula interface: data set for which the respective panel model (see model) is to be evaluated,

model only relevant for formula interface: compute test statistic for model pooling (default), random, or within. When model is used, the data argument needs to be passed as well,

Details

This Lagrange multiplier test uses the auxiliary model on (quasi-)demeaned data taken from a model of class plm which may be a pooling (default for formula interface), random or within model. It performs a Breusch–Godfrey test (using bgtest from package \texttt{lmtest} on the residuals of the (quasi-)demeaned model, which should be serially uncorrelated under the null of no serial correlation in idiosyncratic errors, as illustrated in Wooldridge (2010). The function takes the demeaned data, estimates the model and calls bgtest.

Unlike most other tests for serial correlation in panels, this one allows to choose the order of correlation to test for.

Value

An object of class "htest".

Note

The argument order defaults to the minimum number of observations over the time dimension, while for \texttt{lmtest::bgtest} it defaults to 1.

Author(s)

Giovanni Millo

References


See Also

For the original test in package \texttt{lmtest} see \texttt{lmtest::bgtest().} See \texttt{pdwtest()} for the analogous panel Durbin–Watson test. See \texttt{pbltest()}, \texttt{pbsytest()}, \texttt{pwartest()} and \texttt{pwfdtest()} for other serial correlation tests for panel models.
Examples

data("Grunfeld", package = "plm")
g <- plm(inv ~ value + capital, data = Grunfeld, model = "random")

# panelmodel interface
pbltest(g)
pbltest(g, order = 4)

# formula interface
pbltest(inv ~ value + capital, data = Grunfeld, model = "random")

# F test statistic (instead of default type="Chisq")
pbltest(g, type="F")
pbltest(inv ~ value + capital, data = Grunfeld, model = "random", type = "F")

---

pbltest  Baltagi and Li Serial Dependence Test For Random Effects Models

Description

Baltagi and Li (1995)'s Lagrange multiplier test for AR(1) or MA(1) idiosyncratic errors in panel models with random effects.

Usage

pbltest(x, ...)

## S3 method for class 'formula'
pbltest(x, data, alternative = c("twosided", "onesided"), index = NULL, ...)

## S3 method for class 'plm'
pbltest(x, alternative = c("twosided", "onesided"), ...)

Arguments

x  a model formula or an estimated random–effects model of class plm,
...
  further arguments.
data  for the formula interface only: a data.frame,
alternative  one of "twosided", "onesided". Selects either $H_A: \rho \neq 0$ or $H_A: \rho = 0$
  (i.e., the Normal or the Chi-squared version of the test),
index  the index of the data.frame,
Details

This is a Lagrange multiplier test for the null of no serial correlation, against the alternative of either an AR(1) or an MA(1) process, in the idiosyncratic component of the error term in a random effects panel model (as the analytical expression of the test turns out to be the same under both alternatives, see Baltagi and Li 1995 and Baltagi and Li 1997). The alternative argument, defaulting to twosided, allows testing for positive serial correlation only, if set to onesided.

Value

An object of class "htest".

Author(s)

Giovanni Millo

References


See Also

`pdltest()`, `bgtest`, `pbsytest()`, `pwaristest()` and `pfdtest()` for other serial correlation tests for panel models.

Examples

```r
data("Grunfeld", package = "plm")

# formula interface
pbltest(inv ~ value + capital, data = Grunfeld)

# plm interface
re_mod <- plm(inv ~ value + capital, data = Grunfeld, model = "random")
pbltest(re_mod)
pbltest(re_mod, alternative = "onesided")
```

Description

Tests for AR(1) disturbances in panel models.
Usage

pbnftest(x, ...)

## S3 method for class 'panelmodel'
pbnftest(x, test = c("bnf", "lbi"), ...)

## S3 method for class 'formula'
pbnftest(x, data, test = c("bnf", "lbi"),
          model = c("pooling", "within", "random"), ...)

Arguments

x an object of class "panelmodel" or of class "formula",
...
only relevant for formula interface: further arguments to specify the model to
test (arguments passed on to plm()), e.g. effect.
test a character indicating the test to be performed, either "bnf" or "lbi" for the
(modified) BNF statistic or Baltagi–Wu’s LBI statistic, respectively.
data a data.frame (only relevant for formula interface),
model a character indicating on which type of model the test shall be performed ("pooling",
"within", "random", only relevant for formula interface).

Details

The default, test = "bnf", gives the (modified) BNF statistic, the generalised Durbin-Watson
statistic for panels. For balanced and consecutive panels, the reference is Bhargava/Franzini/Narendranathan
(1982). The modified BNF is given for unbalanced and/or non-consecutive panels (d1 in formula
16 of Baltagi and Wu (1999)).
test = "lbi" yields Baltagi–Wu’s LBI statistic (Baltagi and Wu 1999), the locally best invariant
test which is based on the modified BNF statistic.

No specific variants of these tests are available for random effect models. As the within estimator is
consistent also under the random effects assumptions, the test for random effect models is performed
by taking the within residuals.

No p-values are given for the statistics as their distribution is quite difficult. Bhargava et al. (1982)
supply tabulated bounds for p = 0.05 for the balanced case and consecutive case.

For large N, (Bhargava et al. 1982) suggest it is sufficient to check whether the BNF statistic is < 2
to test against positive serial correlation.

Value

An object of class "htest".

Author(s)

Kevin Tappe
References


See Also

pdwtest() for the original Durbin–Watson test using (quasi-)demeaned residuals of the panel model without taking the panel structure into account. pbltest(), pbsytest(), pwartest() and pwfdtest() for other serial correlation tests for panel models.

Examples

data("Grunfeld", package = "plm")

# formula interface, replicate Baltagi/Wu (1999), table 1, test case A:
data_A <- Grunfeld[!Grunfeld["year"] %in% c("1943", "1944"), ]
pbnftest(inv ~ value + capital, data = data_A, model = "within")
pbnftest(inv ~ value + capital, data = data_A, test = "lbi", model = "within")

# replicate Baltagi (2013), p. 101, table 5.1:
re <- plm(inv ~ value + capital, data = Grunfeld, model = "random")
pbnftest(re)
pbnftest(re, test = "lbi")

pbsytest

*Bera, Sosa-Escudero and Yoon Locally–Robust Lagrange Multiplier Tests for Panel Models and Joint Test by Baltagi and Li*

Description

Test for residual serial correlation (or individual random effects) locally robust vs. individual random effects (serial correlation) for panel models and joint test of serial correlation and the random effect specification by Baltagi and Li.

Usage

```r
pbsytest(x, ...)
```

## S3 method for class 'formula'
pbsytest(x, data, ..., test = c("ar", "re", "j"),
          re.normal = if (test == "re") TRUE else NULL)
## S3 method for class 'panelmodel'

```r
pbsytest(x, test = c("ar", "re", "j"),
  re.normal = if (test == "re") TRUE else NULL, ...)
```

### Arguments

- **x**: an object of class `formula` or of class `panelmodel`,
- **...**: further arguments.
- **data**: a `data.frame`,
- **test**: a character string indicating which test to perform: first-order serial correlation ("ar"), random effects ("re") or joint test for either of them ("j"),
- **re.normal**: logical, only relevant for `test = "re"`: TRUE (default) computes the one-sided "re" test, FALSE the two-sided test (see also Details); not relevant for other values of `test` and, thus, should be NULL.

### Details

These Lagrange multiplier tests are robust vs. local misspecification of the alternative hypothesis, i.e. they test the null of serially uncorrelated residuals against AR(1) residuals in a pooling model, allowing for local departures from the assumption of no random effects; or they test the null of no random effects allowing for local departures from the assumption of no serial correlation in residuals. They use only the residuals of the pooled OLS model and correct for local misspecification as outlined in Bera et al. (2001).

For `test = "re"`, the default (`re.normal = TRUE`) is to compute a one-sided test which is expected to lead to a more powerful test (asymptotically N(0,1) distributed). Setting `re.normal = FALSE` gives the two-sided test (asymptotically chi-squared(2) distributed). Argument `re.normal` is irrelevant for all other values of `test`.

The joint test of serial correlation and the random effect specification (`test = "j"`) is due to Baltagi and Li (1991) (also mentioned in Baltagi and Li (1995), pp. 135–136) and is added for convenience under this same function.

The unbalanced version of all tests are derived in Sosa-Escudero and Bera (2008). The functions implemented are suitable for balanced as well as unbalanced panel data sets. A concise treatment of the statistics for only balanced panels is given in Baltagi (2013), p. 108.

Here is an overview of how the various values of the `test` argument relate to the literature:

- **test = "ar"**:  
  - $RS_\rho^*$ in Bera et al. (2001), p. 9 (balanced)  
  - $LM_\rho^*$ in Baltagi (2013), p. 108 (balanced)  
  - $RS_{\lambda}$ in Sosa-Escudero/Bera (2008), p. 73 (unbalanced)
- **test = "re", re.normal = TRUE** (default) (one-sided test, asymptotically N(0,1) distributed):
  - $RSO_{\mu}^*$ in Bera et al. (2001), p. 11 (balanced)  
  - $RSO_{\mu}^*$ in Sosa-Escudero/Bera (2008), p. 75 (unbalanced)
- **test = "re", re.normal = FALSE** (two-sided test, asymptotically chi-squared(2) distributed):
- \( RS_{*\mu} \) in Bera et al. (2001), p. 7 (balanced)
- \( LM_{*\mu} \) in Baltagi (2013), p. 108 (balanced)
- \( RS_{*\mu} \) in Sosa-Escudero/Bera (2008), p. 73 (unbalanced)

- \( test = "j" \):
  - \( RS_{\mu\rho} \) in Bera et al. (2001), p. 10 (balanced)
  - \( LM \) in Baltagi/Li (2001), p. 279 (balanced)
  - \( LM_1 \) in Baltagi and Li (1995), pp. 135–136 (balanced)
  - \( LM_1 \) in Baltagi (2013), p. 108 (balanced)
  - \( RS_{\lambda\rho} \) in Sosa-Escudero/Bera (2008), p. 74 (unbalanced)

**Value**

An object of class "htest".

**Author(s)**

Giovanni Millo (initial implementation) & Kevin Tappe (extension to unbalanced panels)

**References**


**See Also**

`plmtest()` for individual and/or time random effects tests based on a correctly specified model; `pbltest()`, `pbgtest()` and `pdwtest()` for serial correlation tests in random effects models.

**Examples**

```r
## Bera et. al (2001), p. 13, table 1 use
## a subset of the original Grunfeld
## data which contains three errors --> construct this subset:
data("Grunfeld", package = "plm")
Grunsubset <- rbind(Grunfeld[1:80, ], Grunfeld[141:160, ])
Grunsubset[Grunsubset$firm == 2 & Grunsubset$year %in% c(1940, 1952), ]["inv"] <- c(261.6, 645.2)
Grunsubset[Grunsubset$firm == 2 & Grunsubset$year == 1946, ]["capital"] <- 232.6
```

## default is AR testing (formula interface)

```r
pbsytest(inv ~ value + capital, data = Grunsubset, index = c("firm", "year"))
pbsytest(inv ~ value + capital, data = Grunsubset, index = c("firm", "year"), test = "re")
pbsytest(inv ~ value + capital, data = Grunsubset, index = c("firm", "year"),
  test = "re", re.normal = FALSE)
pbsytest(inv ~ value + capital, data = Grunsubset, index = c("firm", "year"), test = "j")
```

## plm interface

```r
mod <- plm(inv ~ value + capital, data = Grunsubset, model = "pooling")
pbsytest(mod)
```

---

### pcce

**Common Correlated Effects estimators**

**Description**

Common Correlated Effects Mean Groups (CCEMG) and Pooled (CCEP) estimators for panel data with common factors (balanced or unbalanced)

**Usage**

```r
pcce(formula, data, subset, na.action, model = c("mg", "p"),
  index = NULL, trend = FALSE, ...)
```

**S3 method for class 'pcce'**

```r
summary(object, vcov = NULL, ...)
```

**S3 method for class 'summary.pcce'**

```r
print(x, digits = max(3, getOption("digits") - 2),
  width = getOption("width"), ...)
```

**S3 method for class 'pcce'**

```r
residuals(object, type = c("defactored", "standard"), ...)
```

**S3 method for class 'pcce'**

```r
model.matrix(object, ...)
```

**S3 method for class 'pcce'**

```r
pmodel.response(object, ...)
```

**Arguments**

- `formula` a symbolic description of the model to be estimated,
- `data` a `data.frame`,
- `subset` see `lm`,
- `na.action` see `lm`,
- `model` a `c("mg","p")`,
- `index` see `lm`,
- `trend` see `lm`,
- `vcov` see `lm`,
pcce

na.action see `lm`,
model one of "mg", "p", selects Mean Groups vs. Pooled CCE model,
index the indexes, see `pdata.frame()`,
trend logical specifying whether an individual-specific trend has to be included,
... further arguments.
object, x an object of class "pcce",
vcov a variance–covariance matrix furnished by the user or a function to calculate one,
digits digits,
width the maximum length of the lines in the print output,
type one of "defactored" or "standard".

Details

`pcce` is a function for the estimation of linear panel models by the Common Correlated Effects Mean Groups or Pooled estimator, consistent under the hypothesis of unobserved common factors and idiosyncratic factor loadings. The CCE estimator works by augmenting the model by cross-sectional averages of the dependent variable and regressors in order to account for the common factors, and adding individual intercepts and possibly trends.

Value

An object of class `c("pcce","panelmodel")` containing:

- `coefficients` the vector of coefficients,
- `residuals` the vector of (defactored) residuals,
- `stdres` the vector of (raw) residuals,
- `tr.model` the transformed data after projection on H,
- `fitted.values` the vector of fitted values,
- `vcov` the covariance matrix of the coefficients,
- `df.residual` degrees of freedom of the residuals,
- `model` a data.frame containing the variables used for the estimation,
- `call` the call,
- `sigma` always NULL, `sigma` is here only for compatibility reasons (to allow using the same summary and print methods as `pggls`),
- `indcoef` the matrix of individual coefficients from separate time series regressions.

Author(s)

Giovanni Millo
References


Examples

data("Produc", package = "plm")
ccepmod <- pcce(log(gsp) ~ log(pcap) + log(pc) + log(emp) + unemp, data = Produc, model="p")
summary(ccepmod)

summary(ccepmod, vcov = vcovHC) # use argument vcov for robust std. errors

ccemgmod <- pcce(log(gsp) ~ log(pcap) + log(pc) + log(emp) + unemp, data = Produc, model="mg")
summary(ccemgmod)

pcdtest

Tests of cross-section dependence for panel models

Description

Pesaran’s CD or Breusch–Pagan’s LM (local or global) tests for cross sectional dependence in panel models

Usage

pcdtest(x, ...)

## S3 method for class 'formula'
pcdtest(x, data, index = NULL, model = NULL, 
    test = c("cd", "sclm", "bcsclm", "lm", "rho", "absrho"), w = NULL, 
    ...)

## S3 method for class 'panelmodel'
pcdtest(x, test = c("cd", "sclm", "bcsclm", "lm", 
                   "rho", "absrho"), w = NULL, ...)

## S3 method for class 'pseries'
pcdtest(x, test = c("cd", "sclm", "bcsclm", "lm", 
                 "rho", "absrho"), w = NULL, ...)

Arguments

x an object of class formula, panelmodel, or pseries (depending on the respective interface) describing the model to be tested,

... further arguments to be passed on to plm, such as effect or random.method.

data a data.frame,
index
an optional numerical index, if NULL, the first two columns of the data.frame provided in argument data are assumed to be the index variables; for further details see pdata.frame(),
model
an optional character string indicating which type of model to estimate; if left to NULL, the original heterogeneous specification of Pesaran is used,
test
the type of test statistic to be returned. One of
• "cd" for Pesaran’s CD statistic,
• "lm" for Breusch and Pagan’s original LM statistic,
• "sclm" for the scaled version of Breusch and Pagan’s LM statistic,
• "bcslm" for the bias-corrected scaled version of Breusch and Pagan’s LM statistic,
• "rho" for the average correlation coefficient,
• "absrho" for the average absolute correlation coefficient,
w
either NULL (default) for the global tests or – for the local versions of the statistics – a n x n matrix describing proximity between individuals, with \( w_{ij} = a \) where \( a \) is any number such that \( \text{as.logical}(a) \rightarrow \text{TRUE} \) if \( i,j \) are neighbours, \( 0 \) or any number \( b \) such that \( \text{as.logical}(b) \rightarrow \text{FALSE} \) elsewhere. Only the lower triangular part (without diagonal) of \( w \) after coercing by as.logical() is evaluated for neighbouring information (but \( w \) can be symmetric). See also Details and Examples.

Details
These tests are originally meant to use the residuals of separate estimation of one time–series regression for each cross-sectional unit in order to check for cross–sectional dependence. If a different model specification (within, random, ...) is assumed consistent, one can resort to its residuals for testing (which is common, e.g., when the time dimension’s length is insufficient for estimating the heterogeneous model). If the time dimension is insufficient and model=NULL, the function defaults to estimation of a within model and issues a warning. The main argument of this function may be either a model of class panelmodel or a formula and dataframe; in the second case, unless model is set to NULL, all usual parameters relative to the estimation of a plm model may be passed on. The test is compatible with any consistent panelmodel for the data at hand, with any specification of effect. E.g., specifying effect="time" or effect="twoways" allows to test for residual cross-sectional dependence after the introduction of time fixed effects to account for common shocks.

A local version of either test can be computed by supplying a proximity matrix (elements coercible to logical) with argument \( w \) which provides information on whether any pair of individuals are neighbours or not. If \( w \) is supplied, only neighbouring pairs will be used in computing the test; else, \( w \) will default to NULL and all observations will be used. The matrix need not be binary, so commonly used “row–standardized” matrices can be employed as well. nb objects from spdep7 must instead be transformed into matrices by spdep8’s function nb2mat before using.

The methods implemented are suitable also for unbalanced panels.

Pesaran’s CD test (test="cd"), Breusch and Pagan’s LM test (test="lm"), and its scaled version (test="sclm") are all described in Pesaran (2004) (and complemented by Pesaran (2005)).

---

7https://CRAN.R-project.org/package=spdep
8https://CRAN.R-project.org/package=spdep
The bias-corrected scaled test (test="bcslm") is due to (Baltagi et al. 2012) and only valid for within models including the individual effect (it’s unbalanced version uses max(Tij) for T) in the bias-correction term. Breusch and Pagan (1980) is the original source for the LM test.

The test on a pseries is the same as a test on a pooled regression model of that variable on a constant, i.e. pcdtest(some_pseries) is equivalent to pcdtest(plm(some_var ~ 1, data = some_pdata.frame, model = "pooling") and also equivalent to pcdtest(some_var ~ 1, data = some_data), where some_var is the variable name in the data which corresponds to some_pseries.

Value

An object of class "htest".

References


Examples

data("Grunfeld", package = "plm")
## test on heterogeneous model (separate time series regressions)
pcdtest(inv ~ value + capital, data = Grunfeld,
    index = c("firm", "year"))

## test on two-way fixed effects homogeneous model
pcdtest(inv ~ value + capital, data = Grunfeld, model = "within",
    effect = "twoways", index = c("firm", "year"))

## test on panelmodel object
g <- plm(inv ~ value + capital, data = Grunfeld, index = c("firm", "year"))
pcdtest(g)

## scaled LM test
pcdtest(g, test = "sclm")

## test on pseries
pGrunfeld <- pdata.frame(Grunfeld)
pcdtest(pGrunfeld$value)

9https://doi.org/10.1080/07474938.2014.956623
## local test
## define neighbours for individual 2: 1, 3, 4, 5 in lower triangular matrix
w <- matrix(0, ncol = 10, nrow = 10)
pcdtest(g, w = w)

---

**pdata.frame**

**data.frame for panel data**

**Description**

An object of class ’pdata.frame’ is a data.frame with an index attribute that describes its individual and time dimensions.

**Usage**

```r
pdata.frame(x, index = NULL, drop.index = FALSE, row.names = TRUE,
            stringsAsFactors = default.stringsAsFactors(),
            replace.non.finite = FALSE, drop.NA.series = FALSE,
            drop.const.series = FALSE, drop.unused.levels = FALSE)
```

## S3 replacement method for class ’pdata.frame’

```r
x$name <- value
```

## S3 method for class ’pdata.frame’

```r
x[i, j, drop]
```

## S3 method for class ’pdata.frame’

```r
x[[y]]
```

## S3 method for class ’pdata.frame’

```r
x$y
```

## S3 method for class ’pdata.frame’

```r
print(x, ...)
```

## S3 method for class ’pdata.frame’

```r
as.list(x, keep.attributes = FALSE, ...)
```

## S3 method for class ’pdata.frame’

```r
as.data.frame(x, row.names = NULL,
              optional = FALSE, keep.attributes = TRUE, ...)
```
Arguments

- **x**: A data.frame for the pdata.frame function and a pdata.frame for the methods,
- **index**: This argument indicates the individual and time indexes. See Details,
- **drop.index**: Logical, indicates whether the indexes are to be excluded from the resulting pdata.frame,
- **row.names**: NULL or logical, indicates whether “fancy” row names (a combination of individual index and time index) are to be added to the returned (p)data.frame (NULL and ‘FALSE’ have the same meaning),
- **stringsAsFactors**: Logical, indicating whether character vectors are to be converted to factors,
- **replace.non.finite**: Logical, indicating whether values for which is.finite() yields TRUE are to be replaced by NA values, except for character variables (defaults to FALSE),
- **drop.NA.series**: Logical, indicating whether all-NA columns are to be removed from the pdata.frame (defaults to FALSE),
- **drop.const.series**: Logical, indicating whether constant columns are to be removed from the pdata.frame (defaults to FALSE),
- **drop.unused.levels**: Logical, indicating whether unused levels of factors are to be dropped (defaults to FALSE) (unused levels are always dropped from variables serving to construct the index variables),
- **name**: The name of the data.frame,
- **value**: The name of the variable to include,
- **i**: See Extract(),
- **j**: See Extract(),
- **drop**: See Extract(),
- **y**: One of the columns of the data.frame,
- **...**: Further arguments.
- **keep.attributes**: Logical, only for as.list and as.data.frame methods, indicating whether the elements of the returned list/columns of the data.frame should have the pdata.frame’s attributes added (default: FALSE for as.list, TRUE for as.data.frame),
- **optional**: See as.data.frame(),

Details

The index argument indicates the dimensions of the panel. It can be:

- A vector of two character strings which contains the names of the individual and of the time indexes,
a character string which is the name of the individual index variable. In this case, the time index is created automatically and a new variable called "time" is added, assuming consecutive and ascending time periods in the order of the original data,

an integer, the number of individuals. In this case, the data need to be a balanced panel and be organized as a stacked time series (successive blocks of individuals, each block being a time series for the respective individual) assuming consecutive and ascending time periods in the order of the original data. Two new variables are added: "id" and "time" which contain the individual and the time indexes.

The "[" and "$" extract a series from the pdata.frame. The "index" attribute is then added to the series and a class attribute "pseries" is added. The "[" method behaves as for data.frame, except that the extraction is also applied to the index attribute. A safe way to extract the index attribute is to use the function index() for 'pdata.frames' (and other objects). as.data.frame removes the index from the pdata.frame and adds it to each column. as.list behaves by default identical to base::as.list.data.frame() which means it drops the attributes specific to a data.frame; if a list of pseries is wanted, the attribute keep.attributes can to be set to TRUE. This also makes lapply work as expected on a pdata.frame (see also Examples).

Value

a pdata.frame object: this is a data.frame with an index attribute which is a data.frame with two variables, the individual and the time indexes, both being factors. The resulting pdata.frame is sorted by the individual index, then by the time index.

Author(s)

Yves Croissant

See Also

index() to extract the index variables from a 'pdata.frame' (and other objects), pdim() to check the dimensions of a 'pdata.frame' (and other objects), pvar() to check for each variable if it varies cross-sectionally and over time. To check if the time periods are consecutive per individual, see is.pconsecutive().

Examples

# Gasoline contains two variables which are individual and time # indexes
data("Gasoline", package = "plm") Gas <- pdata.frame(Gasoline, index = c("country", "year"), drop.index = TRUE)

# Hedonic is an unbalanced panel, townid is the individual index data("Hedonic", package = "plm") Hed <- pdata.frame(Hedonic, index = "townid", row.names = FALSE)

# In case of balanced panel, it is sufficient to give number of # individuals data set 'Wages' is organized as a stacked time
# series
data("Wages", package = "plm")
Wag <- pdata.frame(Wages, 595)

# lapply on a pdata.frame by making it a list of pseries first
lapply(as.list(Wag[, c("ed", "lwage")], keep.attributes = TRUE), lag)

---

### pdim

**Check for the Dimensions of the Panel**

**Description**

This function checks the number of individuals and time observations in the panel and whether it is balanced or not.

**Usage**

```
pdim(x, ...)
```

```
## Default S3 method:
pdim(x, y, ...)

## S3 method for class 'data.frame'
pdim(x, index = NULL, ...)

## S3 method for class 'pdata.frame'
pdim(x, ...)

## S3 method for class 'pseries'
pdim(x, ...)

## S3 method for class 'panelmodel'
pdim(x, ...)

## S3 method for class 'pgmm'
pdim(x, ...)

## S3 method for class 'pdim'
print(x, ...)
```

**Arguments**

- `x`: a `data.frame`, `pdata.frame`, `pseries`, `panelmodel`, or `pgmm` object,
- `...`: further arguments.
- `y`: a vector,
- `index`: see `pdata.frame()`,
Details

pdim is called by the estimation functions and can be also used stand-alone.

Value

An object of class pdim containing the following elements:

- nT: a list containing n, the number of individuals, T, the number of time observations, N, the total number of observations,
- Tint: a list containing two vectors (of type integer): Ti gives the number of observations for each individual and nt gives the number of individuals observed for each period,
- balanced: a logical value: TRUE for a balanced panel, FALSE for an unbalanced panel,
- panel.names: a list of character vectors: id.names contains the names of each individual and time.names contains the names of each period.

Note

Calling pdim on an estimated panelmodel object and on the corresponding (p)data.frame used for this estimation does not necessarily yield the same result. When called on an estimated panelmodel, the number of observations (individual, time) actually used for model estimation are taken into account. When called on a (p)data.frame, the rows in the (p)data.frame are considered, disregarding any NA values in the dependent or independent variable(s) which would be dropped during model estimation.

Author(s)

Yves Croissant

See Also

is.pbalanced() to just determine balancedness of data (slightly faster than pdim),
punbalancedness() for measures of unbalancedness,
nobs(), pdata.frame(),
pvar() to check for each variable if it varies cross-sectionally and over time.

Examples

# There are 595 individuals
data("Wages", package = "plm")
pdim(Wages, 595)

# Gasoline contains two variables which are individual and time
# indexes and are the first two variables
data("Gasoline", package="plm")
pdim(Gasoline)

# Hedonic is an unbalanced panel, townid is the individual index
data("Hedonic", package = "plm")
pdim(Hedonic, "townid")

# An example of the panelmodel method
data("Produc", package = "plm")
z <- plm(log(gsp)~log(pcap)+log(pc)+log(emp)+unemp, data=Produc,
       model="random", subset = gsp > 5000)
pdim(z)

---

**pdwtest**  
*Durbin–Watson Test for Panel Models*

**Description**
Test of serial correlation for (the idiosyncratic component of) the errors in panel models.

**Usage**

```r
pdwtest(x, ...)
```

### S3 method for class 'panelmodel'

```r
pdwtest(x, ...)
```

### S3 method for class 'formula'

```r
pdwtest(x, data, ...)
```

**Arguments**

- `x`  
an object of class "panelmodel" or of class "formula",  
- `...`  
further arguments to be passed on to `dwtest`, e.g. `alternative`, see `lmtest::dwtest()` for further details.  
- `data`  
a `data.frame`,

**Details**
This Durbin–Watson test uses the auxiliary model on (quasi-)demeaned data taken from a model of class `plm` which may be a pooling (the default), random or within model. It performs a Durbin–Watson test (using `dwtest` from package `lmtest`) on the residuals of the (quasi-)demeaned model, which should be serially uncorrelated under the null of no serial correlation in idiosyncratic errors. The function takes the demeaned data, estimates the model and calls `dwtest`. Thus, this test does not take the panel structure of the residuals into consideration; it shall not be confused with the generalized Durbin-Watson test for panels in `pbnftest`.

**Value**

An object of class "htest".

---

10[https://CRAN.R-project.org/package=lmtest](https://CRAN.R-project.org/package=lmtest)
Author(s)

Giovanni Millo

References


See Also

`lmtest::dwtest()` for the Durbin–Watson test in *lmtest*12, `pbgtest()` for the analogous Breusch–Godfrey test for panel models, `lmtest::bgtest()` for the Breusch–Godfrey test for serial correlation in the linear model. `pbltest()`, `pbsytest()`, `pwartest()` and `pwfptest()` for other serial correlation tests for panel models.

For the Durbin-Watson test generalized to panel data models see `pbnftest()`.

Examples

```r

data("Grunfeld", package = "plm")
g <- plm(inv ~ value + capital, data = Grunfeld, model="random")
pdwtest(g)
pdwtest(g, alternative="two.sided")
## formula interface
pdwtest(inv ~ value + capital, data=Grunfeld, model="random")
```

pFtest

*F Test for Individual and/or Time Effects*

Description

Test of individual and/or time effects based on the comparison of the *within* and the *pooling* model.

---

11https://doi.org/10.1093/biomet/38.1-2.159
12https://CRAN.R-project.org/package=lmtest
Usage

pFtest(x, ...)  

## S3 method for class 'formula'
pFtest(x, data, ...)

## S3 method for class 'plm'
pFtest(x, z, ...)

Arguments

x
  an object of class "plm" or of class "formula",

...  
  further arguments.

data  
  a data.frame,

z
  an object of class "plm",

Details

For the plm method, the argument of this function is two plm objects, the first being a within model, the second a pooling model. The effects tested are either individual, time or two-ways, depending on the effects introduced in the within model.

Value

An object of class "htest".

Author(s)

Yves Croissant

See Also

plmtest() for Lagrange multiplier tests of individuals and/or time effects.

Examples

data("Grunfeld", package="plm")
gp <- plm(inv ~ value + capital, data = Grunfeld, model = "pooling")
gi <- plm(inv ~ value + capital, data = Grunfeld,  
  effect = "individual", model = "within")
gt <- plm(inv ~ value + capital, data = Grunfeld,  
  effect = "time", model = "within")
gd <- plm(inv ~ value + capital, data = Grunfeld,  
  effect = "twoways", model = "within")
pFtest(gi, gp)
pFtest(gt, gp)
pFtest(gd, gp)
pFtest(inv ~ value + capital, data = Grunfeld, effect = "twoways")
pggls

General FGLS Estimators

Description

General FGLS estimators for panel data (balanced or unbalanced)

Usage

pggls(formula, data, subset, na.action, effect = c("individual", "time"),
      model = c("within", "random", "pooling", "fd"), index = NULL, ...)

## S3 method for class 'pggls'
summary(object, ...)

## S3 method for class 'summary.pggls'
print(x, digits = max(3, getOption("digits") - 2),
      width = getOption("width"), ...)  

## S3 method for class 'pggls'
residuals(object, ...)

Arguments

formula a symbolic description of the model to be estimated,
data a data.frame,
subset see lm(),
na.action see lm(),
effect the effects introduced in the model, one of "individual" or "time",
model one of "within", "pooling", "random" or "fd",
index the indexes, see pdata.frame(),
... further arguments.
object, x an object of class pggls,
digits digits,
width the maximum length of the lines in the print output,

Details

pggls is a function for the estimation of linear panel models by general feasible generalized
least squares, either with or without fixed effects. General FGLS is based on a two-step estima-
tion process: first a model is estimated by OLS (model = "pooling"), fixed effects (model = 
"within") or first differences (model = "fd"), then its residuals are used to estimate an error
covariance matrix for use in a feasible-GLS analysis. This framework allows the error covariance
structure inside every group (if effect = "individual", else symmetric) of observations to
be fully unrestricted and is therefore robust against any type of intragroup heteroskedasticity and serial correlation. Conversely, this structure is assumed identical across groups and thus general FGLS estimation is inefficient under groupwise heteroskedasticity. Note also that this method requires estimation of \( T(T + 1)/2 \) variance parameters, thus efficiency requires \( N > T \) (if effect = "individual", else the opposite). Setting model = "random" or model = "pooling", both produce an unrestricted FGLS model as in Wooldridge, Ch. 10.5, although the former is deprecated and included only for retro-compatibility reasons. If model = "within" (the default) then a FEGLS (fixed effects GLS, see ibid.) is estimated; if model = "fd" a FDGLS (first-difference GLS).

Value

An object of class \( \text{c("pggls","panelmodel")} \) containing:

- **coefficients** the vector of coefficients,
- **residuals** the vector of residuals,
- **fitted.values** the vector of fitted values,
- **vcov** the covariance matrix of the coefficients,
- **df.residual** degrees of freedom of the residuals,
- **model** a data.frame containing the variables used for the estimation,
- **call** the call,
- **sigma** the estimated intragroup (or cross-sectional, if effect = "time") covariance of errors,

Author(s)

Giovanni Millo

References


Examples

data("Produc", package = "plm")
zz_wi <- pggls(log(gsp) ~ log(pcap) + log(pc) + log(emp) + unemp,
              data = Produc, model = "within")
summary(zz_wi)
zz_pool <- pggls(log(gsp) ~ log(pcap) + log(pc) + log(emp) + unemp,
    data = Produc, model = "pooling")
summary(zz_pool)

zz_fd <- pggls(log(gsp) ~ log(pcap) + log(pc) + log(emp) + unemp,
    data = Produc, model = "fd")
summary(zz_fd)

---

pgmm

*Generalized Method of Moments (GMM) Estimation for Panel Data*

**Description**

Generalized method of moments estimation for static or dynamic models with panel data.

**Usage**

```r
pgmm(formula, data, subset, na.action, effect = c("twoways", 
    "individual"), model = c("onestep", "twosteps"), collapse = FALSE, 
    lost.ts = NULL, transformation = c("d", "ld"), fsm = NULL, 
    index = NULL, ...)
```

### S3 method for class 'pgmm'

ccoef(object, ...)

### S3 method for class 'pgmm'

summary(object, robust = TRUE, time.dummies = FALSE, 
    ...)

### S3 method for class 'summary.pgmm'

print(x, digits = max(3, getOption("digits") - 2),
    width = getOption("width"), ...)

**Arguments**

- **formula**: a symbolic description for the model to be estimated. The preferred interface is now to indicate a multi–part formula, the first two parts describing the covariates and the GMM instruments and, if any, the third part the ’normal’ instruments,
- **data**: a *data.frame* (neither factors nor character vectors will be accepted in *data.frame*),
- **subset**: see *lm()*,
- **na.action**: see *lm()*,
- **effect**: the effects introduced in the model, one of "twoways" (the default) or "individual",
- **model**: one of "onestep" (the default) or "twosteps",
- **collapse**: if TRUE, the GMM instruments are collapsed,
lost.ts the number of lost time series: if NULL, this is automatically computed. Otherwise, it can be defined by the user as a numeric vector of length 1 or 2. The first element is the number of lost time series in the model in difference, the second one in the model in level. If the second element is missing, it is set to the first one minus one.

transformation the kind of transformation to apply to the model: either "d" (the default value) for the "difference GMM" model or "ld" for the "system GMM",

fsm the matrix for the one step estimator: one of "I" (identity matrix) or "G" (= \(D'D\) where \(D\) is the first–difference operator) if transformation="d", one of "GI" or "full" if transformation="ld",

index the indexes,

... further arguments.

object, x an object of class "pgmm",

robust if TRUE, robust inference is performed in the summary,

time.dummies if TRUE, the estimated coefficients of time dummies are present in the table of coefficients,

digits digits,

width the maximum length of the lines in the print output.

Details

pgmm estimates a model for panel data with a generalized method of moments (GMM) estimator. The description of the model to estimate is provided with a multi–part formula which is (or which is coerced to) a Formula object. The first right–hand side part describes the covariates. The second one, which is mandatory, describes the GMM instruments. The third one, which is optional, describes the 'normal' instruments. By default, all the variables of the model which are not used as GMM instruments are used as normal instruments with the same lag structure as the one specified in the model.

\[ y \sim \text{lag}(y, 1:2) + \text{lag}(x_1, 0:1) + \text{lag}(x_2, 0:2) \mid \text{lag}(y, 2:99) \] is similar to

\[ y \sim \text{lag}(y, 1:2) + \text{lag}(x_1, 0:1) + \text{lag}(x_2, 0:2) \mid \text{lag}(y, 2:99) \mid \text{lag}(x_1, 0:1) + \text{lag}(x_2, 0:2) \]

and indicates that all lags from 2 of \( y \) are used as GMM instruments.

transformation indicates how the model should be transformed for the estimation. "d" gives the "difference GMM" model (see Arellano and Bond 1991), "ld" the "system GMM" model (see Blundell and Bond 1998).

pgmm is an attempt to adapt GMM estimators available within the DPD library for GAUSS (see Arellano and Bond 1998) and Ox (see Arellano and Bond 2012) and within the xtabond2 library for Stata (see Roodman 2009).

Value

An object of class c("pgmm", "panelmodel"), which has the following elements:

coefficients the vector (or the list for fixed effects) of coefficients,

residuals the vector of residuals,
vcov the covariance matrix of the coefficients,
fitted.values the vector of fitted values,
df.residual degrees of freedom of the residuals,
model a list containing the variables used for the estimation for each individual,
W a list containing the instruments for each individual (two lists in case of "sys-GMM"),
A1 the weighting matrix for the one-step estimator,
A2 the weighting matrix for the two-steps estimator,
call the call.

It has print, summary and print.summary methods.

Author(s)
Yves Croissant

References


See Also
sargan() for the Hansen–Sargan test and mtest() for Arellano–Bond’s test of serial correlation. dynformula() for dynamic formulas (deprecated).

Examples

data("EmplUK", package = "plm")

## Arellano and Bond (1991), table 4 col. b
z1 <- pgmm(log(emp) ~ lag(log(emp), 1:2) + lag(log(wage), 0:1) + log(capital) + lag(log(output), 0:1) | lag(log(emp), 2:99),
data = EmplUK, effect = "twoways", model = "twosteps")
summary(z1, robust = FALSE)

## Blundell and Bond (1998) table 4 (cf. DPD for OX p. 12 col. 4)
z2 <- pgmm(log(emp) ~ lag(log(emp), 1) +
lag(log(capital), 0:1) | lag(log(emp), 2:99) +
lag(log(wage), 2:99) + lag(log(capital), 2:99),
data = EmplUK, effect = "twoways", model = "onestep",
transformation = "ld")
summary(z2, robust = TRUE)

## Not run:
## Same with the old formula or dynformula interface
## Arellano and Bond (1991), table 4, col. b
z1 <- pgmm(log(emp) ~ log(wage) + log(capital) + log(output),
lag.form = list(2,1,0,1), data = EmplUK,
effect = "twoways", model = "twosteps",
gmm.inst = ~log(emp), lag.gmm = list(c(2,99)))
summary(z1, robust = FALSE)

## Blundell and Bond (1998) table 4 (cf DPD for OX p. 12 col. 4)
z2 <- pgmm(dynformula(log(emp) ~ log(wage) + log(capital), list(1,1,1)),
data = EmplUK, effect = "twoways", model = "onestep",
gmm.inst = ~log(emp) + log(wage) + log(capital),
lag.gmm = c(2,99), transformation = "ld")
summary(z2, robust = TRUE)

## End(Not run)

---

**pgrangertest**

*Panel Granger (Non-)Causality Test (Dumitrescu/Hurlin (2012))*

**Description**

Test for Granger (non-)causality in panel data.

**Usage**

```
pgrangertest(formula, data, test = c("Ztilde", "Zbar", "Wbar"),
order = 1L, index = NULL)
```

**Arguments**

- `formula` a formula object to describe the direction of the hypothesized Granger causation.
- `data` a `pdata.frame` or a `data.frame`.
- `test` a character to request the statistic to be returned, either "Ztilde" (default), or "Zbar".
order

integer(s) giving the number of lags to include in the test’s auxiliary regressions, the length of order must be either 1 (same lag order for all individuals) or equal to the number of individuals (to specify a lag order per individual).

index

only relevant if data is data.frame and not a pdata.frame; if NULL, the first two columns of the data.frame are assumed to be the index variables, for further details see pdata.frame().

Details

independence

The panel Granger (non-)causality test is a combination of Granger tests (Granger 1969) performed per individual. The test is developed by Dumitrescu and Hurlin (2012), a shorter exposition is given in Lopez and Weber (2017).

The formula formula describes the direction of the (panel) Granger causation where \( y \sim x \) means "x (panel) Granger causes y".

By setting argument test to either "\( \tilde{Z} \)" (default) or "\( \bar{Z} \)", two different statistics can be requested. "\( \tilde{Z} \)" gives the standardised statistic recommended by Dumitrescu/Hurlin (2012) for fixed T samples. If set to "\( \bar{W} \)"; the intermediate \( \bar{W} \) statistic (average of individual Granger chi-square statistics) is given which is used to derive the other two.

The Zbar statistic is not suitable for unbalanced panels. For the Wbar statistic, no p-value is available.

The implementation uses lmtest::grangertest() from package lmtest\(^{13}\) to perform the individual Granger tests.

Value

An object of class c("pgrangertest", "htest"). Besides the usual elements of a htest object, it contains the data frame indgranger which carries the Granger test statistics per individual along the associated p-values, degrees of freedom and the specified lag order.

Author(s)

Kevin Tappe

References


---

\(^{13}\)https://CRAN.R-project.org/package=lmtest
See Also

`lmtest::grangertest()` for the original (non-panel) Granger causality test in `lmtest`\(^\text{14}\).

Examples

```r
## not meaningful, just to demonstrate usage
## H0: 'value' Granger causes 'inv' for all individuals

data("Grunfeld", package = "plm")
pgrangertest(inv ~ value, data = Grunfeld)
pgrangertest(inv ~ value, data = Grunfeld, order = 2L)
pgrangertest(inv ~ value, data = Grunfeld, order = 2L, test = "Zbar")

# varying lag order (last individual lag order 3, others lag order 2)
pgrangertest(inv ~ value, data = Grunfeld, order = c(rep(2L, 9), 3L))
```

---

### Hausman–Taylor Estimator for Panel Data

**Description**

The Hausman–Taylor estimator is an instrumental variable estimator without external instruments (function deprecated).

**Usage**

```r
pht(formula, data, subset, na.action, model = c("ht", "am", "bms"),
     index = NULL, ...)
```

```r
## S3 method for class 'pht'
summary(object, ...)
```

```r
## S3 method for class 'summary.pht'
print(x, digits = max(3, getOption("digits") - 2),
      width = getOption("width"), subset = NULL, ...)
```

**Arguments**

- `formula`: a symbolic description for the model to be estimated,
- `data`: a data.frame,
- `subset`: see `lm()` for "plm", a character or numeric vector indicating a subset of the table of coefficient to be printed for "print.summary.plm".

\(^\text{14}\)https://CRAN.R-project.org/package=lmtest


da.action see \texttt{lm()},

model one of "ht" for Hausman–Taylor, "am" for Amemiya–MaCurdy and "bms" for Breusch–Mizon–Schmidt,

index the indexes,

... further arguments.

object, x an object of class \texttt{"plm"},

digits digits,

width the maximum length of the lines in the print output,

Details

\texttt{pht} estimates panels models using the Hausman–Taylor estimator, Amemiya–MaCurdy estimator, or Breusch–Mizon–Schmidt estimator, depending on the argument \texttt{model}. The model is specified as a two–part formula, the second part containing the exogenous variables.

Value

An object of class \texttt{c("pht","plm","panelmodel").}

A \"pht\" object contains the same elements as \texttt{plm} object, with a further argument called \texttt{varlist} which describes the typology of the variables. It has \texttt{summary} and \texttt{print.summary} methods.

Note

The function \texttt{pht} is deprecated. Please use function \texttt{plm} to estimate Taylor–Hausman models like this with a three-part formula as shown in the example:

\begin{verbatim}
plm(<formula>,random.method = "ht",model = "random",inst.method = "baltagi").
\end{verbatim}

The Amemiya–MaCurdy estimator and the Breusch–Mizon–Schmidt estimator is computed likewise with \texttt{plm}.

Author(s)

Yves Croissant

References

(Amemiya and MaCurdy 1986)

(Baltagi 2013)

(Breusch et al. 1989)

(Hausman and Taylor 1981)

Examples

\begin{verbatim}
## replicates Baltagi (2005, 2013), table 7.4
## preferred way with \texttt{plm()}
data(\texttt{"Wages"}, package = \"plm")
ht <- plm(lwage ~ wks + south + smsa + married + exp + I(exp^2) +
\end{verbatim}
The `phtest` function is used for Hausman Test for Panel Models. It performs a specification test for panel models. The function can be used on objects of class `formula` or `panelmodel`. The `summary` method provides a summary of the test results.

**Description**

Specification test for panel models.

**Usage**

```r
phtest(x, ...)  # S3 method for class 'formula'
phtest(x, data, model = c("within", "random"),
       method = c("chisq", "aux"), index = NULL, vcov = NULL, ...)
```

## deprecated way with pht() for HT
#ht <- pht(lwage ~ wks + south + smsa + married + exp + I(exp^2) +
#         bluecol + ind + union + sex + black + ed |
#         sex + black + bluecol + south + smsa + ind,
#         data = Wages, model = "ht", index = 595)
#summary(ht)
# deprecated way with pht() for AM
#am <- pht(lwage ~ wks + south + smsa + married + exp + I(exp^2) +
#         bluecol + ind + union + sex + black + ed |
#         sex + black + bluecol + south + smsa + ind,
#         data = Wages, model = "am", index = 595)
#summary(am)
Arguments

x an object of class "panelmodel" or "formula", 
... further arguments to be passed on. For the formula method, place argument 
effect here to compare e.g. twoway models (effect = "twoways") Note: 
Argument effect is not respected in the panelmodel method.
data a data.frame, 
model a character vector containing the names of two models (length(model) must be 2), 
method one of "chisq" or "aux", 
index an optional vector of index variables, 
vcov an optional covariance function, 
x2 an object of class "panelmodel",

Details

The Hausman test (sometimes also called Durbin–Wu–Hausman test) is based on the difference 
of the vectors of coefficients of two different models. The panelmodel method computes the 
original version of the test based on a quadratic form (Hausman 1978). The formula method, if 
method = "chisq" (default), computes the original version of the test based on a quadratic form; 
if method = "aux" then the auxiliary-regression-based version in Wooldridge (2010, Sec. 10.7.3.) 
is computed instead (WOOL:10 Sec.10.7.3). Only the latter can be robustified by specifying a 
robust covariance estimator as a function through the argument vcov (see Examples).

The equivalent tests in the one-way case using a between model (either "within vs. between" 
or "random vs. between") (see Hausman and Taylor 1981 or Baltagi 2013 Sec.4.3) can also be 
performed by phtest, but only for test = "chisq", not for the regression-based test. NB: 
These equivalent tests using the between model do not extend to the two-ways case. There are, 
however, some other equivalent tests, (see Kang 1985 or Baltagi 2013 Sec.4.3.7), but those are 
unsupported by phtest.

Value

An object of class "htest".

Author(s)

Yves Croissant, Giovanni Millo

References

49, 1377–1398.
variance components model.” Journal of Econometrics, 28(2), 193 - 203. ISSN 0304-4076, http: 
Examples

```r
data("Gasoline", package = "plm")
form <- lgaspcar ~ lincomep + lrpmg + lcarpcap
wi <- plm(form, data = Gasoline, model = "within")
re <- plm(form, data = Gasoline, model = "random")
phtest(wi, re)
phtest(form, data = Gasoline)
phtest(form, data = Gasoline, method = "aux")

# robust Hausman test (regression-based)
phtest(form, data = Gasoline, method = "aux", vcov = vcovHC)

# robust Hausman test with vcov supplied as a
# function and additional parameters
phtest(form, data = Gasoline, method = "aux",
       vcov = function(x) vcovHC(x, method="white2", type="HC3"))
```

---

**piest**  
*Chamberlain estimator and test for fixed effects*

Description

General estimator useful for testing the within specification

Usage

```r
piest(formula, data, subset, na.action, index = NULL, robust = TRUE, ...)
```

## S3 method for class 'piest'

```r
print(x, ...)
```

## S3 method for class 'piest'

```r
summary(object, ...)
```

## S3 method for class 'summary.piest'

```r
print(x, ...)
```

Arguments

- `formula` a symbolic description for the model to be estimated,
- `data` a `data.frame`,
- `subset` see `lm()`,
- `na.action` see `lm()`,
- `index` the indexes,
robust: if FALSE, the error is assumed to be spherical, otherwise, a robust estimation of the covariance matrix is computed.

Details
The Chamberlain method consists on using the covariates of all the periods as regressors. It allows to test the within specification.

Value
An object of class "piest".

Author(s)
Yves Croissant

References

See Also
aneweytest()

Examples

data("RiceFarms", package = "plm")
pirice <- piest(log(goutput) ~ log(seed) + log(totlabor) + log(size), RiceFarms, index = "id")
summary(pirice)
Arguments

- `formula`: a symbolic description for the model to be estimated,
- `data`: a `data.frame`,
- `subset`: see `lm`,
- `weights`: see `lm`,
- `na.action`: see `lm`,
- `model`: one of "fd", "random" or "pooling",
- `index`: the indexes, see `pdata.frame()`,
- `R`: the number of points for the gaussian quadrature,
- `start`: a vector of starting values,
- `lower`: the lower bound for the censored/truncated dependent variable,
- `upper`: the upper bound for the censored/truncated dependent variable,
- `objfun`: the objective function for the fixed effect model, one of "lsq" for least squares and "lad" for least absolute deviations,
- `sample`: "cens" for a censored (tobit-like) sample, "trunc" for a truncated sample,
- `...`: further arguments.

Details

`pldv` computes two kinds of models: maximum likelihood estimator with an assumed normal distribution for the individual effects and a LSQ/LAD estimator for the first-difference model.

Value

An object of class `c("plm", "panelmodel")`.

Author(s)

Yves Croissant

References

Panel Data Estimators

Description

Linear models for panel data estimated using the \texttt{lm} function on transformed data.

Usage

\begin{verbatim}
plm(formula, data, subset, weights, na.action, effect = c("individual", "time", "twoways", "nested"), model = c("within", "random", "ht", "between", "pooling", "fd"), random.method = NULL, random.models = NULL, random.dfcor = NULL, inst.method = c("bvk", "baltagi", "am", "bms"), restrict.matrix = NULL, restrict.rhs = NULL, index = NULL, ...)

## S3 method for class 'panelmodel'
terms(x, ...)

## S3 method for class 'panelmodel'
vcov(object, ...)

## S3 method for class 'panelmodel'
fitted(object, ...)

## S3 method for class 'panelmodel'
residuals(object, ...)

## S3 method for class 'panelmodel'
df.residual(object, ...)

## S3 method for class 'panelmodel'
coef(object, ...)

## S3 method for class 'panelmodel'
print(x, digits = max(3, getOption("digits") - 2), width = getOption("width"), ...)

## S3 method for class 'panelmodel'
update(object, formula., ..., evaluate = TRUE)

## S3 method for class 'panelmodel'
deviance(object, model = NULL, ...)

## S3 method for class 'plm'
predict(object, newdata = NULL, ...)\end{verbatim}
## S3 method for class 'plm'
formula(x, ...)

## S3 method for class 'plm'
plot(x, dx = 0.2, N = NULL, seed = 1, within = TRUE,
     pooling = TRUE, between = FALSE, random = FALSE, ...)

## S3 method for class 'plm'
residuals(object, model = NULL, effect = NULL, ...)

## S3 method for class 'plm'
fitted(object, model = NULL, effect = NULL, ...)

Arguments

**formula** a symbolic description for the model to be estimated,

**data** a data.frame,

**subset** see stats::lm(),

**weights** see stats::lm(),

**na.action** see stats::lm(); currently, not fully supported,

**effect** the effects introduced in the model, one of "individual", "time", "twoways", or "nested",

**model** one of "pooling", "within", "between", "random", "fd", or "ht",

**random.method** method of estimation for the variance components in the random effects model, one of "swar" (default), "amemiya", "walhus", or "nerlove",

**random.models** an alternative to the previous argument, the models used to compute the variance components estimations are indicated,

**random.dfcor** a numeric vector of length 2 indicating which degree of freedom should be used,

**inst.method** the instrumental variable transformation: one of "bvk", "baltagi", "am", or "bms" (see also Details),

**restrict.matrix** a matrix which defines linear restrictions on the coefficients,

**restrict.rhs** the right hand side vector of the linear restrictions on the coefficients,

**index** the indexes,

... further arguments.

**x, object** an object of class "plm",

**digits** number of digits for printed output,

**width** the maximum length of the lines in the printed output,

**formula.** a new formula for the update method,

**evaluate** a boolean for the update method, if TRUE the updated model is returned, if FALSE the call is returned,
newdata     the new data set for the predict method,
dx         the half–length of the individual lines for the plot method (relative to x range),
N          the number of individual to plot,
seed       the seed which will lead to individual selection,
within     if TRUE, the within model is plotted,
pooling    if TRUE, the pooling model is plotted,
between    if TRUE, the between model is plotted,
random     if TRUE, the random effect model is plotted,

Details

plm is a general function for the estimation of linear panel models. It supports the following estimation methods: pooled OLS (model = "pooling"), fixed effects ("within"), random effects ("random"), first–differences ("fd"), and between ("between"). It supports unbalanced panels and two–way effects (although not with all methods).

For random effects models, four estimators of the transformation parameter are available by setting random.method to one of "swar" (Swamy and Arora 1972) (default), "amemiya" (Amemiya 1971), "walhus" (Wallace and Hussain 1969), or "nerlove" (Nerlove 1971).

For first–difference models, the intercept is maintained (which from a specification viewpoint amounts to allowing for a trend in the levels model). The user can exclude it from the estimated specification the usual way by adding "–1" to the model formula.

Instrumental variables estimation is obtained using two–part formulas, the second part indicating the instrumental variables used. This can be a complete list of instrumental variables or an update of the first part. If, for example, the model is y ~ x1 + x2 + x3, with x1 and x2 endogenous and z1 and z2 external instruments, the model can be estimated with:

- formula = y~x1+x2+x3 | x3+z1+z2,
- formula = y~x1+x2+x3 | .-x1-x2+z1+z2.

If an instrument variable estimation is requested, argument inst.method selects the instrument variable transformation method:

- "bvk" (default) for Balestra and Varadharajan–Krishnakumar (1987),
- "baltagi" for Baltagi (1981),
- "am" for Amemiya and MaCurdy (1986),
- "bms" for Breusch et al. (1989).

The Hausman–Taylor estimator (Hausman and Taylor 1981) is computed with arguments random.method = "ht", model = "random", inst.method = "baltagi" (the other way with only model = "ht" is deprecated).
Value

An object of class "plm".

A "plm" object has the following elements:

- **coefficients**: the vector of coefficients,
- **vcov**: the variance-covariance matrix of the coefficients,
- **residuals**: the vector of residuals (these are the residuals of the (quasi-)demeaned model),
- **weights**: (only for weighted estimations) weights as specified,
- **df.residual**: degrees of freedom of the residuals,
- **formula**: an object of class "pFormula" describing the model,
- **model**: the model frame as a "pdata.frame" containing the variables used for estimation: the response is in first column followed by the other variables, the individual and time indexes are in the 'index' attribute of model,
- **ercomp**: an object of class "ercomp" providing the estimation of the components of the errors (for random effects models only),
- **aliased**: named logical vector indicating any aliased coefficients which are silently dropped by **plm** due to linearly dependent terms (see also detect.lindep()),
- **call**: the call.

It has print, summary and print.summary methods. The summary method creates an object of class "summary.plm" that extends the object it is run on with information about (inter alia) F statistic and (adjusted) R-squared of model, standard errors, t–values, and p–values of coefficients, (if supplied) the furnished vcov, see summary.plm() for further details.

Author(s)

Yves Croissant

References


See Also

`summary.plm()` for further details about the associated summary method and the "summary.plm" object both of which provide some model tests and tests of coefficients. `fixef()` to compute the fixed effects for "within" models (=fixed effects models).

Examples

data("Produc", package = "plm")
zz <- plm(log(gsp) ~ log(pcap) + log(pc) + log(emp) + unemp, 
    data = Produc, index = c("state","year"))
summary(zz)

# replicates some results from Baltagi (2013), table 3.1

data("Grunfeld", package = "plm")
p <- plm(inv ~ value + capital, 
    data = Grunfeld, model = "pooling")

wi <- plm(inv ~ value + capital, 
    data = Grunfeld, model = "within", effect = "twoways")

swar <- plm(inv ~ value + capital, 
    data = Grunfeld, model = "random", effect = "twoways")

amemiya <- plm(inv ~ value + capital, 
    data = Grunfeld, model = "random", random.method = "amemiya", 
    effect = "twoways")

walhus <- plm(inv ~ value + capital, 
    data = Grunfeld, model = "random", random.method = "walhus", 
    effect = "twoways")

# summary and summary with a furnished vcov (passed as matrix, 
# as function, and as function with additional argument)

summary(wi)
summary(wi, vcov = vcovHC(wi))
summary(wi, vcov = vcovHC)
summary(wi, vcov = function(x) vcovHC(x, method = "white2"))

# nested random effect model
# replicate Baltagi/Song/Jung (2001), p. 378 (table 6), columns SA, WH
# == Baltagi (2013), pp. 204-205
data("Produc", package = "plm")
pProduc <- pdata.frame(Produc, index = c("state", "year", "region"))
form <- log(gsp) ~ log(pc) + log(emp) + log(hwy) + log(water) + log(util) + unemp
summary(plm(form, data = pProduc, model = "random", effect = "nested"))
summary(plm(form, data = pProduc, model = "random", effect = "nested",
    random.method = "walhus"))

## Hausman-Taylor estimator and Amemiya-MacCurdy estimator
## replicate Baltagi (2005, 2013), table 7.4
data("Wages", package = "plm")
ht <- plm(lwage ~ wks + south + smsa + married + exp + I(exp ^ 2) +
    bluecol + ind + union + sex + black + ed |
    bluecol + south + smsa + ind + sex + black |
    wks + married + union + exp + I(exp ^ 2),
data = Wages, index = 595,
    random.method = "ht", model = "random", inst.method = "baltagi")
summary(ht)
am <- plm(lwage ~ wks + south + smsa + married + exp + I(exp ^ 2) +
    bluecol + ind + union + sex + black + ed |
    bluecol + south + smsa + ind + sex + black |
    wks + married + union + exp + I(exp ^ 2),
data = Wages, index = 595,
    random.method = "ht", model = "random", inst.method = "am")
summary(am)

---

**plm-deprecated**

** Deprecated functions of plm **

**Description**

dynformula, pht, plm.data, and pvcovHC are deprecated functions which could be removed from plm in a near future.

**Usage**

pvcovHC(x, ...)

plm.data(x, indexes = NULL)

dynformula(formula, lag.form = NULL, diff.form = NULL,
    log.form = NULL)

pFormula(object)

## S3 method for class 'pFormula'
as.Formula(x, ...) 

## S3 method for class 'pFormula'
as.Formula(x, ...)

## S3 method for class 'pFormula'
model.frame(formula, data, ..., lhs = NULL, 
            rhs = NULL)

## S3 method for class 'pFormula'
model.matrix(object, data, model = c("pooling", 
               "within", "Between", "Sum", "between", "mean", "random", "fd"),
            effect = c("individual", "time", "twoways", "nested"), rhs = 1,
            theta = NULL, cstcovar.rm = NULL, ...)

detect_lin_dep(object, ...)

Arguments

... further arguments.
indexes a vector (of length one or two) indicating the (individual and time) indexes (see Details);
formula a formula,
lag.form a list containing the lag structure of each variable in the formula,
diff.form a vector (or a list) of logical values indicating whether variables should be differenced,
log.form a vector (or a list) of logical values indicating whether variables should be in logarithms.
object, x an object of class "plm",
data a data.frame,
lhs see Formula
rhs see Formula
model see plm
effect see plm
theta the parameter of transformation for the random effect model
cstcovar.rm remove the constant columns or not

Details
dynformula was used to construct a dynamic formula which was the first argument of pgmm.
pgmm uses now multi-part formulas.
pht estimates the Hausman-Taylor model, which can now be estimated using the more general plm function.
plm.data is replaced by pdata.frame.
plmtest is replaced by vcovHC.
detect_lin_dep is replaced by detect.lindep.

plmtest

Lagrange FF Multiplier Tests for Panel Models

Description

Test of individual and/or time effects for panel models.

Usage

plmtest(x, ...)

## S3 method for class 'plm'
plmtest(x, effect = c("individual", "time", "twoways")
          , type = c("honda", "bp", "ghm", "kw"), ...)

## S3 method for class 'formula'
plmtest(x, data, ..., effect = c("individual", "time", "twoways")
          , type = c("honda", "bp", "ghm", "kw"))

Arguments

x an object of class "plm" or a formula of class "formula",
... further arguments passed to plmtest.
effect a character string indicating which effects are tested: individual effects ("individual"),
time effects ("time") or both ("twoways"),
type a character string indicating the test to be performed:
  • "honda" (default) for Honda (1985),
  • "bp" for Breusch and Pagan (1980),
  • "kw" for King and Wu (1997), or
  • "ghm" for Gourieroux et al. (1982) for unbalanced panel data sets, the respective unbalanced version of the tests are computed,
data a data.frame,

Details

These Lagrange multiplier tests use only the residuals of the pooling model. The first argument of this function may be either a pooling model of class plm or an object of class formula describing the model. For inputted within (fixed effects) or random effects models, the corresponding pooling model is calculated internally first as the tests are based on the residuals of the pooling model.

The "bp" test for unbalanced panels was derived in Baltagi and Li (1990) (1990), the "kw" test for unbalanced panels in Baltagi et al. (1998).

The "ghm" test and the "kw" test were extended to two-way effects in Baltagi et al. (1992).

For a concise overview of all these statistics see Baltagi (2003), Sec. 4.2, pp. 68–76 (for balanced panels) and Sec. 9.5, pp. 200–203 (for unbalanced panels).
Value

An object of class "htest".

Note

For the King-Wu statistics ("kw"), the oneway statistics ("individual" and "time") coincide with the respective Honda statistics ("honda"); two-way statistics of "kw" and "honda" differ.

Author(s)

Yves Croissant (initial implementation), Kevin Tappe (generalization to unbalanced panels)

References


See Also

pFtest() for individual and/or time effects tests based on the within model.

Examples

data("Grunfeld", package = "plm")
g <- plm(inv ~ value + capital, data = Grunfeld, model = "pooling")
plmtest(g)
plmtest(g, effect="time")
plmtest(inv ~ value + capital, data = Grunfeld, type = "honda")
plmtest(inv ~ value + capital, data = Grunfeld, type = "bp")
plmtest(inv ~ value + capital, data = Grunfeld, type = "bp", effect = "twoways")
plmtest(inv ~ value + capital, data = Grunfeld, type = "ghm", effect = "twoways")
plmtest(inv ~ value + capital, data = Grunfeld, type = "kw", effect = "twoways")
Grunfeld_unbal <- Grunfeld[1:(nrow(Grunfeld)-1), ] # create an unbalanced panel data set
g_unbal <- plm(inv ~ value + capital, data = Grunfeld_unbal, model = "pooling")
plmtest(g_unbal) # unbalanced version of test is indicated in output

---

**pmg**  
*Mean Groups (MG), Demeaned MG and CCE MG estimators*

**Description**

Mean Groups (MG), Demeaned MG (DMG) and Common Correlated Effects MG (CCEMG) estimators for heterogeneous panel models, possibly with common factors (CCEMG)

**Usage**

\[
\text{pmg}(\text{formula, data, subset, na.action, model = c("mg", "cmg", "dmg"),}
\text{index = NULL, trend = FALSE, ...})
\]

```r
## S3 method for class 'pmg'
summary(object, ...)
## S3 method for class 'summary.pmg'
print(x, digits = max(3, getOption("digits") - 2),
      width = getOption("width"), ...)
## S3 method for class 'pmg'
residuals(object, ...)
```

**Arguments**

- **formula** a symbolic description of the model to be estimated,
- **data** a data.frame,
- **subset** see `lm()`,
- **na.action** see `lm()`,
- **model** one of c("mg", "cmg", "dmg").
- **index** the indexes, see `pdata.frame()`,
- **trend** logical specifying whether an individual-specific trend has to be included,
- **...** further arguments.
- **object, x** an object of class `pmg`,
- **digits** digits,
- **width** the maximum length of the lines in the print output,
Details

`pmg` is a function for the estimation of linear panel models with heterogeneous coefficients by the Mean Groups estimator. `model = "mg"` specifies the standard Mean Groups estimator, based on the average of individual time series regressions. If `model = "dmg"` the data are demeaned cross-sectionally, which is believed to reduce the influence of common factors (and is akin to what is done in homogeneous panels when `model = "within"` and `effect = "time"`). Lastly, if `model = "cmg"` the CCEMG estimator is employed: this latter is consistent under the hypothesis of unobserved common factors and idiosyncratic factor loadings; it works by augmenting the model by cross-sectional averages of the dependent variable and regressors in order to account for the common factors, and adding individual intercepts and possibly trends.

Value

An object of class `c("pmg","panelmodel")` containing:

- `coefficients` the vector of coefficients,
- `residuals` the vector of residuals,
- `fitted.values` the vector of fitted values,
- `vcov` the covariance matrix of the coefficients,
- `df.residual` degrees of freedom of the residuals,
- `model` a data.frame containing the variables used for the estimation,
- `call` the call,
- `sigma` always NULL, `sigma` is here only for compatibility reasons (to allow using the same summary and print methods as `pggls`),
- `indcoef` the matrix of individual coefficients from separate time series regressions.

Author(s)

Giovanni Millo

References


Examples

data("Produc", package = "plm")
## Mean Groups estimator
mgmod <- pmg(log(gsp) ~ log(pcap) + log(pc) + log(emp) + unemp, data = Produc)
summary(mgmod)

## demeaned Mean Groups
dmgmod <- pmg(log(gsp) ~ log(pcap) + log(pc) + log(emp) + unemp, data = Produc, model = "dmg")
summary(dmgmod)
## Common Correlated Effects Mean Groups

ccemgmod <- pmg(log(gsp) ~ log(pcap) + log(pc) + log(emp) + unemp,
          data = Produc, model = "cmg")

summary(ccemgmod)

---

**pmodel.response**  
*A function to extract the model.response*

### Description

pmodel.response has several methods to conveniently extract the response of several objects.

### Usage

```r
pmodel.response(object, ...)  
norm S3 method for class 'plm'
pmodel.response(object, ...)
norm S3 method for class 'data.frame'
pmodel.response(object, ...)
norm S3 method for class 'formula'
pmodel.response(object, data, ...)
```

### Arguments

- `object`  
an object of class "plm", or a formula of class "pFormula".
- `...`  
further arguments.
- `data`  
a data.frame

### Details

The model response is extracted from a `pdata.frame` (where the response must reside in the first column; this is the case for a model frame), a `pFormula + data` or a `plm` object, and the transformation specified by `effect` and `model` is applied to it.  
Constructing the model frame first ensures proper NA handling and the response being placed in the first column, see also **Examples** for usage.

### Value

A `pseries` except if model responses’ of a "between" or "fd" model as these models "compress" the data (the number of observations used in estimation is smaller than the original data due to the specific transformation). A numeric is returned for the "between" and "fd" model.
pooltest

Author(s)

Yves Croissant

See Also

plm's model.matrix() for (transformed) model matrix and the corresponding model.frame() method to construct a model frame.

Examples

# First, make a pdata.frame
data("Grunfeld", package = "plm")
pGrunfeld <- pdata.frame(Grunfeld)

# then make a model frame from a pFormula and a pdata.frame

form <- inv ~ value + capital
mf <- model.frame(pGrunfeld, form)
# construct (transformed) response of the within model
resp <- pmodel.response(form, data = mf, model = "within", effect = "individual")
# retrieve (transformed) response directly from model frame
resp_mf <- pmodel.response(mf, model = "within", effect = "individual")

# retrieve (transformed) response from a plm object, i.e. an estimated model
fe_model <- plm(form, data = pGrunfeld, model = "within")
pmodel.response(fe_model)

# same as constructed before
all.equal(resp, pmodel.response(fe_model), check.attributes = FALSE) # TRUE

---

pooltest

Test of Poolability

Description

A Chow test for the poolability of the data.

Usage

pooltest(x, ...)

## S3 method for class 'plm'
pooltest(x, z, ...)

## S3 method for class 'formula'
pooltest(x, data, ...)
Arguments

- `x`: an object of class "plm" for the `plm` method; an object of class "formula" for the formula interface.
- `...`: further arguments passed to `plm`.
- `z`: an object of class "pvcm" obtained with `model="within"`.
- `data`: a `data.frame`.

Details

`pooltest` is a $F$ test of stability (or Chow test) for the coefficients of a panel model. For argument `x`, the estimated `plm` object should be a "pooling" model or a "within" model (the default); intercepts are assumed to be identical in the first case and different in the second case.

Value

An object of class "htest".

Author(s)

Yves Croissant

Examples

```r
data("Gasoline", package = "plm")
form <- lgaspcar ~ lincomep + lrpmg + lcarpcap
gasw <- plm(form, data = Gasoline, model = "within")
gasp <- plm(form, data = Gasoline, model = "pooling")
gasnp <- pvcm(form, data = Gasoline, model = "within")
pooltest(gasw, gasnp)
pooltest(gasp, gasnp)

pooltest(form, data = Gasoline, effect = "individual", model = "within")
pooltest(form, data = Gasoline, effect = "individual", model = "pooling")
```

---

### Produc

#### US States Production

Description

A panel of 48 observations from 1970 to 1986
Produc

Format

A data frame containing:

- **state** the state
- **year** the year
- **region** the region
- **pcap** public capital stock
- **hwy** highway and streets
- **water** water and sewer facilities
- **util** other public buildings and structures
- **pc** private capital stock
- **gsp** gross state product
- **emp** labor input measured by the employment in non-agricultural payrolls
- **unemp** state unemployment rate

Details

- **total number of observations**: 816
- **observation**: regional
- **country**: United States

Source

Online complements to Baltagi (2001):
http://www.wiley.com/legacy/wileychi/baltagi/

Online complements to Baltagi (2013):
http://bcs.wiley.com/he-bcs/Books?action=resource&bcsId=4338&itemId=1118672321&resourceId=13452

References


panel series

Description

A class for panel series for which several useful computations and data transformations are available.

Usage

```r
## S3 method for class 'pseries'
print(x, ...)

## S3 method for class 'pseries'
as.matrix(x, idbyrow = TRUE, ...)

## S3 method for class 'pseries'
plot(x, plot = c("lattice", "superposed"),
     scale = FALSE, transparency = TRUE, col = "blue", lwd = 1, ...)

## S3 method for class 'pseries'
summary(object, ...)

## S3 method for class 'summary.pseries'
plot(x, ...)

## S3 method for class 'summary.pseries'
print(x, ...)

Between(x, ...)

## Default S3 method:
Between(x, effect, ...)

## S3 method for class 'pseries'
Between(x, effect = c("individual", "time", "group"),
        ...)

## S3 method for class 'matrix'
Between(x, effect, ...)

between(x, ...)

## Default S3 method:
between(x, effect, ...)

## S3 method for class 'pseries'
```

between(x, effect = c("individual", "time", "group"),
    ...)  
## S3 method for class 'matrix'
between(x, effect, ...)

Within(x, ...)

## Default S3 method:
Within(x, effect, ...)

## S3 method for class 'pseries'
Within(x, effect = c("individual", "time", "group", "twoways"), ...)

## S3 method for class 'matrix'
Within(x, effect, rm.null = TRUE, ...)

Arguments

x, object
  a pseries or a summary.pseries object,

... further arguments, e.g. na.rm = TRUE for transformation functions like between, see Details and Examples.

idbyrow
  if TRUE in the as.matrix method, the lines of the matrix are the individuals,

plot, scale, transparency, col, lwd
  plot arguments,

effect
  character string indicating the "individual" or "time" effect,

rm.null
  if TRUE, for the Within.matrix method, remove the empty columns.

Details

The functions between, Between, and Within perform specific data transformations, i.e. the between and within transformation.

between returns a vector containing the individual means (over time) with the length of the vector equal to the number of individuals (if effect = "individual" (default); if effect = "time", it returns the time means (over individuals)). Between duplicates the values and returns a vector which length is the number of total observations. Within returns a vector containing the values in deviation from the individual means (if effect = "individual", from time means if effect = "time"), the so called demeaned data.

For between, Between, and Within in presence of NA values it can be useful to supply na.rm = TRUE as an additional argument to keep as many observations as possible in the resulting transformation, see also Examples.

Value

All these functions return an object of class pseries, except:

between, which returns a numeric vector, as.matrix, which returns a matrix.
Author(s)

Yves Croissant

See Also

is.pseries() to check if an object is a pseries. For more functions on class 'pseries' see lag(), lead(), diff() for lagging values, leading values (negative lags) and differencing.

Examples

# First, create a pdata.frame
data("EmplUK", package = "plm")
Em <- pdata.frame(EmplUK)

# Then extract a series, which becomes additionally a pseries
z <- Em$output
class(z)

# obtain the matrix representation
as.matrix(z)

# compute the between and within transformations
between(z)
Within(z)

# Between replicates the values for each time observation
Between(z)

# between, Between, and Within transformations on other dimension
between(z, effect = "time")
Between(z, effect = "time")
Within(z, effect = "time")

# NA treatment for between, Between, and Within
z2 <- z
z2[length(z2)] <- NA # set last value to NA
between(z2, na.rm = TRUE) # non-NA value for last individual
Between(z2, na.rm = TRUE) # only the NA observation is lost
Within(z2, na.rm = TRUE) # only the NA observation is lost

sum(is.na(Between(z2))) # 9 observations lost due to one NA value
sum(is.na(Between(z2, na.rm = TRUE))) # only the NA observation is lost
sum(is.na(Within(z2))) # 9 observations lost due to one NA value
sum(is.na(Within(z2, na.rm = TRUE))) # only the NA observation is lost
punbalancedness  Measures for Unbalancedness of Panel Data

Description

This function reports unbalancedness measures for panel data as defined in Ahrens and Pincus (1981) and Baltagi et al. (2001).

Usage

punbalancedness(x, ...)

## S3 method for class 'pdata.frame'
punbalancedness(x, ...)

## S3 method for class 'data.frame'
punbalancedness(x, index = NULL, ...)

## S3 method for class 'panelmodel'
punbalancedness(x, ...)

Arguments

x  a panelmodel, a data.frame, or a pdata.frame object,
...
  further arguments.
index  only relevant for data.frame interface, for details see pdata.frame().

Details

punbalancedness returns measures for the unbalancedness of a panel data set.

- For two-dimensional data:
  The two measures of Ahrens and Pincus (1981) are calculated, called "gamma" ($\gamma$) and "nu" ($\nu$).

  If the panel data are balanced, both measures equal 1. The more "unbalanced" the panel data, the lower the measures (but > 0). The upper and lower bounds as given in Ahrens and Pincus (1981) are:
  $0 < \gamma, \nu \leq 1$, and for $\nu$ more precisely $\frac{1}{n} < \nu \leq 1$, with $n$ being the number of individuals (as in pdim(x)$nT$n).

- For nested panel data (meaning including a grouping variable):
  The extension of the above measures by Baltagi et al. (2001), p. 368, are calculated:

  - c1: measure of subgroup (individual) unbalancedness,
    - c2: measure of time unbalancedness,
    - c3: measure of group unbalancedness due to each group size.
Values are 1 if the data are balanced and become smaller as the data become more unbalanced.

An application of the measure "gamma" is found in e. g. Baltagi et al. (2001), pp. 488-491, and Baltagi and Chang (1994), pp. 78–87, where it is used to measure the unbalancedness of various unbalanced data sets used for Monte Carlo simulation studies. Measures c1, c2, c3 are used for similar purposes in Baltagi et al. (2001).

In the two-dimensional case, `punbalancedness` uses output of `pdim()` to calculate the two unbalancedness measures, so inputs to `punbalancedness` can be whatever `pdim` works on. `pdim` returns detailed information about the number of individuals and time observations (see `pdim()`).

**Value**

A named numeric containing either two or three entries, depending on the panel structure inputted:

- For the two-dimensional panel structure, the entries are called `gamma` and `nu`,
- For a nested panel structure, the entries are called `c1`, `c2`, `c3`.

**Note**

Calling `punbalancedness` on an estimated `panelmodel` object and on the corresponding (p)data.frame used for this estimation does not necessarily yield the same result (true also for `pdim`). When called on an estimated `panelmodel`, the number of observations (individual, time) actually used for model estimation are taken into account. When called on a (p)data.frame, the rows in the (p)data.frame are considered, disregarding any NA values in the dependent or independent variable(s) which would be dropped during model estimation.

**Author(s)**

Kevin Tappe

**References**


**See Also**

`nobs()`, `pdim()`, `pdata.frame()`

\(^{15}\)https://doi.org/10.1002/bimj.4710230302
**Examples**

```r
# Grunfeld is a balanced panel, Hedonic is an unbalanced panel
data(list=c("Grunfeld", "Hedonic"), package="plm")

# Grunfeld has individual and time index in first two columns
punbalancedness(Grunfeld) # c(1,1) indicates balanced panel
pdim(Grunfeld)$balanced # TRUE

# Hedonic has individual index in column "townid" (in last column)
punbalancedness(Hedonic, index="townid") # c(0.472, 0.519)
pdim(Hedonic, index="townid")$balanced # FALSE

# punbalancedness on estimated models
plm_mod_pool <- plm(inv ~ value + capital, data = Grunfeld)
punbalancedness(plm_mod_pool)
plm_mod_fe <- plm(inv ~ value + capital, data = Grunfeld[1:99,], model = "within")
punbalancedness(plm_mod_fe)

# replicate results for panel data design no. 1 in Ahrens/Pincus (1981), p. 234
ind_d1 <- c(1,1,2,3,3,3,4,4,4,4,4,4,5,5,5,5,5,5,5,5,6,6,6,6,6,6,6)
time_d1 <- c(1,2,3,1,2,3,1,2,3,4,5,1,2,3,4,5,6,7,1,2,3,4,5,6,7)
df_d1 <- data.frame(individual = ind_d1, time = time_d1)
punbalancedness(df_d1) # c(0.868, 0.887)

# example for a nested panel structure with a third index variable
# specifying a group (states are grouped by region) and without grouping
data("Produc", package = "plm")
punbalancedness(Produc, index = c("state", "year", "region"))
punbalancedness(Produc, index = c("state", "year"))
```

---

**purtest**  
*Unit root tests for panel data*

**Description**

*purtest* implements several testing procedures that have been proposed to test unit root hypotheses with panel data.

**Usage**

```r
purtest(object, data = NULL, index = NULL, test = c("levinlin",
"ips", "madwu", "Pm", "invnormal", "logit", "hadri"), exo = c("none",
"intercept", "trend"), lags = c("SIC", "AIC", "Hall"), pmax = 10,
Hcons = TRUE, q = NULL, dfcor = FALSE, fixedT = TRUE, ...)
```

```r
## S3 method for class 'purtest'
```

---

**Examples**

```r
# Grunfeld is a balanced panel, Hedonic is an unbalanced panel
data(list=c("Grunfeld", "Hedonic"), package="plm")

# Grunfeld has individual and time index in first two columns
punbalancedness(Grunfeld) # c(1,1) indicates balanced panel
pdim(Grunfeld)$balanced # TRUE

# Hedonic has individual index in column "townid" (in last column)
punbalancedness(Hedonic, index="townid") # c(0.472, 0.519)
pdim(Hedonic, index="townid")$balanced # FALSE

# punbalancedness on estimated models
plm_mod_pool <- plm(inv ~ value + capital, data = Grunfeld)
punbalancedness(plm_mod_pool)
plm_mod_fe <- plm(inv ~ value + capital, data = Grunfeld[1:99,], model = "within")
punbalancedness(plm_mod_fe)

# replicate results for panel data design no. 1 in Ahrens/Pincus (1981), p. 234
ind_d1 <- c(1,1,2,2,3,3,3,3,4,4,4,4,4,4,5,5,5,5,5,5,5,6,6,6,6,6,6,6)
time_d1 <- c(1,2,3,1,2,3,1,2,3,4,5,1,2,3,4,5,6,7,1,2,3,4,5,6,7)
df_d1 <- data.frame(individual = ind_d1, time = time_d1)
punbalancedness(df_d1) # c(0.868, 0.887)

# example for a nested panel structure with a third index variable
# specifying a group (states are grouped by region) and without grouping
data("Produc", package = "plm")
punbalancedness(Produc, index = c("state", "year", "region"))
punbalancedness(Produc, index = c("state", "year"))
```

---

**purtest**  
*Unit root tests for panel data*

**Description**

*purtest* implements several testing procedures that have been proposed to test unit root hypotheses with panel data.

**Usage**

```r
purtest(object, data = NULL, index = NULL, test = c("levinlin",
"ips", "madwu", "Pm", "invnormal", "logit", "hadri"), exo = c("none",
"intercept", "trend"), lags = c("SIC", "AIC", "Hall"), pmax = 10,
Hcons = TRUE, q = NULL, dfcor = FALSE, fixedT = TRUE, ...)
```

```r
## S3 method for class 'purtest'
```
print(x, ...)

## S3 method for class 'purtest'
summary(object, ...)

## S3 method for class 'summary.purtest'
print(x, ...)

Arguments

object, x    Either a "data.frame" or a matrix containing the time series, a "pseries" object, a formula, or the name of a column of a "data.frame", or a "pdata.frame" on which the test has to be computed; a "purtest" object for the print and summary methods,
data    a "data.frame" or a "pdata.frame" object,
index    the indexes,
test    the test to be computed: one of "levinlin" for Levin et al. (2002), "ips" for Im et al. (2003), "madwu" for Maddala and Wu (1999), "Pm", "invnormal", or "logit" for various tests as in Choi (2001), or "hadri" for Hadri (2000), see Details,
exo    the exogenous variables to introduce in the augmented Dickey–Fuller (ADF) regressions, one of: no exogenous variables ("none"), individual intercepts ("intercept"), or individual intercepts and trends ("trend"), but see Details,
lags    the number of lags to be used for the augmented Dickey-Fuller regressions: either an integer (the number of lags for all time series), a vector of integers (one for each time series), or a character string for an automatic computation of the number of lags, based on either the AIC ("AIC"), the SIC ("SIC"), or on the method by Hall (1994) ("Hall"),
pmax    maximum number of lags,
Hcons    logical, only relevant for test = "hadri", indicating whether the heteroskedasticity-consistent test of Hadri (2000) should be computed,
q    the bandwidth for the estimation of the long-run variance,
dfcor    logical, indicating whether the standard deviation of the regressions is to be computed using a degrees-of-freedom correction,
fixedT    logical, indicating whether the different ADF regressions are to be computed using the same number of observations,
...    further arguments.

Details

All these tests except "hadri" are based on the estimation of augmented Dickey-Fuller (ADF) regressions for each time series. A statistic is then computed using the t-statistics associated with the lagged variable. The Hadri residual-based LM statistic is the cross-sectional average of the individual KPSS statistics (Kwiatkowski et al. 1992), standardized by their asymptotic mean and standard deviation.
Several Fisher-type tests that combine p-values from tests based on ADF regressions per individual are available:

- "madwu" is the inverse chi-squared test (Maddala and Wu 1999), also called P test by Choi (2001).
- "Pm" is the modified P test proposed by Choi (2001) for large N,
- "invnormal" is the inverse normal test by (Choi 2001), and
- "logit" is the logit test by (Choi 2001).

The individual p-values for the Fisher-type tests are approximated as described in MacKinnon (1994).

The kind of test to be computed can be specified in several ways, depending on how the data is handed over to the function:

- For the formula/data interface (if data is a data.frame, an additional index argument should be specified); the formula should be of the form: y ~ 0, y ~ 1, or y ~ trend for a test with no exogenous variables, with an intercept, or with individual intercepts and time trend, respectively. The exo argument is ignored in this case.
- For the data.frame, matrix, and pseries interfaces: in these cases, the exogenous variables are specified using the exo argument.

With the associated summary and print methods, additional information can be extracted/displayed (see also Value).

**Value**

An object of class "purtest": a list with the elements "statistic" (a "htest" object), "call", "args", "idres" (containing results from the individual regressions), and "adjval" (containing the simulated means and variances needed to compute the statistic).

**Author(s)**

Yves Croissant and for "Pm", "invnormal", and "logit" Kevin Tappe

**References**


See Also

*cipstest()*

Examples

data("Grunfeld", package = "plm")
y <- data.frame(split(Grunfeld$inv, Grunfeld$firm))

purtest(y, pmax = 4, exo = "intercept", test = "madwu")

## same via formula interface

purtest(inv ~ 1, data = Grunfeld, index = c("firm", "year"), pmax = 4, test = "madwu")

---

**pvar**

*Check for Cross-Sectional and Time Variation*

**Description**

This function checks for each variable of a panel if it varies cross-sectionally and over time.

**Usage**

\[
\text{pvar}(x, \ldots)
\]

\[
\text{## S3 method for class 'matrix'}
\]

\[
\text{pvar}(x, \text{index = NULL}, \ldots)
\]

\[
\text{## S3 method for class 'data.frame'}
\]

\[
\text{pvar}(x, \text{index = NULL}, \ldots)
\]

\[
\text{## S3 method for class 'pdata.frame'}
\]
pvar(x, ...)

## S3 method for class 'pseries'
pvar(x, ...)

## S3 method for class 'pvar'
print(x, ...)

Arguments

x  a (p)data.frame or a matrix,
...	  further arguments.
index	  see pdata.frame(),

Details

For (p)data.frame and matrix interface: All-NA columns are removed prior to calculation of variation due to coercing to pdata.frame first.

Value

An object of class pvar containing the following elements:

id.variation  a logical vector with TRUE values if the variable has individual variation, FALSE if not,
time.variation  a logical vector with TRUE values if the variable has time variation, FALSE if not,
id.variation_anyNA  a logical vector with TRUE values if the variable has at least one individual-time combination with all NA values in the individual dimension for at least one time period, FALSE if not,
time.variation_anyNA  a logical vector with TRUE values if the variable has at least one individual-time combination with all NA values in the time dimension for at least one individual, FALSE if not.

Note

pvar can be time consuming for “big” panels.

Author(s)

Yves Croissant

See Also

pdim() to check the dimensions of a 'pdata.frame' (and other objects),
Examples

# Gasoline contains two variables which are individual and time
# indexes and are the first two variables
data("Gasoline", package = "plm")
pvar(Gasoline)

# Hedonic is an unbalanced panel, townid is the individual index;
# the drop.index argument is passed to pdata.frame
data("Hedonic", package = "plm")
pvar(Hedonic, "townid", drop.index = TRUE)

# same using pdata.frame
Hed <- pdata.frame(Hedonic, "townid", drop.index = TRUE)
pvar(Hed)

# Gasoline with pvar's matrix interface
Gasoline_mat <- as.matrix(Gasoline)
pvar(Gasoline_mat)
pvar(Gasoline_mat, index=c("country", "year"))

---

**pvcm**  
*Variable Coefficients Models for Panel Data*

**Description**

Estimators for random and fixed effects models with variable coefficients.

**Usage**

\[
pvcm(formula, data, subset, na.action, effect = c("individual", "time"),
    model = c("within", "random"), index = NULL, ...)
\]

## S3 method for class 'pvcm'

summary(object, ...)

## S3 method for class 'summary.pvcm'

print(x, digits = max(3,getOption("digits") - 2),
    width = getOption("width"), ...)

**Arguments**

- **formula**: a symbolic description for the model to be estimated,
- **data**: a data.frame,
- **subset**: see lm,
- **na.action**: see lm,
effect       the effects introduced in the model: one of "individual", "time",
model        one of "within", "random",
index        the indexes, see `pdata.frame()`,
...           further arguments.
object, x    an object of class "pvcm",
digits       digits,
width         the maximum length of the lines in the print output,

Details

`pvcm` estimates variable coefficients models. Time or individual effects are introduced, respectively, if `effect = "time"` or `effect = "individual"` (the default value).

Coefficients are assumed to be fixed if `model = "within"` and random if `model = "random"`. In the first case, a different model is estimated for each individual (or time period). In the second case, the Swamy (1970) model is estimated. It is a generalized least squares model which uses the results of the previous model.

Value

An object of class c("pvcm", "panelmodel"), which has the following elements:

coefficients the vector (or the data frame for fixed effects) of coefficients,
residuals    the vector of residuals,
fitted.values the vector of fitted values,
vcov         the covariance matrix of the coefficients (a list for fixed effects),
df.residual  degrees of freedom of the residuals,
model        a data frame containing the variables used for the estimation,
call         the call,
Delta        the estimation of the covariance matrix of the coefficients (random effect models only).
std.error    a data frame containing standard errors for all coefficients for each individual (within models only).

`pvcm` objects have `print`, `summary` and `print.summary` methods.

Author(s)

Yves Croissant

References

Examples

data("Produc", package = "plm")
zw <- pvcm(log(gsp) ~ log(pcap) + log(pc) + log(emp) + unemp, data = Produc, model = "within")
Zr <- pvcm(log(gsp) ~ log(pcap) + log(pc) + log(emp) + unemp, data = Produc, model = "random")

## replicate Greene (2012), p. 419, table 11.14
summary(pvcm(log(gsp) ~ log(pc) + log(hwy) + log(water) + log(util) + log(emp) + unemp,
data = Produc, model = "random"))

## Not run:
# replicate Swamy (1970), p. 166, table 5.2
data(Grunfeld, package = "AER") # 11 firm Grunfeld data needed from package AER
gw <- pvcm(invest ~ value + capital, data = Grunfeld, index = c("firm", "year"))

## End(Not run)

---

**pwaldtest**

*Wald-style Chi-square Test and F Test*

**Description**

Wald-style Chi-square test and F test of slope coefficients being zero jointly, including robust versions of the tests.

**Usage**

pwaldtest(x, ...)

## S3 method for class 'plm'
pwaldtest(x, test = c("Chisq", "F"), vcov = NULL,
df2adj = (test == "F" && !is.null(vcov) && missing(.df2)), .df1, .df2,
...)

## S3 method for class 'pvcm'
pwaldtest(x, ...)

**Arguments**

- **x**: an estimated model of which the coefficients should be tested (usually of class "plm"/"pvcm")
- **...**: further arguments (currently none).
- **test**: a character, indicating the test to be performed, may be either "Chisq" or "F" for the Wald-style Chi-square test or F test, respectively.
vcov

NULL by default; a matrix giving a variance–covariance matrix or a function which computes such; if supplied (non NULL), the test is carried out using the variance–covariance matrix indicated resulting in a robust test.

df2adj

logical, only relevant for test = "F", indicating whether the adjustment for clustered standard errors for the second degrees of freedom parameter should be performed (see Details, also for further requirements regarding the variance–covariance matrix in vcov for the adjustment to be performed).

.df1

a numeric, used if one wants to overwrite the first degrees of freedom parameter in the performed test (usually not used).

.df2

a numeric, used if one wants to overwrite the second degrees of freedom parameter for the F test (usually not used).

Details

pwaldtest can be used stand–alone with a plm object or a pvcm object (for the latter only the 'random' type is valid and no further arguments are processed). It is also used in summary.plm() to produce the F statistic and the Chi-square statistic for the joint test of coefficients.

pwaldtest performs the test if the slope coefficients of a panel regression are jointly zero. It does not perform general purpose Wald-style tests (for those, see lmtest::waldtest() (from package lmtest\(^1\)) or car::linearHypothesis() (from package car\(^2\)).

If a user specified variance-covariance matrix/function is given in argument vcov, the robust version of the tests are carried out. In that case, if the F test is requested (test = "F") and no overwriting of the second degrees of freedom parameter is given (by supplying argument (.df2)), the adjustment of the second degrees of freedom parameter is performed by default. The second degrees of freedom parameter is adjusted to be the number of unique elements of the cluster variable - 1, e. g. the number of individuals -

1. For the degrees of freedom adjustment of the F test in general, see e. g. Cameron and Miller (2015), section VII; (Andreß et al. 2013), pp. 126, footnote 4.

The degrees of freedom adjustment requires the vcov object supplied or created by a supplied function to carry an attribute called "cluster" with a known clustering described as a character (for now this could be either "group" or "time"). The vcovXX functions of the package plm provide such an attribute for their returned variance–covariance matrices. No adjustment is done for unknown descriptions given in the attribute "cluster" or when the attribute "cluster" is not present. Robust vcov objects/functions from package clubSandwich\(^3\) work as inputs to pwaldtest's F test because a they are translated internally to match the needs described above.

Value

An object of class "htest".

Author(s)

Yves Croissant (initial implementation) and Kevin Tappe (extensions: vcov argument and F test's df2 adjustment)

---

\(^1\)https://CRAN.R-project.org/package=lmtest
\(^2\)https://CRAN.R-project.org/package=car
\(^3\)https://CRAN.R-project.org/package=clubSandwich
References


See Also

vcovHC() for an example of the vcovXX functions, a robust estimation for the variance–covariance matrix; summary.plm()

Examples

data("Grunfeld", package = "plm")
mod_fe <- plm(inv ~ value + capital, data = Grunfeld, model = "within")
mod_re <- plm(inv ~ value + capital, data = Grunfeld, model = "random")
pwaldtest(mod_fe, test = "F")
pwaldtest(mod_re, test = "Chisq")

# with robust vcov (matrix, function)
pwaldtest(mod_fe, vcov = vcovHC(mod_fe))
pwaldtest(mod_fe, vcov = function(x) vcovHC(x, type = "HC3"))

pwaldtest(mod_fe, vcov = vcovHC(mod_fe), df2adj = FALSE) # w/o df2 adjustment

# example without attribute "cluster" in the vcov
vcov_mat <- vcovHC(mod_fe)
attr(vcov_mat, "cluster") <- NULL # remove attribute
pwaldtest(mod_fe, vcov = vcov_mat) # no df2 adjustment performed

---

**pwartest**

*Wooldridge Test for AR(1) Errors in FE Panel Models*

Description

Test of serial correlation for (the idiosyncratic component of) the errors in fixed–effects panel models.

19https://doi.org/10.1007/978-3-642-32914-2
Usage

pwartest(x, ...)

## S3 method for class 'formula'
pwartest(x, data, ...)

## S3 method for class 'panelmodel'
pwartest(x, ...)

Arguments

x an object of class formula or of class panelmodel,
... further arguments to be passed on to vcovHC (see Details and Examples).
data a data.frame,

Details

As Wooldridge (2010), Sec. 10.5.4 observes, under the null of no serial correlation in the errors, the residuals of a FE model must be negatively serially correlated, with \( \text{cor}(\hat{u}_{it}, \hat{u}_{is}) = -1/(T-1) \) for each \( t, s \). He suggests basing a test for this null hypothesis on a pooled regression of FE residuals on their first lag: \( \hat{u}_{it} = \alpha + \delta \hat{u}_{it-1} + \eta_{it} \). Rejecting the restriction \( \delta = -1/(T-1) \) makes us conclude against the original null of no serial correlation.

\( \text{pwartest} \) estimates the within model and retrieves residuals, then estimates an AR(1) pooling model on them. The test statistic is obtained by applying a F test to the latter model to test the above restriction on \( \delta \), setting the covariance matrix to \( \text{vcovHC} \) with the option \text{method}="arellano" to control for serial correlation.

Unlike the \text{pbgtest()} and \text{pdwtest()} , this test does not rely on large–T asymptotics and has therefore good properties in "short" panels. Furthermore, it is robust to general heteroskedasticity.

Value

An object of class "htest".

Author(s)

Giovanni Millo

References


See Also

\text{pwfhtest()}, \text{pdwhtest()}, \text{pbgtest()}, \text{pblhtest()}, \text{pbsytest()}.
Examples

data("EmplUK", package = "plm")
pwartest(log(emp) ~ log(wage) + log(capital), data = EmplUK)

# pass argument 'type' to vcovHC used in test
pwartest(log(emp) ~ log(wage) + log(capital), data = EmplUK, type = "HC3")

pwfdtest  

Wooldridge first–difference–based test for AR(1) errors in levels or first–differenced panel models

Description

First–differencing–based test of serial correlation for (the idiosyncratic component of) the errors in either levels or first–differenced panel models.

Usage

pwfdtest(x, ...)

## S3 method for class 'formula'
pwfdtest(x, data, ..., h0 = c("fd", "fe"))

## S3 method for class 'panelmodel'
pwfdtest(x, ..., h0 = c("fd", "fe"))

Arguments

x      an object of class formula or a "fd"-model (plm object),
...    further arguments to be passed on to vcovHC (see Details and Examples).
data    a data.frame,
h0      the null hypothesis: one of "fd", "fe",

Details

As Wooldridge (2010), Sec. 10.6.3 observes, if the idiosyncratic errors in the model in levels are uncorrelated (which we label hypothesis "fe"), then the errors of the model in first differences (FD) must be serially correlated with \( \text{cor}(\hat{e}_{it}, \hat{e}_{is}) = -0.5 \) for each \( t, s \). If on the contrary the levels model’s errors are a random walk, then there must be no serial correlation in the FD errors (hypothesis "fd"). Both the fixed effects (FE) and the first–differenced (FD) estimators remain consistent under either assumption, but the relative efficiency changes: FE is more efficient under "fe", FD under "fd".

Wooldridge (ibid.) suggests basing a test for either hypothesis on a pooled regression of FD residuals on their first lag: \( \hat{e}_{it} = \alpha + \rho \hat{e}_{i,t-1} + \eta_{it} \). Rejecting the restriction \( \rho = -0.5 \) makes us conclude
against the null of no serial correlation in errors of the levels equation ("fe"). The null hypothesis of no serial correlation in differenced errors ("fd") is tested in a similar way, but based on the zero restriction on $\rho (\rho = 0)$. Rejecting "fe" favours the use of the first-differences estimator and the contrary, although it is possible that both be rejected.

`pwfdtest` estimates the fd model (or takes an fd model as input for the panelmodel interface) and retrieves its residuals, then estimates an AR(1) pooling model on them. The test statistic is obtained by applying a F test to the latter model to test the relevant restriction on $\rho$, setting the covariance matrix to `vcovHC` with the option `method="arellano"` to control for serial correlation.

Unlike the `pbgtest` and `pdwtest`, this test does not rely on large-T asymptotics and has therefore good properties in "short" panels. Furthermore, it is robust to general heteroskedasticity. The "fe" version can be used to test for error autocorrelation regardless of whether the maintained specification has fixed or random effects (see Drukker 2003).

**Value**

An object of class "htest".

**Author(s)**

Giovanni Millo

**References**


**See Also**

`pdwtest`, `pbgtest`, `pwartest`,

**Examples**

```r
data("EmplUK", package = "plm")
pwfdtest(log(emp) ~ log(wage) + log(capital), data = EmplUK)
pwfdtest(log(emp) ~ log(wage) + log(capital), data = EmplUK, h0 = "fe")

# pass argument 'type' to vcovHC used in test
pwfdtest(log(emp) ~ log(wage) + log(capital), data = EmplUK, type = "HC3", h0 = "fe")
```

# same with panelmodel interface
mod <- plm(log(emp) ~ log(wage) + log(capital), data = EmplUK, model = "fd")
pwfdtest(mod)
```
pwfdtest(mod, h0 = "fe")
pwfdtest(mod, type = "HC3", h0 = "fe")

pwtest

Wooldridge’s Test for Unobserved Effects in Panel Models

Description
Semi-parametric test for the presence of (individual or time) unobserved effects in panel models.

Usage

pwtest(x, ...)

## S3 method for class 'formula'
pwtest(x, data, effect = c("individual", "time"), ...)

## S3 method for class 'panelmodel'
pwtest(x, effect = c("individual", "time"), ...)

Arguments

x an object of class "formula", or an estimated model of class panelmodel,
... further arguments passed to plm.
data a data.frame,
effect the effect to be tested for, one of "individual" (default) or "time",

Details
This semi-parametric test checks the null hypothesis of zero correlation between errors of the same group. Therefore, it has power both against individual effects and, more generally, any kind of serial correlation.
The test relies on large-N asymptotics. It is valid under error heteroskedasticity and departures from normality.
The above is valid if effect="individual", which is the most likely usage. If effect="time", symmetrically, the test relies on large-T asymptotics and has power against time effects and, more generally, against cross-sectional correlation.
If the panelmodel interface is used, the inputted model must be a pooling model.

Value
An object of class "htest".
**r.squared**  

*R squared and adjusted R squared for panel models*

**Description**

This function computes R squared or adjusted R squared for plm objects. It allows to define on which transformation of the data the (adjusted) R squared is to be computed and which method for calculation is used.

**Usage**

```r
r.squared(object, model = NULL, type = c("cor", "rss", "ess"), dfcor = FALSE)
```

**Author(s)**

Giovanni Millo

**References**


**See Also**

`pbltest()`, `pbgtest()`, `pdwtest()`, `pbsytest()`, `pwarstest()`, `pwfdtest()` for tests for serial correlation in panel models. `plmtest()` for tests for random effects.

**Examples**

```r
data("Produc", package = "plm")
## formula interface
pwtest(log(gsp) ~ log(pcap) + log(pc) + log(emp) + unemp, data = Produc)
pwtest(log(gsp) ~ log(pcap) + log(pc) + log(emp) + unemp, data = Produc, effect = "time")

## panelmodel interface
# first, estimate a pooling model, than compute test statistics
form <- formula(log(gsp) ~ log(pcap) + log(pc) + log(emp) + unemp)
pool_prodc <- plm(form, data = Produc, model = "pooling")
pwtest(pool_prodc) # == effect="individual"
pwtest(pool_prodc, effect="time")
```
ranef.plm

Arguments

- **object**: an object of class "plm",
- **model**: on which transformation of the data the R-squared is to be computed. If NULL, the transformation used to estimate the model is also used for the computation of R squared,
- **type**: indicates method which is used to compute R squared. One of "rss" (residual sum of squares), "ess" (explained sum of squares), or "cor" (coefficient of correlation between the fitted values and the response),
- **dfcor**: if TRUE, the adjusted R squared is computed.

Value

A numerical value. The R squared or adjusted R squared of the model estimated on the transformed data, e. g. for the within model the so called "within R squared".

See Also

plm() for estimation of various models; summary.plm() which makes use of r.squared.

Examples

data("Grunfeld", package = "plm")
p <- plm(inv ~ value + capital, data = Grunfeld, model = "pooling")
r.squared(p)
r.squared(p, dfcor = TRUE)

---

ranef.plm

Extract the Random Effects

Description

Function to calculate the random effects from a plm object (random effects model).

Usage

```r
## S3 method for class 'plm'
ranef(object, effect = NULL, ...)
```

Arguments

- **object**: an object of class "plm", needs to be a fitted random effects model,
- **effect**: NULL, "individual", or "time", the effects to be extracted, see Details,
- **...**: further arguments (currently not used).
Details

Function `ranef` calculates the random effects of a fitted random effects model. For one-way models, the effects of the estimated model are extracted (either individual or time effects). For two-way models, extracting the individual effects is the default (both, argument `effect = NULL` and `effect = "individual"` will give individual effects). Time effects can be extracted by setting `effect = "time"`.

Not all random effect model types are supported (yet?).

Value

A named numeric with the random effects per dimension (individual or time).

Author(s)

Kevin Tappe

See Also

`fixef()` to extract the fixed effects from a fixed effects model (within model).

Examples

data("Grunfeld", package = "plm")
m1 <- plm(inv ~ value + capital, data = Grunfeld, model = "random")
ranef(m1) # individual random effects

# compare to random effects by ML estimation via lmer from package lme4
## Not run:
library(lme4)
m2 <- lmer(inv ~ value + capital + (1 | firm), data = Grunfeld)
cbind("plm" = ranef(m1), "lmer" = unname(ranef(m2)$firm))
## End(Not run)

# two-ways RE model, calculate individual and time random effects
data("Cigar", package = "plm")
tw <- plm(sales ~ pop + price, data = Cigar, model = "random", effect = "twoways")
ranef(tw) # individual random effects
ranef(tw, effect = "time") # time random effects
RiceFarms  
Production of Rice in Indonesia

Description

a panel of 171 observations

Format

A dataframe containing:

- **id** the farm identifier
- **size** the total area cultivated with rice, measured in hectares
- **status** land status, one of 'owner' (non sharecroppers, owner operators or leaseholders or both), 'share' (sharecroppers), 'mixed' (mixed of the two previous status)
- **varieties** one of 'trad' (traditional varieties), 'high' (high yielding varieties) and 'mixed' (mixed varieties)
- **bimas** bIMAS is an intensification program; one of 'no' (non-bimas farmer), 'yes' (bimas farmer) or 'mixed' (part but not all of farmer’s land was registered to be in the bimas program)
- **seed** seed in kilogram
- **urea** urea in kilogram
- **phosphate** phosphate in kilogram
- **pesticide** pesticide cost in Rupiah
- **pseed** price of seed in Rupiah per kg
- **purea** price of urea in Rupiah per kg
- **pphosph** price of phosphate in Rupiah per kg
- **hiredlabor** hired labor in hours
- **famlabor** family labor in hours
- **totlabor** total labor (excluding harvest labor)
- **wage** labor wage in Rupiah per hour
- **goutput** gross output of rice in kg
- **noutput** net output, gross output minus harvesting cost (paid in terms of rice)
- **price** price of rough rice in Rupiah per kg
- **region** one of 'wargabinangun','langan','gunungwangi','malausma','sukaambit','ciwangi'

Details

- number of observations : 1026
- observation : farms
- country : Indonesia
Hansen–Sargan Test of Overidentifying Restrictions

Description
A test of overidentifying restrictions for models estimated by GMM.

Usage
sargan(object, weights = c("twosteps", "onestep"))

Arguments
- object: an object of class "pgmm",
- weights: the weighting matrix to be used for the computation of the test.

Details
The Hansen–Sargan test calculates the quadratic form of the moment restrictions that is minimized while computing the GMM estimator. It follows asymptotically a chi-square distribution with number of degrees of freedom equal to the difference between the number of moment conditions and the number of coefficients.

Value
An object of class "htest".

Author(s)
Yves Croissant

References
(Hansen 1982)
(Sargan 1958)

See Also
pgmm()

---

Source
Examples

```r
data("EmplUK", package = "plm")
ar <- pgmm(log(emp) ~ lag(log(emp), 1:2) + lag(log(wage), 0:1) +
    lag(log(capital), 0:2) + lag(log(output), 0:2) | lag(log(emp), 2:99),
    data = EmplUK, effect = "twoways", model = "twosteps")
sargan(ar)
```

Snmesp  
Employment and Wages in Spain

Description

A panel of 738 observations from 1983 to 1990

Format

A data frame containing:

- `firm`  firm index
- `year`  year
- `n`  log of employment
- `w`  log of wages
- `y`  log of real output
- `i`  log of intermediate inputs
- `k`  log of real capital stock
- `f`  real cash flow

Details

- total number of observations: 5904
- observation: firms
- country: Spain

Source

Journal of Business Economics and Statistics data archive:
http://amstat.tandfonline.com/loi/ubes20/

References

Description
A panel of 125 observations from 1960 to 1985

Format
A data frame containing:

- `year` the year
- `country` the country name (factor)
- `opec` OPEC member?
- `com` communist regime?
- `pop` country's population (in thousands)
- `gdp` real GDP per capita (in 1985 US dollars)
- `sr` saving rate (in percent)

Details

- `total number of observations`: 3250
- `observation`: country
- `country`: World

Source
Online supplements to Hayashi (2000).
http://fhayashi.fc2web.com/datasets.htm

References


21https://doi.org/10.2307/2937941
**Summary for plm objects**

**Description**

The summary method for plm objects generates some more information about estimated plm models.

**Usage**

```r
## S3 method for class 'plm'
summary(object, vcov = NULL, ...)

## S3 method for class 'summary.plm'
print(x, digits = max(3, getOption("digits") - 2),
       width = getOption("width"), subset = NULL, ...)
```

**Arguments**

- `object`: an object of class "plm",
- `vcov`: a variance–covariance matrix furnished by the user or a function to calculate one (see Examples),
- `...`: further arguments.
- `x`: an object of class "summary.plm",
- `digits`: number of digits for printed output,
- `width`: the maximum length of the lines in the printed output,
- `subset`: a character or numeric vector indicating a subset of the table of coefficients to be printed for "print.summary.plm".

**Details**

The summary method for plm objects (summary.plm) creates an object of class c("summary.plm", "plm", "panelmodel") that extends the plm object it is run on with various information about the estimated model like (inferential) statistics, see Value. It has an associated print method (print.summary.plm).

**Value**

An object of class c("summary.plm", "plm", "panelmodel"). Some of its elements are carried over from the associated plm object and described there (plm()). The following elements are new or changed relative to the elements of a plm object:

- `fstatistic`: 'htest' object: joint test of significance of coefficients (F or Chi-square test) (robust statistic in case of supplied argument vcov, see pwaldtest() for details),
coefficients  a matrix with the estimated coefficients, standard errors, t–values, and p–values, if argument \texttt{vcov} was set to non-NULL the standard errors (and t– and p–values) in their respective robust variant,

\texttt{vcov}  the "regular" variance–covariance matrix of the coefficients (class "matrix"),

\texttt{rvcov}  only present if argument \texttt{vcov} was set to non-NULL: the furnished variance–covariance matrix of the coefficients (class "matrix"),

\texttt{r.squared}  a named numeric containing the R-squared ("rsq") and the adjusted R-squared ("adjrsq") of the model,

\texttt{df}  an integer vector with 3 components, (p, n-p, p*), where p is the number of estimated (non-aliased) coefficients of the model, n-p are the residual degrees of freedom (n being number of observations), and p* is the total number of coefficients (incl. any aliased ones).

Author(s)
Yves Croissant

See Also

\texttt{plm()} for estimation of various models; \texttt{vcovHC()} for an example of a robust estimation of variance–covariance matrix; \texttt{r.squared()} for the function to calculate R-squared; \texttt{stats::print.power.htest()} for some information about class "htest"; \texttt{fixef()} to compute the fixed effects for "within" (=fixed effects) models and \texttt{within_intercept()} for an "overall intercept" for such models; \texttt{pwaldtest()}.

Examples

data("Produc", package = "plm")
zz <- \texttt{plm(log(gsp) \sim log(pcap) + log(pc) + log(emp) + unemp,}
  \texttt{data = Produc, index = c("state","year"))}
summary(zz)

# summary with a furnished vcov, passed as matrix, as function, and
# as function with additional argument
data("Grunfeld", package = "plm")
wi <- \texttt{plm(inv \sim value + capital,}
  \texttt{data = Grunfeld, model="within", effect = "individual")}
summary(wi, \texttt{vcov = vcovHC(wi)})
summary(wi, \texttt{vcov = vcovHC})
summary(wi, \texttt{vcov = function(x) vcovHC(x, method = "white2")})

# extract F statistic
\texttt{wi_summary <- summary(wi)}
\texttt{Fstat <- wi_summary["fstatistic"]}

# extract estimates and p-values
\texttt{est <- wi_summary["coefficients"][, "Estimate"]}
\texttt{pval <- wi_summary["coefficients"][, "Pr>|t|"]}
# print summary only for coefficient "value"
print(wi_summary, subset = "value")

vcovBK

## S3 method for class 'plm'
vcovBK(x, type = c("HC0", "HC1", "HC2", "HC3", "HC4"),
       cluster = c("group", "time"), diagonal = FALSE, ...)

Arguments

- **x**: an object of class "plm",
- **...**: further arguments,
- **type**: the weighting scheme used, one of "HC0", "HC1", "HC2", "HC3", "HC4",
- **cluster**: one of "group", "time",
- **diagonal**: a logical value specifying whether to force nondiagonal elements to zero.

Details

vcovBK is a function for estimating a robust covariance matrix of parameters for a panel model according to the Beck and Katz (1995) method, a.k.a. Panel Corrected Standard Errors (PCSE), which uses an unconditional estimate of the error covariance across time periods (groups) inside the standard formula for coefficient covariance. Observations may be clustered either by "group" to account for timewise heteroskedasticity and serial correlation or by "time" to account for cross-sectional heteroskedasticity and correlation. It must be borne in mind that the Beck and Katz formula is based on N- (T-) asymptotics and will not be appropriate elsewhere.

The diagonal logical argument can be used, if set to TRUE, to force to zero all nondiagonal elements in the estimated error covariances; this is appropriate if both serial and cross–sectional correlation are assumed out, and yields a timewise- (groupwise-) heteroskedasticity–consistent estimator.

Weighting schemes specified by type are analogous to those in sandwich::vcovHC() in package sandwich\(^{22}\) and are justified theoretically (although in the context of the standard linear model) by MacKinnon and White (1985) and Cribari–Neto (2004) (see Zeileis 2004).

\(^{22}\)https://CRAN.R-project.org/package=sandwich
The main use of `vcovBK` is to be an argument to other functions, e.g. for Wald–type testing: argument `vcov` to `coeftest()`, argument `vcov` to `waldtest()` and other methods in the `lmtest` package; and argument `vcov` to `linearHypothesis()` in the `car` package (see the examples). Notice that the `vcov` and `vcov.` arguments allow to supply a function (which is the safest) or a matrix (see Zeileis 2004, 4.1-2 and examples below).

**Value**

An object of class "matrix" containing the estimate of the covariance matrix of coefficients.

**Author(s)**

Giovanni Millo

**References**


**See Also**

- `sandwich::vcovHC()` from the `sandwich` package for weighting schemes (type argument).

**Examples**

```r
library(lmtest)
library(car)
data("Produc", package="plm")
zz <- plm(log(gsp)~log(pcap)+log(pc)+log(emp)+unemp, data=Produc, model="random")
## standard coefficient significance test
coefftest(zz)
## robust significance test, cluster by group
## (robust vs. serial correlation), default arguments
coefftest(zz, vcov.=vcovBK)
## idem with parameters, pass vcov as a function argument
coefftest(zz, vcov.=function(x) vcovBK(x, type="HC1"))
## idem, cluster by time period
## (robust vs. cross-sectional correlation)
```

23[https://CRAN.R-project.org/package=lmtest](https://CRAN.R-project.org/package=lmtest)

24[https://CRAN.R-project.org/package=car](https://CRAN.R-project.org/package=car)

25[https://CRAN.R-project.org/package=sandwich](https://CRAN.R-project.org/package=sandwich)
vcovDC

coeftest(zz, vcov.=function(x) vcovBK(x,
  type="HC1", cluster="time"))
## idem with parameters, pass vcov as a matrix argument
coeftest(zz, vcov.=vcovBK(zz, type="HC1"))
## joint restriction test
waldtest(zz, update(zz, .~-log(emp)-unemp), vcov=vcovBK)
## test of hyp.: 2*log(pc)=log(emp)
linearHypothesis(zz, "2*log(pc)=log(emp)", vcov.=vcovBK)

v covDC

Double-Clustering Robust Covariance Matrix Estimator

Description

High-level convenience wrapper for double-clustering robust covariance matrix estimators a la Thompson (2011) and Cameron et al. (2011) for panel models.

Usage

vcovDC(x, ...)

## S3 method for class 'plm'
vcovDC(x, type = c("HC0", "sss", "HC1", "HC2", "HC3",
  "HC4"), ...)

Arguments

x an object of class "plm" or "pcce"
... further arguments
type the weighting scheme used, one of "HC0", "sss", "HC1", "HC2", "HC3",
  "HC4", see Details,

Details

vcovDC is a function for estimating a robust covariance matrix of parameters for a panel model with errors clustering along both dimensions. The function is a convenience wrapper simply summing a group- and a time-clustered covariance matrix and subtracting a diagonal one a la White.

Weighting schemes specified by type are analogous to those in sandwich::vcovHC() in package sandwich26 and are justified theoretically (although in the context of the standard linear model) by MacKinnon and White (1985) and Cribari–Neto (2004) (see Zeileis 2004).

The main use of vcovDC is to be an argument to other functions, e.g. for Wald-type testing: argument vcov. to coeftest(), argument vcov to waldtest() and other methods in the lmtest27 package; and argument vcov. to linearHypothesis() in the car28 package (see the examples). Notice that the vcov and vcov. arguments allow to supply a function (which is the safest) or a matrix (see Zeileis 2004, 4.1-2 and examples below).

References

26https://CRAN.R-project.org/package=sandwich
27https://CRAN.R-project.org/package=lmtest
28https://CRAN.R-project.org/package=car
Value

An object of class "matrix" containing the estimate of the covariance matrix of coefficients.

Author(s)

Giovanni Millo

References


See Also

`sandwich::vcovHC()` from the *sandwich* package for weighting schemes (type argument).

Examples

```r
library(lmtest)
library(car)
data("Produc", package="plm")
zz <- plm(log(gsp)~log(pcap)+log(pc)+log(emp)+unemp, data=Produc, model="pooling")
## standard coefficient significance test
coeftest(zz)
## DC robust significance test, default
coeftest(zz, vcov.=vcovDC)
## idem with parameters, pass vcov as a function argument
coeftest(zz, vcov.=function(x) vcovDC(x, type="HC1", maxlag=4))
## joint restriction test
waldtest(zz, update(zz, .~-log(emp)-unemp), vcov=vcovDC)
## test of hyp.: 2*log(pc)=log(emp)
linearHypothesis(zz, "2*log(pc)=log(emp)", vcov.=vcovDC)
```

[29]https://CRAN.R-project.org/package=sandwich
Generic Lego building block for Robust Covariance Matrix Estimators

Description

Generic Lego building block for robust covariance matrix estimators of the vcovXX kind for panel models.

Usage

vcovG(x, ...)

## S3 method for class 'plm'
vcovG(x, type = c("HC0", "sss", "HC1", "HC2", "HC3", "HC4"), cluster = c("group", "time"), l = 0, inner = c("cluster", "white", "diagavg"), ...)

## S3 method for class 'pcce'
vcovG(x, type = c("HC0", "sss", "HC1", "HC2", "HC3", "HC4"), cluster = c("group", "time"), l = 0, inner = c("cluster", "white", "diagavg"), ...)

Arguments

x an object of class "plm" or "pcce"

... further arguments

type the weighting scheme used, one of "HC0", "sss", "HC1", "HC2", "HC3", "HC4";

cluster one of "group", "time".

l lagging order, defaulting to zero

inner the function to be applied to the residuals inside the sandwich: one of "cluster" or "white" or "diagavg".

Details

vcovG is the generic building block for use by higher–level wrappers vcovHC(), vcovSCC(), vcovDC(), and vcovNW(). The main use of vcovG is to be used internally by the former, but it is made available in the user space for use in non–standard combinations. For more documentation, see see wrapper functions mentioned.

Value

An object of class "matrix" containing the estimate of the covariance matrix of coefficients.

Author(s)

Giovanni Millo
References


See Also

vcovHC(), vcovSCC(), vcovDC(), vcovNW(), and vcovBK() albeit the latter does not make use of vcovG.

Examples

data("Produc", package="plm")
zz <- plm(log(gsp)~log(pcap)+log(pc)+log(emp)+unemp, data=Produc, model="pooling")
## reproduce Arellano's covariance matrix
vcovG(zz, cluster="group", inner="cluster", l=0)
## use in coefficient significance test
library(lmtest)
## define custom covariance function
## (in this example, same as vcovHC)
myvcov <- function(x) vcovG(x, cluster="group", inner="cluster", l=0)
## robust significance test
coeftest(zz, vcov.=myvcov)
Arguments

- **x**: an object of class "plm" which should be the result of a random effects or a within model or a model of class "pgmm" or an object of class "pcce",
- **method**: one of "arellano", "white1", "white2",
- **type**: the weighting scheme used, one of "HC0", "sss", "HC1", "HC2", "HC3", "HC4", see Details,
- **cluster**: one of "group", "time",
- **...**: further arguments.

Details

vcovHC is a function for estimating a robust covariance matrix of parameters for a fixed effects or random effects panel model according to the White method (White 1980, 1984; Arellano 1987). Observations may be clustered by "group" ("time") to account for serial (cross-sectional) correlation.

All types assume no intragroup (serial) correlation between errors and allow for heteroskedasticity across groups (time periods). As for the error covariance matrix of every single group of observations, "white1" allows for general heteroskedasticity but no serial (cross-sectional) correlation; "white2" is "white1" restricted to a common variance inside every group (time period) (see Greene 2003, Sec. 13.7.1-2, Greene 2012, Sec. 11.6.1-2 and Wooldridge 2002, Sec. 10.7.2); "arellano" (see ibid. and the original ref. Arellano 1987) allows a fully general structure w.r.t. heteroskedasticity and serial (cross-sectional) correlation.

Weighting schemes specified by **type** are analogous to those in sandwich::vcovHC() in package sandwich30 and are justified theoretically (although in the context of the standard linear model) by MacKinnon and White (1985) and Cribari–Neto (2004) (Zeileis 2004). type = "sss" employs the small sample correction as used by Stata. elaborate why different result for FE models (intercept)

The main use of vcovHC is to be an argument to other functions, e.g. for Wald–type testing: argument vcov. to coeftest(), argument vcov to waldtest() and other methods in the lmtest31 package; and argument vcov. to linearHypothesis() in the car32 package (see the examples). Notice that the vcov and vcov. arguments allow to supply a function (which is the safest) or a matrix (ZEIL:04, 4.1-2 and examples below).

A special procedure for pgmm objects, proposed by Windmeijer (2005), is also provided.

Value

An object of class "matrix" containing the estimate of the asymptotic covariance matrix of coefficients.

Note

The function pvcovHC is deprecated. Use vcovHC for the same functionality.

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30https://CRAN.R-project.org/package=sandwich
31https://CRAN.R-project.org/package=lmtest
32https://CRAN.R-project.org/package=car
vcovHC.plm

Author(s)

Giovanni Millo & Yves Croissant

References


See Also

sandwich::vcovHC() from the sandwich package for weighting schemes (type argument).

Examples

```r
library(lmtest)
library(car)
data("Produc", package = "plm")
zz <- plm(log(gsp) ~ log(pcap) + log(pc) + log(emp) + unemp,
data = Produc, model = "random")
## standard coefficient significance test
coeftest(zz)
## robust significance test, cluster by group
## (robust vs. serial correlation)
coeftest(zz, vcov.=vcovHC)
## idem with parameters, pass vcov as a function argument
coeftest(zz, vcov.=function(x) vcovHC(x, method="arellano", type="HC1"))
## idem, cluster by time period
## (robust vs. cross-sectional correlation)
coeftest(zz, vcov.=function(x) vcovHC(x, method="arellano",
type="HC1", cluster="group"))
## idem with parameters, pass vcov as a matrix argument
```

33https://CRAN.R-project.org/package=sandwich
```r
coefest(zz, vcov.=vcovHC(zz, method="arellano", type="HC1"))
## joint restriction test
waldtest(zz, update(zz, .~.-log(emp)-unemp), vcov=vcovHC)
## test of hyp.: 2*log(pc)=log(emp)
linearHypothesis(zz, "2*log(pc)=log(emp)", vcov.=vcovHC)

## Robust inference for CCE models
data("Produc", package = "plm")
ccepmod <- pcce(log(gsp) ~ log(pcap) + log(pc) + log(emp) + unemp, data = Produc, model="p")
summary(ccepmod, vcov = vcovHC)

## Robust inference for GMM models
data("EmplUK", package="plm")
ar <- pgmm(log(emp) ~ lag(log(emp), 1:2) + lag(log(wage), 0:1)
   + log(capital) + lag(log(capital), 2) + log(output)
   + lag(log(output),2) | lag(log(emp), 2:99),
data = EmplUK, effect = "twoways", model = "twosteps")
rv <- vcovHC(ar)
mtest(ar, order = 2, vcov = rv)
```

---

**vcovNW**

*Newey and West (1987) Robust Covariance Matrix Estimator*

**Description**

Nonparametric robust covariance matrix estimators a la Newey and West for panel models with serial correlation.

**Usage**

```r
vcovNW(x, ...)  
```

## S3 method for class 'plm'
```r
vcovNW(x, type = c("HC0", "sss", "HC1", "HC2", "HC3",  
                   "HC4"), maxlag = NULL, wj = function(j, maxlag) 1 - j/(maxlag + 1),  
                   ...)  
```  
## S3 method for class 'pcce'
```r
vcovNW(x, type = c("HC0", "sss", "HC1", "HC2", "HC3",  
                   "HC4"), maxlag = NULL, wj = function(j, maxlag) 1 - j/(maxlag + 1),  
                   ...)  
```

**Arguments**

- **x** an object of class "plm" or "pcce"
- **...** further arguments
- **type** the weighting scheme used, one of "HC0", "sss", "HC1", "HC2", "HC3", "HC4", see Details,
maxlag

either NULL or a positive integer specifying the maximum lag order before truncation.

wj

weighting function to be applied to lagged terms.

Details

vcovNW is a function for estimating a robust covariance matrix of parameters for a panel model according to the Newey and West (1987) method. The function works as a restriction of the Driscoll and Kraay (1998) covariance (see vcovSCC()) to no cross-sectional correlation.

Weighting schemes specified by type are analogous to those in sandwich::vcovHC() in package sandwich34 and are justified theoretically (although in the context of the standard linear model) by MacKinnon and White (1985) and Cribari–Neto (2004) (see Zeileis 2004).

The main use of vcovNW is to be an argument to other functions, e.g. for Wald–type testing: argument vcov. to coeftest(), argument vcov to waldtest() and other methods in the lmtest35 package; and argument vcov. to linearHypothesis() in the car36 package (see the examples). Notice that the vcov and vcov. arguments allow to supply a function (which is the safest) or a matrix (see Zeileis 2004, 4.1-2 and examples below).

Value

An object of class "matrix" containing the estimate of the covariance matrix of coefficients.

Author(s)

Giovanni Millo

References


See Also

sandwich::vcovHC() from the sandwich37 package for weighting schemes (type argument).

---

34https://CRAN.R-project.org/package=sandwich
35https://CRAN.R-project.org/package=lmtest
36https://CRAN.R-project.org/package=car
37https://CRAN.R-project.org/package=sandwich
Examples

```r
library(lmtest)
library(car)
data("Produc", package="plm")
zz <- plm(log(gsp)~log(pcap)+log(pc)+log(emp)+unemp, data=Produc, model="pooling")
## standard coefficient significance test
coeftest(zz)
## NW robust significance test, default
coeftest(zz, vcov.=vcovNW)
## idem with parameters, pass vcov as a function argument
coeftest(zz, vcov.=function(x) vcovNW(x, type="HC1", maxlag=4))
## joint restriction test
waldtest(zz, update(zz, .~.-log(emp)-unemp), vcov=vcovNW)
## test of hyp.: 2*log(pc)=log(emp)
linearHypothesis(zz, "2*log(pc)=log(emp)", vcov.=vcovNW)
```

vcovSCC

Driscoll and Kraay (1998) Robust Covariance Matrix Estimator

Description

Nonparametric robust covariance matrix estimators *a la Driscoll and Kraay* for panel models with cross-sectional and serial correlation.

Usage

```r
vcovSCC(x, ...)
```

Arguments

- `x` an object of class "plm" or "pcce"
- `...` further arguments
- `type` the weighting scheme used, one of "HC0", "sss", "HC1", "HC2", "HC3", "HC4"
- `cluster` switch for vcovG; set at "time" here,
vcovSCC

maxlag
either NULL or a positive integer specifying the maximum lag order before truncation

inner
the function to be applied to the residuals inside the sandwich: "cluster" for SCC, "white" for Newey-West, ("diagavg" for compatibility reasons)

wj
weighting function to be applied to lagged terms,

Details

vcovSCC is a function for estimating a robust covariance matrix of parameters for a panel model according to the Driscoll and Kraay (1998) method, which is consistent with cross-sectional and serial correlation in a T-asymptotic setting and irrespective of the N dimension. The use with random effects models is undocumented.

Weighting schemes specified by type are analogous to those in sandwich::vcovHC() in package sandwich and are justified theoretically (although in the context of the standard linear model) by MacKinnon and White (1985) and Cribari–Neto (2004) (see Zeileis 2004)).

The main use of vcovSCC is to be an argument to other functions, e.g. for Wald–type testing: argument vcov. to coeftest(), argument vcov to waldtest() and other methods in the lmtest package; and argument vcov to linearHypothesis() in the car package (see the examples). Notice that the vcov and vcov. arguments allow to supply a function (which is the safest) or a matrix (see Zeileis 2004, 4.1-2 and examples below).

Value

An object of class "matrix" containing the estimate of the covariance matrix of coefficients.

Author(s)

Giovanni Millo, partially ported from Daniel Hoechle’s (2007) Stata code

References


---

38https://CRAN.R-project.org/package=sandwich
39https://CRAN.R-project.org/package=lmtest
40https://CRAN.R-project.org/package=car
See Also

`sandwich::vcovHC()` from the `sandwich` package for weighting schemes (type argument).

Examples

```r
library(lmtest)
library(car)
data("Produc", package="plm")
zz <- plm(log(gsp)-log(pcap)+log(pc)+log(emp)+unemp, data=Produc, model="pooling")
## standard coefficient significance test
coeftest(zz)
## SCC robust significance test, default
coeftest(zz, vcov.=vcovSCC)
## idem with parameters, pass vcov as a function argument
coeftest(zz, vcov.=function(x) vcovSCC(x, type="HC1", maxlag=4))
## joint restriction test
waldtest(zz, update(zz, .~.-log(emp)-unemp), vcov=vcovSCC)
## test of hyp.: 2*log(pc)=log(emp)
linearHypothesis(zz, "2*log(pc)=log(emp)", vcov.=vcovSCC)
```

---

Wages

### Panel Data of Individual Wages

**Description**


The data are organized as a stacked time series/balanced panel, see Examples on how to convert to a `pdata.frame`.

**Format**

A data frame containing:

- `exp` years of full-time work experience.
- `wks` weeks worked.
- `bluecol` blue collar?
- `ind` works in a manufacturing industry?
- `south` resides in the south?
- `smsa` resides in a standard metropolitan statistical area?
- `married` married?
- `sex` a factor with levels "male" and "female"

---

41[https://CRAN.R-project.org/package=sandwich](https://CRAN.R-project.org/package=sandwich)
**union** individual’s wage set by a union contract?
**ed** years of education.
**black** is the individual black?
**lwage** logarithm of wage.

**Details**

- total number of observations : 4165
- observation : individuals
- country : United States

**Source**

Online complements to Baltagi (2001):
http://www.wiley.com/legacy/wileychi/baltagi/
Online complements to Baltagi (2013):
http://bcs.wiley.com/he-bcs/Books?action=resource&bcsId=4338&itemId=1118672321&resourceId=13452

**References**


**Examples**

```r
# data set 'Wages' is organized as a stacked time series/balanced panel
data("Wages", package = "plm")
Wag <- pdata.frame(Wages, index=595)
```

---

**within_intercept**

*Overall Intercept for Within Models Along its Standard Error*

**Description**

This function gives an overall intercept for within models and its accompanying standard error

**Usage**

```r
within_intercept(object, ...)
```

```r
# S3 method for class 'plm'
within_intercept(object, vcov = NULL, ...)
```
within_intercept

Arguments

object object of class plm which must be a within model (fixed effects model),
... further arguments (currently none).
vcov if not NULL (default), a function to calculate a user defined variance–covariance matrix (function for robust vcov),

Details

The (somewhat artificial) intercept for within models (fixed effects models) was made popular by Stata of StataCorp (see Gould 2013), EViews of IHS, and gretl (gretl p. 160-161, example 18.1), see for treatment in the literature, e.g. Greene (2012), Ch. 11.4.4, p. 364. It can be considered an overall intercept in the within model framework and is the weighted mean of fixed effects (see Examples for the relationship).

within_intercept estimates a new model which is computationally more demanding than just taking the weighted mean. However, with within_intercept one also gets the associated standard error and it is possible to get an overall intercept for two-way fixed effect models.

Users can set argument vcov to a function to calculate a specific (robust) variance–covariance matrix and get the respective (robust) standard error for the overall intercept, e.g. the function vcovHC(), see examples for usage. Note: The argument vcov must be a function, not a matrix, because the model to calculate the overall intercept for the within model is different from the within model itself.

Value

A named numeric of length one: The overall intercept for the estimated within model along attribute "se" which contains the standard error for the intercept.

Author(s)

Kevin Tappe

References


See Also

fixef() to extract the fixed effects of a within model.

Examples

# TODO: two-way unbalanced case, once fixef() produces results that are compatible estimate within model (unbalanced data)
data("Hedonic", package = "plm")
mod_fe <- plm(mv ~ age + crim, data = Hedonic, index = "townid")
overallint <- within_intercept(mod_fe)
attr(overallint, "se") # standard error

# overall intercept is the weighted mean of fixed effects in the
# one-way case
weighted.mean(fixef(mod_fe), as.numeric(table(index(mod_fe)[[1]])))

# relationship of type="dmean", "level" and within_intercept in the
# one-way case
data("Grunfeld", package = "plm")
gi <- plm(inv ~ value + capital, data = Grunfeld, model = "within")
fx_level <- fixef(gi, type = "level")
fx_dmean <- fixef(gi, type = "dmean")
overallint <- within_intercept(gi)
all.equal(overallint + fx_dmean, fx_level, check.attributes = FALSE) # TRUE

# overall intercept with robust standard error
within_intercept(gi, vcov = function(x) vcovHC(x, method="arellano", type="HC0"))