# Package 'PanelTM'

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**Type** Package

**Title** Two- And Three-Way Dynamic Panel Threshold Regression Model for Change Point Detection

**Version** 1.2

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**Description** Estimation of two-way and three-way dynamic panel threshold regression models using the first-differenced instrumental-variable generalized method of moments (FD-IV-GMM) estimator. The implementation builds on Seo and Shin (2016) <doi:10.1016/j.jeconom.2016.03.005> and Di Lascio and Perazzini (2026) <doi:10.1007/s10260-026-00842-3>. The models accommodate time-varying exogenous and endogenous regressors and allow the lagged dependent variable to serve as the threshold variable. The package includes a bootstrap-based test for threshold effects, a procedure for identifying change points in individual time series, functions for simulating two-way and three-way panel data with regime changes, and tools for evaluating estimator performance through bias and root mean squared error measures.

**License** GPL (>= 2)

**Depends** R (>= 4.3.0), methods, stats, pracma, MASS

**NeedsCompilation** no

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banana *Biompedance measurements on bananas.*

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## Description

Bioimpedance measurements and weight of a production batch of 50 bananas observed for 11 days. Bioimpedance has been measured at 3 different electrical frequencies of a portable electrical impedance spectroscopy device, called Fruit Meter. The experiment has been conducted by the Sensing Technologies Laboratory https://sensingtechnologies.groups.unibz.it/ of the Faculty of Engineering (ex Fac. Science and Technology) at the Free University of Bozen-Bolzano (Unibz, Italy) in the context of an interdisciplinary research project with the Faculty of Economics and Management (Unibz, Italy).

## Format

A matrix containing three-way observations.

## References

Ibba, P., Falco, A., Abera, B., Cantarella, G., Petti, L., and Lugli, P. (2019). Bio-impedance and circuit parameters: An analysis for tracking fruit ripening. Postharvest Biology and Technology, 159. DOI: 10.1016/j.postharvbio.2019.110978.

Ibba P., et al. (2021). Design and Validation of a Portable AD5933-Based Impedance Analyzer for Smart Agriculture, in IEEE Access, 9, pp. 63656-63675. DOI: 10.1109/ACCESS.2021.3074269.

Ibba, P. (2021). Fruit quality evaluation using electrical impedance spectroscopy. PhD thesis, 196, Supervisor: Lugli P., Free University of Bozen-Bolzano.

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cpoint *Computation of the regime switch time in a (two-way or three-way) panel threshold regression model.*

---

## Description

A measure for computing the time at which a regime changes, i.e. the change point.

## Usage

```
cpoint(data., nameI=NA, nameT=NA, nameJ=NA, nameY=NA, thresholds)
```

## Arguments

| | |
|---|---|
| `data.` | A (two-way or three-way) panel dataset. It can be either a $N \times T$ matrix of the dependent variable(s) where the row represents the statistical unit ($i$) and the column the time ($t$) or a `data.frame` containing columns `nameI`, `nameT`, `nameJ`, and `nameY`, which should all be specified. |
| `nameI` | If data. is a `data.frame`, the name of the (numerical) variable that identifies the statistical units. Otherwise, it is `NULL`. |
| `nameT` | If data. is a `data.frame`, the name of the (numerical) time variable. Otherwise, it is `NULL`. |
| `nameJ` | If data. is a `data.frame`, the name of the (numerical/categorical) variable that indicates the third dimension. Otherwise, it is `NULL`. |
| `nameY` | If data. is a `data.frame`, the name of the (numerical) dependent variable. Otherwise, it is `NULL`. |
| `thresholds` | The vector of estimated threshold value(s). If data. is a `matrix`, the object should contain one value $\gamma$. If data. is a `data.frame`, the vector should contain one threshold value per each value of j, i.e. $\gamma_j$. |

## Details

`cpoint` identifies the change point in a variable time series for each statistical unit $(i, j)$, given the observed values of $Y$ and the estimated threshold parameter $\widehat{\gamma}_j$. The regime is determined by comparing the threshold variable $q_{ijt}$ with the estimated threshold $\widehat{\gamma}_j$: observations satisfying $q_{ijt} \leq \widehat{\gamma}_j$ belong to the lower regime, whereas observations satisfying $q_{ijt} > \widehat{\gamma}_j$ belong to the upper regime. Following the identification criterion in Di Lascio and Perazzini (2026), the change point depends on the regime occurring at the beginning of the time series. When the series starts in the lower regime, the change point is associated with the transition to the upper regime, identified by

$$\mathrm{CP}_{ij} = \min\{t \in \{1, \ldots, T\} : q_{ijt} > \widehat{\gamma}_j\}.$$

Conversely, when the series starts in the upper regime, the change point is associated with the transition to the lower regime, identified by

$$\mathrm{CP}_{ij} = \min\{t \in \{1, \ldots, T\} : q_{ijt} < \widehat{\gamma}_j\}.$$

Since a time series may cross the estimated threshold more than once, `cpoint` identifies the beginning of the longest uninterrupted sequence of observations in the relevant regime, according to the initial regime of the series. If a unique change point cannot be identified the function returns `NA`.

## Value

An object of S4 class "cpoint", which is a `matrix` reporting the change point per each statistical unit $i$ and each $j$.

## Note

The change point is detected in $t > 4$ since the criterion has been inspired by the (two-way or three-way) dynamic panel threshold regression model that requires at least 6 times of observation: four lags of the dependent and independent variables are used as instruments and two more are necessary to identify the regime switch (i.e., one per regime).

## Author(s)

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## References

Di Lascio, F.M.L. and Perazzini, S. (2026) A three-way dynamic panel threshold regression model for change point detection in bioimpedance data. Stat Methods Appl 35, 849-867.

Di Lascio, F.M.L. and Perazzini, S. (2022) Change point detection in fruit bioimpedance using a three-way panel model. Book of short papers - SIS2022, p.1184-1189, Eds. A. Balzanella, M. Bini, C. Cavicchia, R. Verde. Pearson. ISBN: 978-88-9193-231-0.

## See Also

See also banana, ptm2, and ptm3.

## Examples

```
# Import data
data(banana)

## Example 1: Application to a three-way panel data

# Select data for all the three levels of the third way
bioimp.df2 <- banana

# Estimation: three-way ptm on bioimpedance data with the lagged
# dependent variable as transition variable
estimates2 <- ptm3(data.=bioimp.df2, nameI="i", nameT="t",
                   nameJ="j", nameY="bioimpedance", nameTV=NULL,
                   nameXexo="weight", nameIV=NULL, trimrate=0.4,
                   ngrid=100, h0=1.5, Iweight=FALSE,
                   test.lin=FALSE)

# Change point computation using a data frame (unique input choice)
CP3 <- cpoint(data.=bioimp.df2, nameI="i", nameT="t", nameJ="j",
              nameY="bioimpedance",
              thresholds=estimates2@"threshold"[,2])

## NOT RUN
### Example 2: Application to a two-way panel data
#
## Select data for a specific level of the third way
#bioimp.df <- banana[which(banana$j==1),]
#
## Prepare input matrix for ptm2
#bioimp.m <-  matrix(bioimp.df$bioimpedance,
#                    ncol=length(unique(bioimp.df$t)), byrow=TRUE)
#
## Estimation: two-way ptm on bioimpedance data with the lagged
## dependent variable as transition variable
```

```
#estimates <- ptm2(Y=bioimp.m, TV=NULL, Xendo=NULL, Xexo=NULL,
#                  IV=NULL, trimrate=0.4, ngrid=100, h0=1.5,
#                  Iweight=FALSE, test.lin=FALSE)
#
## Change point computation using a data frame as input
#CP1 <- cpoint(data.=bioimp.df, nameI="i", nameT="t", nameJ="j",
#              nameY="bioimpedance",
#              thresholds=estimates@"threshold"[[1]])
#
## Change point computation using a data matrix as input
#CP2 <- cpoint(data.=bioimp.m, nameI=NA, nameT=NA, nameJ=NA,
#              nameY=NA, thresholds=estimates@"threshold"[[1]])
##
```

---

`cpoint-class` *Class "cpoint"*

---

## Description

A class for `cpoint` and its extensions

## Objects from the Class

Objects can be created by calls of the form `new("cpoint", ...)`.

## Slots

`CP`: Object of class `matrix`. A matrix reporting the computed change point per each statistical unit and each level/category/value of the third way.

## Methods

No methods defined with class "cpoint" in the signature.

## Author(s)

Selene Perazzini <selene.perazzini@alumni.imtlucca.it>

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## References

Di Lascio, F.M.L. and Perazzini, S. (2026) A three-way dynamic panel threshold regression model for change point detection in bioimpedance data. Stat Methods Appl 35, 849-867.

Di Lascio, F.M.L. and Perazzini, S. (2022) Change point detection in fruit bioimpedance using a three-way panel model. Book of short papers - SIS2022, p.1184-1189, Eds. A. Balzanella, M. Bini, C. Cavicchia, R. Verde. Pearson. ISBN: 978-88-9193-231-0.

## See Also

See also ptm2 and ptm3.

## Examples

```
showClass("cpoint")
```

---

perfm — *Performance measures of the (two-way or three-way) panel threshold regression model estimated on simulated data.*

---

## Description

Computes the relative bias, the bias, the root mean squared error, and the relative root mean squared error.

## Usage

```
perfm(truepar,estpar)
```

## Arguments

| | |
|---|---|
| truepar | True value of the parameter. |
| estpar | Vector of the estimated parameters (one value per each simulated dataset). |

## Details

perfm computes the following performance measures: the relative bias, the bias, the root mean squared error, and the relative root mean squared error.

## Value

An object of S4 class "perfm", which is a list with the following values: the true value of the parameters, the relative bias, the bias, the root relative mean squared error, the relative root relative means squared error.

## Note

The vector of the estimated parameters can contain missing values that are excluded from the computation of the performance mesaures.

## Author(s)

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## References

Di Lascio, F.M.L. and Perazzini, S. (2026) A three-way dynamic panel threshold regression model for change point detection in bioimpedance data. Stat Methods Appl 35, 849-867.

Di Lascio, F.M.L. and Perazzini, S. (2022) Change point detection in fruit bioimpedance using a three-way panel model. Book of short papers - SIS2022, p.1184-1189, Eds. A. Balzanella, M. Bini, C. Cavicchia, R. Verde. Pearson. ISBN: 978-88-9193-231-0.

## See Also

See also ptm2, ptm3 and simptm.

## Examples

```
# Simulation of the two-way panel threshold model
# y_{it} = (-0.7-0.5*x_{it})1(y_{it-1}<=0) + (1.8+0.8*x_{it})1(y_{it-1}>0)
# Two datasets with 20 individuals observed over 15 times with change
# point at time 12 and an autoregressive error term (with parameter 0.7
# and unit error variance).

sims <- simptm(n=20, T.=15, J=1, CP=12, gamma=c(0),
               phi_c=matrix(c(-0.7,1.8), nrow=1, byrow=TRUE),
               phi_X=matrix(c(-0.5,0.8), nrow=1, byrow=TRUE), sigmau=1,
               parAR=0.2, B=2, seedstart=1)

# Estimate the two simulated two-way panel threshold models

estimates1 <- ptm3(sims@simulation[[1]], nameI="i", nameT="t", nameJ="j",
                   nameY="Y", nameXexo="X1", nameXendo=NULL, nameTV=NULL,
                   nameIV=NULL, trimrate=0.4, ngrid=100, h0=1.5,
                   Iweight=FALSE, test.lin=FALSE)

estimates2 <- ptm3(sims@simulation[[2]], nameI="i", nameT="t", nameJ="j",
                   nameY="Y", nameXexo="X1", nameXendo=NULL, nameTV=NULL,
                   nameIV=NULL, trimrate=0.4, ngrid=100, h0=1.5,
                   Iweight=FALSE, test.lin=FALSE)

# Compute performance measures for the parameter beta of the exogenous
# regressor (for details see refs)
pm1 <- perfm(truepar=-0.5, estpar=c(estimates1@param[,2],
             estimates2@param[,2]))
pm1

# Compute performance measures for the delta corresponding to the
# difference between the constants of the model (for details see refs)
pm2 <- perfm(truepar=c(1.8+0.7), estpar=c(estimates1@param[,4],
             estimates2@param[,4]))
pm2

# Compute performance measures for the delta corresponding to the
# difference between the regressors coefficients of the model
# (for details see refs)
```

```
pm3 <- perfm(truepar=c(0.8+0.5), estpar=c(estimates1@param[,6],
             estimates2@param[,6]))
pm3
```

---

perfm-class *Class "perfm"*

---

## Description

A class for perfm and its extensions

## Objects from the Class

Objects can be created by calls of the form new("perfm", ...).

## Slots

trueval Object of class numeric. The true value of the parameter.

rb Object of class numeric. The relative bias.

nrb Object of class numeric. The bias.

rrmse Object of class numeric. The relative root mean squared error.

rmse Object of class numeric. The root mean squared error.

## Methods

No methods defined with class "perfm" in the signature.

## Author(s)

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## References

Di Lascio, F.M.L. and Perazzini, S. (2026) A three-way dynamic panel threshold regression model for change point detection in bioimpedance data. Stat Methods Appl 35, 849-867.

Di Lascio, F.M.L. and Perazzini, S. (2022) Change point detection in fruit bioimpedance using a three-way panel model. Book of short papers - SIS2022, p.1184-1189, Eds. A. Balzanella, M. Bini, C. Cavicchia, R. Verde. Pearson. ISBN: 978-88-9193-231-0.

## See Also

See also perfm.

## Examples

```
showClass("perfm")
```

ptm2 *Two-way panel threshold regression model.*

## Description

Two-way panel threshold regression model with the 2-step GMM estimator.

## Usage

```
ptm2(Y, TV=NULL, Xendo=NULL, Xexo=NULL, IV=NULL, trimrate=0.4,
    ngrid=100, h0=1.5, Iweight=FALSE, test.lin=TRUE, B=1000)
```

## Arguments

| | |
|---|---|
| Y | a $N \times T$ matrix of the dependent variable where the rows represent the statistical units and the columns the time. |
| TV | a $N \times T$ transition variable matrix where the rows represent the statistical units and the columns the time. If not specified, the first lag of $Y$ is taken. |
| Xendo | a $Nk_{endo} \times T$ matrix of the independent variables (if any). The rows contain in order $X_{1i=1}, X_{1i=2}, \ldots, X_{1i=N}, X_{2i=1}, X_{2i=2}, \ldots, X_{2i=N}, \ldots, X_{k_{endo}i=1}$, $X_{k_{endo}i=2}, \ldots, X_{k_{endo}i=N}$. |
| Xexo | a $Nk_{exo} \times T$ matrix of the independent variables (if any). The rows contain in order $X_{1i=1}, X_{1i=2}, \ldots, X_{1i=N}, X_{2i=1}, X_{2i=2}, \ldots, X_{2i=N}, \ldots, X_{k_{exo}i=1}$, $X_{k_{exo}i=2}, \ldots, X_{k_{exo}i=N}$. |
| IV | a matrix of the additional instrumental variables to include in the analysis. The rows contain in order $z_{1i=1}, z_{1i=2}, \ldots, z_{1i=N}, z_{2i=1}, z_{2i=2}, \ldots, z_{2i=N}, \ldots$, $z_{li=1}, z_{li=2}, \ldots, z_{li=N}$. The lagged dependent and independent variables are automatically included in the estimation and should not be specified in IV. If not specified, only the lags of the dependent and independent variables are taken as instrumental variables. |
| trimrate | the trim rate when constructing the grid for estimating the threshold. Default is set to 0.4. |
| ngrid | the number of grid points to estimate the threshold. Default is set to 100. |
| h0 | the parameter for Silverman's rule of thumb for kernel estimation. The default is set to 1.5. |
| Iweight | the 1-st step weight matrix. If TRUE, the identity matrix is used. If FALSE, the 1-st step weight matrix is constructed from the instrumental variables and the moments matrix. Default is set to FALSE. |
| test.lin | if TRUE (default), the linearity test is performed; if FALSE, not. |
| B | if test.lin=TRUE, it is the number of bootstrap iterations for the linearity test. |

## Details

`ptm2` estimates a two-way panel threshold regression model using the first-difference instrumental-variable generalized method of moments (FD-IV-GMM) estimator proposed by Seo and Shin (2016).

Let $i = 1, \ldots, n$ index individuals and $t = 1, \ldots, T$ index time periods. The model is

$$y_{it} = (1, x_{it}')\phi_1 I(q_{it} \leq \gamma) + (1, x_{it}')\phi_2 I(q_{it} > \gamma) + \varepsilon_{it},$$

where $y_{it}$ is the dependent variable, $x_{it}$ is a vector of time-varying regressors, $q_{it}$ is the threshold variable, $\gamma$ is the threshold parameter, and $I(\cdot)$ is the indicator function. The parameter vectors $\phi_1$ and $\phi_2$ contain the intercept and slope coefficients in the lower and upper regimes, respectively. The error term is

$$\varepsilon_{it} = \mu_i + \nu_{it},$$

where $\mu_i$ is an unobserved individual-specific effect and $\nu_{it}$ is an idiosyncratic error. The threshold variable can be specified by the user. If it is not provided, the first lag of the dependent variable is used. If no regressors are supplied, the model includes an intercept only. Regressors can be specified as exogenous or endogenous. Additional instruments can be supplied through the `IV` argument, while lagged values of the dependent variable and regressors are also used as instruments.

The following steps are performed in the estimation algorithm:

1. Define the first-differenced model:

$$\Delta y_{it} = \beta' \Delta x_{it} + \delta' X_{it}' I_{it}(\gamma) + \Delta \nu_{it},$$

   where $\delta = \phi_2 - \phi_1$, $\beta$ contains the lower-regime slope coefficients, $X_{it}$ collects the regressors and intercept at periods $t$ and $t-1$, and $I_{it}(\gamma)$ indicates whether the transition variable is above the threshold at those two periods.

2. Define the instrumental variables matrix, which includes the lagged dependent and independent variables, and the additional instrumental variables in the IV matrix (if specified).
3. Construct the 1-st step weight matrix according to the Iweight option.
4. Identify a set of equally distant points between quantiles (`trimrate`/2) and 1-(`trimrate`/2) of the threshold variable vector. The number of points is specified in the option ngrid.
5. Compute the GMM estimator setting the threshold equal to each selected point and computes the residuals. Identify the 1st-step estimator by minimizing the residual.
6. Construct the 2nd-step weight matrix from the residuals associated with the 1st-step estimator.
7. Repeat steps 4. and 5. and return the 2nd-step estimator of the 1st-differenced parameters $\widehat{\delta}$, the threshold $\widehat{\gamma}$, the associated pvalues, and the covariance matrix.

The regressors in the output are always ordered with the exogenous variables first, followed by the endogenous variables. Within each group, the variables retain the same order as specified by the user in the input arguments. Therefore, the estimated coefficients and their associated p-values should be interpreted according to this ordering.

When `test.lin = TRUE`, the function also performs a bootstrap-based test for the presence of a threshold effect. The null hypothesis is that the regime-specific coefficient difference is zero, $H_0 : \delta = 0$, against the alternative that it differs from zero. The test uses a supremum Wald statistic over the threshold grid, with the number of bootstrap replications controlled by `B`.

## Value

An object of S4 class "ptm2", which is a list with the following elements:

| | |
|---|---|
| `threshold` | the estimated threshold and the associated p-value. |
| `estimates` | the `matrix` of the estimated first-differenced parameters (i.e. parameter(s) estimated for the lower regime, the difference between the parameter(s) estimated for the upper and the lower regime) and the associated p-values. |
| `cov.` | the sample version of covariance matrix of the estimated paramaters. |
| `residuals.` | the `matrix` of the first-differenced residuals. |
| `test.lin.` | the `list` of the linearity test results containing: the name of the test; the number of bootstrap iterations carried out; the p-value of the test. |

## Note

The method requires at least 6 times of observation: four lags of the dependent and independent variables are used as instruments, and two more are necessary to identify the regime switch (i.e., one per regime).

## Author(s)

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## References

Seo, M.H. and Shin, Y. (2016) Dynamic panels with threshold effect and endogeneity. Journal of Econometrics, 195(2), p.169-186.

Seo, M.H., Kim, S. and Kim Y.-J. (2019) Estimation of dynamic panel threshold model using Stata. The Stata Journal, 19(3), p.685-697.

## See Also

See also `ptm3` and `simptm`.

## Examples

```
## Select data
data(banana)
data <- banana[which(banana$j==1),]

# Prepare input matrices for ptm2
bioimpedance <-  matrix(data$bioimpedance, ncol=length(unique(data$t)),
                        byrow=TRUE)

weight <-  matrix(data$weight, ncol=length(unique(data$t)), byrow=TRUE)

## Estimation

# Model on bioimpedance y_{it} with transition variable y_{i(t-1)}
```

```
# y_{it}= (phi1_c)1(y_{it-1}<= gamma) + (phi2_c)1(y_{it-1}>gamma)
# Estimation and linear test
p2 <- ptm2(Y=bioimpedance, TV=NULL, Xendo=NULL, Xexo=NULL, IV=NULL,
     trimrate=0.4, ngrid=100, h0=1.5, Iweight=FALSE, test.lin=TRUE,
     B=100)

# Show main output
show(p2)

## NOT RUN
## Model on bioimpedance y_{it} with transition variable y_{i(t-1)} and
## weight as regressor x_{it}:
## y_{it}= (phi1_c + phi1_X*x_{it})1(y_{it-1}<= gamma) +
##         (phi2_c + phi2_X*x_{it})1(y_{it-1}>gamma)
#ptm2(Y=bioimpedance, TV=NULL, Xendo=weight, Xexo=NULL, IV=NULL,
#     trimrate=0.4, ngrid=100, h0=1.5, Iweight=FALSE, test.lin=FALSE)
##
```

---

`ptm2-class` *Class "ptm2"*

---

## Description

A class for `ptm2` and its extensions

## Objects from the Class

Objects can be created by calls of the form `new("ptm2", ...)`.

## Slots

`threshold`**:** Object of class `numeric`. The estimated threshold and the associated p-value.

`estimates`**:** Object of class `numeric`. The vector of the parameter(s) estimated for the lower regime, the difference between the parameter(s) estimated for the upper and the lower regime, and the associated p-values.

`cov.`**:** Object of class `matrix`. The sample version of covariance matrix of the estimated paramaters.

`residuals.`**:** Object of class `matrix`. A matrix of the first-differenced residuals.

`test.lin.`**:** Object of class `list`. Result of the linearity test.

## Methods

No methods defined with class "ptm2" in the signature.

## Author(s)

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## References

Seo, M.H. and Shin, Y. (2016) Dynamic panels with threshold effect and endogeneity. Journal of Econometrics, 195(2), p.169-186.

Seo, M.H., Kim, S. and Kim Y.-J. (2019) Estimation of dynamic panel threshold model using Stata. The Stata Journal, 19(3), p.685-697.

## See Also

See also `ptm2`.

## Examples

```
showClass("ptm2")
```

---

`ptm3` *Three-way panel threshold regression model.*

---

## Description

Three-way panel threshold regression model and its estimation through the 2-step GMM estimator.

## Usage

```
ptm3(data., nameI, nameT, nameJ, nameY, nameTV=NULL, nameXendo=NULL,
    nameXexo=NULL, nameIV=NULL, trimrate=0.4, ngrid=100, h0=1.5,
    Iweight=FALSE, test.lin=TRUE, B=1000)
```

## Arguments

| | |
|---|---|
| `data.` | a `data.frame` with the following variables (by cols): $I$ (statistical units ID), $T$ (time), $J$ (third-level), $Y$ (dependent variable), and if not null, $TV$ (threshold variable), $Xendo$ (endogenous regressor(s)), $Xexo$ (exogenous regressor(s)), $IV$ (instruments). |
| `nameI` | the name of the (numerical) variable that identifies the statistical units. |
| `nameT` | the name of the (numerical) time variable. |
| `nameJ` | the name of the (numerical) variable that indicates the third dimension. |
| `nameY` | the name of the (numerical) dependent variable. |
| `nameTV` | the name of the (numerical) transition variable. If not specified, the first lag of $Y$ is taken. |
| `nameXendo` | the names of the (numerical) independent endogenous variables (if any). |
| `nameXexo` | the names of the (numerical) independent exogenous variables (if any). |
| `nameIV` | the names of the (numerical) instrumental variables (if any). |
| `trimrate` | the trim rate when constructing the grid for estimating the threshold. The default value is set to 0.4. |

| | |
|---|---|
| ngrid | the number of grid points to estimate the threshold. The default is set to 100. |
| h0 | the parameter for Silverman's rule of thumb for kernel estimation. The default is set to 1.5. |
| Iweight | the 1-st step weight matrix. If TRUE, the identity matrix is used. If FALSE, the 1-st step weight matrix is constructed from the instrumental variables. The default is set to FALSE. |
| test.lin | if TRUE (default), the linearity test is performed; if FALSE, not. |
| B | if test.lin=TRUE, the number of bootstrap iterations for the linearity test. |

## Details

ptm3 estimates a three-way dynamic panel threshold regression model using the first-difference instrumental-variable generalized method of moments (FD-IV-GMM) estimator in Di Lascio and Perazzini (2026).

Let $i = 1, \ldots, n$ index individuals, $t = 1, \ldots, T$ index time periods, and $j = 1, \ldots, J$ index levels of the third dimension. The model is

$$y_{ijt} = (1, x'_{ijt})\phi_{1j} I(q_{ijt} \leq \gamma_j) + (1, x'_{ijt})\phi_{2j} I(q_{ijt} > \gamma_j) + \varepsilon_{ijt},$$

where $y_{ijt}$ is the dependent variable, $x_{ijt}$ is a vector of time-varying regressors, $q_{ijt}$ is the threshold variable, $\gamma_j$ is the threshold parameter specific to level $j$, and $I(\cdot)$ is the indicator function. The parameter vectors $\phi_{1j}$ and $\phi_{2j}$ contain the intercept and slope coefficients in the lower and upper regimes, respectively. The error term is

$$\varepsilon_{ijt} = \mu_i + \lambda_j + \nu_{ijt},$$

where $\mu_i$ is an unobserved individual-specific effect, $\lambda_j$ is an unobserved effect associated with the third dimension, and $\nu_{ijt}$ is an idiosyncratic error.

The model is estimated separately for each level $j$, allowing the regression coefficients and threshold parameter to vary across levels of the third dimension. The threshold variable can be specified by the user. If it is not provided, the first lag of the dependent variable is used. Regressors can be specified as exogenous or endogenous. If no regressors are supplied, the model includes an intercept only. Lagged values of the dependent variable and regressors are also used as instruments and additional instruments can be supplied through the nameIV argument.

Once fixed $j$, the steps to estimate the model for the specific level $j$ coincide with the ones described in the Details section of the ptm2 documentation.

The regressors in the output are always ordered with the exogenous variables first, followed by the endogenous variables. Within each group, the variables retain the same order as specified by the user in the input arguments. Therefore, the estimated coefficients and their associated p-values should be interpreted according to this ordering.

When test.lin = TRUE, the function also performs a bootstrap-based test for the presence of a threshold effect separately for each level $j$. The null hypothesis is that the regime-specific coefficient difference is zero, $H0 : \delta_j = 0$ against $H1 : \delta_j \neq 0$. The test uses a supremum Wald statistic over the threshold grid, with the number of bootstrap replications controlled by B.

If $J = 1$, the function estimates a two-way panel threshold model as implemented in ptm2.

## Value

An object of S4 class "ptm3", which is a list with the following elements:

| | |
|---|---|
| `threshold` | the `matrix` of the estimated thresholds and the associated p-values. |
| `param` | the `matrix` of the estimated first-differenced parameters of the model and the associated p-values. |
| `cov.` | the `array` containing the estimated covariance matrix per each value of the third way. |
| `residuals.` | the `list` containing the estimated first-differenced residuals per each value of the third way. |
| `test.lin.` | the `list` of the linearity test results containing: the name of the test; the number of bootstrap iterations carried out; the p-value of the test per each value of the third way. |

## Note

The estimation method requires at least $t \geq 6$: four lags of the dependent and independent variables are used as instruments, and two more are necessary to identify the regime switch (i.e., one per regime). Note that the instant times in the nameT variable are automatically ordered increasingly.

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## References

Di Lascio, F.M.L. and Perazzini, S. (2026) A three-way dynamic panel threshold regression model for change point detection in bioimpedance data. Stat Methods Appl 35, 849-867.

Di Lascio, F.M.L. and Perazzini, S. (2022) Change point detection in fruit bioimpedance using a three-way panel model. Book of short papers - SIS2022, p.1184-1189, Eds. A. Balzanella, M. Bini, C. Cavicchia, R. Verde. Pearson. ISBN: 978-88-9193-231-0.

## See Also

See also `ptm2` and `simptm`.

## Examples

```
# Import data
data(banana)

## NOT RUN
## Model on bioimpedance y_{ijt} with transition variable y_{ij(t-1)}
## y_{ijt} = (phi1_{jc})1(y_{ijt-1}<=gamma_j) +
##           (phi2_{jc})1(y_{ijt-1}>gamma_j)
#
#ptm3(data.=banana, nameI="i", nameT="t", nameJ="j",
```

```
#    nameY="bioimpedance", nameTV=NULL, nameXendo=NULL, nameXexo=NULL,
#    nameIV=NULL, trimrate=0.4, ngrid=100, h0=1.4, Iweight=FALSE,
#    test.lin=FALSE)
##

# Model on bioimpedance y_{ijt} with transition variable y_{ij(t-1)}
# and time-varying regressor x_{ijt}:
# y_{it}=(phi1_{jc}+phi1_{jX}*x_{ijt})1(y_{ijt-1}<=gamma_j) +
# (phi2_{jc}+phi2_{jX}*x_{ijt})1(y_{ijt-1}>gamma_j)

p3 <- ptm3(data.=banana, nameI="i", nameT="t", nameJ="j",nameY="bioimpedance",
    nameTV=NULL, nameXendo="weight", nameXexo=NULL, nameIV=NULL,
    trimrate=0.4, ngrid=100, h0=1.5, Iweight=FALSE, test.lin=FALSE)

# Show main output
show(p3)
```

---

`ptm3-class` *Class "ptm3"*

---

## Description

A class for `ptm3` and its extensions

## Objects from the Class

Objects can be created by calls of the form `new("ptm3", ...)`.

## Slots

`threshold`**:** Object of class `numeric`. A vector of the estimated thresholds and the associated p-values.

`param`**:** Object of class `matrix`. A matrix of the estimated first-differenced parameters of the model and the associated p-values.

`cov.`**:** Object of class `array`. The sample covariance matrix of the estimated parameters per each value of the third way.

`residuals.`**:** Object of class `list`. The estimated first-differenced residuals per each value of the third way.

`test.lin.`**:** Object of class `list`. Result of the linearity test.

## Methods

No methods defined with class "ptm3" in the signature.

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## References

Di Lascio, F.M.L. and Perazzini, S. (2026) A three-way dynamic panel threshold regression model for change point detection in bioimpedance data. Stat Methods Appl 35, 849-867.

Di Lascio, F.M.L. and Perazzini, S. (2022) Change point detection in fruit bioimpedance using a three-way panel model. Book of short papers - SIS2022, p.1184-1189, Eds. A. Balzanella, M. Bini, C. Cavicchia, R. Verde. Pearson. ISBN: 978-88-9193-231-0.

## See Also

See also `ptm3`.

## Examples

```
showClass("ptm3")
```

---

`simptm` *Data simulation from two- or three-way panel threshold regression model.*

---

## Description

Random generation of data from two- or three-way panel threshold regression model with or without a time-varying regressor.

## Usage

```
simptm(n, T., J=2, CP, gamma.=c(0,0),
        phi_c=matrix(c(-1,1,-0.7,1.8), nrow=2, byrow=TRUE),
        phi_X=matrix(c(-0.2,0.2,-0.5,0.8), nrow=2, byrow=TRUE),
        sigmau=1, parAR=c(0.7,0.5), B=200, seedstart=1)
```

## Arguments

| | |
|---|---|
| `n` | number of statistical units. |
| `T.` | number of times. |
| `J` | number of third way's values. |
| `CP` | vector of times of regime switch (one per each $j$). If vector of length 1, the same change point is taken for all the $j$s. |
| `gamma.` | vector of length J of threshold values. |
| `phi_c` | matrix $J \times 2$ of the constant parameters of the two regimes; first column for lower (upper) regime and second column for upper (lower) regime. |
| `phi_X` | matrix $J \times 2$ of the regressor parameter of the two regimes; first column for lower (upper) regime and second column for upper (lower) regime. |
| `sigmau` | possible constant to be applied to the error term distributed as a Gaussian white noise. |

| | |
|---|---|
| B | number of datasets to be drawn. |
| parAR | vector of autoregressive parameter(s) (one for each $j$) to generate a (exogenous) time-varying regressor. |
| seedstart | number of the initial seed. |

## Details

simptm generates B datasets from a three-way panel threshold regression model.

Let $i = 1, \ldots, n$ index statistical units, $t = 1, \ldots, T$ index time periods, and $j = 1, \ldots, J$ index levels of the third dimension. The data-generating process is

$$y_{ijt} = \begin{cases} \phi_{1j}^{(1)} + \phi_{1j}^{(2)} x_{ijt} + \sigma \varepsilon_{ijt}, & \text{if } y_{ij(t-1)} \leq \gamma_j, \quad t \leq CP_j, \\ \phi_{2j}^{(1)} + \phi_{2j}^{(2)} x_{ijt} + \sigma \varepsilon_{ijt}, & \text{if } y_{ij(t-1)} > \gamma_j, \quad t > CP_j. \end{cases}$$

where $CP_j$ is the change point, $\phi_{1j}^{(1)}$ and $\phi_{2j}^{(1)}$ are the intercepts in the two regimes, and $\phi_{1j}^{(2)}$ and $\phi_{2j}^{(2)}$ are the corresponding slope coefficients. The regime switch is determined by the lagged dependent variable, with threshold value $\gamma_j$. The variable $x_{ijt}$ denotes the exogenous regressor for unit $i$, level $j$, and time $t$. When included, it follows an autoregressive process of order one:

$$x_{ijt} = \rho_j x_{ij(t-1)} + \eta_{ijt},$$

where $\rho_j$ is the autoregressive coefficient for level $j$, specified through parAR, and $\eta_{ijt}$ is a Gaussian white noise process. The errors $\varepsilon_{ijt}$ are also generated from Gaussian white noise, and $\sigma$ is a user-defined scaling constant specified through sigmau.

If $J = 1$, the function simulates a two-way panel threshold model.

## Value

An object of S4 class "simptm", which is a list of simulated data matrices.

## Note

The estimation method requires at least $T. \geq 6$: four lags of the dependent and independent variables are used as instruments, and two more are necessary to identify the regime switch (i.e., one per regime). The output is a list of B dataframes. Each dataframe contains columns: $i$, $j$, $t$, $Y$ and possibly $X$.

## Author(s)

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## References

Di Lascio, F.M.L. and Perazzini, S. (2026) A three-way dynamic panel threshold regression model for change point detection in bioimpedance data. Stat Methods Appl 35, 849-867.

Di Lascio, F.M.L. and Perazzini, S. (2022) Change point detection in fruit bioimpedance using a three-way panel model. Book of short papers - SIS2022, p.1184-1189, Eds. A. Balzanella, M. Bini, C. Cavicchia, R. Verde. Pearson. ISBN: 978-88-9193-231-0.

Seo, M.H. and Shin, Y. (2016) Dynamic panels with threshold effect and endogeneity, Journal of Econometrics, 195(2), p.169-186.

## See Also

See also `ptm2` and `ptm3`.

## Examples

```
## NOT RUN
#
## Simulation of 10 two-way panels
## y_{it} = (-1-0.2*x_{it})1(y_{it-1}<=0) + (1+0.2*x_{it})1(y_{it-1}>0)
## with 50 statistical units observed for 50 times with change point at
## time 20, autoregressive parameter 0.7, and sigmau=1.
#
DB1 <- simptm(n=50, T.=11, J=1, CP=8, gamma.=0, phi_c=matrix(c(-1,1),
     nrow=1, byrow=TRUE), phi_X=matrix(c(-0.2,0.2), nrow=1, byrow=TRUE),
     sigmau=1, parAR=0.7, B=10, seedstart=1)
#head(DB1@simulation)
#str(DB1@simulation)

## Simulation of 10 three-way panels
## y_{i1t} = (-1-0.2*x_{i1t})1(y_{i1t-1}<=0) +
##           (1+0.2*x_{i1t})1(y_{i1t-1}>0)
## y_{i2t} = (-0.7-0.5*x_{i2t})1(y_{i2t-1}<=0) +
##           (1.8+0.8*x_{i2t})1(y_{i2t-1}>0)
## with 50 statistical units, 50 times, J=2, change point corresponding to
## time 20, with autoregressive parameter 0.7, and sigmau=1.
#
#DB2 <- simptm(n=50, T.=20, J=2, CP=10, gamma.=c(0,0),
#    phi_c=matrix(c(-1,1,-0.7,1.8), nrow=2, byrow=TRUE),
#    phi_X=matrix(c(-0.2,0.2,-0.5,0.8), nrow=2, byrow=TRUE), sigmau=1,
#    parAR=rep(0.7,2), B=5, seedstart=1)
#head(DB2@simulation)
#str(DB2@simulation)
#
##
```

`simptm-class` *Class "simptm"*

## Description

A class for `simptm` and its extensions

## Objects from the Class

Objects can be created by calls of the form `new("simptm", ...)`.

## Slots

`simulation` Object of class `"list"`. A list of dataframes of simulated data. The list contains `B` dataframes, one for each replication. Each dataframe contains columns: $i$, $j$, $t$, $Y$ and possibly $X$.

## Methods

No methods defined with class "simptm" in the signature.

## Author(s)

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## References

Di Lascio, F.M.L. and Perazzini, S. (2026) A three-way dynamic panel threshold regression model for change point detection in bioimpedance data. Stat Methods Appl 35, 849-867.

Di Lascio, F.M.L. and Perazzini, S. (2022) Change point detection in fruit bioimpedance using a three-way panel model. Book of short papers - SIS2022, p.1184-1189, Eds. A. Balzanella, M. Bini, C. Cavicchia, R. Verde. Pearson. ISBN: 978-88-9193-231-0.

Seo, M. and Shin, Y. (2016) Dynamic panels with threshold effect and endogeneity. Journal of Econometrics, 195(2), p.169-186.

## See Also

See also `simptm`.

## Examples

```
showClass("simptm")
```

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