Package ‘tsDyn’

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Description Implements nonlinear autoregressive (AR) time series models. For univariate se-
       ries, a non-parametric approach is available through additive nonlinear AR. Parametric modeling
       and testing for regime switching dynamics is available when the transition is either di-
       rect (TAR: threshold AR) or smooth (STAR: smooth transition AR, LSTAR). For multivariate se-
       ries, one can estimate a range of TVAR or threshold cointegration TVECM mod-
       els with two or three regimes. Tests can be conducted for TVAR as well as for TVECM (Hansen and Seo 2002 and Seo 2006).
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R topics documented:

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Description

Getting started with the tsDyn package

Details

This package provides some tools inspired by nonlinear dynamics for the analysis-modelling of observed time series.

For loading the package, type:

library(tsDyn)

A good place to start learning the package usage, is the vignette. It contains a more detailed guide on package contents, and an applied case study. At the R prompt, write:

vignette("tsDyn")

For a full list of functions exported by the package, type:

ls("package:tsDyn")

There is also an experimental GUI for built-in NLAR models. Call it with:

nlarDialog(timeSeries)

where timeSeries is an available time series object.

Each exported function has a corresponding man page (some man pages are in common to more functions). Display it by typing

help(functionName)
Additive nonlinear autoregressive model

**Description**

Additive nonlinear autoregressive model.

**Usage**

```
aar(x, m, d=1, steps=d, series)
```

**Arguments**

- `x`: time series
- `m, d, steps`: embedding dimension, time delay, forecasting steps
- `series`: time series name (optional)

**Details**

Nonparametric additive autoregressive model of the form:

\[
x_{t+s} = \mu + \sum_{j=1}^{m} s_j(x_{t-(j-1)d})
\]

where \( s_j \) are nonparametric univariate functions of lagged time series values. They are represented by cubic regression splines. \( s_j \) are estimated together with their level of smoothing using routines in the `mgcv` package (see references).

**Value**

An object of class `nlar`, subclass `aar`, i.e. a list with mostly internal structures for the fitted `gam` object.

**Author(s)**

Antonio, Fabio Di Narzo
accuracy_stat

References
Wood and Augustin, GAMs with integrated model selection using penalized regression splines and

Examples
\begin{verbatim}
# fit an AAR model:
mod <- aar(log(lynx), m=3)
# Summary informations:
summary(mod)
# Diagnostic plots:
plot(mod)
\end{verbatim}

accuracy_stat Forecasting accuracy measures.

Description
Compute forecasting accuracies. This is very similar ot the accuracy method from forecast.

Usage
accuracy_stat(object, ...)

## Default S3 method:
accuracy_stat(object, true, ...)

## S3 method for class 'pred_roll'
accuracy_stat(object, w, ...)

Arguments

object      A data-frame, matrix, or object of class pred_roll
...         Not used currently.
true        If object is just a matrix or data-frame, true values to be compared to should be supplied
w           Optional. For objects of class pred_roll containing multiple variables, user can specify the way to aggregate the specific x-step-ahead into the ‘all’ category

Details
The function works either for a simple data.frame or for objects pred_roll. For simple data.frames, the argument true, i.e. a data frame containing the true values, has to be provided. For pred_roll objects, the true values are contained in the object, so no need (nor possibility) to provide the true values.
addRegime

Value
A data-frame containing the forecasting accuracy measures.

Author(s)
Matthieu Stigler

Examples

```r
## univariate:
mod_ar <- linear(lynx[1:100], m=1)
mod_ar_pred <- predict_rolling(mod_ar, newdata=lynx[101:114])
accuracy_stat(object=mod_ar_pred$pred, true=mod_ar_pred$true)

## multivariate
data(barry)
mod_var <- lineVar(barry, lag=1)

mod_var_pred <- predict_rolling(object=mod_var, nroll=10, n.ahead=1:3)
accuracy_stat(object=mod_var_pred)
accuracy_stat(object=mod_var_pred, w=c(0.7, 0.2, 0.1))
```

---

addRegime (addRegime test)

Description
addRegime test

Usage
addRegime(object, ...)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>object</td>
<td>fitted model object with at least 2 regimes</td>
</tr>
<tr>
<td>...</td>
<td>arguments to and from other methods</td>
</tr>
</tbody>
</table>

Value
A list containing the p-value of the F statistic and a boolean, true if there is some remaining nonlinearity and false otherwise.
autopairs

Author(s)
J. L. Aznarte

References
TODO

See Also
star

Examples

```r
# TODO
```

<table>
<thead>
<tr>
<th>autopairs</th>
<th>Bivariate time series plots</th>
</tr>
</thead>
</table>

Description

Bivariate time series plots: scatterplots, directed lines and kernel density estimations using functions in the `sm` package.

Usage

```r
autopairs(x, lag = 1, h, type = c("levels", "persp", "image", "lines", "points", "regression"))
```

Arguments

- `x` : time series
- `lag` : time lag
- `h` : kernel window (useful only for kernel estimations)
- `type` : type of plot: contour levels, perspective plots, image, directed lines, points or points with superposed kernel regression

Details

Bivariate time series plots: scatterplots, directed lines and kernel density and regression functions estimations using functions in the package `sm`. In particular, for kernel density estimation `sm.density` is used, with smoothing parameter `h` defaulting to `hnorm`. For kernel regression, `sm.regression` is used.
Value
None. Plots are produced on the default graphical device.

Author(s)
Wrappers to sm by Antonio, Fabio Di Narzo

See Also
For finer control on density estimation, consider using directly sm.density and, especially, sm.ts.pdf from package sm.

Examples

```r
x <- log10(lynx)
autopairs(x, lag=2, type="lines")
```

---

autotriples  Trivariate time series plots

Description
Trivariate time series plots: kernel autoregression using functions in the sm package

Usage
```r
autotriples(x, lags = 1:2, h, type = c("levels", "persp", "image", "lines", "points"))
```

Arguments
- `x` time series
- `lags` vector of regressors lags
- `h` kernel window
- `type` type of plot: contour levels, perspective plots, image

Details
This function displays trivariate time series plots, i.e. kernel regression of \( x[t - lags[1]], x[t - lags[2]] \) against \( x[t] \) using functions in the package sm. In particular, sm.regression is used, with smoothing parameter defaulting to hnorm(x).

Value
None. Plots are produced on the default graphical device.
Author(s)

Wrappers to \texttt{sm} by Antonio, Fabio Di Narzo

See Also

For finer control on kernel regression, consider using directly \texttt{sm.regression} and, especially, \texttt{sm.autoregression} in package \texttt{sm}.

Examples

\begin{verbatim}
autotriples(log(lynx))
autotriples(log(lynx), type="persp")
autotriples(log(lynx), type="image")
\end{verbatim}

Description

Interactive trivariate time series plots

Usage

\texttt{autotriples.rgl(x, lags = 1:2, type = c("lines", "points"))}

Arguments

\begin{itemize}
\item \texttt{x} \hspace{1cm} time series
\item \texttt{lags} \hspace{1cm} vector of regressors lags
\item \texttt{type} \hspace{1cm} type of plot: contour levels, perspective plots, image
\end{itemize}

Details

This function displays interactive trivariate time series plots \(x[t-lags[1]], x[t-lags[2]]\) against \(x[t]\) using the interactive \texttt{rgl} device.

Value

None. A plot is produced on the current \texttt{rgl} device.

Author(s)

Wrapper to ‘sm’ and GUI by Antonio, Fabio Di Narzo
availableModels

See Also

autotriples for 3d visualization via scatterplot3d package and for kernel post-processing of the cloud for nonparametric autoregression functions estimates.

Examples

if(interactive())
  autotriples.rgl(log(lynx))

---

availableModels: Available models

Description

Available built-in time series models

Usage

availableModels()

Details

Return the list of built-in available 'nlar' time series models

Value

A character vector containing built-in time series models. For help on a specific model, type: help(modelName).

Author(s)

Antonio, Fabio Di Narzo

Examples

availableModels()
**barry**

*Time series of PPI used as example in Bierens and Martins (2010)*

**Description**

This data set contains the series used by *Bierens and Martins* for testing for PPI between Canada and US.

**Usage**

```r
data(barry)
```

**Format**

A data frame with 324 monthly observations, ranging from 1973:M1 until 1999:M12.

- `dolcan` Exchange rate US/Can dollar.
- `cpiUSA` US Consumer Price Index.
- `cpiCAN` Canada Consumer Price Index.

**Author(s)**

Matthieu Stigler

**Source**


---

**BBCTest**

*Test of unit root against SETAR alternative*

**Description**

Test of unit root against a stationnary three regime SETAR alternative

**Usage**

```r
BBCTest(x, m, series, testStat = c("LR", "Wald", "LM"), trim = 0.1, 
grid = c("minPerc", "minObs"))
```
Arguments

- `x`: time series
- `m`: Number of lags under the alternative
- `series`: time series name (optional)
- `testStat`: Type of test statistic to use
- `trim`: trimming parameter indicating the minimal percentage of observations in each regime
- `grid`: Whether a minimal number of percentage or observations should be imposed. See details

Details

TODO

Value

A object of class "BBC2004Test" containing:
- The value of the sup Test
- The version of test used (either Wald, LM or LR).

Author(s)

Matthieu Stigler

See Also

`setarTest` for a test with stationarity as a null.

Examples

```r
BBCTest(lynx, m=3, test="Wald", grid="minPerc")
```

---

### coefB

**Extract cointegration parameters A, B and PI**

**Description**

Extract parameters in VECM: adjustment coefficients A, cointegrating coefficients B, or the composite matrix PI

---
Usage

coefB(object, ...)

## S3 method for class 'VECM'
coefB(object, ...)

## S3 method for class 'ca.jo'
coefB(object, r = 1, normalize = TRUE, ...)

c coefA(object, ...)

## S3 method for class 'VECM'
coefA(object, ...)

## S3 method for class 'ca.jo'
coefA(object, r = 1, normalize = TRUE, ...)

c coefP1(object, ...)

Arguments

object An object of class VECM, ca.jo
r The cointegrating rank
normalize Whether to normalize the A/B coefficients. See details
... Further arguments passed to methods

Details

The functions extract the parameters from a VECM with $K$ variables and rank $r$:

**A** Adjustment coefficients, of dim $K \times r$

**B** Cointegrating coefficients, of dim $K \times r$

**Pi** Matrix $\Pi = A \hat{B}'$, of dim $K \times K$

Coefficients are extracted from a VECM in package tsDyn, or from a VECM obtained in package urca from ca.jo or cajorls.

Note that by default, the A and B coefficients returned are normalized (see below). This is the case for results obtained from VECMLineVar and cajorls, while for ca.jo, the user has the choice (but normalize=TRUE by default), in which case the rank $r$ is also to be specified. The normalization is the Phillips triangular representation, as suggested by Johansen (1995, p. 72), standardising the first $r \times r$ coefficients to $I_r$:

**B** $B_{norm} = B(c' B)^{-1}$ with $c = (I_r, 0_{p-r,r})'$

**A** $A_{norm} = B'c$

Finally, note that the function also apply to objects obtained from tests of class ca.jo.test (from blrtest etc...). Care should be taken however, since the normalization might override the restrictions imposed.
Value
A matrix containing the coefficients

Author(s)
Matthieu Stigler

Examples

data(barry)
vecm <- VECM(barry, lag=1, estim="ML")
vecm_r2 <- VECM(barry, lag=1, estim="ML", r=2)

## extract coefficients:
coefA(vecm)
coefB(vecm)
coefPI(vecm)
coefB(vecm_r2)
coefPI(vecm_r2)

## Beta-Restricted VECM:
beta_vecm2 <- coefB(vecm_r2)
beta_vecm2[3,2] <- 0.02
vecm_r2_rest <- VECM(barry, lag=1, estim="ML", r=2, beta=beta_vecm2)
round(coefB(vecm_r2_rest),5)

## Package vars/urca
if(require(urca)){
  vecm_ur <- ca.jo(barry, K=2)
  coefB(vecm_ur)
  coefB(vecm_ur,r=2)
  coefB(cajorls(vecm_ur, r=2))
  all.equal(coefB(vecm), coefB(vecm_ur), check.attributes=FALSE)
  all.equal(coefB(vecm_r2), coefB(vecm_ur, r=2), check.attributes=FALSE)
}

---

**delta**

*delta test of conditional independence*

Description
delta statistic of conditional independence and associated bootstrap test

Usage
delta(x, m, d = 1, eps)
delta.test(x, m = 2:3, d = 1, eps = seq(0.5 * sd(x), 2 * sd(x), length = 4), B = 49)
**Arguments**

- `x` time series
- `m` vector of embedding dimensions
- `d` time delay
- `eps` vector of length scales
- `B` number of bootstrap replications

**Details**

delta statistic of conditional independence and associated bootstrap test. For details, see Manzan(2003).

**Value**

delta returns the computed delta statistic. delta.test returns the bootstrap based 1-sided p-value.

**Warning**

Results are sensible to the choice of the window `eps`. So, try the test for a grid of `m` and `eps` values. Also, be aware of the course of dimensionality: `m` can’t be too high for relatively small time series. See references for further details.

**Author(s)**

Antonio, Fabio Di Narzo

**References**


**See Also**

- BDS marginal independence test: `bds.test` in package `tseries`
- Teraesvinta’s neural network test for nonlinearity: `terasvirta.test` in package `tseries`
- delta test for nonlinearity: `delta.lin.test`

**Examples**

delta(log10(lynx), m=3, eps=sd(log10(lynx)))
**delta.lin**

*delta test of linearity*

---

**Description**

delta test of linearity based on conditional mutual information

**Usage**

delta.lin(x, m, d = 1)

delta.lin.test(x, m = 2:3, d = 1, eps = seq(0.5 * sd(x), 2 * sd(x), length = 4), B = 49)

**Arguments**

- **x**: time series
- **m**: vector of embedding dimensions
- **d**: time delay
- **eps**: vector of length scales
- **B**: number of bootstrap replications

**Details**

delta test of linearity based on conditional mutual information

**Value**

delta.lin returns the parametrically estimated delta statistic for the given time series (assuming linearity). delta.lin.test returns the bootstrap based 1-sided p-value. The test statistic is the difference between the parametric and nonparametric delta estimators.

**Author(s)**

Antonio, Fabio Di Narzo

**References**


**Examples**

delta.lin(log10(lynx), m=3)
extendBoot

extension of the bootstrap replications

Description
This function updates an existing bootstrap test with new bootstrap replications.

Usage
extendBoot(x, nboot)

Arguments
x
A object from setarTest (hence of class Hansen99Test)
nboot
The number of new bootstrap replications

Details
The plot function will draw the old and new distribution, hence allowing to test the sensitivity of the results obtained.

Value
Returns an object of the same class with same objects but updated values.

Author(s)
Matthieu Stigler

See Also
bbctest for a similar test. setarTest for a test with stationarity as a null.

Examples
## Not run:
# test with 10 bootstrap replications:
a<-setarTest(sun[1:100], m=1, nboot=10)
plot(a)

#use old results and compue 20 new replications
b<-extendBoot(a, n=20)
#see the different distributions:
plot(b)

## End(Not run)
Description

Use the fevd function from package vars to compute the forecast error variance decomposition of a VAR(p) or VECM for n.ahead steps.

Usage

```r
## S3 method for class 'nlVar'
fevd(x, n.ahead=10, ...)
```

Arguments

- `x`: Object of class ‘VAR’ generated by lineVar(), or an object of class ‘VECM’ generated by VECM().
- `n.ahead`: Integer specifying the number of steps.
- `...`: Currently not used.

Details

The function converts the VAR or VECM computed by package tsDyn into an object of class ‘vec2var’, on which then the fevd method is applied. For details, see package vars.

Value

A list with class attribute ‘varFevd’ of length K holding the forecast error variances as matrices.

Author(s)

Bernhard Pfaff

References


See Also

- `plot` for the plot method. `lineVar`, `VECM` for the models.

Examples

```r
data(zeroyld)
mod_vecm <- VECM(zeroyld, lag = 2)
fevd(mod_vecm, n.ahead = 5)
```
fitted.nlVar

fitted.nlVar

fitted method for objects of class nlVar, i.e. VAR and VECM models.

Description

Returns the fitted values of the model, either as computed in the model, or back to the original series level.

Usage

```r
## S3 method for class 'nlVar'
fitted(object, level = c("model", "original"), ...)
```

Arguments

- `object` An object of class `nlVar`; generated by `VECM` or `lineVar`.
- `level` How to return the fitted values. See below.
- `...` Currently not used.

Details

In case of a VAR in differences, in ADF specification, or a VECM, the fitted values are actually in differences. With the option `level="original"`, the function returns the series in the original level.

For VAR in levels, the two arguments are evidently the same and hence it is not taken into account, returning a warning.

Value

A matrix.

Author(s)

Matthieu Stigler

Examples

```r
## estimate models
data(barry)
ve <- VECM(barry, lag=2)
va <- lineVar(barry, lag=1)
va_diff <- lineVar(barry, lag=1, I="diff")
va_ADF <- lineVar(barry, lag=1, I="ADF")
```
### getTh

**Extract threshold(s) coefficient**

**Description**

Extract threshold coefficient(s)

**Usage**

getTh(object, ...)

## Default S3 method:

getTh(object, ...)

**Arguments**

- **object** object of class setar, summary.setar, nlVar
- **...** additional arguments to getTh

**Value**

Threshold value.

**Author(s)**

Matthieu Stigler

**Examples**

```r
set <- setar(lynx, m=3)
getTh(set)
getTh(summary(set))
```
This data, used as example in Hansen (1999), contains the US monthly industrial production.

Usage
data(IIPUs)

Format
A monthly time series of class ts starting in January 1960 and ending in September 1997. Note that the series ends at 1997 and not 1998 as in the paper of Hansen, even if the data was taken from hisite and the graph is exactly the same.

Source

Examples
data(IIPUs)
end(IIPUs) # not same date as in the paper
plot(IIPUs)# exactly same graph as in the paper
sel<-selectSETAR(IIPUs, m=16, thDelay=5, criterion="SSR", trim=0.1, plot=FALSE)
sel # R function obtains a lower SSR with another threshold
plot(sel)
setar(IIPUs, m=16, thDelay=5, trim=0.1, th=sel$th)

set2<-selectSETAR(IIPUs, m=16, thDelay=5, criterion="SSR", trim=0.1, plot=FALSE, nthresh=2)
set2 # all results agree
summary(set2)

# this is obviously a error in Hansen, see:
XX<-embed(IIPUs, 17)
Y<-XX[,1]
X<-XX[,,-1]
dummyDown<-ifelse(X[,6]<= -2.5, 1,0)
sum(dummyDown)
M<-cbind(1*dummyDown,X*dummyDown )
lm(Y~M-1)

## see the test functions (not run, due to long computing time, even with small nboot
## Impulse response function

**Description**

Use the `fevd` function from package `vars` to compute the impulse response coefficients of a VAR(p) (or transformed VECM to VAR(p)) for `n.ahead` steps.

**Usage**

```r
## S3 method for class 'nlVar'
irf(x, impulse = NULL, response = NULL, n.ahead = 10,
    ortho = TRUE, cumulative = FALSE, boot = TRUE, ci = 0.95,
    runs = 100, seed = NULL, ...)
```

**Arguments**

- `x` Object of class `'VAR'`, generated by `lineVar()`, or object of class `'VECM'`; generated by `vecM()`.  
- `impulse` A character vector of the impulses, default is all variables.  
- `response` A character vector of the responses, default is all variables.  
- `n.ahead` Integer specifying the steps.  
- `ortho` Logical, if `TRUE` (the default) the orthogonalised impulse response coefficients are computed (only for objects of class `'varest'`).  
- `cumulative` Logical, if `TRUE` the cumulated impulse response coefficients are computed. The default value is false.  
- `boot` Logical, if `TRUE` (the default) bootstrapped error bands for the impulse response coefficients are computed.  
- `ci` Numeric, the confidence interval for the bootstrapped errors bands.  
- `runs` An integer, specifying the runs for the bootstrap.  
- `seed` An integer, specifying the seed for the `rng` of the bootstrap.  
- `...` Currently not used.

**Details**

The function converts the VAR or VECM computed by package `tsDyn` into an object of class `‘vec2var’`, on which then the `irf` method is applied. For details, see the relevant package.
Value

A list of class ‘varirf’ with the following elements is returned:

- `irf` A list with matrices for each of the impulse variables containing the impulse response coefficients.
- `Lower` If `boot = TRUE`, a list with matrices for each of the impulse variables containing the lower bands.
- `Upper` If `boot = TRUE`, a list with matrices for each of the impulse variables containing the upper bands.
- `response` Character vector holding the names of the response variables.
- `impulse` Character vector holding the names of the impulse variables.
- `ortho` Logical, if `true`, orthogonalised impulse responses have been computed.
- `cumulative` Logical, if `true`, cumulated impulse responses have been computed.
- `runs` An integer, specifying the number of bootstrap runs.
- `ci` Numeric, defining the confidence level.
- `boot` Logical, if `true` bootstrapped error bands have been computed.
- `model` Character, containing ‘class(x)’.

Author(s)

Bernhard Pfaff

References


See Also

`plot` for the plot method. `lineVar`, `VECM` for the models.

Examples

data(barry)

```r
## For VAR
mod_var <- lineVar(barry, lag = 2)
irf(mod_var, impulse = "dolcan", response = c("dolcan", "cpiUSA", "cpiCAN"), boot = FALSE)

## For VECM
mod_VECM <- VECM(barry, lag = 2, estim="ML", r=2)
irf(mod_VECM, impulse = "dolcan", response = c("dolcan", "cpiUSA", "cpiCAN"), boot = FALSE)
```
**KapShinTest**

---

**isLinear**  
**isLinear**

**Description**

Generic NLAR linearity test

**Usage**

```r
isLinear(object, ...)
```

**Arguments**

- `object` : fitted time series model
- `...` : arguments to and from other methods

**Author(s)**

A. F. Di Narzo

---

**KapShinTest**  
*Test of unit root against SETAR alternative with*

**Description**

Test of unit root against a stationnary 3 regime SETAR alternative with random walk in the inner regime

**Usage**

```r
KapShinTest(x, m=1, series, include = c("none","const", "trend", "both"), c=3, delta=0.5, points=NULL,minObsMid=10, trick=c("for", "apply", "mapply"), trace=FALSE)
```

**Arguments**

- `x` : time series
- `m` : Number of lags under the alternative
- `series` : time series name (optional)
- `include` : Whether data should be raw, de-meaned or de-meaned and de-trended
- `c` : Argument for the grid search. See details
- `delta` : Argument for the grid search. See details
- `points` : Points for the grid search. See details
- `minObsMid` : Minimal number of observations in the inner regime
- `trick` : type of internal function used
- `trace` : should additional infos be printed? (logical)
Details

This function is currently spurious.

Value

A object of class KapShin2006Test containing:

- statistic: The three (SupW, AvgW, ExpW) test statistics computed
- case: Whether the data was transformed, corresponds to input argument include
- series: The name of the series

Author(s)

Matthieu Stigler

See Also

BBCTest for a similar test. setarTest for a test with stationarity as a null.

Examples

KapShinTest(lynx, m=1, trace=FALSE, include="none", points=10)

Description

Selection of the cointegrating rank and the lags with Information criterion (AIC, BIC).

Usage

lags.select(data, lag.max = 10, include = c("const", "trend", "none", "both"), fitMeasure = c("SSR", "LL"), sameSample = TRUE)

Arguments

data: multivariate time series.
lag.max: Maximum number of lags to investigate.
include: Type of deterministic regressors to include.
fitMeasure: Whether the AIC/BIC should be based on the full likelihood, or just the SSR. See explanations in logLik.VECM.
sameSample: Logical. Whether the data should be shortened so that the AIC/BIC are estimated on the same sample. Default to TRUE.
Details

This function selects the lag according to AIC, BIC and Hannan-Quinn.

Value

An object of class `rank.select`, with `print` and `summary` methods, containing among other the matrices of AIC/BIC/HQ.

Author(s)

Matthieu Stigler

See Also

`rank.select`, the underlying function, to estimate the rank also.

`VARselect` in package `vars`, does basically the same.

Examples

data(barry)

#
rk_sel <- lags.select(barry)
rk_sel
summary(rk_sel)
Arguments

- x: time series
- m, d, steps: embedding dimension, time delay, forecasting steps
- series: time series name (optional)
- include: Type of deterministic regressors to include
- type: Whether the variable is taken is level, difference or a mix (diff y = y-1, diff lags) as in the ADF test

Details

AR(m) model:

\[ x_{t+s} = \phi_0 + \phi_1 x_t + \phi_2 x_{t-d} + \ldots + \phi_m x_{t-(m-1)d} + \epsilon_{t+s} \]

Value

A \texttt{nlar} object, linear subclass.

Author(s)

Antonio, Fabio Di Narzo

See Also

\texttt{nlar} for fitting this and other models to time series data

Examples

```r
# fit an AR(2) model
mod.linear <- linear(log(lynx), m=2)
mod.linear
summary(mod.linear)
```

Description

Estimate either a VAR or a VECM.

Usage

```r
lineVar(data, lag, r = 1, include = c("const", "trend", "none", "both"),
model = c("VAR", "VECM"), I = c("level", "diff", "ADF"), beta = NULL,
estim = c("20LS", "ML"), LRinclude = c("none", "const", "trend", "both"),
exogen = NULL)
```
Arguments

data multivariate time series (first row being first=oldest value)
lag Number of lags to include in each regime
r Number of cointegrating relationships
include Type of deterministic regressors to include
model Model to estimate. Either a VAR or a VECM
I For VAR only: whether in the VAR the variables are to be taken in levels (original series) or in difference, or similarly to the univariate ADF case.
beta for VECM only: user-specified cointegrating value. If NULL, will be estimated using the estimator specified in estim
estim Type of estimator for the VECM: '2OLS' for the two-step approach or 'ML' for Johansen MLE
LRinclude Possibility to include in the long-run relationship and the ECT a trend, a, constant, etc. Can also be a matrix with exogeneous regressors
exogen Inclusion of exogenous variables (first row being first=oldest value). Is either of same size than data (then automatically cut) or than end-sample.

Details

This function provides basic functionalities for VAR and VECM models. More comprehensive functions are in package vars. A few differences appear in the VECM estimation:

Engle-Granger estimator The Engle-Granger estimator is available
Presentation Results are printed in a different ways, using a matrix form
latex export The matrix of coefficients can be exported to latex, with or without standard-values and significance stars

Two estimators are available: the Engle-Granger two-steps approach (2OLS) or the Johansen (ML). For the 2OLS, deterministic regressors (or external variables if LRinclude is of class numeric) can be added for the estimation of the cointegrating value and for the ECT. This is only working when the beta value is not pre-specified.

The argument beta is only for VECM, look at the specific help page for more details.

Value

Fitted model data

Author(s)

Matthieu Stigler

See Also

VECM which is just a wrapper for lineVar(..., model="VECM"). Methods predict.VAR, VARrep, regime, irf and toLatex.
TVAR and TVECM for the corresponding threshold models. linear for the univariate AR model.
**Examples**

```r
data(zeroyl)

# Fit a VAR
VAR <- lineVar(zeroyl, lag=1)
VAR
summary(VAR)

# Compare results with package vars:
if(require(vars)) {
  a <- VAR(zeroyl, p=1)
  coef_vars <- t(sapply(coef(a), function(x) x[,c(3,1,2),1]))
  all.equal(coef(VAR), coef_vars, check.attributes=FALSE)
}

### VECM
VECM.EG <- lineVar(zeroyl, lag=2, model="VECM")
VECM.EG
summary(VECM.EG)

VECM.ML <- lineVar(zeroyl, lag=2, model="VECM", estim="ML")
VECM.ML
summary(VECM.ML)

### Check Johansen MLE
myVECM <- lineVar(zeroyl, lag=1, include="const", model="VECM", estim="ML")
summary(myVECM, digits=7)
# comparing with vars package
if(require(vars)){
a <- ca.jo(zeroyl, spec="trans")
summary(a)
# same answer also!
}

### Export to Latex
toLatex(VECM.EG)
toLatex(summary(VECM.EG))
options("show.signif.stars"=FALSE)
toLatex(summary(VECM.EG), parenthese="Pvalue")
options("show.signif.stars"=TRUE)
```

---

**llar**

*Locally linear model*
Description

Casdagli test of nonlinearity via locally linear forecasts

Usage

llar(x, m, d=1, steps=d, series, eps.min = sd(x)/2, eps.max = diff(range(x)), neps = 30, trace = 0)

llar.predict(x, m, d=1, steps=d, series, n.ahead=1, eps=stop("you must specify a window value"), onvoid=c("fail","enlarge"), r = 20, trace=1)

llar.fitted(x, m, d=1, steps=d, series, eps, trace=0)

Arguments

x time series
m, d, steps embedding dimension, time delay, forecasting steps
series time series name (optional)
n.ahead n. of steps ahead to forecast
eps.min, eps.max min and max neighbourhood size
neps number of neighbourhood levels along which iterate
eps neighbourhood size
onvoid what to do in case of an isolated point: stop or enlarge neighbourhood size by an r%
r if an isolated point is found, enlarge neighbourhood window by r%
trace tracing level: 0, 1 or more than 1 for llar, 0 or 1 for llar.forecast

Details

llar does the Casdagli test of non-linearity. Given the embedding state-space (of dimension m and time delay d) obtained from time series series, for a sequence of distance values eps, the relative error made by forecasting time series values with a linear autoregressive model estimated on points closer than eps is computed. If minimum error is reached at relatively small length scales, a global linear model may be inappropriate (using current embedding parameters). This was suggested by Casdagli(1991) as a test for non-linearity.

llar.predict tries to extend the given time series by n.ahead points by iteratively fitting locally (in the embedding space of dimension m and time delay d) a linear model. If the spatial neighbourhood window is too small, your time series last point would be probably isolated. You can ask to automatically enlarge the window eps by a factor of r% sequentially, until enough neighbours are found for fitting the linear model.

llar.fitted gives out-of-sample fitted values from locally linear models.
Value

`llar` gives an object of class `llar`. I.e., a list of components:

- **RMSE**: vector of relative errors
- **eps**: vector of neighbourhood sizes (in the same order of RMSE)
- **frac**: vector of fractions of the time series used for RMSE computation
- **avfound**: vector of average number of neighbours for each point in the time series which can be plotted using the `plot` method, and transformed to a regular `data.frame` with the `as.data.frame` function.

Function `llar.forecast` gives the vector of n steps ahead locally linear iterated forecasts.
Function `llar.fitted` gives out-of-sample fitted values from locally linear models.

Warning

For long time series, this can be slow, especially for relatively big neighbourhood sizes.

Note

The C implementation was re-adapted from that in the TISEAN package ("ll-ar" routine, see references). However, here the euclidean norm is used, in place of the max-norm.

Author(s)

Antonio, Fabio Di Narzo

References


Hegger, R., Kantz, H., Schreiber, T., Practical implementation of nonlinear time series methods: The TISEAN package; CHAOS 9, 413-435 (1999)

Examples

```r
res <- llar(log(lynx), m=3, neps=7)
plot(res)

x.new <- llar.predict(log(lynx), n.ahead=20, m=3, eps=1, onvoid="enlarge", r=5)
lag.plot(x.new, labels=FALSE)

x.fitted <- llar.fitted(log(lynx), m=3, eps=1)
lag.plot(x.fitted, labels=FALSE)
```
logLik.nlVar

Extract Log-Likelihood

Description

Log-Likelihood method for VAR models.

Usage

```r
## S3 method for class 'nlVar'
logLik(object, ...)
```

Arguments

- `object`: object of class VAR computed by `lineVar`.
- `...`: additional arguments to `logLik`.

Details

The Log-Likelihood is computed as in Luetkepohl (2006) equ. 3.4.5 (p. 89) and Juselius (2006) p. 56:

\[
LL = -(TK/2) \log(2\pi) - (T/2) \log |\Sigma| - (1/2) \sum_{t=1}^{T} (y_t - A' x_t)' \Sigma^{-1} (y_t - A' x_t)
\]

Where \( \Sigma \) is the Variance matrix of residuals, and \( x_t \) is the matrix stacking the regressors (lags and deterministic).

However, we use a computationally simpler version:

\[
LL = -(TK/2) \log(2\pi) - (T/2) \log |\Sigma| - (TK/2)
\]


(See Hamilton (1994) 11.1.10, p. 293 gives \(+ (T/2) \log |\Sigma^{-1}|, \) which is the same as \(-(T/2) \log |\Sigma|\)).

Value

Log-Likelihood value.

Author(s)

Matthieu Stigler

References

Examples

```r
data(zeroylld)
data<-zeroylld

#Fit a VAR
VAR<-lineVar(data, lag=1)
logLik(VAR)
```

---

**Description**

Log-Likelihood method for VECM models.

**Usage**

```r
## S3 method for class 'VECM'
logLik(object, r, ...)
```

**Arguments**

- `object` : object of class VECM computed by `VECM`.
- `r` : The cointegrating rank. By default the rank specified in the call to `VECM`, but can be set differently by user.
- `...` : additional arguments to `logLik`.

**Details**

The Log-Likelihood is computed in two different ways, depending on whether the VECM was estimated with ML (Johansen) or 2OLS (Engle and Granger).

When the model is estimated with ML, the LL is computed as in Hamilton (1994) 20.2.10 (p. 637):

\[
LL = -(TK/2) \log(2\pi) - (TK/2) - (T/2) \log |\hat{\Sigma}_{UU}| - (T/2) \sum_{i=1}^{r} \log(1 - \hat{\lambda}_i)
\]

Where \(\Sigma_{UU}\) is the variance matrix of residuals from the first auxiliary regression, i.e. regrssing \(\Delta y_t\) on a constant and lags, \(\Delta y_{t-1}, \ldots, \Delta y_{t-p}\). \(\lambda_i\) are the eigenvalues from the \(\hat{\Sigma}_{V\hat{V}^{-1}}, \hat{\Sigma}_{UU}^{-1} \hat{\Sigma}_{UV}\), see 20.2.9 in Hamilton (1994).

When the model is estimated with 2OLS, the LL is computed as:

\[
LL = \log |\Sigma|
\]

Where \(\Sigma\) is the variance matrix of residuals from the VECM model. There is hence no correspondence between the LL from the VECM computed with 2OLS or ML.
Value

Log-Likelihood value.

Author(s)

Matthieu Stigler

References


Examples

```r
data(zeroyld)
data<-zeroyld

#Fit a VAR
vecm<-VECM(data, lag=1, r=1, estim="ML")
loglik(vecm)
```

---

**LSTAR**  
*Logistic Smooth Transition AutoRegressive model*

Description

Logistic Smooth Transition AutoRegressive model.

Usage

```r
lstar(x, m, d=1, steps=d, series, mL, mH, mTh, thDelay, thVar, th, gamma, trace=TRUE, include = c("const", "trend", "none", "both"), control=list(), starting.control=list())
```

Arguments

- `x`  
  time series
- `m, d, steps`  
  embedding dimension, time delay, forecasting steps
- `series`  
  time series name (optional)
- `mL`  
  autoregressive order for 'low' regime (default: `m`). Must be \( \leq m \)
- `mH`  
  autoregressive order for 'high' regime (default: `m`). Must be \( \leq m \)
- `thDelay`  
  'time delay' for the threshold variable (as multiple of embedding time delay `d`)
- `mTh`  
  coefficients for the lagged time series, to obtain the threshold variable
- `thVar`  
  external threshold variable
th, gamma  starting values for coefficients in the LSTAR model. If missing, a grid search is performed.

trace  should additional infos be printed? (logical)

include  Type of deterministic regressors to include

control  further arguments to be passed as control list to optim

starting.control  further arguments for the grid search (dimension, bounds). See details below.

Details

\[ x_{t+s} = (\phi_{1,0} + \phi_{1,1}x_t + \phi_{1,2}x_{t-d} + \ldots + \phi_{1,mL}x_{t-(mL-1)d})G(z_t, th, \gamma) + (\phi_{2,0} + \phi_{2,1}x_t + \phi_{2,2}x_{t-d} + \ldots + \phi_{2,mH}x_{t-(mH-1)d})(1 - G(z_t, th, \gamma)) + \epsilon_t + \text{steps} \]

with z the threshold variable, and G the logistic function, computed as \( plogis(q, \text{location} = \text{th}, \text{scale} = 1/\text{gamma}) \), so see \texttt{plogis} documentation for details on the logistic function formulation and parameters meanings. The threshold variable can alternatively be specified by:

\[
\text{mTh} \quad z[t] = x[t]mTh[1] + x[t-d]mTh[2] + \ldots + x[t-(m-1)d]mTh[m] \\
\text{thDelay} \quad z[t] = x[t - \text{thDelay} \ast d] \\
\text{thVar} \quad z[t] = \text{thVar}[t]
\]

Note that if starting values for phi1 and phi2 are provided, isn’t necessary to specify mL and mH. Further, the user has to specify only one parameter between mTh, thDelay and thVar for indicating the threshold variable.

Estimation of the transition parameters th and gamma, as well as the regression parameters phi1 and phi2, is done using concentrated least squares, as suggested in Leybourne et al. (1996).

Given th and gamma, the model is linear, so regression coefficients can be obtained as usual by OLS. So the nonlinear numerical search needs only to be done for th and gamma; the regression parameters are then recovered by OLS again from the optimal th and gamma.

For the nonlinear estimation of the parameters th and gamma, the program uses the \texttt{optim} function, with optimization method BFGS using the analytical gradient. For the estimation of standard values, \texttt{optim} is re-run using the complete Least Squares objective function, and the standard errors are obtained by inverting the hessian. You can pass further arguments to \texttt{optim} directly with the control list argument. For instance, the option \texttt{maxit} maybe useful when there are convergence issues (see examples).

Starting parameters are obtained doing a simple two-dimensional grid-search over th and gamma. Parameters of the grid (interval for the values, dimension of the grid) can be passed to starting.control.

nTh  The number of threshold values (th) in the grid. Defaults to 200

nGamma  The number of smoothing values (gamma) in the grid. Defaults to 40

trim  The minimal percentage of observations in each regime. Defaults to 10% (possible threshold values are between the 0.1 and 0.9 quantile)

gammaInt  The lower and higher smoothing values of the grid. Defaults to c(1,40)

thInt  The lower and higher threshold values of the grid. When not specified (default, i.e NA), the interval are the trim quantiles above.
Value

An object of class `nlar`, subclass `lstar`, i.e. a list with fitted model informations.

Author(s)

Antonio, Fabio Di Narzo

References


See Also

`plot.lstar` for details on plots produced for this model from the `plot` generic.

Examples

```r
# fit a LSTAR model. Note 'maxit': slow convergence
mod.lstar <- lstar(log10(lynx), m=2, mTh=c(0,1), control=list(maxit=3000))
mod.lstar

# fit a LSTAR model without a constant in both regimes.
mod.lstar2 <- lstar(log10(lynx), m=1, include="none")
mod.lstar2

# Note in example below that the initial grid search seems to be too narrow.
# Extend it, and evaluate more values (slow!):
controls <- list(gammaInt=c(1,2000), nGamma=50)
mod.lstar3 <- lstar(log10(lynx), m=1, include="none", starting.control=controls)
mod.lstar3

# a few methods for lstar:
summary(mod.lstar)
residuals(mod.lstar)
AIC(mod.lstar)
BIC(mod.lstar)
plot(mod.lstar)
predict(mod.lstar, n.ahead=5)
```
m.unrate  

*Monthly US unemployment*

**Description**


**Usage**

data(m.unrate)

**Format**

zoo object

**Source**

http://faculty.chicagobooth.edu/ruey.tsay/teaching/fts2

**References**


---

makethspec  

*Specification of the threshold search*

**Description**

This optional function allows the user to set different restrictions for the threshold grid search in function `selectSETAR`.

**Usage**

`makethspec(ngrid = c("All", "Half", "Third", "Quarter"), exact = NULL, int = c("from", "to"), around = "val", ...)`

**Arguments**

- `ngrid`: The number of values to search for
- `exact`: The user give an exact threshold value
- `int`: The user gives an interval to search inside
- `around`: The user gives an point to search around
- `...`: currently unused
Details

This function is just to check the inputs for the specification of the grid search. If not provided, the search will be in the biggest interval (ngrid = "All") between the minimum and maximum values. The user can reduce it by giving setting "Half" (only every two points is taken) and so on, or setting a number.

The search can also be made around a point, or between two points. When between a point, the argument ngrid is still used, whereas for around, a value of 30 is taken as default value if ngrid is not specified by user.

Value

The input values are given as output after checking for consistency (only one of exact/int/around should be given).

Author(s)

Matthieu Stigler

See Also

selectSETAR

Examples

```r
sun <- (sqrt(sunspot.year+1)-1)*2
selectSETAR(sun, m=3, th=MakeThSpec(exact=10.40967), criterion="SSR", d=1, thDelay=0:2, plot=FALSE, nthresh=1)
# when pre-specified value does not correspond, function will search nearest value
selectSETAR(sun, m=3, th=MakeThSpec(exact=10.4), criterion="SSR", d=1, thDelay=0:2, plot=FALSE, nthresh=1)
# search around:
selectSETAR(sun, m=3, th=MakeThSpec(around=10.40967, ngrid=20), criterion="SSR", d=1, thDelay=0:2, plot=FALSE, nthresh=1)
# search in an interval
selectSETAR(sun, m=3, th=MakeThSpec(int=c(10, 11), ngrid=20), criterion="SSR", d=1, thDelay=0:2, plot=FALSE, nthresh=1)
# reduce size of the grid:
selectSETAR(sun, m=3, th=MakeThSpec(ngrid="Half"), criterion="SSR", d=1, thDelay=0:2, plot=FALSE, nthresh=1)

# 2 thresholds:
selectSETAR(sun, m=3, th=MakeThSpec(ngrid="Half"), criterion="SSR", d=1, thDelay=0:2, plot=FALSE, nthresh=2)
```
MAPE

Mean Absolute Percent Error

Description

Generic function to compute the Mean Absolute Percent Error of a fitted model.

Usage

MAPE(object, ...)

## Default S3 method:
MAPE(object, ...)

Arguments

- object: object of class `nlar.fit`
- ...: additional arguments to `MAPE`

Value

Computed Mean Absolute Percent Error for the fitted model.

Author(s)

Antonio, Fabio Di Narzo

mse

Mean Square Error

Description

Generic function to compute the Mean Squared Error of a fitted model.

Usage

mse(object, ...)

## Default S3 method:
mse(object, ...)

Arguments

- object: object of class `nlar.fit`
- ...: additional arguments to `mse`
**Description**

Generic ‘nlar’ methods. Method ‘nlar’ is described in a separate page: `predict.nlar`

**Usage**

```r
## S3 method for class 'nlar'
AIC(object, k=2, ...)
## S3 method for class 'nlar'
coef(object, ...)
## S3 method for class 'nlar'
fitted(object, ...)
## S3 method for class 'nlar'
MAPE(object, ...)
## S3 method for class 'nlar'
mse(object, ...)
## S3 method for class 'nlar'
print(x, digits = max(3, getOption("digits") - 3), ...)
## S3 method for class 'nlar'
residuals(object, ...)
## S3 method for class 'nlar'
summary(object, ...)
## S3 method for class 'nlar'
plot(x, ask=interactive(), ...)
## S3 method for class 'nlar'
toLatex(object, digits, label, ...)
```

**Arguments**

- `x, object` fitted ‘nlar’ object
- `ask` graphical option. See `par`
- `digits` For print method, see `printCoefmat`
- `k` numeric, the penalty per parameter to be used; the default `k = 2` is the classical AIC
- `label` LaTeX label passed to the equation
- `...` further arguments to be passed to and from other methods
Details

MAPE  Mean Absolute Percent Error
mse  Mean Square Error
plot  Diagnostic plots

Author(s)

Antonio, Fabio Di Narzo

See Also

availableModels for listing all currently available models.

Examples

```r
x <- log10(lynx)
mod.setar <- setar(x, m=2, thDelay=1, th=3.25)
mod.setar
AIC(mod.setar)
mse(mod.setar)
MAPE(mod.setar)
coef(mod.setar)
summary(mod.setar)

e <- residuals(mod.setar)
e <- e[!is.na(e)]
plot(e)
acf(e)

plot(x)
lines(fitted(mod.setar), lty=2)
legend(x=1910, y=3.9, lty=c(1,2), legend=c("observed","fitted"))

plot(mod.setar)
```

Description

Neural Network nonlinear autoregressive model.

Usage

```r
nnetTs(x, m, d = 1, steps = d, series, size, control = list(trace = FALSE))
```
Arguments

x          time series  
m, d, steps embedding dimension, time delay, forecasting steps  
series     time series name (optional)  
size       number of hidden units in the neural network  
control    control list to be passed to nnet::nnet optimizer  

Details

Neural network model with 1 hidden layer and linear output:

\[ x_{t+s} = \beta_0 + \sum_{j=1}^{D} \beta_j g(\gamma_{0j} + \sum_{i=1}^{m} \gamma_{ij} x_{t-(i-1)d}) \]

Model is estimated using the nnet function in nnet package. Optimization is done via the BFGS method of optim. Note that for this model, no additional model-specific summary and plot methods are made available from this package.

Value

An object of class nlar, subclass nnetTs, i.e. a list with mostly nnet::nnet internal structures.

Author(s)

Antonio, Fabio Di Narzo  

References


Examples

# fit a Neural Network model  
mod.nnet <- nnetTs(log(lynx), m=2, size=3)  
mod.nnet
plot methods

Plotting methods for SETAR and LSTAR subclasses

Description

Plotting methods ‘setar’ and ‘lstar’ subclasses

Usage

```r
## S3 method for class 'setar'
plot(x, ask=interactive(), legend=FALSE, regSwStart, regSwStop, ...)
## S3 method for class 'lstar'
plot(x, ask=interactive(), legend=FALSE, regSwStart, regSwStop, ...)
```

Arguments

- `x` : fitted ‘setar’ or ‘lstar’ object
- `ask` : graphical option. See `par`
- `legend` : Should a legend be plotted? (logical)
- `regSwStart, regSwStop` : optional starting and stopping time indices for regime switching plot
- `...` : further arguments to be passed to and from other methods

Details

These plot methods produce a plot which gives to you an idea of the behaviour of the fitted model. Firstly, if embedding dimension is, say, $m$, $m$ scatterplots are produced. On the x axis you have the lagged time series values. On the y axis the ‘response’ time series values. Observed points are represented with different colors/symbols depending on the level of the threshold variable. Specifically, for the setar model, black means ‘low regime’, red means ‘high regime’. For the lstar model, where the self-threshold variable is continuous, threshold values are grouped in 5 different zones with the same number of points in each. Note that if more than 300 points are to be plotted, they all share the same symbol, and regimes can be distinguished only by color. If you want, by specifying `legend=TRUE` a legend is added at the upper-left corner of each scatterplot. To each scatterplot, a dashed line is superposed, which links subsequent fitted values.

Finally, a new time series plot is produced, with lines segments coloured depending on the regime (colors meanings are the same of those in the preceding scatterplots). Optionally, you can specify a starting and ending time indices, for zooming on a particular segment of the time series.

Author(s)

Antonio, Fabio Di Narzo
predict.nlar

See Also

`setar`, `lstar`

`nlar-methods` for other generic available methods for this kind of objects.

Examples

```r
##
##See 'setar' examples
##
```

predict.nlar  

*Predict method for objects of class* `nlar`.*

**Description**

Forecasting a non-linear model object of general class `nlar`, including `setar` and `star`.

**Usage**

```r
## S3 method for class 'nlar'
predict(object, newdata, n.ahead = 1, type = c("naive", "MC", "bootstrap", "block-bootstrap"), nboot = 100, ci = 0.95, block.size = 3, boot1Zero = TRUE, ...)
```

**Arguments**

- `object`  
  An object of class `nlar`; generated by `setar()` or `lstar()`.

- `newdata`  
  Optional. A new data frame to predict from.

- `n.ahead`  
  An integer specifying the number of forecast steps.

- `type`  
  Type of forecasting method used. See details.

- `nboot`  
  The number of replications for type MC or bootstrap.

- `ci`  
  The forecast confidence interval (available only with types MC and bootstrap).

- `block.size`  
  The block size when the block-bootstrap is used.

- `boot1Zero`  
  Whether the first innovation for MC/bootstrap should be set to zero.

- `...`  
  Further arguments passed to the internal `oneStep` function. Mainly argument `thVar` if an external threshold variable was provided.

**Details**

The forecasts are obtained recursively from the estimated model. Given that the models are non-linear, ignoring the residuals in the 2- and more steps ahead forecasts leads to biased forecasts (so-called naive). Different resampling methods, averaging `n.boot` times over future residuals, are available:

- **naive**  
  No residuals
**predict.nl**

MC Monte-Carlo method, where residuals are taken from a normal distribution, with sd. equal to the residuals sd.

**bootstrap** Residuals are resampled from the empirical residuals from the model.

**block-bootstrap** Same as bootstrap, but residuals are resampled in block, with size `block.size`

The MC and bootstrap methods correspond to equations 3.90 and 3.91 of Franses and van Dijk (2000, p. 121). The bootstrap/MC is initiated either from the first forecast, `n.ahead=1` (set with `boot1zero` to TRUE), or from the second only.

When the forecast method is based on resampling, forecast intervals are available. These are obtained simply as empirical ci quantiles of the resampled forecasts (cf Method 2 in Franses and van Dijk, 2000, p. 122).

**Value**

A ‘ts’ object, or, in the case of MC/bootstrap, a list containing the prediction (pred) and the forecast standard errors (se).

**Author(s)**

Matthieu Stigler

**References**


**See Also**

The model fitting functions `setar`, `lstar`.

A more sophisticated predict function, allowing to do sub-sample rolling predictions: `predict_rolling`.

**Examples**

```r
x.train <- window(log10(lynx), end = 1924)
x.test <- window(log10(lynx), start = 1925)

### Use different forecasting methods:
mod.set <- setar(x.train, m=2, thDelay=0)
pred_setar_naive <- predict(mod.set, n.ahead=10)
pred_setar_boot <- predict(mod.set, n.ahead=10, type="bootstrap", n.boot=200)
pred_setar_Bboot <- predict(mod.set, n.ahead=10, type="block-bootstrap", n.boot=200)
pred_setar_MC <- predict(mod.set, n.ahead=10, type="bootstrap", n.boot=200)

### Plot to compare results:
pred_range <- range(pred_setar_naive, pred_setar_boot$pred, pred_setar_MC$pred, na.rm=TRUE)
plot(x.test, ylim=pred_range, main="Comparison of forecasts methods from same SETAR")
lines(pred_setar_naive, lty=2, col=2)
```
predict.TVAR

Predict method for objects of class ‘VAR’, ‘VECM’ or ‘TVAR’

Description

Forecasting the level of a series estimated by ‘VAR’ / ‘VECM’ or ‘TVAR’

Usage

```r
## S3 method for class 'TVAR'
predict(object, newdata, n.ahead = 5, newdataTrendStart, ...)

## S3 method for class 'VAR'
predict(object, newdata, n.ahead = 5, newdataTrendStart,
    exoPred = NULL, ...)
```

Arguments

- `object`: An object of class ‘VAR’, ‘VECM’ or ‘TVAR’
- `newdata`: Optional. A new data frame to predict from. This should contain lags of the level of the original series. See Details.
- `n.ahead`: An integer specifying the number of forecast steps.
- `newdataTrendStart`: If ‘newdata’ is provided by the user, and the estimated model includes a trend, this argument specifies where the trend should start
- `exoPred`: vector/matrix of predictions for the exogeneous variable(s) (with ‘n. ahead’ rows). Only for ‘VAR’/‘VECM’, not for ‘TVAR’.

Details

The forecasts are obtained recursively, and are for the levels of the series.

When providing newdata, newdata has to be ordered chronologically, so that the first row/element is the earliest value.

For VECM, the forecasts are obtained by transforming the VECM to a VAR (using function `VARrep`). Note that a VECM(lag=p) corresponds to a VAR(lag=p+1), so that if the user provides newdata for a VECM(lag=p), newdata should actually contain p+1 rows.
**predict_rolling**

Value

A matrix of predicted values.

Author(s)

Matthieu Stigler

See Also

- `lineVar` and `VECM.VARrep`
- `varrep`

A more sophisticated predict function, allowing to do sub-sample rolling predictions: `predict_rolling`.

Examples

```r
data(barry)
barry_in <- head(barry, -5)
barry_out <- tail(barry, 5)

mod_vecm <- VECM(barry_in, lag=2)
mod_var <- lineVar(barry_in, lag=3)
mod_tvar <- TVAR(barry_in, lag=3, nthresh=1, thDelay=1)

pred_vecm <- predict(mod_vecm)
pred_var <- predict(mod_var)
pred_tvar <- predict(mod_tvar)

## compare forecasts on a plot
n <- 30
plot(1:n, tail(barry[,1], n), type="l", xlab="n", ylim=c(0,n))
lines((n-5+1):n, pred_var[,1], lty=2, col=2)
lines((n-5+1):n, pred_vecm[,1], lty=2, col=3)
lines((n-5+1):n, pred_tvar[,1], lty=2, col=4)
legend("bottomright", lty=c(1,2,2,2), col=1:4, legend=c("true", "var", "vecm", "tvar"))

## example for newdata:
all.equal(predict(mod_vecm), predict(mod_vecm, newdata=barry[c(317, 318, 319),]))
```

---

**Description**

Forecasts a VAR or VECM by discarding a part of the sample, and generating a series of updated forecasts.
predict_rolling

Usage

predict_rolling(object, ...)

## S3 method for class 'nlVar'
predict_rolling(object, nroll = 10, n.ahead = 1, refit.every, newdata, ...)

Arguments

- **object**: A linear object of class 'nlVar'; generated by `lineVar` or `VECM`.
- **...**: Currently not used.
- **nroll**: The number of rolling forecasts.
- **n.ahead**: An integer specifying the number of forecast steps.
- **refit.every**: Determines every how many periods the model is re-estimated.
- **newdata**: In case the model given is already estimated on the sub-sample, the out of sample data can be provided. Note it should contain observations to predict the first values, that are also contained in the in-sample.

Details

This function allows to check the out-of sample forecasting accuracy by estimating the model on a sub-sample of the original, then making `nroll` forecasts of horizon `n.ahead`, each time by updating the sample. In other words, with a given model estimated on 100 observations, the function will estimate it on say 90 first obs (`nroll=10`), generate a say 1 step-ahead `n.ahead=1` from obs 90, then using true value 91, 92,... till full sample.

Unlike usual `predict()` methods, specifying `n.ahead=2` will not generate a 1 step-ahead and a 2 step-ahead forecasts, but only `nroll` 2 step-ahead forecasts.

Note that while the forecasts are updated with new values, the model estimation is (by default) not updated. This can however be done with the argument `fit.every`, specifying at which frequency the model should be re-estimated. By setting it to 1 for example, each time a new observation is taken, the model is reestimated. This is similar to the `ugarchroll` in package `rugarch`.

Value

A matrix containing the forecasts.

Author(s)

Matthieu Stigler

See Also

- `predict.nlar` for the standard predict function.
Examples

data(barry)
  ## model estimated on full sample:
  mod_vec <- VECM(barry, lag=2)

  ## generate 10 1-step-ahead forecasts:
  preds_roll <- predict_rolling(mod_vec, nroll=10)

  ## plot the results:
  plot(window(barry[,”dolcan”], start=1998), type=“l”, ylab=“barry: dolcan”)
  preds_roll_ts <- ts(preds_roll$pred, start=time(barry)[nrow(barry)-10], freq=12)
  lines(preds_roll_ts[,”dolcan”], col=2, lty=2)
  legend(“bottomright”, text=c(1,2), col=1:2, legend=c(“True”, “Fitted”))
  title(“Comparison of true and rolling 1-ahead forecasts

rank.select  Selection of the cointegrating rank with Information criterion.

Description

Selection of the cointegrating rank and the lags with Information criterion (AIC, BIC).

Usage

rank.select(data, lag.max = 10, r.max = ncol(data) - 1,
             include = c(“const”, “trend”, “none”, “both”),
             fitMeasure = c(“SSR”, “LL”),
             sameSample = TRUE, returnModels = FALSE)

## S3 method for class ’rank.select’
print(x, …)

## S3 method for class ’rank.select’
summary(object, …)

Arguments

data multivariate time series.

lag.max Maximum number of lags to investigate.

r.max Maximum rank to investigate.

include Type of deterministic regressors to include. See VECM or lineVar.

fitMeasure Whether the AIC/BIC should be based on the full likelihood, or just the SSR. See explanations in logLik.VECM.
sameSample Logical. Whether the data should be shortened so that the AIC/BIC are estimated on the same sample. Default to TRUE.

returnModels Logical, default to FALSE. Whether the output should also contain the list of each model computed.

x The output from rank.select for the print method.

... Unused.

object The output from rank.select for the summary method.

Details

This function estimates the AIC, BIC and Hannan-Quinn for each rank (up to lags.max) and lags (up to lags.max). This method has been shown to be useful to select simultaneously the rank and the lags, see references.

Value

An object of class ‘rank.select’, with ‘print’ and ‘summary methods’, containing among other the matrices of AIC/BIC/HQ, the Likelihood, and best ranks according to each criterion.

Author(s)

Matthieu Stigler

References


See Also

VECM for estimating a VECM. rank.test (or ca.io in package urca) for the classical Johansen cointegration test.
**Examples**

```r
data(barry)

#
rk_sel <- rank.select(barry)
rk_sel
summary(rk_sel)
```

**Description**

Maximum-likelihood test of the cointegrating rank.

**Usage**

```r
rank.test(vecm, type = c("eigen", "trace"), r_null, cval = 0.05)
```

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

```r
## S3 method for class 'rank.test'
summary(object, digits = max(1,getOption("digits") - 3),
          ...)
```

**Arguments**

- `vecm` ‘VECM’ object computed with the function VECM.
- `type` Type of test, either 'trace' or 'eigenvalue'. See details below.
- `r_null` Rank to test specifically.
- `cval` Critical value level for the automatic test.
- `x` The output from rank.test for the print method.
- `...` Unused.
- `object` The output from rank.test for the summary method.
- `digits` The number of digits to use in format.pval
Details

This function computes the two maximum-likelihood tests for the cointegration rank from Johansen (1996). Tests are:

**trace** Test the hypothesis of rank ‘h’ against rank K, i.e. against the alternative that the system is stationary.

**eigenvalue** Test the hypothesis of rank ‘h’ against rank ‘h+1’.

The test works for five specifications of the deterministic terms as in Doornik et al (1998), to be specified in the previous call to `VECM`:

- **H ql** Unrestricted constant and trend: use `include="both"`
- **H l** Unrestricted constant and restricted trend: use `include="const" and Lrinclude="trend"`
- **H lc** Unrestricted constant and no trend: use `include="const"`
- **H c** Restricted constant and no trend: use `Lrinclude="const"`
- **H z** No constant nor trend: use `include="none"

Two testing procedures can be used:

**Specific test** By specifying a value for ‘r_null’. The ‘pval’ value returned gives the specific p-value.

**Automatic test** If not value is specified for ‘r_null’, the function makes a simple automatic test: returns the rank (slot ‘r’) of the first test not rejected (level specified by arg ‘cval’) as recommend i.a. in Doornik et al (1998, p. 544).

A full table with both test statistics ad their respective p-values is given in the summary method. P-values are obtained from the gamma approximation from Doornik (1998, 1999). Small sample values adjusted for the sample size for the these values is different from output in gretl for example.

Value

An object of class ‘rank.test’, with ‘print’ and ‘summary methods’.

Comparison with urca

While `ca.jo` in package `urca` and `rank.test` both implement Johansen tests, there are a few differences:

- `rank.test` gives p-values, while `ca.jo` gives only critical values.
- `rank.test` allows for five different specifications of deterministic terms (see above), `ca.jo` for only three.
- `ca.jo` allows for seasonal and exogenous regressors, which is not available in `rank.test`.
- The lag is specified differently: K from `ca.jo` corresponds to lag+1 in `rank.test`.

Author(s)

Matthieu Stigler
References


See Also

VECM for estimating a VECM. rank.select to estimate the rank based on information criteria.
caJo in package urca for another implementation of Johansen cointegration test (see section ‘Comparison with urca’ for more info).

Examples

data(barry)

## estimate the VEC with Johansen!
ve <- VECM(barry, lag=1, estim="ML")

## specific test:
ve_test_spec <- rank.test(ve, r_null=1)
ve_test_spec_tr <- rank.test(ve, r_null=1, type="trace")

ve_test_spec
ve_test_spec_tr

## No specific test: automatic method
ve_test_unspec <- rank.test(ve)
ve_test_unspec_tr <- rank.test(ve, type="trace")

ve_test_unspec
ve_test_unspec_tr

## summary method: output will be same for all types/test procedure:
summary(ve_test_unspec_tr)

## The function works for many specification of the VECM(), try:
rack.test(VECM(barry, lag=3, estim="ML"))
rack.test(VECM(barry, lag=3, include="both", estim="ML"))
rack.test(VECM(barry, lag=3, LRinclude="const", estim="ML"))

## Note that the tests are simple likelihood ratio, and hence can be obtained also manually:
-2*(logLik(ve, r=1)-logLik(ve, r=2)) # eigen test, 1 against 2
-2*(logLik(ve, r=1)-logLik(ve, r=3)) # eigen test, 1 against 3
regime

Extract variable showing regime

Description

This function allows to extract the indicator variable specifying the regime in which the process is at time t.

Usage

regime(object, initVal = TRUE, timeAttr = TRUE, ...)

Arguments

object object of class setar or nlVar
initVal Logical. Whether the NA initial values should be returned. Default to TRUE.
timeAttr Logical. Whether the time attributes should be returned. Default to TRUE.
... additional arguments to regime

Value

Time series of same attributes as input to setar.

Author(s)

Matthieu Stigler

Examples

set <- setar(lynx, m=3)
regime(set)
regime(set, time=FALSE, initVal=FALSE)

plot(regime(set))
Description
Extracts the global and regime-dependant variance of the residuals

Usage
```r
resVar(x, adj=c("OLS", "ML"))
```

Arguments
- `x`: setar object
- `adj`: Degrees of freedom adjustment for the variance

Details
The degree of freedom adjustment in the formula for the variance is the number of parameters when `adj="OLS"` or zero when `adj="ML"`.

Value
A vector containing:
- **Total**: The residual variance of the full sample
- **L, M, H**: The residual variance of the lower (L), middle (if two thresholds) (M) and higher (H) regimes

Author(s)
Matthieu Stigler

References

Examples
```r
#Lynx model as in Tong (1980, p. 387)
mod.setar <- setar(log10(lynx), mL=7, mH=2, thDelay=1, th=3.116)
summary(mod.setar)
#coefficients are same for lower regime but differ for higher
resVar(mod.setar, adj="ML")
#variance or the residuals is same for lower regime but differ for higher regime and hence for total
#Lynx model as in Tong (1980, p. 405)
```
selectHyperParms <- setar(log10(lynx), mL=1, mM=7, mH=2, thDelay=1, nthresh=2, th=c(2.373, 3.154))
round(coefficients(mod.setar2), 3)
resVar(mod.setar2, adj="ML")

selectHyperParms  Automatic selection of model hyper-parameters

Description

Automatic selection of model hyper-parameters

Usage

selectLSTAR(x, m, d=1, steps=d, mL = 1:m, mH = 1:m, thDelay=0:(m-1),
fast=TRUE, trace=FALSE)
selectNNET(x, m, d=1, steps=d, size=1:(m+1), maxit=1e3, trace=FALSE)

Arguments

x  time series
m, d, steps  embedding parameters. For their meanings, see help about nlar
mL, mH  Vector of 'low' and 'high' regimes autoregressive orders
thDelay  Vector of 'threshold delay' values
size  Vector of numbers of hidden units in the nnet model
maxit  Max. number of iterations for each model estimation
fast  For LSTAR selection, whether a fast algorithm using starting values from previous models should be used
trace  Logical. Whether informations from each model should be returned.

Details

Functions for automatic selection of LSTAR and NNET models hyper parameters. An exhaustive search over all possible combinations of values of specified hyper-parameters is performed. Embedding parameters m, d, steps are kept fixed.
Selection criterion is the usual AIC.
For the LSTAR model, two methods are offered:

fast=FALSE  Each model is run separately, each time using the full grid search for starting values.
fast=TRUE  Only the first model is run with a full grid search, while the subsequent use the first model results for their starting values.
Value

A data-frame, with columns giving hyper-parameter values and the computed AIC for each row (only the best 10s are returned)

Author(s)

Antonio, Fabio Di Narzo

Examples

```r
lynx <- log10(lynx)
selctLSTAR(lynx, m=2)
selctNNET(lynx, m=3, size=1:5)
```

Description

Automatic selection of SETAR hyper-parameters

Usage

```r
selectSETAR(x, m, d=1, steps=d, series, mL, mM, mH, thDelay=0, mTh, thVar,
               th=MakeThSpec(), trace=TRUE, include = c("const", "trend","none", "both"),
               common=c("none", "include","lags", "both"), model=c("TAR", "MTAR"),
               ML=seq_len(mL), MH=seq_len(mH), MM=seq_len(mM), nthresh=1, trim=0.15,
               criterion = c("pooled-AIC", "AIC","BIC", "SSR"), thSteps = 7, plot=TRUE,
               max.iter=2, type=c("level", "diff", "ADF"), same.lags=FALSE,
               restriction=c("none","OuterSymAll","OuterSymTh"), hpc=c("none", "foreach") )
```

Arguments

- `x` : time series
- `m, d, steps` : embedding parameters. For their meanings, see help about `nlar`
- `series` : time series name (optional)
- `mL, mM, mH` : autoregressive order for 'low' (mL) 'middle' (mM, only useful if nthresh=2) and 'high' (mH) regime (default values: m). Must be <=m. Alternatively, you can specify ML
- `thDelay` : Vector of possible 'threshold delay' values to check for
- `mTh` : coefficients for the lagged time series, to obtain the threshold variable
- `thVar` : external threshold variable
- `th` : Different specifications of the grid search, to pre-specify a value or set the number of points to search. See `MakeThSpec`
- `trace` : should additional infos be printed? (logical)
selectSETAR includes Type of deterministic regressors to include

include

common

Indicates which elements are common to all regimes: no, only the include variables, the lags or both

model

Currently not implemented

ML, MM, MH

vector of lags for order for ‘low’ (ML) ‘middle’ (MM, only useful if nthresh=2) and ‘high’ (MH) regime. Max must be <= m

nthresh

Number of threshold of the model

trim

trimming parameter indicating the minimal percentage of observations in each regime. Default to 0.15

criterion

Model selection criterion

thSteps

Not used

plot

Should a plot showing the criterion values be printed? (logical)

max.iter

Number of iterations for the algorithm

type

Whether the variable is taken is level, difference or a mix (diff y = y-1, diff lags) as in the ADF test

same.lags

Logical. When AIC or pooled-AIC is used and arg m is given, should it search for same number of lags in each regime (TRUE) or allow for different (FALSE) lags in each regime. Different lags involves more computation

restriction

Restriction on the threshold. OuterSymAll will take a symmetric threshold and symmetric coefficients for outer regimes. OuterSymTh currently unavailable

hpc

Possibility to run the bootstrap on parallel core. See details

Details

Routine for automatic selection of SETAR models hyper parameters.

An exhaustive search over all possible combinations of values of specified hyper-parameters is performed. Thus the threshold delay, the number of lags in each regime and the threshold value are computed.

Embedding parameters d, steps are kept fixed.

Possible criteria are the usual SSR, AIC and a pooled AIC formula: \( AIC(lowregimemodel) + AIC(highregimemodel) \). The default criterion is the pooled AIC formula. SSR criterion can’t be used to compare models with different lags.

When two thresholds (nthresh=2) have to be computed, the search for the second is made conditional on results for first threshold as suggested in Gonzalo and Pittaraxis (2002). Refinements can be obtained by using max.iter (first threshold being re-estimated based on the second one). If SSR is used, the number of lags in the inner regime is either the same if only arg m was given, otherwise it has to be pre-specified. Criterion AIC can be used to determine the number of lags in the inner regime, whereas pooled-aic is currently not implemented for nthresh=2.

By default, all threshold values excluding the upper and lower trim of the threshold values are taken as potential threshold. restriction can be made with arg th. See function MakeThSpec.

With the argument hpc, the heavy grid search can be run on parallel cores, thus alleviating the time of computation. Preliminary results indicate however that the length of the series must be very considerable in order that the parallel code becomes advantageous. To use it, the user needs simply to choose a package (among doMC, doMPI, doSNOW or doRedis) and register the backend. See the vignette for more details.
Value

An object of class `selectSETAR` (print and plot methods) with:

- `res`: A data-frame, with columns giving hyper-parameter values and the computed AIC for each row (only the best 10/5s are returned)
- `res2`: Same as `res`, returned if `nthresh=2` otherwise set to `NULL`
- `bests`: estimated hyper-parameters
- `th, firstBests, bests2th, ML, MM, MH`: estimated parameters, from first and conditional search
- `criterion, nthresh, same.lags`: returns args given by user
- `allTh`: all threshold values and corresponding criterion from first search

Author(s)

Antonio, Fabio Di Narzo and Stigler, Matthieu

References


See Also

`selectLSTAR, selectNNET, MakeThSpec`

Examples

```r
lynx <- log10(lynx)
selectSETAR(lynx, m=2)
# Suggested model is the following:
setar(lynx, m=2, thDelay=1, th=3.4)
```

Description

Self Threshold Autoregressive model.

Usage

```r
setar(x, m, d=1, steps=d, series, mL, mM, mH, thDelay=0, mTh, thVar, th, trace=FALSE, nested=FALSE, include = c( "const", "trend","none", "both"), common=c("none", "include","lags", "both"), model=c("TAR", "MTAR"), ML=seq_len(mL), MM=seq_len(mM), MH=seq_len(mH), nthresh=1, trim=0.15, type=c("level", "diff", "ADF"), restriction=c("none","OuterSymAll","OuterSymTh"))
```
Arguments

x  time series
m, d, steps  embedding dimension, time delay, forecasting steps
series  time series name (optional)
ML, mM, mH  autoregressive order for ‘low’ (ML) ‘middle’ (mM, only useful if nthresh=2) and ‘high’ (mH) regime (default values: m). Must be <=m. Alternatively, you can specify ML
thDelay  ‘time delay’ for the threshold variable (as multiple of embedding time delay d)
mTh  coefficients for the lagged time series, to obtain the threshold variable
thVar  external threshold variable
th  threshold value (if missing, a search over a reasonable grid is tried)
trace  should additional infos be printed? (logical)
include  Type of deterministic regressors to include
common  Indicates which elements are common to all regimes: no, only the include variables, the lags or both
ML, mM, mH  vector of lags for order for ‘low’ (ML) ‘middle’ (mM, only useful if nthresh=2) and ‘high’ (mH) regime. Max must be <=m
model  Currently not implemented
nthresh  Number of threshold of the model
trim  trimming parameter indicating the minimal percentage of observations in each regime. Default to 0.15
type  Whether the variable is taken is level, difference or a mix (diff y= y-1, diff lags) as in the ADF test
restriction  Restriction on the threshold. OuterSymAll will take a symmetric threshold and symmetric coefficients for outer regimes. OuterSymTh currently unavailable
nested  Whether is this a nested call? (useful for correcting final model df)
...  further arguments to be passed to nlar

Details

Self Exciting Threshold AutoRegressive model.

\[ X_{t+s} = x_{t+s} = (\phi_{1,0} + \phi_{1,1}x_t + \phi_{1,2}x_{t-d} + \ldots + \phi_{1,mL}x_{t-(mL-1)d})I(z_t \leq th) + (\phi_{2,0} + \phi_{2,1}x_t + \phi_{2,2}x_{t-d} + \ldots + \phi_{2,mH}x_{t-(mH-1)d})I(z_t > th) + \epsilon_t + \text{steps} \]

with \( z \) the threshold variable. The threshold variable can alternatively be specified by (in that order):

thDelay  \( z[t] = x[t - \text{thDelay}*d] \)
mTh  \( z[t] = x[t]\ mTh[1] + x[t-d]\ mTh[2] + \ldots + x[t-(m-1)d]\ mTh[m] \)

thVar  \( z[t] = \text{thVar}[t] \)

For fixed \( th \) and threshold variable, the model is linear, so \( \phi1 \) and \( \phi2 \) estimation can be done directly by CLS (Conditional Least Squares). Standard errors for \( \phi1 \) and \( \phi2 \) coefficients provided by the \texttt{summary} method for this model are taken from the linear regression theory, and are to be considered asymptoticals.
Value

An object of class nlar, subclass setar

Author(s)

Antonio, Fabio Di Narzo

References


See Also

plot.setar for details on plots produced for this model from the plot generic.

Examples

# fit a SETAR model, with threshold as suggested in Tong (1990, p 377)
mod.setar <- setar(log10(lynx), m=2, thDelay=1, th=3.25)
summary(mod.setar)

## example in Tsay (2005)
data(m.unrate)
setar(diff(m.unrate), ML=c(2,3,4,12), MH=c(2,4,12), th=0.1, include="none")

setar.sim

Simulation and bootstrap of Threshold Autoregressive model

Description

Simulate or bootstrap a Threshold VAR

Usage

setar.sim(data, B, setarObject, n = 200, lag = 1, trend = TRUE,
nthresh = 0, thDelay = 0, Thresh, type = c("boot", "simul", "check"),
starting = NULL, rand.gen = rnorm, innov = rand.gen(n, ...), ...)
Arguments

data  
vector of coefficients to simulate

setarObject  
Object of class linear or setar to be bootstrapped

n  
Number of observations to create when type="simul"

lag  
Number of lags to include in each regime

trend  
If a trend should be included in the model

nthresh  
number of threshold (see details)

thDelay  
'time delay' for the threshold variable (as multiple of embedding time delay d).

Thresh  
The threshold value(s). Vector of length nthresh

type  
Whether a bootstrap or simulation is to employ. See details

starting  
Starting values when a simulation with given parameter matrix is made

rand.gen  
optional: a function to generate the innovations.

innov  
an optional times series of innovations. If not provided, rand.gen is used.

...  
additional arguments for rand.gen. Most usefully, the standard deviation of the
innovations generated by rnorm can be specified by sd.

Details

This function offers the possibility to generate series following a TAR from two approaches: bootstrap or simulation. When the data is given, one can use a simple residual bootstrap or simulate a series from the parameter matrix and with normal distributed residuals (with variance pre-specified). The choice "check" is just there to check the function: one should obtain the same values as the given values. Please report if different. When the parameter matrix is given, there is only the possibility to simulate series. The starting values (of length equal to the number of lags) can be given. The user should take care for the choice of the starting values and parameters values, since it is not sure that the simulated values will cross the threshold even once.

Value

a list with the simulated/bootstrapped data and the parameter matrix used.

Author(s)

Matthieu Stigler

See Also

setar to estimate a SETAR, arima.sim to simulate an ARMA.
Examples

```r
#Simulation of a TAR with 1 threshold
TvarMat <- c(2.9,-0.4,-0.1,-1.5, 0.2,0.3)
sim<-setar.sim(B=TvarMat,lag=2, type="simul", nthresh=1, Thresh=2, starting=c(2.8,2.2))$serie
mean(ifelse(sim>2,1,0)) #approximation of values over the threshold

#check the result
selectSETAR(sim, m=2)

#Bootstrap a TAR with two threshold (three regimes)
sun<-(sqrt(sunspot.year+1)-1)*2
setar.sim(data=sun,nthresh=2,n=500, type="boot", Thresh=c(6,9))$serie

#Check the bootstrap
cbind(setar.sim(data=sun,nthresh=2,n=500, type="check", Thresh=c(6,9))$serie,sun)
```

Description

Test of linearity against threshold of Hansen (1999) with bootstrap distribution

Usage

```r
setarTest(x, m, d = 1, steps = d, series, thDelay = 0, nboot=10, trim=0.1, test=c("1vs", "2vs3"), hpc=c("none", "foreach"),check=FALSE)
```

Arguments

- **x**: time series
- **m, d, steps**: embedding dimension, time delay, forecasting steps
- **series**: time series name (optional)
- **thDelay**: 'time delay' for the threshold variable (as multiple of embedding time delay d)
- **nboot**: number of bootstrap replications
- **trim**: trimming parameter indicating the minimal percentage of observations in each regime
- **test**: Type of test. See details
- **hpc**: Possibility to run the bootstrap on parallel core. See details in TVECM.HTest
- **check**: Possibility to check if the bootstrap is correct by not sampling the residuals. The result given should be the same as in the original data
Details

Estimation of the first threshold parameter is made with CLS, a conditional search with one iteration is made for the second threshold. The Ftest comparing the residual sum of squares (SSR) of each model is computed.

\[ F_{ij} = T((S_i - S_j)/S_j) \]

where \( S_i \) is the SSR of the model with \( i \) regimes (and so \( i-1 \) thresholds).

Three test are available. The both first can be seen as linearity test, whereas the third can be seen as a specification test: once the 1vs2 or/and 1vs3 rejected the linearity and henceforth accepted the presence of a threshold, is a model with one or two thresholds preferable?

Test 1vs2: Linear AR versus 1 threshold TAR
Test 1vs3: Linear AR versus 2 threshold TAR
Test 2vs3: 1 threshold TAR versus 2 threshold TAR

The both first are computed together and available with test="1vs". The third test is available with test="2vs3".

The homoskedastic bootstrap distribution is based on resampling the residuals from H0 model (ar for test 1vs, and setar(1) for test 2vs3), estimating the threshold parameter and then computing the Ftest, so it involves many computations and is pretty slow.

Value

A object of class "Hansen99Test" containing:

- SSRs: The residual Sum of squares of model AR, 1 threshold TAR and 2 thresholds TAR
- Ftests: The Ftest statistic for the test
- PvalBoot: The bootstrap p-values for the test selected
- CriticalValBoot: The critical values for the test selected
- Ftestboot: All the F-test computed
- firstBests, secBests: The thresholds for the original series, obtained from search for 1 thresh (firstBests) and conditional search for 2 thresh (secBests)
- nboot, m, type: The number of bootstrap replications (nboot), the lags used (m) and the type of test (type)

Author(s)

Matthieu Stigler

References

See Also

`TVAR.LRtest` for the multivariate version. `SETAR` for estimation of the model.

Examples

```r
# Data used by Hansen
sun <- (sqrt(sunspot.year + 1) - 1) * 2

# Test 1 vs 2 and 1 vs 3
setarTest(sun, m = 11, thDelay = 0:1, nboot = 5, trim = 0.1, test = "1vs")
```

Description

Some sigmoid functions. See R sources for their definition.

Usage

```
sigmoid(x)
dsigmoid(x)
```

Arguments

- **x**: numeric vector

Author(s)

J. L. Aznarte

Description

STAR model fitting with automatic selection of the number of regimes based on LM tests.

Usage

```
star(x, m = 2, noRegimes = 1, steps = d, series = rob = FALSE, mTh, thDelay, thVar, sig = 0.05, trace = TRUE, control = list(), ...)
```
Arguments

x                         time series
m, d, steps               embedding dimension, time delay, forecasting steps
noRegimes                 max number of regimes
series                    time series name (optional)
rob                       perform robust test (not implemented)
thDelay                   'time delay' for the threshold variable (as multiple of embedding time delay d)
mTh                       coefficients for the lagged time series, to obtain the threshold variable
thVar                     external threshold variable
sig                       significance level for the tests to select the number of regimes.
control                   further arguments to be passed as control list to optim
trace                     should additional infos be printed out?
...                       currently unused

Details

The function star implements the iterative building strategy described in [1] to identify and estimate Smooth Transition AutoRegressive models.


Value

star returns an object of class nlar, subclass star, i.e. a list with informations about the fitted model.

Author(s)

J. L. Aznarte M.

See Also

addRegime

Examples

mod.star <- star(log10(lynx), mTh=c(0,1), control=list(maxit=3000))
mod.star

addRegime(mod.star)
**toLatex.setar**  

*Latex representation of fitted setar models*

---

### Description

Produce LaTeX output of the SETAR model.

### Usage

```r
## S3 method for class 'setar'
toLatex(object, digits = 3, label, ...)
```

### Arguments

- `object` fitted setar model (using `nlar`)
- `digits` options to be passed to `format` for formatting numbers
- `label` LaTeX label passed to the equation
- `...` Not used

### Author(s)

Antonio, Fabio Di Narzo

### See Also

`setar, nlar-methods`

### Examples

```r
mod.setar <- setar(log10(lynx), m=2, thDelay=1, th=3.25)
toLatex(mod.setar)
```

---

**tVAR**  

*Multivariate Threshold Autoregressive model*

---

### Description

Estimate a multivariate Threshold VAR
Usage

TVAR(data, lag, include = c("const", "trend", "none", "both"),
model = c("TAR", "MTAR"), commonInter = FALSE, nthresh = 1,
thDelay = 1, mTh = 1, thVar, trim = 0.1, ngrid, gamma = NULL, around,
plot = FALSE, dummyToBothRegimes = TRUE, trace = TRUE, trick = "for",
max.iter = 2)

Arguments

data: time series
lag: Number of lags to include in each regime
include: Type of deterministic regressors to include
model: Whether the transition variable is taken in levels (TAR) or difference (MTAR)
commonInter: Whether the deterministic regressors are regime specific (commonInter=FALSE) or not.
nthresh: Number of thresholds
thDelay: 'time delay' for the threshold variable (as multiple of embedding time delay d)
PLEASE NOTE that the notation is currently different to univariate models in tsDyn. The left side variable is taken at time t, and not t+1 as in univariate cases.
mTh: combination of variables with same lag order for the transition variable. Either a single value (indicating which variable to take) or a combination
thVar: external transition variable
trim: trimming parameter indicating the minimal percentage of observations in each regime
ngrid: number of elements of the grid, especially for nthresh=3
gamma: prespecified threshold values
around: The grid search is restricted to ngrid values around this point. Especially useful for nthresh=3.
plot: Whether a plot showing the results of the grid search should be printed
dummyToBothRegimes: Whether the dummy in the one threshold model is applied to each regime or not.
trace: should additional infos be printed out?
trick: type of R function called: for or mapply
max.iter: Number of iterations for the algorithm

Details

For fixed th and threshold variable, the model is linear, so estimation can be done directly by CLS (Conditional Least Squares). The search of the parameters values is made upon a grid of potential values. So it is pretty slow.
nthresh=1: estimation of one threshold model (two regimes) upon a grid of ngrid values (default to ALL) possible thresholds and delays values.
nthresh=2: estimation of two thresholds model (three regimes) Conditional on the threshold found in model where nthresh=1, the second threshold is searched. When both are found, a second grid search is made with 30 values around each threshold.

nthresh=3: DOES NOT estimate a 3 thresholds model, but a 2 thresholds model with a whole grid over the thresholds parameters (so is really slow) with a given delay, is there rather to check the consistency of the method nthresh=2

Value

An object of class TVAR, with standard methods.

Author(s)

Matthieu Stigler

References


See Also

`lineVar` for the linear VAR/VECM, `TVAR.LRtest` to test for TVAR, `TVAR.sim` to simulate/bootstrap a TVAR.

Examples

data(zeroylld)

tv <- TVAR(zeroylld, lag=2, nthresh=2, thDelay=1, trim=0.1, mTh=1, plot=FALSE)

print(tv)
summary(tv)

# a few useful methods:
plot(tv)
predict(tv)
c(AIC(tv), BIC(tv), logLik(tv))

Description

Multivariate extension of the linearity against threshold test from Hansen (1999) with bootstrap distribution
Usage

TVAR.LRtest(data, lag = 1, trend = TRUE, series, thDelay = 1:m, mTh = 1, thVar, nboot = 10, plot = FALSE, trim = 0.1, test = c("1vs", "2vs3"), model = c("TAR", "MTAR"), hpc = c("none", "foreach"), trace = FALSE, check = FALSE)

Arguments

data multivariate time series
lag Number of lags to include in each regime
trend whether a trend should be added
series name of the series
thDelay 'time delay' for the threshold variable (as multiple of embedding time delay d)
PLease note that the notation is currently different to univariate models in tsDyn. The left side variable is taken at time t, and not t+1 as in univariate cases.
mTh combination of variables with same lag order for the transition variable. Either a single value (indicating which variable to take) or a combination
thVar external transition variable
nboot Number of bootstrap replications
plot Whether a plot showing the results of the grid search should be printed
trim trimming parameter indicating the minimal percentage of observations in each regime
test Type of usual and alternative hypothesis. See details
model Whether the threshold variable is taken in level (TAR) or difference (MTAR)
hpc Possibility to run the bootstrap on parallel core. See details in TVECM.HStest
trace should additional infos be printed? (logical)
check Possibility to check the function by no sampling: the test value should be the same as in the original data

Details

This test is just the multivariate extension proposed by Lo and Zivot of the linearity test of Hansen (1999). As in univariate case, estimation of the first threshold parameter is made with CLS, for the second threshold a conditional search with one iteration is made. Instead of a Ftest comparing the SSR for the univariate case, a Likelihood Ratio (LR) test comparing the covariance matrix of each model is computed.

\[
LR_{ij} = T(ln(\det \hat{\Sigma}_i) - ln(\det \hat{\Sigma}_j))
\]

where \(\hat{\Sigma}_i\) is the estimated covariance matrix of the model with i regimes (and so i-1 thresholds).

Three test are available. The both first can be seen as linearity test, whereas the third can be seen as a specification test: once the 1vs2 or/and 1vs3 rejected the linearity and henceforth accepted the presence of a threshold, is a model with one or two thresholds preferable?
Test 1vs2: Linear VAR versus 1 threshold TVAR
Test 1vs3: Linear VAR versus 2 threshold2 TVAR
Test 2vs3: 1 threshold TAR versus 2 threshold2 TAR

The both first are computed together and available with test="1vs". The third test is available with test="2vs3".

The homoskedastik bootstrap distribution is based on resampling the residuals from H0 model, estimating the threshold parameter and then computing the Ftest, so it involves many computations and is pretty slow.

Value

A list containing:
- The values of each LR test
- The bootstrap Pvalues and critical values for the test selected

Author(s)

Matthieu Stigler

References


See Also

setartest for the univariate version. 01sTVar for estimation of the model.

Examples

data(zeroyld)
data<-zeroyld

TVAR.LRtest(data, lag=2, mTh=1, thDelay=1:2, nboot=3, plot=FALSE, trim=0.1, test="1vs")
**Simulation of a multivariate Threshold Autoregressive model (TVAR)**

**Description**

Simulate a multivariate Threshold VAR (TVAR)

**Usage**

```r
tVAR.sim(B, Thresh, nthresh = 1, n = 200, lag = 1, include = c("const", "trend", "none", "both"), thDelay = 1, mTh = 1, starting = NULL, innov = rnorm(n, varcov = varcov), varcov = diag(1, nrow(B)), show.parMat = FALSE, ...)

tVAR.boot(TVARobject, innov, seed, boot.scheme = c("resample", "wild1", "wild2", "check"), ...)
```

**Arguments**

- **B**
  - Matrix of coefficients to simulate
- **Thresh**
  - The threshold value(s). Vector of length nthresh
- **nthresh**
  - number of threshold (see details)
- **n**
  - Number of observations to create when type="simul"
- **lag**
  - Number of lags to include in each regime
- **include**
  - Type of deterministic regressors to include. NOT WORKING PROPERLY CURRENTLY if not const
- **thDelay**
  - 'time delay' for the threshold variable (as multiple of embedding time delay d)
  - PLEASE NOTE that the notation is currently different to univariate models in tsDyn. The left side variable is taken at time t, and not t+1 as in univariate cases.
- **mTh**
  - combination of variables with same lag order for the transition variable. Either a single value (indicating which variable to take) or a combination
- **starting**
  - Starting values (matrix of dimension lag x k). If not given, set to zero.
- **innov**
  - Innovations used for simulation. Should be matrix of dim n x k. By default multivariate normal. For the bootstrap case TVAR.boot, residuals are resampled if argument is missing.
- **varcov**
  - Variance-covariance matrix for the innovations. By default identity matrix.
- **show.parMat**
  - Logical. Should the parameter matrix be shown? Useful to understand how to give right input
- **...**
  - Further arguments passed to the underlying (un-exported) TVAR.gen function
- **TVARobject**
  - Object of class TVAR generated by function TVAR
- **seed**
  - Optional. Seed for the random resampling function.
- **boot.scheme**
  - The bootstrap scheme.
Details

This function offers the possibility to generate series following a TVAR.

By giving a matrix of coefficients, one can only simulate a VAR (\(nthresh=0\)) or TVAR (\(nthresh=1\) or 2). One can have a specification with constant (default), trend, both or none (see arg include). Order in parameters is include/lags (VECM) and include/lags/include/lags for TVECM, hence, a matrix for a TVECM with 3 regimes, a const and a 2 lags would have 2 lines and 2*(1+4) columns. The innovations can be given by the user (a matrix of dim nxk, here n does not include the starting values!), by default it uses a multivariate normal distribution, with covariance matrix specified by varcov. The starting values (of dim lags x k) can be given. The user should take care for their choice, since it is not sure that the simulated values will cross the threshold even once.

The matrix ‘B’ has to be in the form: constant, trend, lags, then repeated if many regimes. In case of uncertainty, using \(\text{who\_par\_Mat}\_\text{TRUE}\) will print the matrix as interpreted by the function, helping the user to feed the right input.

For the bootstrap, the function resamples data from a given TVAR model generated by TVAR, returning the resampled data. A residual recursive bootstrap is used, where one uses either a simple resampling, or the Wild bootstrap, either with a normal distribution (\text{wild1}) or inverting the sign randomly (\text{wild2}).

Value

A matrix with the simulated/bootstrapped series.

Author(s)

Matthieu Stigler

See Also

TVAR to estimate the TVAR. Similar TVECM.sim and TVECM.boot for TVECM, VAR.sim and VAR.boot for VAR models estimated with lineVar.

Examples

```r
## TVAR.sim: Simulation of a TVAR with 1 threshold
B <- rbind(c(0.11928245, 1.00880447, -0.009974585, -0.089316, 0.95425564, 0.02592617),
          c(0.25283578, 0.09182279, 0.914763741, -0.0530613, 0.02248586, 0.94309347))
colnames(B) <- paste(rep(c("Const", "Lag_1_var1", "Lag_1_var2"), 2), c("Low", "High"), sep="_")
sim <- TVAR.sim(B=B, nthresh=1, n=500, mTh=1, Thresh=5, starting=matrix(c(5.2, 5.5), nrow=1))

#estimate the new serie
TVAR(sim, lag=1, dummyToBothRegimes=TRUE)
```
## Threshold Vector Error Correction model (VECM)

**Description**

Estimate a Threshold Vector Error Correction model (VECM)

**Usage**

```r
tvecm(data, lag = 1, nthresh = 1, trim = 0.05, ngridBeta = 50, ngridTh = 50, plot = TRUE, th1 = list(exact = NULL, int = c("from", "to"), around = "val"), th2 = list(exact = NULL, int = c("from", "to"), around = "val"), beta = list(exact = NULL, int = c("from", "to"), around = c("val", "by")), restr = c("none", "equal", "signOp"), common = c("All", "only_ECT"), include = c("const", "trend", "none", "both"), dummyToBothRegimes = TRUE, beta0 = 0, methodMapply = FALSE, trace = TRUE)
```

**Arguments**

- `data`: time series
- `lag`: Number of lags to include in each regime
- `nthresh`: number of threshold (see details)
- `trim`: trimming parameter indicating the minimal percentage of observations in each regime
- `ngridBeta`: number of elements to search for the cointegrating value
- `ngridTh`: number of elements to search for the threshold value
- `plot`: Whether the grid with the SSR of each threshold should be plotted.
- `th1`: different possibilities to pre-specify an exact value, an interval or a central point for the search of the threshold (or first threshold if `nthresh`=2)
- `th2`: different possibilities to pre-specify an exact value or a central point for the search of the second threshold (used only if `nthresh`=2)
- `beta`: different possibilities to pre-specify an exact value, an interval or a central point for the search of the cointegrating value
- `restr`: Currently not available
- `common`: Whether the regime-specific dynamics are only for the ECT or for the ECT and the lags
- `include`: Type of deterministic regressors to include
dummyToBothRegimes
Whether the dummy in the one threshold model is applied to each regime or not.

betaP
Additional regressors to include in the cointegrating relation

methodMapply
only for programming. Is to make the choice between a for loop or mapply implementation

trace
should additional infos be printed? (logical)

Details
For fixed threshold and cointegrating vector, the model is linear, so estimation of the regression parameters can be done directly by CLS (Conditional Least Squares). The search of the threshold and cointegrating parameters values which minimize the residual sum of squares (SSR) is made on a grid of potential values. For specification of the grids, see below.

The function can estimate one as well as two thresholds:

nthresh=1: estimation of one threshold model (two regimes) upon a grid of ngridTh values (default to ALL) possible thresholds and delays values.

nthresh=2: estimation of two thresholds model (three regimes). Conditional on the threshold found in model where nthresh=1, the second threshold is searched. When both are found, a second grid search is made with 30 values around each threshold.

The model can be either with a threshold effect on all variables ("All") or only on the error correction term (ECT) (argument "only ECT"). In the second case, the value for the middle threshold is taken a null, as in Balke and Fomby (1997).

The grid for the threshold parameters can be set in different ways, through the argument th1, th2 and beta:

exact: Pre-specified value (for beta: cointegrating vector will be c(1,-beta))

int: Specify an interval (of length ngridTh) in which to search.

around: Specify to take ngridTh points around the value given.

The default is to do an interval search. Interval bounds for the threshold interval are simply the trim and 1-trim percents of the sorted error correction term. For the cointegrating parameter, bounds of the interval are obtained from the (OLS) confidence interval of the linear cointegration case. It is often found however that this interval is too tight. It is hence recommended to inspect the plot of the grid search.

Value
Fitted model data

Author(s)
Matthieu Stigler
References


See Also

vecm for the linear VECM, TVAR for the threshold VAR, TVECM.SeoTest to test for TVECM, TVECM.sim to simulate/bootstrap a TVECM.

Examples

data(zeroyld)

# Estimate a TVECM (we use here minimal grid, it should be usually much bigger!)

tvec <- TVECM(zeroyld, nthresh=2, lag=1, ngridBeta=20, ngridTh=30, plot=TRUE, trim=0.05, common="All")

print(tvec)
summary(tvec)

# Obtain diverse infos:
AIC(tvec)
BIC(tvec)

res.tvec<-residuals(tvec)

# Export the equations as Latex:
toLatex(tvec)

TVECM.HStest  Test of linear cointegration vs threshold cointegration

Description

Tests the null of linear cointegration against threshold cointegration following Hansen and Seo (2002). Fixed regressor and residual bootstrap are available.

Usage

TVECM.HStest(data, lag=1, ngridTh=300, trim=0.05, nboot=100, fixed.beta=NULL, intercept=TRUE, boot.type=c("FixedReg", "ResBoot"), hpc=c("none", "foreach"))
Arguments

- **data**: Time series
- **lag**: Number of lags to include in each regime
- **ngridTh**: Number of threshold grid points to evaluate the optimal threshold.
- **trim**: Trimming parameter indicating the minimal percentage of observations in each regime
- **nboot**: Number of bootstrap replications
- **fixed.beta**: Numeric. User pre-specified cointegrating value, as in VECM (i.e. cointegrating vector will be c(1, -beta.fixed)). When NULL (default), the value is estimated from the linear VECM.
- **intercept**: Logical. Whether an intercept has to be included in the VECM
- **boot.type**: Character. Type of bootstrap simulation (only if nboot>0)
- **hpc**: Possibility to run the bootstrap on parallel core. See details

Details

This test follows the implementation done by Hansen and Seo (2002). The cointegrating value is estimated from the linear VECM. Then, conditional on this value, the LM test is run for a range of different threshold values. The maximum of those LM test values is reported.

Two bootstrap are available: a fixed regressor, as well as a usual residual bootstrap (using the function TVECM.sim).

Available methods are print(), summary() and plot().

With the argument hpc, the burdensome bootstrap replication can be run on parallel cores, thus alleviating the time of computation. The user needs simply to choose a package (among doMC, doMPI, doSNOW or doRedis) and register the backend. See the vignette for more details.

Value

A list containing diverse values:

- **stat**: The sup-LM statistic.
- **values**: The whole LM values.
- **PvalBoot**: The bootstrap p-value
- **CriticalValBoot**: The bootstrap critical values
- **allBoots**: The boot sup-LM values
- **args**: Some user given args (nboot, boot.type)

Reproducibility

Comparison with original paper is made difficult as values of the test are not shown in the paper, only their critical values, which depend on random bootstrap.

Comparison is done with the GAUSS code available on the page of Bruce Hansen. Running tar_ci, we have the same sup-LM value when lags=1 and lags=2, a higher value with lag=3. When the test is run with pre-specified beta values, we have different results, sometimes higher but also smaller sup-LM value.
Author(s)

Matthieu Stigler

References


See Also

zeroyld: data used in the original paper of Hansen and Seo.

TVECM.SeoTest: a similar test, but with null hypothesis of no-cointegration.

TVECM for estimating a TVECM, TVECM.sim for simulating/bootstrap a TVECM.

Examples

# Use original data from paper:
data(zeroylld)
dataPaper<-zeroyld
# Test: nboot, number of bootstrap replications, should be high
## Not run:
test1<-TVECM.HStest(dataPaper, lag=1, intercept=TRUE, nboot=1000)

## End(Not run)

# we use here for the example a much smaller number of bootstrap:
test1<-TVECM.HStest(dataPaper, lag=1, intercept=TRUE, nboot=10)

test1
summary(test1)
plot(test1)

# can have only specific plots:
plot(test1, which="LM values")
plot(test1, which="Density")

## Run the function in parallel:
## Not run:
# we show here the use with package doMC
library(doMC)
registerDoMC(2) # Number of cores
test1<-TVECM.HStest(dataPaper, lag=1, intercept=TRUE, nboot=1000, hpc="foreach")

## End(Not run)
TVECM.SeoTest

No cointegration vs threshold cointegration test

Description
Test the null of no cointegration against threshold cointegration with bootstrap distribution of Seo (2006)

Usage
TVECM.SeoTest(data, lag, beta, trim = 0.1, nboot, plot = FALSE, hpc = c("none", "foreach"), check = FALSE)

Arguments
data time series
lag Number of lags to include in each regime
beta Pre-specified cointegrating value (i.e. cointegrating vector will be c(1, -beta))
trim trimming parameter indicating the minimal percentage of observations in each regime
nboot Number of bootstrap replications
plot Whether a grid with the SSR of each threshold should be printed
hpc Possibility to run the bootstrap on parallel core. See details in TVECM.Htest
check Possibility to check the function by no sampling: the test value should be the same as in the original data

Details
For this test, the cointegrating value has to be specified by the user.

The model used is one where the threshold effect concerns only the cointegrating vector, and only in the outer regimes.

Due to the presence of parameters unidentified under the null hypothesis, the test employed is a Sup-Wald test, that means that for each combination of the thresholds, a Wald Test is computed and the supremum of all tests is taken. For each bootstrap replication, this approach is taken, so that the test is really slow.

Value
A list containing diverse informations:
Estimated threshold parameters and usual slope parameters.
Value of the test.
Critical and P-value from bootstrap distribution.
Author(s)
Matthieu Stigler

References

See Also
TVECM for estimating a TVECM, TVECM.sim for simulating/bootstrap a TVECM,

Examples

# As the function takes long long time to be executed, we show in in don't run environement
## Not run:
data(zeroyld)

# can be useful to check whether the bootstrap is working:
# without sampling, results of boot should be same as original
# this is indeed not always the case due to floating point algorithm
TVECM.SeoTest(zeroyld,lag=2, beta=1, trim=0.1,nboot=2, plot=FALSE,check=TRUE)

# then run the function:
TVECM.SeoTest(zeroyld,lag=2, beta=1, trim=0.1,nboot=100, plot=FALSE,check=FALSE)

## End(Not run)

---

Data

Description
This data, used as example in Caner and Hansen (2001), contains the monthly US adult male unemployment from 1956 to 1999.

Usage
data(UsUnemp)

Format
A monthly time series of class ts starting in January 1956 and ending in August 1999.

Source
VAR.sim

**Simulate or bootstrap a VAR model**

**Description**

Allow to either simulate from scratch (by providing coefficients) or bootstrap from an estimated VAR model.

**Usage**

```r
VAR.sim(b, n = 200, lag = 1, include = c("const", "trend", "none", "both"), starting = NULL, innov = rmnorm(n, varcov = varcov), varcov = diag(1, nrow(b)), show.parMat = FALSE, returnStarting = FALSE, ...)

VAR.boot(VARobject, boot.scheme = c("resample", "wild1", "wild2", "check"), seed, ...)
```

**Arguments**

- `b` Matrix of coefficients.
- `n` Number of observations to simulate
- `lag` Number of lags of the VAR to simulate
- `include` Type of deterministic regressors to include in the VAR to simulate
- `starting` Starting values (matrix of dimension lag x k) for the VAR to simulate. If not given, set to zero.
- `innov` Innovations used for in the VAR to simulate. Should be matrix of dim n x k. By default multivariate normal.
- `varcov` Variance-covariance matrix for the innovations. By default identity matrix.
- `show.parMat` Logical. Should the parameter matrix be shown? Useful to understand how to give right input
- `returnStarting` Whether starting values are returned. Default to FALSE
- `...` Further arguments passed to the underlying (un-exported) VAR.gen function
- `VARobject` Object of class VAR generated by function `lineVar`
- `boot.scheme` The bootstrap scheme. See details.
- `seed` Optional. Seed for the random resampling function.

**Details**

For the bootstrap, the function resamples data from a given VAR model generated by `lineVar`, returning the resampled data. A residual recursive bootstrap is used, where one uses either a simple resampling, or the Wild bootstrap, either with a normal distribution (wild1) or inverting the sign randomly (wild2)
Value

A matrix with the resampled series.

Author(s)

Matthieu Stigler

See Also

lineVar to estimate the VAR. Similar TVECM.sim and TVECM.boot for TVECM, TVAR.sim and TVAR.boot for TVAR models.

Examples

```r
## VAR.sim: simulate VAR as in Enders 2004, p 268
B1 <- matrix(c(0.7, 0.2, 0.2, 0.7), 2)
var1 <- VAR.sim(B=B1, n=100, include="none")
ts.plot(var1, type="l", col=c(1,2))

B2=rbind(c(0.5, 0.5, 0.5),
c(0, 0.5, 0.5))
varcov<-matrix(c(1,0.2, 0.3, 1),2)
var2 <- VAR.sim(B=B2, n=100, include="const", varcov=varcov)
ts.plot(var2, type="l", col=c(1,2))

## VAR.boot: Bootstrap a VAR
data(zeroyl)
mod <- lineVar(data=zeroyl,lag=1)
VAR.boot(mod)
```

### VARrep

**VAR representation**

**Description**

Show the VAR representation of a VECM

**Usage**

VARrep(object, ...)

```r
## S3 method for class 'VECM'
VARrep(object, ...)

## S3 method for class 'VAR'
VARrep(object, ...)
```
**VECM**

**Arguments**

- `object` An object of class ‘VECM’ created by `vecm`, or of class ‘VAR’ created by `linevar`.

  ... Currently not used

**Value**

A matrix containing the parameters of the VECM under their VAR representation.

**Author(s)**

Matthieu Stigler

**References**


**Examples**

```r
data(barry)

# VECM model:
mod_vecm <- VECM(barry, lag=2, estim="ML")
VARrep(mod_vecm)

# VAR model:
mod_var <- lineVar(barry, lag=2, I="diff")
VARrep(mod_var)
```

---

**Description**

Estimate a VECM by either Engle-Granger (2OLS) or Johansen (MLE) method.

**Usage**

```r
VECM(data, lag, r = 1, include = c("const", "trend", "none", "both"),
    beta = NULL, estim = c("2OLS", "ML"), LRinclude = c("none", "const",
    "trend", "both"), exogen = NULL)
```
Arguments

- **data**: multivariate time series (first row being first=oldest value)
- **lag**: Number of lags (in the VECM representation, see Details)
- **r**: Number of cointegrating relationships
- **include**: Type of deterministic regressors to include
- **beta**: for VECM only: user-specified cointegrating values, the cointegrating vector will be taken as: \((1, -\beta)\) If NULL, will be estimated using the estimator specified in **estim**
- **estim**: Type of estimator: 2OLS for the two-step approach or ML for Johansen MLE
- **LRIinclude**: Type of deterministic regressors to include in the long-term relationship. Can also be a matrix with exogeneous regressors (2OLS only).
- **exogen**: Inclusion of exogeneous variables (first row being first=oldest value). Is either of same size than data (then automatically cut) or than end-sample.

Details

This function is just a wrapper for the lineVar, with model="VECM".

More comprehensive functions for VECM are in package vars. Differences with that package are:

**Engle-Granger estimator** The Engle-Granger estimator is available

**Presentation** Results are printed in a different ways, using a matrix form

**latex export** The matrix of coefficients can be exported to latex, with or without standard-values and significance stars

**Prediction** The predict method contains a newdata argument allowing to compute rolling forecasts.

Two estimators are available: the Engle-Granger two step approach (2OLS) or the Johansen (ML). For the 2OLS, deterministics regressors (or external variables if LRIinclude is of class numeric) can be added for the estimation of the cointegrating value and for the ECT. This is only working when the beta value is not pre-specified.

The arg beta is the cointegrating value, the cointegrating vector will be taken as: \((1, -\beta)\).

Note that the lag specification corresponds to the lags in the VECM representation, not in the VAR (as is done in package vars or software GRETL). Basically, a VAR with 2 lags corresponds here to a VECM with 1 lag. The lag can be set to 0, although some methods (irf, fevd) won’t work for this case.

The arg beta allows to specify constrained cointegrating values, leading to \(ECT = \beta’ X_{t-1}\). It should be specified as a \(K \times r\) matrix. In case of \(r = 1\), can also be specified as a vector. Note that the vector should be normalised, with the first value to 1, and the next values showing the opposite sign in the long-run relationship \(-\beta\). In case the vector has \(K - 1\) values, this is what lineVar is doing, setting \((1, -\beta)\). Note finally one should provide values for all the coefficients (eventually except for special case of r=1 and k-1), if you want to provide only part of the parameters, and let the others be estimated, look at the functions in package urca.

The eigenvector matrix \(\beta\) is normalised using the Phillips triangular representation, see Hamilton (1994, p. 576) and Juselius (2006, p. 216), see coefA for more details.
Value

An object of class VECM (and higher classes VAR and nlVar) with methods:

**Usual methods** Print, summary, plot, residuals, fitted, vcov

**Fit criteria** AIC, BIC, MAPE, mse, logLik (latter only for models estimated with MLE)

**Prediction** Predict and predict_rolling

**VAR/VECM methods** Impulse response function (irf) and forecast error variance decomposition (fevd)

**LaTeX** toLatex

Author(s)

Matthieu Stigler

References


See Also

coefA, coefB and coefPI to extract the relevant parameter matrices.

lineVar TVAR and TVECM for the corresponing threshold models. linear for the univariate AR model.

Examples

data(zeroyld)
data<-zeroyld

#Fit a VECM with Engle-Granger 2OLS estimator:
vecm.eg<-VECM(zeroyld, lag=2)

#Fit a VECM with Johansen MLE estimator:
vecm.jo<-VECM(zeroyld, lag=2, estim="ML")

#compare results with package vars:
if(require(vars)) {
data(finland)
#check long coint values
all.equal(VECM(finland, lag=2, estim="ML", r=2)$model.specific$beta,
cajorls(ca.jo(finland, K=3, spec="transitory"), r=2) $beta, check.attributes=FALSE)
# check OLS parameters
all.equal(t(coefficients(VECM(finland, lag=2, estim="ML", r=2))),
coefficients(cajorls(ca.jo(finland, K=3, spec="transitory"), r=2)$rlm), check.attributes=FALSE)
}

VECM.sim

Simulation and bootstrap a VECM or bivariate TVECM

Description

Estimate or bootstraps a multivariate Threshold VAR

Usage

VECM.sim(data, B, VECMObject, beta, n = 200, lag = 1, type = c("simul", "boot", "check"), include = c("const", "trend", "none", "both"), starting = NULL, innov = rmnorm(n, varcov = varcov), varcov = diag(1, k), show.parMat = FALSE, seed)

VECM.boot(VECMObject, show.parMat = FALSE, seed, check = TRUE)

TVECM.boot(TVECMObject, show.parMat = FALSE, seed, check = TRUE)

TVECM.sim(data, B, TVECMObject, nthresh = 1, Thresh, beta, n = 200, lag = 1, type = c("simul", "boot", "check"), include = c("const", "trend", "none", "both"), starting = NULL, innov = rmnorm(n, varcov = varcov), varcov = diag(1, k), show.parMat = FALSE, seed)

Arguments

data matrix of parameter to simulate
B Matrix of coefficients to simulate
beta The cointegrating value
n Number of observations to create when type="simul"
lag Number of lags to include in each regime
type Whether a bootstrap or simulation is to employ. See details
include Type of deterministic regressors to include. NOT WORKING PROPERLY CURRENTLY if not const
starting Starting values when a simulation with given parameter matrix is made
### VECM.sim

**innov**  
Innovations used for simulation. Should be matrix of dim nxk. By default multivariate normal.

**varcov**  
Variance-covariance matrix for the innovations. By default multivariate normal is used.

**show.parMat**  
Logical. Should the parameter matrix be shown? Useful to understand how to give right input.

**seed**  
Optional. Seed for the random number generation.

**check**  
When performing a bootstrap replication, check if taking original residuals (instead of resampled) leads to the original data.

**TVECMobject, VECMobject**  
Object computed by function TVECM or linear VECM.

**nthresh**  
number of threshold (see details)

**thresh**  
The threshold value(s). Vector of length nthresh.

### Details

This function offers the possibility to generate series following a VECM/TVECM from two approaches: bootstrap or simulation. VECM.sim is just a wrapper for TVECM.sim.

When the argument matrix is given, on can only simulate a VECM (nthresh=0) or TVECM (nthresh=1 or 2). One can have a specification with constant ("const"), "trend", "both" or "none" (see argument include). Order for the parameters is ECT/include/lags for VECM and ECT1/include1/lags1/ECT2/include2/lags2 for TVECM. To be sure that once is using it correctly, setting show.parMat = TRUE will show the matrix of parameters together with their values and names.

The argument beta is the cointegrating value on the right side of the long-run relationship, and hence the function use the vector (1,-beta). The innov argument specifies the innovations. It should be given as a matrix of dim nxk, (here n does not include the starting values!), by default it uses a multivariate normal distribution, with covariance matrix specified by varcov.

The starting values (of dim lags x k) can be given through argument starting. The user should take care for their choice, since it is not sure that the simulated values will cross the threshold even once. Notice that only one cointegrating value is allowed. User interested in simulating a VECM with more cointegrating values should do use the VAR representation and use TVAR.sim.

The second possibility is to bootstrap series. This is done on a object generated by TVECM (or VECM). A simple residual bootstrap is done, or one can simulate a series with the same parameter matrix and with normal distributed residuals (with variance pre-specified), corresponding to Monte-carlo simulations.

One can alternatively give only the series, and then the function will call internally TVAECM.

### Value

A matrix with the simulated/bootstraped series.

### Author(s)

Matthieu Stigler
VECM or TVECM to estimate the VECM or TVECM. Similar TVAR.sim and TVAR.boot for TVAR, VAR.sim and VAR.boot for VAR models estimated with lineVar models.

Examples

```r
### reproduce example in Enders (2004, 2 edition) p. 350,  
# (similar example in Enders (2010, 3 edition) 301-302).

if(require(mnormt)){
  # see that the full "VAR" coefficient matrix is:
  A <- matrix(c(-0.2, 0.2, 0.2, -0.2), byrow=TRUE, ncol=2)
  # but this is not the input of VECM.sim. You should decompose into the a and b matrix:
  a <- matrix(c(-0.2, 0.2), ncol=1)
  b <- matrix(c(1,-1), nrow=1)
  # so that:
  a%*%b
  # The a matrix is the input under argument B, while the b matrix is under argument beta:
  # (the other zeros in B are for the not-specified lags)
  innov <- rmnorm(100, varcov=diag(2))
  startVal <- matrix(0, nrow=2, ncol=1)
  Bvecm <- rbind(c(-0.2, 0, 0), c(0.2, 0, 0))
  vecm1 <- VECM.sim(B=Bvecm, beta=1, n=100, lag=1, include="none", innov=innov, starting=startVal)
  ECT <- vecm1[,1]-vecm1[,2]
  # add an intercept as in panel B
  Bvecm2 <- rbind(c(-0.2, 0.1, 0, 0), c(0.2, 0.4, 0, 0))
  vecm2 <- VECM.sim(B=Bvecm2, n=100, beta=1, lag=1, include="const", innov=innov, starting=startVal)
  par(mfrow=c(2,1))
  plot(vecm1[,1], type="l", main="Panel a: no drift or intercept", ylab="", xlab="")
  lines(vecm1[,2], lty=2)
  plot(vecm2[,1], type="l", main="Panel b: drift terms (0.1)", ylab="", xlab="")
  lines(vecm2[,2], lty=2)
}
### bootstrap a TVAR with 1 threshold (two regimes)
data(zeroYld)
dat <- zeroYld
TVECMObject <- TVECM(dat, nthresh=1, lag=1, ngridBeta=20, ngridTh=20, plot=FALSE)
TVECM.sim(TVECMObject, type="boot")

### Check the bootstrap
TVECM.sim.check <- TVECM.sim(TVECMObject=TVECMObject, type="check")
all(TVECM.sim.check==dat)
```
VECM_symbolic

Virtua VECM model

Description

Pedagogical tool to create a symbolic VECM model, i.e. just for representation purpose.

Usage

VECM_symbolic(alpha, beta, lags, inc, include = c("none", "const", "trend", "both"))

Arguments

alpha Matrix of alpha speed adjustment coefficients.
beta Matrix of alpha, cointegrating coefficients.
lags Matrix containing the lags coefficients.
inc Matrix containing the include (see following arg) coefficients.
include Character indicating the type of deterministic term included, if any.

Value

An object of class ‘VECM’, without however any data.

Examples

a <- matrix(c(-0.4, 0.1), ncol=1)
b <- matrix(c(1, -2), ncol=2)

# VECM_symb(alpha=a, beta=t(b))
d <- VECM_symbolic(alpha=a, beta=t(b))
VARrep(d)
d <- VECM_symbolic(alpha=a, beta=t(b), lags=matrix(0, ncol=2, nrow=2))
VARrep(d)
LagMat <- matrix(c(0.1, 0.3, 0.1, 0.2), ncol=2, nrow=2)
incMat <- matrix(c(0.5, 0.1), ncol=1)
d3 <- VECM_symbolic(alpha=a, beta=t(b), lags=LagMat, inc=incMat, include="const")
VARrep(d3)
Description


Format

A data frame with 482 observations on 2 variables.

```
[,1] short.run numeric Short term, 12 month
[,2] long.run numeric Long term, 120 month
```

Source


The data can be downloaded from: http://www.ssc.wisc.edu/~bhansen/progs/joe_02r.zip.

The authors themselves took the data from the webpage of Huston McCulloch: http://www.econ.ohio-state.edu/jhm/ts/mcckwon/mccull.htm

See Also

TVECM.HStest: Hansen and Seo test.
TVECM for estimating a TVECM.
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