

Package ‘uGMAR’

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Title Estimate Univariate Gaussian or Student's t Mixture
Autoregressive Model

Version 3.3.0

Description Maximum likelihood estimation of univariate Gaussian Mixture Autoregressive (GMAR), Student's t Mixture Autoregressive (StMAR), and Gaussian and Student's t Mixture Autoregressive (G-StMAR) models, quantile residual tests, graphical diagnostics, forecast and simulate from GMAR, StMAR and G-StMAR processes.
Leena Kalliovirta, Mika Meitz, Pentti Saikkonen (2015) <doi:10.1111/jtsa.12108>,
Mika Meitz, Daniel Preve, Pentti Saikkonen (2018) <arXiv:1805.04010>,
Savi Virolainen (2020) <arXiv:2003.05221>.

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Author Savi Virolainen [aut, cre]

Maintainer Savi Virolainen <savi.virolainen@helsinki.fi>

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add_data	<i>Add data to object of class 'gsmar' defining a GMAR, StMAR, or G-StMAR model</i>
----------	---

Description

add_data adds or updates data to object of class 'gsmar' that defines a GMAR, StMAR, or G-StMAR model. Also calculates empirical mixing weights, conditional moments, and quantile residuals accordingly.

Usage

```

add_data(
  data,
  gsmar,
  calc_qresiduals = TRUE,
  calc_cond_moments = TRUE,
  calc_std_errors = FALSE,
  custom_h = NULL
)

```

Arguments

<code>data</code>	a numeric vector or class 'ts' object containing the data. NA values are not supported.
<code>gsmar</code>	object of class 'gsmar' created with the function <code>fitGSMAR</code> or <code>GSMAR</code> .
<code>calc_qresiduals</code>	should quantile residuals be calculated? Default is TRUE iff the model contains data.
<code>calc_cond_moments</code>	should conditional means and variances be calculated? Default is TRUE iff the model contains data.
<code>calc_std_errors</code>	should approximate standard errors be calculated?
<code>custom_h</code>	A numeric vector with same the length as the parameter vector: i :th element of <code>custom_h</code> is the difference used in central difference approximation for partial differentials of the log-likelihood function for the i :th parameter. If NULL (default), then the difference used for differentiating overly large degrees of freedom parameters is adjusted to avoid numerical problems, and the difference is $6e-6$ for the other parameters.

Value

Returns an object of class 'gsmar' defining the GMAR, StMAR, or G-StMAR model with the data added to the model. If the object already contained data, the data will be updated. Does not modify the 'gsmar' object given as argument!

References

- Kalliovirta L., Meitz M. and Saikkonen P. 2015. Gaussian Mixture Autoregressive model for univariate time series. *Journal of Time Series Analysis*, **36**, 247-266.
- Meitz M., Preve D., Saikkonen P. 2018. A mixture autoregressive model based on Student's t-distribution. arXiv:1805.04010 [econ.EM].
- Virolainen S. 2020. A mixture autoregressive model based on Gaussian and Student's t-distribution. arXiv:2003.05221 [econ.EM].

See Also

[fitGSMAR](#), [GSMAR](#), [iterate_more](#), [get_gradient](#), [get_regime_means](#), [swap_parametrization](#), [stmar_to_gstmar](#)

Examples

```
# G-StMAR model without data
params42gs <- c(0.04, 1.34, -0.59, 0.54, -0.36, 0.01, 0.06, 1.28, -0.36,
               0.2, -0.15, 0.04, 0.19, 9.75)
gstmar42 <- GSMAR(p=4, M=c(1, 1), params=params42gs, model="G-StMAR")
gstmar42

# Add data to the model
gstmar42 <- add_data(data=M10Y1Y, gsmar=gstmar42)
gstmar42
```

add_dfs *Add random dfs to a vector*

Description

add_dfs adds random degrees of freedom parameters to a vector.

Usage

```
add_dfs(x, how_many)
```

Arguments

x	a vector to add the dfs to
how_many	how many dfs?

Details

Read the source code for details.

Value

Returns `c(x, dfs)` with `how_many` dfs-elements.

all_pos_ints	<i>Check whether all arguments are strictly positive natural numbers</i>
--------------	--

Description

all_pos_ints tells whether all the elements in a vector are strictly positive natural numbers.

Usage

```
all_pos_ints(x)
```

Arguments

x a vector containing the elements to be tested.

Value

Returns TRUE or FALSE accordingly.

alt_gsmar	<i>Construct a GSMAR model based on results from an arbitrary estimation round of fitGSMAR</i>
-----------	--

Description

alt_gsmar constructs a GSMAR model based on results from an arbitrary estimation round of fitGSMAR.

Usage

```
alt_gsmar(
  gsmar,
  which_round = 1,
  which_largest,
  calc_qresiduals = TRUE,
  calc_cond_moments = TRUE,
  calc_std_errors = TRUE,
  custom_h = NULL
)
```

Arguments

gsmar	object of class 'gsmar' created with the function <code>fitGSMAR</code> or <code>GSMAR</code> .
which_round	based on which estimation round should the model be constructed? An integer value in 1,...,ncalls.
which_largest	based on estimation round with which largest log-likelihood should the model be constructed? An integer value in 1,...,ncalls. For example, <code>which_largest=2</code> would take the second largest log-likelihood and construct the model based on the corresponding estimates. If used, then <code>which_round</code> is ignored.
calc_qresiduals	should quantile residuals be calculated? Default is TRUE iff the model contains data.
calc_cond_moments	should conditional means and variances be calculated? Default is TRUE iff the model contains data.
calc_std_errors	should approximate standard errors be calculated?
custom_h	A numeric vector with same the length as the parameter vector: <code>i</code> :th element of <code>custom_h</code> is the difference used in central difference approximation for partial differentials of the log-likelihood function for the <code>i</code> :th parameter. If NULL (default), then the difference used for differentiating overly large degrees of freedom parameters is adjusted to avoid numerical problems, and the difference is $6e-6$ for the other parameters.

Details

It's sometimes useful to examine other estimates than the one with the highest log-likelihood value. This function is just a simple wrapper to `GSMAR` that picks the correct estimates from an object returned by `fitGSMAR`.

Value

Returns an object of class 'gsmar' defining the specified GMAR, StMAR, or G-StMAR model. If data is supplied, the returned object contains (by default) empirical mixing weights, some conditional and unconditional moments, and quantile residuals. Note that the first `p` observations are taken as the initial values so the mixing weights, conditional moments, and quantile residuals start from the `p+1`:th observation (interpreted as `t=1`).

References

- Kalliovirta L., Meitz M. and Saikkonen P. 2015. Gaussian Mixture Autoregressive model for univariate time series. *Journal of Time Series Analysis*, **36**, 247-266.
- Meitz M., Preve D., Saikkonen P. 2018. A mixture autoregressive model based on Student's t-distribution. arXiv:1805.04010 [econ.EM].
- Virolainen S. 2020. A mixture autoregressive model based on Gaussian and Student's t-distribution. arXiv:2003.05221 [econ.EM].

See Also

[fitGSMAR](#), [GSMAR](#), [iterate_more](#), [get_gradient](#), [get_regime_means](#), [swap_parametrization](#), [stmar_to_gstmar](#)

Examples

```
# These are long running examples that take approximately ...
fit42t <- fitGSMAR(data=M10Y1Y, p=4, M=2, model="StMAR", ncalls=2,
                  seeds=c(1, 6))
fit42t # Bad estimate in the boundary of the stationarity region!

# So we build a model based on the next-best local maximum point:
fit42t_alt <- alt_gsmar(fit42t, which_largest=2)
fit42t_alt # Overly large degrees of freedom paramter estimate

# Switch to the appropriate G-StMAR model:
fit42gs <- stmar_to_gstmar(fit42t_alt)
fit42gs
```

calc_gradient

Calculate gradient or Hessian matrix

Description

calc_gradient or calc_hessian calculates the gradient or Hessian matrix of the given function at the given point using central difference numerical approximation. get_gradient (and get_foc) or get_hessian calculates the gradient or Hessian matrix of the log-likelihood function at the parameter values of a class 'gsmar' object. get_soc returns eigenvalues of the Hessian matrix.

Usage

```
calc_gradient(x, fn, h = 6e-06, varying_h = NULL, ...)
```

```
calc_hessian(x, fn, h = 6e-06, varying_h = NULL, ...)
```

```
get_gradient(gsmar, custom_h = NULL)
```

```
get_foc(gsmar, custom_h = NULL)
```

```
get_hessian(gsmar, custom_h = NULL)
```

```
get_soc(gsmar, custom_h = NULL)
```


Arguments

x	a numeric vector specifying the point at which the gradient or Hessian should be evaluated.
fn	a function that takes in the argument x as the first argument.
h	the difference used to approximate the derivatives.
varying_h	a numeric vector with the same length as x specifying the difference h for each dimension separately. If NULL (default), then the difference given as parameter h will be used for all dimensions.
...	other arguments passed to fn.
gsmar	object of class 'gsmar' created with the function fitGSMAR or GSMAR.
custom_h	same as varying_h but if NULL (default), then the difference h used for differentiating overly large degrees of freedom parameters is adjusted to avoid numerical problems, and the difference is 6e-6 for the other parameters.

Details

In particular, the functions `get_foc` and `get_soc` can be used to check whether the found estimates denote a (local) maximum point, a saddle point, or something else.

Value

The gradient functions return numerical approximation of the gradient, and the Hessian functions return numerical approximation of the Hessian. `get_soc` returns eigenvalues of the Hessian matrix, `get_foc` is the same as `get_gradient` but named conveniently.

Warning

No argument checks!

See Also

[profile_logliks](#)

Examples

```
# Simple function
foo <- function(x) x^2 + x
calc_gradient(x=1, fn=foo)
calc_gradient(x=-0.5, fn=foo)
calc_hessian(x=2, fn=foo)

# More complicated function
foo <- function(x, a, b) a*x[1]^2 - b*x[2]^2
calc_gradient(x=c(1, 2), fn=foo, a=0.3, b=0.1)
calc_hessian(x=c(1, 2), fn=foo, a=0.3, b=0.1)

# GMAR model
params12 <- c(1.70, 0.85, 0.30, 4.12, 0.73, 1.98, 0.63)
```

```

gmar12 <- GSMAR(data=simudata, p=1, M=2, params=params12, model="GMAR")
get_gradient(gmar12)
get_foc(gmar12)
get_hessian(gmar12)
get_soc(gmar12)

```

change_parametrization

Change parametrization of a parameter vector

Description

change_parametrization changes the parametrization of the given parameter vector to change_to.

Usage

```

change_parametrization(
  p,
  M,
  params,
  model = c("GMAR", "StMAR", "G-StMAR"),
  restricted = FALSE,
  constraints = NULL,
  change_to = c("intercept", "mean")
)

```

Arguments

- p** a positive integer specifying the autoregressive order of the model.
- M** **For GMAR and StMAR models:** a positive integer specifying the number of mixture components.
For G-StMAR models: a size (2x1) integer vector specifying the number of *GMAR type* components M1 in the first element and *StMAR type* components M2 in the second element. The total number of mixture components is M=M1+M2.
- params** a real valued parameter vector specifying the model.
For non-restricted models: For GMAR model: Size $(M(p+3) - 1 \times 1)$ vector $\theta = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1})$, where $v_m = (\phi_{m,0}, \phi_m, \sigma_m^2)$ and $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$, $m = 1, \dots, M$.
For StMAR model: Size $(M(p+4) - 1 \times 1)$ vector $(\theta, \nu) = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.
For G-StMAR model: Size $(M(p+3) + M2 - 1 \times 1)$ vector $(\theta, \nu) = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_{M1+1}, \dots, \nu_M)$.
With linear constraints: Replace the vectors ϕ_m with vectors ψ_m and provide a list of constraint matrices **C** that satisfy $\phi_m = R_m \psi_m$ for all $m = 1, \dots, M$, where $\psi_m = (\psi_{m,1}, \dots, \psi_{m,q_m})$.

For restricted models: For GMAR model: Size $(3M + p - 1 \times 1)$ vector $\theta = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1})$, where $\phi = (\phi_1, \dots, \phi_p)$.

For StMAR model: Size $(4M + p - 1 \times 1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.

For G-StMAR model: Size $(3M + M2 + p - 1 \times 1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.

With linear constraints: Replace the vector ϕ with vector ψ and provide a constraint matrix C that satisfies $\phi = R\psi$, where $\psi = (\psi_1, \dots, \psi_q)$.

Symbol ϕ denotes an AR coefficient, σ^2 a variance, α a mixing weight, and ν a degrees of freedom parameter. If parametrization=="mean", just replace each intercept term $\phi_{m,0}$ with regimewise mean $\mu_m = \phi_{m,0} / (1 - \sum \phi_{i,m})$. In the **G-StMAR** model, the first M1 components are *GMAR type* and the rest M2 components are *StMAR type*. Note that in the case **M=1**, the parameter α is dropped, and in the case of **StMAR** or **G-StMAR** model, the degrees of freedom parameters ν_m have to be larger than 2.

model is "GMAR", "StMAR", or "G-StMAR" model considered? In the G-StMAR model, the first M1 components are *GMAR type* and the rest M2 components are *StMAR type*.

restricted a logical argument stating whether the AR coefficients $\phi_{m,1}, \dots, \phi_{m,p}$ are restricted to be the same for all regimes.

constraints specifies linear constraints applied to the autoregressive parameters.

For non-restricted models: a list of size (pxq_m) constraint matrices C_m of full column rank satisfying $\phi_m = C_m \psi_m$ for all $m = 1, \dots, M$, where $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$ and $\psi_m = (\psi_{m,1}, \dots, \psi_{m,q_m})$.

For restricted models: a size (pxq) constraint matrix C of full column rank satisfying $\phi = C\psi$, where $\phi = (\phi_1, \dots, \phi_p)$ and $\psi = (\psi_1, \dots, \psi_q)$.

Symbol ϕ denotes an AR coefficient. Note that regardless of any constraints, the nominal autoregressive order is always p for all regimes. Ignore or set to NULL if applying linear constraints is **not** desired.

change_to either "intercept" or "mean" specifying to which parametrization it should be switched to. If set to "intercept", it's assumed that params is mean-parametrized, and if set to "mean" it's assumed that params is intercept-parametrized.

Value

Returns parameter vector described in params but with parametrization changed from intercept to mean (when change_to==mean) or from mean to intercept (when change_to==intercept).

Warning

No argument checks!

References

- Kalliovirta L., Meitz M. and Saikkonen P. 2015. Gaussian Mixture Autoregressive model for univariate time series. *Journal of Time Series Analysis*, **36**, 247-266.
- Meitz M., Preve D., Saikkonen P. 2018. A mixture autoregressive model based on Student's t-distribution. arXiv:1805.04010 [**econ.EM**].

- Virolainen S. 2020. A mixture autoregressive model based on Gaussian and Student's t-distribution. arXiv:2003.05221 [econ.EM].

change_regime	<i>Change the specified regime of parameter vector to the given regime-parameter vector</i>
---------------	---

Description

change_regime changes the specified regime of the parameter vector to correspond the given regime-parameter vector and returns the modified parameter vector. Does not affect mixing weight parameters.

Usage

```
change_regime(
  p,
  M,
  params,
  model = c("GMAR", "StMAR", "G-StMAR"),
  restricted = FALSE,
  constraints = NULL,
  regime_params,
  regime
)
```

Arguments

- p** a positive integer specifying the autoregressive order of the model.
- M** **For GMAR and StMAR models:** a positive integer specifying the number of mixture components.
For G-StMAR models: a size (2x1) integer vector specifying the number of *GMAR type* components M1 in the first element and *StMAR type* components M2 in the second element. The total number of mixture components is $M=M1+M2$.
- params** a real valued parameter vector specifying the model.
For non-restricted models: For GMAR model: Size $(M(p+3) - 1x1)$ vector $\theta=(v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1})$, where $v_m = (\phi_{m,0}, \phi_m, \sigma_m^2)$ and $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$, $m = 1, \dots, M$.
For StMAR model: Size $(M(p+4) - 1x1)$ vector $(\theta, \nu) = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.
For G-StMAR model: Size $(M(p+3) + M2 - 1x1)$ vector $(\theta, \nu) = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_{M1+1}, \dots, \nu_M)$.
With linear constraints: Replace the vectors ϕ_m with vectors ψ_m and provide a list of constraint matrices **C** that satisfy $\phi_m = R_m \psi_m$ for all $m = 1, \dots, M$, where $\psi_m = (\psi_{m,1}, \dots, \psi_{m,q_m})$.

	<p>For restricted models: For GMAR model: Size $(3M + p - 1 \times 1)$ vector $\theta = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1})$, where $\phi = (\phi_1, \dots, \phi_p)$.</p> <p>For StMAR model: Size $(4M + p - 1 \times 1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1}, \nu)$.</p> <p>For G-StMAR model: Size $(3M + M2 + p - 1 \times 1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1}, \nu)$.</p> <p>With linear constraints: Replace the vector ϕ with vector ψ and provide a constraint matrix C that satisfies $\phi = R\psi$, where $\psi = (\psi_1, \dots, \psi_q)$.</p> <p>Symbol ϕ denotes an AR coefficient, σ^2 a variance, α a mixing weight, and ν a degrees of freedom parameter. If parametrization=="mean", just replace each intercept term $\phi_{m,0}$ with regimewise mean $\mu_m = \phi_{m,0} / (1 - \sum \phi_{i,m})$. In the G-StMAR model, the first M1 components are <i>GMAR type</i> and the rest M2 components are <i>StMAR type</i>. Note that in the case M=1, the parameter α is dropped, and in the case of StMAR or G-StMAR model, the degrees of freedom parameters ν_m have to be larger than 2.</p>
model	is "GMAR", "StMAR", or "G-StMAR" model considered? In the G-StMAR model, the first M1 components are <i>GMAR type</i> and the rest M2 components are <i>StMAR type</i> .
restricted	a logical argument stating whether the AR coefficients $\phi_{m,1}, \dots, \phi_{m,p}$ are restricted to be the same for all regimes.
constraints	specifies linear constraints applied to the autoregressive parameters. <p>For non-restricted models: a list of size (pxq_m) constraint matrices C_m of full column rank satisfying $\phi_m = C_m \psi_m$ for all $m = 1, \dots, M$, where $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$ and $\psi_m = (\psi_{m,1}, \dots, \psi_{m,q_m})$.</p> <p>For restricted models: a size (pxq) constraint matrix C of full column rank satisfying $\phi = C\psi$, where $\phi = (\phi_1, \dots, \phi_p)$ and $\psi = (\psi_1, \dots, \psi_q)$.</p> <p>Symbol ϕ denotes an AR coefficient. Note that regardless of any constraints, the nominal autoregressive order is always p for all regimes. Ignore or set to NULL if applying linear constraints is not desired.</p>
regime_params	a numeric vector specifying the parameter values that should be inserted to the specified regime. <p>For non-restricted models: For GMAR model: Size $(p+2 \times 1)$ vector $(\phi_{m,0}, \phi_{m,1}, \dots, \phi_{m,p}, \sigma_m^2)$.</p> <p>For StMAR model: Size $(p+3 \times 1)$ vector $(\phi_{m,0}, \phi_{m,1}, \dots, \phi_{m,p}, \sigma_m^2, \nu_m)$.</p> <p>For G-StMAR model: Same as GMAR for GMAR-components and same as StMAR for StMAR-components.</p> <p>With linear constraints: Parameter vector as described above, but vector ϕ_m replaced with vector ψ_m that satisfies $\phi_m = R_m \psi_m$.</p> <p>For restricted models: For GMAR model: Size (2×1) vector $(\phi_{m,0}, \sigma_m^2)$.</p> <p>For StMAR model: Size (3×1) vector $(\phi_{m,0}, \sigma_m^2, \nu_m)$.</p> <p>For G-StMAR model: Same as GMAR for GMAR-components and same as StMAR for StMAR-components.</p> <p>With linear constraints: Parameter vector as described above.</p>
regime	a positive integer in the interval $[1, M]$ defining which regime should be changed.
Value	Returns modified parameter vector of the form described in params.

 check_and_correct_data

Check that the data is set correctly and correct if not

Description

check_and_correct_data checks that the data is set correctly and throws an error if there is something wrong with the data.

Usage

```
check_and_correct_data(data, p)
```

Arguments

data a numeric vector or class 'ts' object containing the data. NA values are not supported.

p a positive integer specifying the autoregressive order of the model.

Value

Returns the data as a class 'ts' object.

 check_constraint_mat *Check the constraint matrices*

Description

check_constraint_mat checks for some parts that the constraint matrices are correctly set.

Usage

```
check_constraint_mat(p, M, restricted = FALSE, constraints = NULL)
```

Arguments

p a positive integer specifying the autoregressive order of the model.

M **For GMAR and StMAR models:** a positive integer specifying the number of mixture components.
For G-StMAR models: a size (2x1) integer vector specifying the number of *GMAR type* components M1 in the first element and *StMAR type* components M2 in the second element. The total number of mixture components is $M=M1+M2$.

restricted a logical argument stating whether the AR coefficients $\phi_{m,1}, \dots, \phi_{m,p}$ are restricted to be the same for all regimes.

constraints specifies linear constraints applied to the autoregressive parameters.

For non-restricted models: a list of size (pxq_m) constraint matrices C_m of full column rank satisfying $\phi_m = C_m \psi_m$ for all $m = 1, \dots, M$, where $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$ and $\psi_m = (\psi_{m,1}, \dots, \psi_{m,q_m})$.

For restricted models: a size (pxq) constraint matrix C of full column rank satisfying $\phi = C\psi$, where $\phi = (\phi_1, \dots, \phi_p)$ and $\psi = (\psi_1, \dots, \psi_q)$.

Symbol ϕ denotes an AR coefficient. Note that regardless of any constraints, the nominal autoregressive order is always p for all regimes. Ignore or set to NULL if applying linear constraints is **not** desired.

Value

Doesn't return anything but throws an informative error if finds out that something is wrong.

check_data	<i>Check that given object contains data</i>
------------	--

Description

check_data checks that a given object contains data.

Usage

```
check_data(object)
```

Arguments

object an object to be tested

Value

Doesn't return anything but throws and error if something is wrong.

check_gsmar	<i>Check that given object has class attribute 'gsmar'</i>
-------------	--

Description

check_gsmar checks that the given object has class attribute 'gsmar'.

Usage

```
check_gsmar(object, object_name = "gsmar")
```

Arguments

object an object to be tested
 object_name the name of the tested object

Value

Doesn't return anything but throws an error if something is wrong.

check_model *Check that the argument 'model' is correctly specified.*

Description

check_model checks that the argument 'model' is correctly specified.

Usage

```
check_model(model)
```

Arguments

model is "GMAR", "StMAR", or "G-StMAR" model considered? In the G-StMAR model, the first M1 components are *GMAR type* and the rest M2 components are *StMAR type*.

Value

Doesn't return anything but throws an error if something is wrong.

check_params_length *Check that the parameter vector has the correct dimension*

Description

check_model checks that the parameter vector has the correct dimension.

Usage

```
check_params_length(  
  p,  
  M,  
  params,  
  model = c("GMAR", "StMAR", "G-StMAR"),  
  restricted = FALSE,  
  constraints = NULL  
)
```


Arguments

p	a positive integer specifying the autoregressive order of the model.
M	<p>For GMAR and StMAR models: a positive integer specifying the number of mixture components.</p> <p>For G-StMAR models: a size (2×1) integer vector specifying the number of <i>GMAR type</i> components M1 in the first element and <i>StMAR type</i> components M2 in the second element. The total number of mixture components is $M=M1+M2$.</p>
params	<p>a real valued parameter vector specifying the model.</p> <p>For non-restricted models: For GMAR model: Size $(M(p+3) - 1 \times 1)$ vector $\theta=(v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1})$, where $v_m = (\phi_{m,0}, \phi_m, \sigma_m^2)$ and $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$, $m = 1, \dots, M$.</p> <p>For StMAR model: Size $(M(p+4) - 1 \times 1)$ vector $(\theta, \nu) = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.</p> <p>For G-StMAR model: Size $(M(p+3) + M2 - 1 \times 1)$ vector $(\theta, \nu) = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_{M1+1}, \dots, \nu_M)$.</p> <p>With linear constraints: Replace the vectors ϕ_m with vectors ψ_m and provide a list of constraint matrices C that satisfy $\phi_m = R_m \psi_m$ for all $m = 1, \dots, M$, where $\psi_m = (\psi_{m,1}, \dots, \psi_{m,q_m})$.</p> <p>For restricted models: For GMAR model: Size $(3M + p - 1 \times 1)$ vector $\theta = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1})$, where $\phi = (\phi_1, \dots, \phi_p)$.</p> <p>For StMAR model: Size $(4M + p - 1 \times 1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.</p> <p>For G-StMAR model: Size $(3M + M2 + p - 1 \times 1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1}, \nu_{M1+1}, \dots, \nu_M)$.</p> <p>With linear constraints: Replace the vector ϕ with vector ψ and provide a constraint matrix C that satisfies $\phi = R\psi$, where $\psi = (\psi_1, \dots, \psi_q)$.</p> <p>Symbol ϕ denotes an AR coefficient, σ^2 a variance, α a mixing weight, and ν a degrees of freedom parameter. If parametrization="mean", just replace each intercept term $\phi_{m,0}$ with regimewise mean $\mu_m = \phi_{m,0} / (1 - \sum \phi_{i,m})$. In the G-StMAR model, the first M1 components are <i>GMAR type</i> and the rest M2 components are <i>StMAR type</i>. Note that in the case M=1, the parameter α is dropped, and in the case of StMAR or G-StMAR model, the degrees of freedom parameters ν_m have to be larger than 2.</p>
model	is "GMAR", "StMAR", or "G-StMAR" model considered? In the G-StMAR model, the first M1 components are <i>GMAR type</i> and the rest M2 components are <i>StMAR type</i> .
restricted	a logical argument stating whether the AR coefficients $\phi_{m,1}, \dots, \phi_{m,p}$ are restricted to be the same for all regimes.
constraints	<p>specifies linear constraints applied to the autoregressive parameters.</p> <p>For non-restricted models: a list of size $(p \times q_m)$ constraint matrices C_m of full column rank satisfying $\phi_m = C_m \psi_m$ for all $m = 1, \dots, M$, where $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$ and $\psi_m = (\psi_{m,1}, \dots, \psi_{m,q_m})$.</p> <p>For restricted models: a size $(p \times q)$ constraint matrix C of full column rank satisfying $\phi = C\psi$, where $\phi = (\phi_1, \dots, \phi_p)$ and $\psi = (\psi_1, \dots, \psi_q)$.</p> <p>Symbol ϕ denotes an AR coefficient. Note that regardless of any constraints, the nominal autoregressive order is always p for all regimes. Ignore or set to NULL if applying linear constraints is not desired.</p>

Value

Doesn't return anything but throws an error if something is wrong.

check_pM	<i>Check that p and M are correctly set</i>
----------	---

Description

check_pM checks that the arguments p and M are correctly set.

Usage

```
check_pM(p, M, model = c("GMAR", "StMAR", "G-StMAR"))
```

Arguments

p	a positive integer specifying the autoregressive order of the model.
M	For GMAR and StMAR models: a positive integer specifying the number of mixture components. For G-StMAR models: a size (2x1) integer vector specifying the number of <i>GMAR type</i> components M1 in the first element and <i>StMAR type</i> components M2 in the second element. The total number of mixture components is $M=M1+M2$.
model	is "GMAR", "StMAR", or "G-StMAR" model considered? In the G-StMAR model, the first M1 components are <i>GMAR type</i> and the rest M2 components are <i>StMAR type</i> .

Value

Doesn't return anything but throws an informative error if something is wrong.

condmomentPlot	<i>DEPRECATED, USE cond_moment_plot INSTEAD! Conditional mean or variance plot for GMAR, StMAR, and G-StMAR models</i>
----------------	--

Description

condmomentPlot plots the one-step in-sample conditional means/variances of the model along with the time series contained in the model (e.g. the time series the model was fitted to). Also plots the regimewise conditional means/variances multiplied with the mixing weights. **DEPRECATED, USE cond_moment_plot INSTEAD!**

Usage

```
condmomentPlot(gsmar, which_moment = c("mean", "variance"))
```

Arguments

gsmar object of class 'gsmar' created with the function fitGSMAR or GSMAR.
 which_moment should conditional means or variances be plotted?

Details

DEPRECATED, USE cond_moment_plot INSTEAD!

Value

cond_moment_plot only plots to a graphical device and does not return anything. Numerical values of the conditional means/variances can be extracted from the model with the dollar sign.

References

- Galbraith, R., Galbraith, J. 1974. On the inverses of some patterned matrices arising in the theory of stationary time series. *Journal of Applied Probability* **11**, 63-71.
- Kalliovirta L. (2012) Misspecification tests based on quantile residuals. *The Econometrics Journal*, **15**, 358-393.
- Kalliovirta L., Meitz M. and Saikkonen P. 2015. Gaussian Mixture Autoregressive model for univariate time series. *Journal of Time Series Analysis*, **36**, 247-266.
- Meitz M., Preve D., Saikkonen P. 2018. A mixture autoregressive model based on Student's t-distribution. arXiv:1805.04010 [econ.EM].
- Virolainen S. 2020. A mixture autoregressive model based on Gaussian and Student's t-distribution. arXiv:2003.05221 [econ.EM].

See Also

[profile_logliks](#), [diagnostic_plot](#), [fitGSMAR](#), [GSMAR](#), [quantile_residual_tests](#), [quantileResidualPlot](#)

condMoments	<i>DEPRECATED, USE cond_moments INSTEAD! Calculate conditional moments of GMAR, StMAR, or G-StMAR model</i>
-------------	---

Description

condMoments calculates the regime specific conditional means and variances and total conditional means and variances of the specified GMAR, StMAR or G-StMAR model. DEPRECATED, USE cond_moments INSTEAD!

Usage

```
condMoments(
  data,
  p,
  M,
  params,
  model = c("GMAR", "StMAR", "G-StMAR"),
  restricted = FALSE,
  constraints = NULL,
  parametrization = c("intercept", "mean"),
  to_return = c("regime_cmeans", "regime_cvars", "total_cmeans", "total_cvars")
)
```

Arguments

data a numeric vector or class 'ts' object containing the data. NA values are not supported.

p a positive integer specifying the autoregressive order of the model.

M **For GMAR and StMAR models:** a positive integer specifying the number of mixture components.

For G-StMAR models: a size (2x1) integer vector specifying the number of *GMAR type* components M1 in the first element and *StMAR type* components M2 in the second element. The total number of mixture components is $M=M1+M2$.

params a real valued parameter vector specifying the model.

For non-restricted models: For GMAR model: Size $(M(p+3) - 1x1)$ vector $\theta=(v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1})$, where $v_m = (\phi_{m,0}, \phi_m, \sigma_m^2)$ and $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$, $m = 1, \dots, M$.

For StMAR model: Size $(M(p+4) - 1x1)$ vector $(\theta, \nu) = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.

For G-StMAR model: Size $(M(p+3) + M2 - 1x1)$ vector $(\theta, \nu) = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_{M1+1}, \dots, \nu_M)$.

With linear constraints: Replace the vectors ϕ_m with vectors ψ_m and provide a list of constraint matrices **C** that satisfy $\phi_m = R_m \psi_m$ for all $m = 1, \dots, M$, where $\psi_m = (\psi_{m,1}, \dots, \psi_{m,q_m})$.

For restricted models: For GMAR model: Size $(3M + p - 1x1)$ vector $\theta = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1})$, where $\phi = (\phi_1, \dots, \phi_p)$.

For StMAR model: Size $(4M + p - 1x1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.

For G-StMAR model: Size $(3M + M2 + p - 1x1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1}, \nu_{M1+1}, \dots, \nu_M)$.

With linear constraints: Replace the vector ϕ with vector ψ and provide a constraint matrix **C** that satisfies $\phi = R\psi$, where $\psi = (\psi_1, \dots, \psi_q)$.

Symbol ϕ denotes an AR coefficient, σ^2 a variance, α a mixing weight, and ν a degrees of freedom parameter. If parametrization=="mean", just replace each intercept term $\phi_{m,0}$ with regimewise mean $\mu_m = \phi_{m,0} / (1 - \sum \phi_{i,m})$. In the **G-StMAR** model, the first M1 components are *GMAR type* and the rest M2 components are *StMAR type*. Note that in the case **M=1**, the parameter α is

	dropped, and in the case of StMAR or G-StMAR model, the degrees of freedom parameters ν_m have to be larger than 2.
model	is "GMAR", "StMAR", or "G-StMAR" model considered? In the G-StMAR model, the first M1 components are <i>GMAR type</i> and the rest M2 components are <i>StMAR type</i> .
restricted	a logical argument stating whether the AR coefficients $\phi_{m,1}, \dots, \phi_{m,p}$ are restricted to be the same for all regimes.
constraints	specifies linear constraints applied to the autoregressive parameters. For non-restricted models: a list of size (pxq_m) constraint matrices C_m of full column rank satisfying $\phi_m = C_m \psi_m$ for all $m = 1, \dots, M$, where $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$ and $\psi_m = (\psi_{m,1}, \dots, \psi_{m,q_m})$. For restricted models: a size (pxq) constraint matrix C of full column rank satisfying $\phi = C\psi$, where $\phi = (\phi_1, \dots, \phi_p)$ and $\psi = (\psi_1, \dots, \psi_q)$. Symbol ϕ denotes an AR coefficient. Note that regardless of any constraints, the nominal autoregressive order is always p for all regimes. Ignore or set to NULL if applying linear constraints is not desired.
parametrization	is the model parametrized with the "intercepts" $\phi_{m,0}$ or "means" $\mu_m = \phi_{m,0} / (1 - \sum \phi_{i,m})$?
to_return	calculate regimewise conditional means (regime_cmeans), regimewise conditional variances (regime_cvars), total conditional means (total_cmeans), or total conditional variances (total_cvars)?

Value

Note that the first p observations are taken as the initial values so the conditional moments start from the p+1:th observation (interpreted as t=1).

- if to_return=="regime_cmeans":** a size $((n_obs-p) \times M)$ matrix containing the regime specific conditional means.
- if to_return=="regime_cvars":** a size $((n_obs-p) \times M)$ matrix containing the regime specific conditional variances.
- if to_return=="total_cmeans":** a size $((n_obs-p) \times 1)$ vector containing the total conditional means.
- if to_return=="total_cvars":** a size $((n_obs-p) \times 1)$ vector containing the total conditional variances.

References

- Galbraith, R., Galbraith, J. 1974. On the inverses of some patterned matrices arising in the theory of stationary time series. *Journal of Applied Probability* **11**, 63-71.
- Kalliovirta L. (2012) Misspecification tests based on quantile residuals. *The Econometrics Journal*, **15**, 358-393.
- Kalliovirta L., Meitz M. and Saikkonen P. 2015. Gaussian Mixture Autoregressive model for univariate time series. *Journal of Time Series Analysis*, **36**, 247-266.
- Meitz M., Preve D., Saikkonen P. 2018. A mixture autoregressive model based on Student's t-distribution. arXiv:1805.04010 [**econ.EM**].

- Virolainen S. 2020. A mixture autoregressive model based on Gaussian and Student's t-distribution. arXiv:2003.05221 [econ.EM].

cond_moments	<i>Calculate conditional moments of GMAR, StMAR, or G-StMAR model</i>
--------------	---

Description

cond_moments calculates the regime specific conditional means and variances and total conditional means and variances of the specified GMAR, StMAR or G-StMAR model.

Usage

```
cond_moments(
  data,
  p,
  M,
  params,
  model = c("GMAR", "StMAR", "G-StMAR"),
  restricted = FALSE,
  constraints = NULL,
  parametrization = c("intercept", "mean"),
  to_return = c("regime_cmeans", "regime_cvars", "total_cmeans", "total_cvars")
)
```

Arguments

data a numeric vector or class 'ts' object containing the data. NA values are not supported.

p a positive integer specifying the autoregressive order of the model.

M **For GMAR and StMAR models:** a positive integer specifying the number of mixture components.

For G-StMAR models: a size (2x1) integer vector specifying the number of *GMAR type* components M1 in the first element and *StMAR type* components M2 in the second element. The total number of mixture components is $M=M1+M2$.

params a real valued parameter vector specifying the model.

For non-restricted models: For GMAR model: Size $(M(p+3) - 1x1)$ vector $\theta=(v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1})$, where $v_m = (\phi_{m,0}, \phi_m, \sigma_m^2)$ and $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$, $m = 1, \dots, M$.

For StMAR model: Size $(M(p+4) - 1x1)$ vector $(\theta, \nu) = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.

For G-StMAR model: Size $(M(p+3) + M2 - 1x1)$ vector $(\theta, \nu) = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_{M1+1}, \dots, \nu_M)$.

With linear constraints: Replace the vectors ϕ_m with vectors ψ_m and provide a list of constraint matrices **C** that satisfy $\phi_m = R_m \psi_m$ for all $m = 1, \dots, M$, where $\psi_m = (\psi_{m,1}, \dots, \psi_{m,q_m})$.

For restricted models: For GMAR model: Size $(3M + p - 1 \times 1)$ vector $\theta = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1})$, where $\phi = (\phi_1, \dots, \phi_p)$.

For StMAR model: Size $(4M + p - 1 \times 1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_{M-1})$.

For G-StMAR model: Size $(3M + M2 + p - 1 \times 1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_{M-1})$.

With linear constraints: Replace the vector ϕ with vector ψ and provide a constraint matrix C that satisfies $\phi = R\psi$, where $\psi = (\psi_1, \dots, \psi_q)$.

Symbol ϕ denotes an AR coefficient, σ^2 a variance, α a mixing weight, and ν a degrees of freedom parameter. If parametrization=="mean", just replace each intercept term $\phi_{m,0}$ with regimewise mean $\mu_m = \phi_{m,0} / (1 - \sum \phi_{i,m})$. In the **G-StMAR** model, the first M1 components are *GMAR type* and the rest M2 components are *StMAR type*. Note that in the case **M=1**, the parameter α is dropped, and in the case of **StMAR** or **G-StMAR** model, the degrees of freedom parameters ν_m have to be larger than 2.

model	is "GMAR", "StMAR", or "G-StMAR" model considered? In the G-StMAR model, the first M1 components are <i>GMAR type</i> and the rest M2 components are <i>StMAR type</i> .
restricted	a logical argument stating whether the AR coefficients $\phi_{m,1}, \dots, \phi_{m,p}$ are restricted to be the same for all regimes.
constraints	specifies linear constraints applied to the autoregressive parameters. For non-restricted models: a list of size (pxq_m) constraint matrices C_m of full column rank satisfying $\phi_m = C_m\psi_m$ for all $m = 1, \dots, M$, where $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$ and $\psi_m = (\psi_{m,1}, \dots, \psi_{m,q_m})$. For restricted models: a size (pxq) constraint matrix C of full column rank satisfying $\phi = C\psi$, where $\phi = (\phi_1, \dots, \phi_p)$ and $\psi = (\psi_1, \dots, \psi_q)$.
parametrization	Symbol ϕ denotes an AR coefficient. Note that regardless of any constraints, the nominal autoregressive order is always p for all regimes. Ignore or set to NULL if applying linear constraints is not desired.
to_return	is the model parametrized with the "intercepts" $\phi_{m,0}$ or "means" $\mu_m = \phi_{m,0} / (1 - \sum \phi_{i,m})$? calculate regimewise conditional means (regime_cmeans), regimewise conditional variances (regime_cvars), total conditional means (total_cmeans), or total conditional variances (total_cvars)?

Value

Note that the first p observations are taken as the initial values so the conditional moments start from the p+1:th observation (interpreted as t=1).

if to_return=="regime_cmeans": a size $((n_obs-p) \times M)$ matrix containing the regime specific conditional means.

if to_return=="regime_cvars": a size $((n_obs-p) \times M)$ matrix containing the regime specific conditional variances.

if to_return=="total_cmeans": a size $((n_obs-p) \times 1)$ vector containing the total conditional means.

if to_return=="total_cvars": a size $((n_obs-p) \times 1)$ vector containing the total conditional variances.

References

- Galbraith, R., Galbraith, J. 1974. On the inverses of some patterned matrices arising in the theory of stationary time series. *Journal of Applied Probability* **11**, 63-71.
- Kalliovirta L. (2012) Misspecification tests based on quantile residuals. *The Econometrics Journal*, **15**, 358-393.
- Kalliovirta L., Meitz M. and Saikkonen P. 2015. Gaussian Mixture Autoregressive model for univariate time series. *Journal of Time Series Analysis*, **36**, 247-266.
- Meitz M., Preve D., Saikkonen P. 2018. A mixture autoregressive model based on Student's t-distribution. arXiv:1805.04010 [econ.EM].
- Virolainen S. 2020. A mixture autoregressive model based on Gaussian and Student's t-distribution. arXiv:2003.05221 [econ.EM].

See Also

Other moment functions: [get_regime_autocovs\(\)](#), [get_regime_means\(\)](#), [get_regime_vars\(\)](#), [uncond_moments\(\)](#)

Examples

```
# GMAR model, regimewise conditional means and variances
params12 <- c(1.70, 0.85, 0.30, 4.12, 0.73, 1.98, 0.63)
cond_moments(simudata, p=1, M=2, params=params12, model="GMAR",
             to_return="regime_cmeans")
cond_moments(simudata, p=1, M=2, params=params12, model="GMAR",
             to_return="regime_cvars")

# G-StMAR-model, total conditional means and variances
params42gs <- c(0.04, 1.34, -0.59, 0.54, -0.36, 0.01, 0.06, 1.28, -0.36,
              0.2, -0.15, 0.04, 0.19, 9.75)
cond_moments(M10Y1Y, p=4, M=c(1, 1), params=params42gs, model="G-StMAR",
             to_return="total_cmeans")
cond_moments(M10Y1Y, p=4, M=c(1, 1), params=params42gs, model="G-StMAR",
             to_return="total_cvars")
```

cond_moment_plot	<i>Conditional mean or variance plot for GMAR, StMAR, and G-StMAR models</i>
------------------	--

Description

cond_moment_plot plots the one-step in-sample conditional means/variances of the model along with the time series contained in the model (e.g. the time series the model was fitted to). Also plots the regimewise conditional means/variances multiplied with the mixing weights.

Usage

```
cond_moment_plot(gsmar, which_moment = c("mean", "variance"))
```


Arguments

gsmar object of class 'gsmar' created with the function `fitGSMAR` or `GSMAR`.
 which_moment should conditional means or variances be plotted?

Details

The conditional mean plot works best if the data contains positive values only.

Value

`cond_moment_plot` only plots to a graphical device and does not return anything. Numerical values of the conditional means/variances can be extracted from the model with the dollar sign.

References

- Galbraith, R., Galbraith, J. 1974. On the inverses of some patterned matrices arising in the theory of stationary time series. *Journal of Applied Probability* **11**, 63-71.
- Kalliovirta L. (2012) Misspecification tests based on quantile residuals. *The Econometrics Journal*, **15**, 358-393.
- Kalliovirta L., Meitz M. and Saikkonen P. 2015. Gaussian Mixture Autoregressive model for univariate time series. *Journal of Time Series Analysis*, **36**, 247-266.
- Meitz M., Preve D., Saikkonen P. 2018. A mixture autoregressive model based on Student's t-distribution. arXiv:1805.04010 [econ.EM].
- Virolainen S. 2020. A mixture autoregressive model based on Gaussian and Student's t-distribution. arXiv:2003.05221 [econ.EM].

See Also

[profile_logliks](#), [diagnostic_plot](#), [fitGSMAR](#), [GSMAR](#), [quantile_residual_tests](#), [quantile_residual_plot](#)

Examples

```
# GMAR model
params12 <- c(1.70, 0.85, 0.30, 4.12, 0.73, 1.98, 0.63)
gmar12 <- GSMAR(data=simudata, p=1, M=2, params=params12, model="GMAR")
cond_moment_plot(gmar12, which_moment="mean")
cond_moment_plot(gmar12, which_moment="variance")

# G-StMAR model
params42gs <- c(0.04, 1.34, -0.59, 0.54, -0.36, 0.01, 0.06, 1.28, -0.36,
               0.2, -0.15, 0.04, 0.19, 9.75)
gstmar42 <- GSMAR(data=M10Y1Y, p=4, M=c(1, 1), params=params42gs,
                  model="G-StMAR")
cond_moment_plot(gstmar42, which_moment="mean")
cond_moment_plot(gstmar42, which_moment="variance")
```

diagnosticPlot	<i>DEPRECATED, USE diagnostic_plot INSTEAD! Quantile residual based diagnostic plots for GMAR, StMAR, and G-StMAR models</i>
----------------	--

Description

diagnosticPlot plots quantile residual time series, normal QQ-plot, autocorrelation function, and squared quantile residual autocorrelation function. There is an option to also plot the individual statistics associated with the quantile residual tests (for autocorrelation and conditional heteroskedasticity) divided by their approximate standard errors with their approximate 95% critical bounds (see Kalliovirta 2012, Section 3). DEPRECATED, USE diagnostic_plot INSTEAD!

Usage

```
diagnosticPlot(gsmar, nlags = 20, nsimu = 1, plot_indstats = FALSE)
```

Arguments

gsmar	object of class 'gsmar' created with the function fitGSMAR or GSMAR.
nlags	a positive integer specifying how many lags should be calculated for the autocorrelation and conditional heteroscedasticity statistics.
nsimu	a positive integer specifying to how many simulated values from the process the covariance matrix "Omega" (used to compute the tests) should be based on. Larger number of simulations may result more reliable tests but takes longer to compute. If smaller than data size, then "Omega" will be based on the given data. Ignored if plot_indstats==FALSE.
plot_indstats	set TRUE if the individual statistics discussed in Kalliovirta (2012) should be plotted with their approximate 95% critical bounds (this may take some time).

Details

DEPRECATED, USE diagnostic_plot INSTEAD!

Sometimes the individual statistics are not plotted because it was not (numerically) possible to calculate all the required statistics. This may suggest that the model is misspecified.

The dashed lines plotted with autocorrelation functions (for quantile residuals and their squares) are plus-minus $1.96 * T^{-1/2}$ where T is the sample size (minus the p initial values for conditional models).

Value

diagnostic_plot only plots to a graphical device and does not return anything. Use the function quantile_residual_tests in order to obtain the individual statistics.

Suggested packages

Install the suggested package "gsl" for faster evaluations in the cases of StMAR and G-StMAR models. For large StMAR and G-StMAR models with large data the calculations to obtain the individual statistics may take a significantly long time without the package "gsl".

References

- Galbraith, R., Galbraith, J. 1974. On the inverses of some patterned matrices arising in the theory of stationary time series. *Journal of Applied Probability* **11**, 63-71.
- Kalliovirta L. (2012) Misspecification tests based on quantile residuals. *The Econometrics Journal*, **15**, 358-393.
- Kalliovirta L., Meitz M. and Saikkonen P. 2015. Gaussian Mixture Autoregressive model for univariate time series. *Journal of Time Series Analysis*, **36**, 247-266.
- Meitz M., Preve D., Saikkonen P. 2018. A mixture autoregressive model based on Student's t-distribution. arXiv:1805.04010 [econ.EM].
- Virolainen S. 2020. A mixture autoregressive model based on Gaussian and Student's t-distribution. arXiv:2003.05221 [econ.EM].

See Also

[profile_logliks](#), [get_foc](#), [fitGSMAR](#), [cond_moment_plot](#), [quantile_residual_tests](#), [quantile_residual_plot](#), [simulateGSMAR](#), [LR_test](#), [Wald_test](#)

diagnostic_plot	<i>Quantile residual based diagnostic plots for GMAR, StMAR, and G-StMAR models</i>
-----------------	---

Description

diagnostic_plot plots quantile residual time series, normal QQ-plot, autocorrelation function, and squared quantile residual autocorrelation function. There is an option to also plot the individual statistics associated with the quantile residual tests (for autocorrelation and conditional heteroskedasticity) divided by their approximate standard errors with their approximate 95% critical bounds (see Kalliovirta 2012, Section 3).

Usage

```
diagnostic_plot(gsmar, nlags = 20, nsimu = 1, plot_indstats = FALSE)
```

Arguments

gsmar	object of class 'gsmar' created with the function fitGSMAR or GSMAR.
nlags	a positive integer specifying how many lags should be calculated for the autocorrelation and conditional heteroscedasticity statistics.

nsimu	a positive integer specifying to how many simulated values from the process the covariance matrix "Omega" (used to compute the tests) should be based on. Larger number of simulations may result more reliable tests but takes longer to compute. If smaller than data size, then "Omega" will be based on the given data. Ignored if plot_indstats==FALSE.
plot_indstats	set TRUE if the individual statistics discussed in Kalliovirta (2012) should be plotted with their approximate 95% critical bounds (this may take some time).

Details

Sometimes the individual statistics are not plotted because it was not (numerically) possible to calculate all the required statistics. This may suggest that the model is misspecified.

The dashed lines plotted with autocorrelation functions (for quantile residuals and their squares) are plus-minus $1.96 * T^{-1/2}$ where T is the sample size (minus the p initial values for conditional models).

Value

diagnostic_plot only plots to a graphical device and does not return anything. Use the function quantile_residual_tests in order to obtain the individual statistics.

Suggested packages

Install the suggested package "gsl" for faster evaluations in the cases of StMAR and G-StMAR models. For large StMAR and G-StMAR models with large data the calculations to obtain the individual statistics may take a significantly long time without the package "gsl".

References

- Galbraith, R., Galbraith, J. 1974. On the inverses of some patterned matrices arising in the theory of stationary time series. *Journal of Applied Probability* **11**, 63-71.
- Kalliovirta L. (2012) Misspecification tests based on quantile residuals. *The Econometrics Journal*, **15**, 358-393.
- Kalliovirta L., Meitz M. and Saikkonen P. 2015. Gaussian Mixture Autoregressive model for univariate time series. *Journal of Time Series Analysis*, **36**, 247-266.
- Meitz M., Preve D., Saikkonen P. 2018. A mixture autoregressive model based on Student's t-distribution. arXiv:1805.04010 [econ.EM].
- Virolainen S. 2020. A mixture autoregressive model based on Gaussian and Student's t-distribution. arXiv:2003.05221 [econ.EM].

See Also

[profile_logliks](#), [get_foc](#), [fitGSMAR](#), [cond_moment_plot](#), [quantile_residual_tests](#), [quantile_residual_plot](#), [simulateGSMAR](#), [LR_test](#), [Wald_test](#)

Examples

```
## The below examples take approximately 30 seconds to run.

# G-StMAR model with one GMAR type and one StMAR type regime
fit42gs <- fitGSMAR(M10Y1Y, p=4, M=c(1, 1), model="G-StMAR",
                  ncalls=1, seeds=4)
diagnostic_plot(fit42gs)

# Restricted StMAR model: plot also the individual statistics with
# their approximate critical bounds using the given data (and not
# simulation procedure)
fit42tr <- fitGSMAR(M10Y1Y, p=4, M=2, model="StMAR", restricted=TRUE,
                  ncalls=1, seeds=1)
diagnostic_plot(fit42tr, nlags=10, nsimu=1, plot_indstats=TRUE)

# GMAR model, plot 30 lags.
fit12 <- fitGSMAR(data=simudata, p=1, M=2, model="GMAR", ncalls=1, seeds=1)
diagnostic_plot(fit12, nlags=30)
```

extract_regime

Extract regime from a parameter vector

Description

extract_regime extracts the specified regime from the GMAR, StMAR, or G-StMAR model parameter vector. Doesn't extract mixing weight parameter α .

Usage

```
extract_regime(
  p,
  M,
  params,
  model = c("GMAR", "StMAR", "G-StMAR"),
  restricted = FALSE,
  constraints = NULL,
  regime,
  with_dfs = TRUE
)
```

Arguments

p a positive integer specifying the autoregressive order of the model.

M **For GMAR and StMAR models:** a positive integer specifying the number of mixture components.

	<p>For G-StMAR models: a size (2×1) integer vector specifying the number of <i>GMAR type</i> components $M1$ in the first element and <i>StMAR type</i> components $M2$ in the second element. The total number of mixture components is $M=M1+M2$.</p>
params	<p>a real valued parameter vector specifying the model.</p> <p>For non-restricted models: For GMAR model: Size $(M(p+3) - 1 \times 1)$ vector $\theta=(v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1})$, where $v_m = (\phi_{m,0}, \phi_m, \sigma_m^2)$ and $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$, $m = 1, \dots, M$.</p> <p>For StMAR model: Size $(M(p+4) - 1 \times 1)$ vector $(\theta, \nu) = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.</p> <p>For G-StMAR model: Size $(M(p+3) + M2 - 1 \times 1)$ vector $(\theta, \nu) = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_{M1+1}, \dots, \nu_M)$.</p> <p>With linear constraints: Replace the vectors ϕ_m with vectors ψ_m and provide a list of constraint matrices \mathbf{C} that satisfy $\phi_m = R_m \psi_m$ for all $m = 1, \dots, M$, where $\psi_m = (\psi_{m,1}, \dots, \psi_{m,q_m})$.</p> <p>For restricted models: For GMAR model: Size $(3M + p - 1 \times 1)$ vector $\theta = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1})$, where $\phi = (\phi_1, \dots, \phi_p)$.</p> <p>For StMAR model: Size $(4M + p - 1 \times 1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.</p> <p>For G-StMAR model: Size $(3M + M2 + p - 1 \times 1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1}, \nu_{M1+1}, \dots, \nu_M)$.</p> <p>With linear constraints: Replace the vector ϕ with vector ψ and provide a constraint matrix C that satisfies $\phi = R\psi$, where $\psi = (\psi_1, \dots, \psi_q)$.</p> <p>Symbol ϕ denotes an AR coefficient, σ^2 a variance, α a mixing weight, and ν a degrees of freedom parameter. If parametrization="mean", just replace each intercept term $\phi_{m,0}$ with regimewise mean $\mu_m = \phi_{m,0} / (1 - \sum \phi_{i,m})$. In the G-StMAR model, the first $M1$ components are <i>GMAR type</i> and the rest $M2$ components are <i>StMAR type</i>. Note that in the case $\mathbf{M=1}$, the parameter α is dropped, and in the case of StMAR or G-StMAR model, the degrees of freedom parameters ν_m have to be larger than 2.</p>
model	<p>is "GMAR", "StMAR", or "G-StMAR" model considered? In the G-StMAR model, the first $M1$ components are <i>GMAR type</i> and the rest $M2$ components are <i>StMAR type</i>.</p>
restricted	<p>a logical argument stating whether the AR coefficients $\phi_{m,1}, \dots, \phi_{m,p}$ are restricted to be the same for all regimes.</p>
constraints	<p>specifies linear constraints applied to the autoregressive parameters.</p> <p>For non-restricted models: a list of size (pxq_m) constraint matrices C_m of full column rank satisfying $\phi_m = C_m \psi_m$ for all $m = 1, \dots, M$, where $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$ and $\psi_m = (\psi_{m,1}, \dots, \psi_{m,q_m})$.</p> <p>For restricted models: a size (pxq) constraint matrix C of full column rank satisfying $\phi = C\psi$, where $\phi = (\phi_1, \dots, \phi_p)$ and $\psi = (\psi_1, \dots, \psi_q)$.</p> <p>Symbol ϕ denotes an AR coefficient. Note that regardless of any constraints, the nominal autoregressive order is always p for all regimes. Ignore or set to NULL if applying linear constraints is not desired.</p>
regime	<p>a positive integer in the interval $[1, M]$ defining which regime should be extracted.</p>
with_dfs	<p>Should the degrees of freedom parameter (if any) be included?</p>

Value

Returns a numeric vector corresponding to the regime with...

For non-restricted models: For GMAR model: Size $(p+2x1)$ vector $(\phi_{m,0}, \phi_{m,1}, \dots, \phi_{m,p}, \sigma_m^2)$.

For StMAR model: Size $(p + 3x1)$ vector $(\phi_{m,0}, \phi_{m,1}, \dots, \phi_{m,p}, \sigma_m^2, \nu_m)$.

For G-StMAR model: Same as GMAR for GMAR-components and same as StMAR for StMAR-components.

With linear constraints: Parameter vector as described above, but vector ϕ_m replaced with vector ψ_m that satisfies $\phi_m = R_m \psi_m$.

For restricted models: For GMAR model: Size $(2x1)$ vector $(\phi_{m,0}, \sigma_m^2)$.

For StMAR model: Size $(3x1)$ vector $(\phi_{m,0}, \sigma_m^2, \nu_m)$.

For G-StMAR model: Same as GMAR for GMAR-components and same as StMAR for StMAR-components.

With linear constraints: Parameter vector as described above.

 fitGSMAR

Estimate Gaussian or Student's t Mixture Autoregressive model

Description

fitGSMAR estimates GMAR, StMAR, or G-StMAR model in two phases. In the first phase, a genetic algorithm is employed to find starting values for a gradient based method. In the second phase, the gradient based variable metric algorithm is utilized to accurately converge to a local maximum or a saddle point near each starting value. Parallel computing is used to conduct multiple rounds of estimations in parallel.

Usage

```
fitGSMAR(
  data,
  p,
  M,
  model = c("GMAR", "StMAR", "G-StMAR"),
  restricted = FALSE,
  constraints = NULL,
  conditional = TRUE,
  parametrization = c("intercept", "mean"),
  ncalls = round(10 + 9 * log(sum(M))),
  ncores = min(2, ncalls, parallel::detectCores()),
  maxit = 300,
  seeds = NULL,
  print_res = TRUE,
  ...
)
```

Arguments

data	a numeric vector or class 'ts' object containing the data. NA values are not supported.
p	a positive integer specifying the autoregressive order of the model.
M	For GMAR and StMAR models: a positive integer specifying the number of mixture components. For G-StMAR models: a size (2x1) integer vector specifying the number of <i>GMAR type</i> components M1 in the first element and <i>StMAR type</i> components M2 in the second element. The total number of mixture components is $M=M1+M2$.
model	is "GMAR", "StMAR", or "G-StMAR" model considered? In the G-StMAR model, the first M1 components are <i>GMAR type</i> and the rest M2 components are <i>StMAR type</i> .
restricted	a logical argument stating whether the AR coefficients $\phi_{m,1}, \dots, \phi_{m,p}$ are restricted to be the same for all regimes.
constraints	specifies linear constraints applied to the autoregressive parameters. For non-restricted models: a list of size (pxq_m) constraint matrices C_m of full column rank satisfying $\phi_m=C_m\psi_m$ for all $m = 1, \dots, M$, where $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$ and $\psi_m = (\psi_{m,1}, \dots, \psi_{m,q_m})$. For restricted models: a size (pxq) constraint matrix C of full column rank satisfying $\phi=C\psi$, where $\phi = (\phi_1, \dots, \phi_p)$ and $\psi = (\psi_1, \dots, \psi_q)$. Symbol ϕ denotes an AR coefficient. Note that regardless of any constraints, the nominal autoregressive order is always p for all regimes. Ignore or set to NULL if applying linear constraints is not desired.
conditional	a logical argument specifying whether the conditional or exact log-likelihood function should be used.
parametrization	is the model parametrized with the "intercepts" $\phi_{m,0}$ or "means" $\mu_m = \phi_{m,0}/(1 - \sum \phi_{i,m})$?
ncalls	a positive integer specifying how many rounds of estimation should be conducted. The estimation results may vary from round to round because of multimodality of the log-likelihood function and the randomness associated with the genetic algorithm.
ncores	the number of CPU cores to be used in the estimation process.
maxit	the maximum number of iterations for the variable metric algorithm.
seeds	a length ncalls vector containing the random number generator seed for each call to the genetic algorithm, or NULL for not initializing the seed. Exists for the purpose of creating reproducible results.
print_res	should the estimation results be printed?
...	additional settings passed to the function GAFit employing the genetic algorithm.

Details

Because of complexity and multimodality of the log-likelihood function, it's **not guaranteed** that the estimation algorithm will end up in the global maximum point. It's often expected that most of the estimation rounds will end up in some local maximum point instead, and therefore a number of estimation rounds is required for reliable results. Because of the nature of the models, the estimation may fail particularly in the cases where the number of mixture components is chosen too large. Note that the genetic algorithm is designed to avoid solutions with mixing weights of some regimes too close to zero at almost all times ("redundant regimes") but the settings can, however, be adjusted (see ?GAfit).

If the iteration limit for the variable metric algorithm (`maxit`) is reached, one can continue the estimation by iterating more with the function `iterate_more`.

The core of the genetic algorithm is mostly based on the description by *Dorsey and Mayer (1995)*. It utilizes a slightly modified version the individually adaptive crossover and mutation rates described by *Patnaik and Srinivas (1994)* and employs (50%) fitness inheritance discussed by *Smith, Dike and Stegmann (1995)*. Large (in absolute value) but stationary AR parameter values are generated with the algorithm proposed by Monahan (1984).

The variable metric algorithm (or quasi-Newton method, Nash (1990, algorithm 21)) used in the second phase is implemented with function `optim` from the package `stats`.

Additional Notes about the estimates:

Sometimes the found MLE is very close to the boundary of the stationarity region some regime, the related variance parameter is very small, and the associated mixing weights are "spiky". This kind of estimates often maximize the log-likelihood function for a technical reason that induces by the endogenously determined mixing weights. In such cases, it might be more appropriate to consider the next-best local maximum point of the log-likelihood function that is well inside the parameter space. Models based local-only maximum points can be built with the function `alt_gsmar` by adjusting the argument `which_largest` accordingly.

Some mixture components of the StMAR model may sometimes get very large estimates for the degrees of freedom parameters. Such parameters are weakly identified and induce various numerical problems. However, mixture components with large degree of freedom parameters are similar to the mixture components of the GMAR model. It's hence advisable to further estimate a G-StMAR model by allowing the mixture components with large degrees of freedom parameter estimates to be GMAR type with the function `stmar_to_gstmar`.

Value

Returns an object of class 'gsmar' defining the estimated GMAR, StMAR or G-StMAR model. The returned object contains estimated mixing weights, some conditional and unconditional moments, quantile residuals, and quantile residual test results if the tests were performed. Note that the first `p` observations are taken as the initial values so the mixing weights, conditional moments, and quantile residuals start from the `p+1`:th observation (interpreted as `t=1`). In addition, the returned object contains the estimates and log-likelihood values from all of the estimation rounds. The estimated parameter vector can be obtained as `gsmar$params` (and the corresponding approximate standard errors as `gsmar$std_errors`) and it's...

For non-restricted models: For GMAR model: Size $(M(p + 3) - 1 \times 1)$ vector $\theta = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1})$, where $v_m = (\phi_{m,0}, \phi_m, \sigma_m^2)$ and $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$, $m = 1, \dots, M$.

For StMAR model: Size $(M(p+4) - 1 \times 1)$ vector $(\theta, \nu) = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.

For G-StMAR model: Size $(M(p+3)+M2-1x1)$ vector $(\theta, \nu)=(v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_{M1+1}, \dots, \nu_M)$.

With linear constraints: Replace the vectors ϕ_m with vectors ψ_m and provide a list of constraint matrices C that satisfy $\phi_m=C_m\psi_m$ for all $m = 1, \dots, M$, where $\psi_m = (\psi_{m,1}, \dots, \psi_{m,q_m})$.

For restricted models: For GMAR model: Size $(3M+p-1x1)$ vector $\theta = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1})$, where $\phi = (\phi_1, \dots, \phi_p)$.

For StMAR model: Size $(4M+p-1x1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.

For G-StMAR model: Size $(3M+M2+p-1x1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1}, \nu_{M1+1}, \dots, \nu_M)$.

With linear constraints: Replace the vector ϕ with vector ψ and provide a constraint matrix C that satisfies $\phi=C\psi$, where $\psi = (\psi_1, \dots, \psi_q)$.

Symbol ϕ denotes an AR coefficient, σ^2 a variance, α a mixing weight, and ν a degrees of freedom parameter. If parametrization=="mean" just replace each intercept term $\phi_{m,0}$ with regimewise mean $\mu_m = \phi_{m,0}/(1 - \sum \phi_{i,m})$. In the **G-StMAR** model, the first M1 components are *GMAR type* and the rest M2 components are *StMAR type*. Note that in the case **M=1** the parameter α is dropped, and in the case of **StMAR** or **G-StMAR** model the degrees of freedom parameters ν_m have to be larger than 2.

S3 methods

The following S3 methods are supported for class 'gsmar' objects: print, summary, plot, logLik, residuals.

References

- Dorsey R. E. and Mayer W. J. 1995. Genetic algorithms for estimation problems with multiple optima, nondifferentiability, and other irregular features. *Journal of Business & Economic Statistics*, **13**, 53-66.
- Kalliovirta L., Meitz M. and Saikkonen P. 2015. Gaussian Mixture Autoregressive model for univariate time series. *Journal of Time Series Analysis*, **36**, 247-266.
- Meitz M., Preve D., Saikkonen P. 2018. A mixture autoregressive model based on Student's t-distribution. arXiv:1805.04010 [econ.EM].
- Monahan J.F. 1984. A Note on Enforcing Stationarity in Autoregressive-Moving Average Models. *Biometrika* **71**, 403-404.
- Nash J. 1990. Compact Numerical Methods for Computers. Linear algebra and Function Minimization. *Adam Hilger*.
- Patnaik L.M. and Srinivas M. 1994. Adaptive Probabilities of Crossover and Mutation in Genetic Algorithms. *Transactions on Systems, Man and Cybernetics* **24**, 656-667.
- Smith R.E., Dike B.A., Stegmann S.A. 1995. Fitness inheritance in genetic algorithms. *Proceedings of the 1995 ACM Symposium on Applied Computing*, 345-350.
- Virolainen S. 2020. A mixture autoregressive model based on Gaussian and Student's t-distribution. arXiv:2003.05221 [econ.EM].

See Also

[GSMAR](#), [iterate_more](#), [stmar_to_gstmar](#), [add_data](#), [profile_logliks](#), [swap_parametrization](#), [get_gradient](#), [simulateGSMAR](#), [predict.gsmar](#), [diagnostic_plot](#), [quantile_residual_tests](#), [cond_moments](#), [uncond_moments](#), [LR_test](#), [Wald_test](#)

Examples

```

## These are long running examples that use parallel computing.
## The below examples take approximately 90 seconds to run.

## Note that the number of estimation rounds (ncalls) is relatively small
## in the below examples. For reliable results, a large number of estimation
## rounds is recommended!

# GMAR model
fit12 <- fitGSMAR(data=simudata, p=1, M=2, model="GMAR", ncalls=4, seeds=1:4)
summary(fit12)
plot(fit12)
profile_logliks(fit12)
diagnostic_plot(fit12)

# StMAR model (boundary estimate + large degrees of freedom)
fit42t <- fitGSMAR(data=M10Y1Y, p=4, M=2, model="StMAR", ncalls=6, seeds=1:6)
summary(fit42t, digits=4) # Four almost-unit roots in the 2nd regime!
plot(fit42t) # Spiky mixing weights!
fit42t_alt <- alt_gsmar(fit42t, which_largest=2) # Second largest local max
summary(fit42t_alt) # Overly large 2nd regime degrees of freedom estimate!
fit42gs <- stmar_to_gstmar(fit42t_alt) # Switch to G-StMAR model
summary(fit42gs) # Finally, an appropriate model!
plot(fit42gs)

# Restricted StMAR model
fit42r <- fitGSMAR(M10Y1Y, p=4, M=2, model="StMAR", restricted=TRUE,
                  ncalls=2, seeds=1:2)
fit42r

# G-StMAR model with one GMAR type and one StMAR type regime
fit42gs <- fitGSMAR(M10Y1Y, p=4, M=c(1, 1), model="G-StMAR",
                  ncalls=1, seeds=4)
fit42gs

# The following three examples demonstrate how to apply linear constraints
# to the autoregressive (AR) parameters.

# Two-regime GMAR p=2 model with the second AR coefficient of
# of the second regime constrained to zero.
C22 <- list(diag(1, ncol=2, nrow=2), as.matrix(c(1, 0)))
fit22c <- fitGSMAR(M10Y1Y, p=2, M=2, constraints=C22, ncalls=1, seeds=6)
fit22c

# StMAR(3, 1) model with the second order AR coefficient constrained to zero.
C31 <- list(matrix(c(1, 0, 0, 0, 0, 1), ncol=2))
fit31tc <- fitGSMAR(M10Y1Y, p=3, M=1, model="StMAR", constraints=C31,
                  ncalls=1, seeds=1)
fit31tc

# Such StMAR(3, 2) model that the AR coefficients are restricted to be

```

```
# the same for both regimes and the second AR coefficients are
# constrained to zero.
fit32rc <- fitGSMAR(M10Y1Y, p=3, M=2, model="StMAR", restricted=TRUE,
                  constraints=matrix(c(1, 0, 0, 0, 0, 1), ncol=2),
                  ncalls=1, seeds=1)

fit32rc
```

format_valuef	<i>Function factory for formatting values</i>
---------------	---

Description

format_valuef generates functions that format values so that they print out with the desired number of digits.

Usage

```
format_valuef(digits)
```

Arguments

digits	number of digits to use
--------	-------------------------

Value

Returns a function that takes an atomic vector as its argument and returns it formatted to character with digits decimals.

GAfit	<i>Genetic algorithm for preliminary estimation of GMAR, StMAR, or G-StMAR model</i>
-------	--

Description

GAfit estimates specified GMAR, StMAR, or G-StMAR model using a genetic algorithm. The employed genetic algorithm is designed to find starting values for gradient based methods.

Usage

```
GAfit(
  data,
  p,
  M,
  model = c("GMAR", "StMAR", "G-StMAR"),
  restricted = FALSE,
  constraints = NULL,
  parametrization = c("intercept", "mean"),
  conditional = TRUE,
  ngen = 200,
  popsize,
  smart_mu = min(100, ceiling(0.5 * ngen)),
  mu_scale,
  sigma_scale,
  initpop = NULL,
  regime_force_scale = 1,
  red_criteria = c(0.05, 0.01),
  to_return = c("alt_ind", "best_ind"),
  minval,
  seed = NULL,
  ...
)
```

Arguments

data	a numeric vector or class 'ts' object containing the data. NA values are not supported.
p	a positive integer specifying the autoregressive order of the model.
M	For GMAR and StMAR models: a positive integer specifying the number of mixture components. For G-StMAR models: a size (2x1) integer vector specifying the number of <i>GMAR type</i> components M1 in the first element and <i>StMAR type</i> components M2 in the second element. The total number of mixture components is $M=M1+M2$.
model	is "GMAR", "StMAR", or "G-StMAR" model considered? In the G-StMAR model, the first M1 components are <i>GMAR type</i> and the rest M2 components are <i>StMAR type</i> .
restricted	a logical argument stating whether the AR coefficients $\phi_{m,1}, \dots, \phi_{m,p}$ are restricted to be the same for all regimes.
constraints	specifies linear constraints applied to the autoregressive parameters. For non-restricted models: a list of size (pxq_m) constraint matrices C_m of full column rank satisfying $\phi_m=C_m\psi_m$ for all $m = 1, \dots, M$, where $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$ and $\psi_m = (\psi_{m,1}, \dots, \psi_{m,q_m})$. For restricted models: a size (pxq) constraint matrix C of full column rank satisfying $\phi=C\psi$, where $\phi = (\phi_1, \dots, \phi_p)$ and $\psi = \psi_1, \dots, \psi_q$.

Symbol ϕ denotes an AR coefficient. Note that regardless of any constraints, the nominal autoregressive order is always p for all regimes. Ignore or set to NULL if applying linear constraints is **not** desired.

parametrization	is the model parametrized with the "intercepts" $\phi_{m,0}$ or "means" $\mu_m = \phi_{m,0}/(1 - \sum \phi_{i,m})$?
conditional	a logical argument specifying whether the conditional or exact log-likelihood function should be used.
ngen	a positive integer specifying the number of generations to be ran through in the genetic algorithm.
popsize	a positive even integer specifying the population size in the genetic algorithm. Default is $10*d$ where d is the number of parameters.
smart_mu	a positive integer specifying the generation after which the random mutations in the genetic algorithm are "smart". This means that mutating individuals will mostly mutate fairly close (or partially close) to the best fitting individual so far.
mu_scale	a real valued vector of length two specifying the mean (the first element) and standard deviation (the second element) of the normal distribution from which the μ_m mean-parameters are generated in random mutations in the genetic algorithm. Default is $c(\text{mean}(\text{data}), \text{sd}(\text{data}))$. Note that the genetic algorithm optimizes with mean-parametrization even when <code>parametrization=="intercept"</code> , but input (in <code>initpop</code>) and output (return value) parameter vectors may be intercept-parametrized.
sigma_scale	a positive real number specifying the standard deviation of the (zero mean, positive only by taking absolute value) normal distribution from which the component variance parameters are generated in the random mutations in the genetic algorithm. Default is <code>var(stats::ar(data, order.max=10)\$resid, na.rm=TRUE)</code> .
initpop	a list of parameter vectors from which the initial population of the genetic algorithm will be generated from. The parameter vectors should be of form...

For non-restricted models: For GMAR model: Size $(M(p+3) - 1 \times 1)$ vector $\theta = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1})$, where $v_m = (\phi_{m,0}, \phi_m, \sigma_m^2)$ and $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$, $m = 1, \dots, M$.

For StMAR model: Size $(M(p+4) - 1 \times 1)$ vector $(\theta, \nu) = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.

For G-StMAR model: Size $(M(p+3) + M - 1 \times 1)$ vector $(\theta, \nu) = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_{M+1}, \dots, \nu_M)$.

With linear constraints: Replace the vectors ϕ_m with vectors ψ_m and provide a list of constraint matrices \mathbf{C} that satisfy $\phi_m = \mathbf{C}_m \psi_m$ for all $m = 1, \dots, M$, where $\psi_m = (\psi_{m,1}, \dots, \psi_{m,q_m})$.

For restricted models: For GMAR model: Size $(3M + p - 1 \times 1)$ vector $\theta = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1})$, where $\phi = (\phi_1, \dots, \phi_p)$.

For StMAR model: Size $(4M + p - 1 \times 1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.

For G-StMAR model: Size $(3M + M + p - 1 \times 1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1}, \nu_{M+1}, \dots, \nu_M)$.

With linear constraints: Replace the vector ϕ with vector ψ and provide a constraint matrix \mathbf{C} that satisfies $\phi = \mathbf{C}\psi$, where $\psi = (\psi_1, \dots, \psi_q)$.

Symbol ϕ denotes an AR coefficient, σ^2 a variance, α a mixing weight, and ν a degrees of freedom parameter. Note that in the case $\mathbf{M}=\mathbf{1}$, the parameter

α is dropped, and in the case of **StMAR** or **G-StMAR** model, the degrees of freedom parameters ν_m have to be larger than 2. If not specified (or FALSE as default), the initial population will be drawn randomly.

regime_force_scale	a non-negative real number specifying how much should natural selection favour individuals with less regimes that have almost all mixing weights (practically) at zero (see red_criteria), i.e., with less "redundant regimes". Set to zero for no favouring or large number for heavy favouring. Without any favouring the genetic algorithm gets more often stuck in an area of the parameter space where some regimes are wasted, but with too much favouring the best genes might never mix into the population and the algorithm might converge poorly. Default is 1 and it gives $2x$ larger surviving probability weights for individuals with no wasted regimes compared to individuals with one wasted regime. Number 2 would give $3x$ larger probabilities etc.
red_criteria	a length 2 numeric vector specifying the criteria that is used to determine whether a regime is redundant or not. Any regime m which satisfies $\text{sum}(\text{mixing_weights}[,m] > \text{red_criteria}[1]) < \text{red_criteria}[2] * n_obs$ will be considered "redundant". One should be careful when adjusting this argument (set $c(0, 0)$ to fully disable the 'redundant regime' features from the algorithm).
to_return	should the genetic algorithm return the best fitting individual which has the least "redundant" regimes ("alt_ind") or the individual which has the highest log-likelihood in general ("best_ind") but might have more wasted regimes?
minval	a real number defining the minimum value of the log-likelihood function that will be considered. Values smaller than this will be treated as they were minval and the corresponding individuals will never survive. The default is $-(10^{\lceil \log_{10}(\text{length}(\text{data})) + 1 \rceil} - 1)$, and one should be very careful if adjusting this.
seed	a single value, interpreted as an integer, or NULL, that sets seed for the random number generator in the beginning of the function call. If calling GAfit from fitGSMAR, use the argument seeds instead of passing the argument seed.
...	We currently use this to catch deprecated arguments.

Details

The core of the genetic algorithm is mostly based on the description by *Dorsey and Mayer (1995)*. It utilizes a slightly modified version of the individually adaptive crossover and mutation rates described by *Patnaik and Srinivas (1994)* and employs (50%) fitness inheritance discussed by *Smith, Dike and Stegmann (1995)*. Large (in absolute value) but stationary AR parameter values are generated with the algorithm proposed by *Monahan (1984)*.

By "redundant" or "wasted" regimes we mean regimes that have the time varying mixing weights basically at zero for all t . The model with redundant regimes would have approximately the same log-likelihood value without the redundant regimes and there is no purpose to have redundant regimes in the model.

Value

Returns estimated parameter vector with the form described in `initpop`.

References

- Dorsey R. E. and Mayer W. J. 1995. Genetic algorithms for estimation problems with multiple optima, nondifferentiability, and other irregular features. *Journal of Business & Economic Statistics*, **13**, 53-66.
- Kalliovirta L., Meitz M. and Saikkonen P. 2015. Gaussian Mixture Autoregressive model for univariate time series. *Journal of Time Series Analysis*, **36**, 247-266.
- Meitz M., Preve D., Saikkonen P. 2018. A mixture autoregressive model based on Student's t-distribution. arXiv:1805.04010 [econ.EM].
- Monahan J.F. 1984. A Note on Enforcing Stationarity in Autoregressive-Moving Average Models. *Biometrika* **71**, 403-404.
- Patnaik L.M. and Srinivas M. 1994. Adaptive Probabilities of Crossover and Mutation in Genetic Algorithms. *Transactions on Systems, Man and Cybernetics* **24**, 656-667.
- Smith R.E., Dike B.A., Stegmann S.A. 1995. Fitness inheritance in genetic algorithms. *Proceedings of the 1995 ACM Symposium on Applied Computing*, 345-350.
- Virolainen S. 2020. A mixture autoregressive model based on Gaussian and Student's t-distribution. arXiv:2003.05221 [econ.EM].

get_alpha_mt

Get mixing weights alpha_mt (this function is for internal use)

Description

get_alpha_mt computes the mixing weights based on the logarithm of the multivariate normal densities in the definition of the mixing weights.

Usage

```
get_alpha_mt(
  M,
  log_mvnvalues,
  alphas,
  epsilon,
  conditional,
  to_return,
  also_l_0 = FALSE
)
```

Arguments

M **For GMAR and StMAR models:** a positive integer specifying the number of mixture components.

For G-StMAR models: a size (2x1) integer vector specifying the number of *GMAR type* components M1 in the first element and *StMAR type* components M2 in the second element. The total number of mixture components is $M=M1+M2$.

log_mvvalues	$T \times M$ matrix containing the log multivariate normal densities.
alphas	$M \times 1$ vector containing the mixing weight pa
epsilon	the smallest number such that its exponent is wont classified as numerically zero (around -698 is used).
conditional	a logical argument specifying whether the conditional or exact log-likelihood function should be used.
to_return	should the returned object be the log-likelihood value, mixing weights, mixing weights including value for $\alpha_{m,T+1}$, a list containing log-likelihood value and mixing weights, the terms $l_t : t = 1, \dots, T$ in the log-likelihood function (see <i>KMS 2015, eq.(13)</i>), regimewise conditional means, regimewise conditional variances, total conditional means, total conditional variances, or quantile residuals? Default is the log-likelihood value ("loglik").
also_l_0	return also l_0 (the first term in the exact log-likelihood function)?

Details

Note that we index the time series as $-p + 1, \dots, 0, 1, \dots, T$ as in Kalliovirta et al. (2015).

Value

Returns the mixing weights a matrix of the same dimension as log_mvvalues so that the t:th row is for the time point t and m:th column is for the regime m.

References

- Galbraith, R., Galbraith, J. 1974. On the inverses of some patterned matrices arising in the theory of stationary time series. *Journal of Applied Probability* **11**, 63-71.
- Kalliovirta L. (2012) Misspecification tests based on quantile residuals. *The Econometrics Journal*, **15**, 358-393.
- Kalliovirta L., Meitz M. and Saikkonen P. 2015. Gaussian Mixture Autoregressive model for univariate time series. *Journal of Time Series Analysis*, **36**, 247-266.
- Meitz M., Preve D., Saikkonen P. 2018. A mixture autoregressive model based on Student's t-distribution. arXiv:1805.04010 [econ.EM].
- Virolainen S. 2020. A mixture autoregressive model based on Gaussian and Student's t-distribution. arXiv:2003.05221 [econ.EM].

See Also

[loglikelihood_int](#)

get_ar_roots	<i>Calculate absolute values of the roots of the AR characteristic polynomials</i>
--------------	--

Description

get_ar_roots calculates the absolute values of the roots of the AR characteristic polynomials for each mixture component.

Usage

```
get_ar_roots(gsmar)
```

Arguments

gsmar object of class 'gsmar' created with the function fitGSMAR or GSMAR.

Value

Returns a list with M elements each containing the absolute values of the roots of the AR characteristic polynomial corresponding to each mixture component.

References

- Kalliovirta L., Meitz M. and Saikkonen P. 2015. Gaussian Mixture Autoregressive model for univariate time series. *Journal of Time Series Analysis*, **36**, 247-266.
- Meitz M., Preve D., Saikkonen P. 2018. A mixture autoregressive model based on Student's t-distribution. arXiv:1805.04010 [[econ.EM](#)].
- Virolainen S. 2020. A mixture autoregressive model based on Gaussian and Student's t-distribution. arXiv:2003.05221 [[econ.EM](#)].

Examples

```
params12 <- c(1.70, 0.85, 0.30, 4.12, 0.73, 1.98, 0.63)
gmar12 <- GSMAR(data=simudata, p=1, M=2, params=params12, model="GMAR")
get_ar_roots(gmar12)
```

get_IC	<i>Calculate AIC, HQIC and BIC</i>
--------	------------------------------------

Description

get_IC calculates AIC, HQIC and BIC

Usage

```
get_IC(loglik, npars, obs)
```

Arguments

loglik	log-likelihood value
npars	the number of (freely estimated) parameters in the model.
obs	the number of observations with initial values excluded for conditional models.

Value

Returns a data frame containing the information criteria values.

get_minval	<i>Returns the default smallest allowed log-likelihood for given data.</i>
------------	--

Description

get_minval returns the default smallest allowed log-likelihood for given data.

Usage

```
get_minval(data)
```

Arguments

data	a numeric vector or class 'ts' object containing the data. NA values are not supported.
------	---

Details

This function exists simply to avoid duplication inside the package.

Value

Returns $-(10^{\lceil \log_{10}(\text{length}(\text{data})) \rceil} + 1) - 1$

See Also

[fitGSMAR](#), [Gafit](#)

get_regime_autocovs Calculate regime specific autocovariances $\gamma_{m,p}$

Description

get_regime_autocovs calculates the first p regime specific autocovariances $\gamma_{m,p}$ for the given GMAR, StMAR, or G-StMAR model.

Usage

```
get_regime_autocovs(gsmar)
```

Arguments

gsmar object of class 'gsmar' created with the function fitGSMAR or GSMAR.

Value

Returns a size $(p \times M)$ matrix containing the first p autocovariances of the components processes: i :th autocovariance in the i :th row and m :th component process in the m :th column.

References

- Kalliovirta L., Meitz M. and Saikkonen P. 2015. Gaussian Mixture Autoregressive model for univariate time series. *Journal of Time Series Analysis*, **36**, 247-266.
- Meitz M., Preve D., Saikkonen P. 2018. A mixture autoregressive model based on Student's t -distribution. arXiv:1805.04010 [econ.EM].
- There are currently no published references for the G-StMAR model, but it's a straightforward generalization with theoretical properties similar to the GMAR and StMAR models.
- Lutkepohl H. 2005. New Introduction to Multiple Time Series Analysis. *Springer*.

See Also

Other moment functions: [cond_moments\(\)](#), [get_regime_means\(\)](#), [get_regime_vars\(\)](#), [uncond_moments\(\)](#)

Examples

```
# GMAR model
params13 <- c(1.4, 0.88, 0.26, 2.46, 0.82, 0.74, 5.0, 0.68, 5.2, 0.72, 0.2)
gmar13 <- GSMAR(p=1, M=3, params=params13, model="GMAR")
get_regime_autocovs(gmar13)

# StMAR model
params12t <- c(1.38, 0.88, 0.27, 3.8, 0.74, 3.15, 0.8, 100, 3.6)
stmar12t <- GSMAR(p=1, M=2, params=params12t, model="StMAR")
get_regime_autocovs(stmar12t)

# G-StMAR model (similar to the StMAR model above)
```

```
params12gs <- c(1.38, 0.88, 0.27, 3.8, 0.74, 3.15, 0.8, 3.6)
gstmar12 <- GSMAR(p=1, M=c(1, 1), params=params12gs, model="G-StMAR")
get_regime_autocovs(gstmar12)
```

get_regime_means *Calculate regime specific means μ_m*

Description

get_regime_means calculates the regime means $\mu_m = \phi_{m,0}/(1 - \sum \phi_{i,m})$ for the given GMAR, StMAR, or G-StMAR model

Usage

```
get_regime_means(gsmar)
```

Arguments

gsmar object of class 'gsmar' created with the function fitGSMAR or GSMAR.

Value

Returns a length M vector containing the regime mean μ_m in the m:th element.

References

- Kalliovirta L., Meitz M. and Saikkonen P. 2015. Gaussian Mixture Autoregressive model for univariate time series. *Journal of Time Series Analysis*, **36**, 247-266.
- Meitz M., Preve D., Saikkonen P. 2018. A mixture autoregressive model based on Student's t-distribution. arXiv:1805.04010 [[econ.EM](#)].
- Virolainen S. 2020. A mixture autoregressive model based on Gaussian and Student's t-distribution. arXiv:2003.05221 [[econ.EM](#)].

See Also

[cond_moments](#), [uncond_moments](#), [get_regime_vars](#), [get_regime_autocovs](#)

Other moment functions: [cond_moments\(\)](#), [get_regime_autocovs\(\)](#), [get_regime_vars\(\)](#), [uncond_moments\(\)](#)

Examples

```
# GMAR model
params13 <- c(1.4, 0.88, 0.26, 2.46, 0.82, 0.74, 5.0, 0.68, 5.2, 0.72, 0.2)
gmar13 <- GSMAR(p=1, M=3, params=params13, model="GMAR")
get_regime_means(gmar13)
```

```
# StMAR model
params12t <- c(1.38, 0.88, 0.27, 3.8, 0.74, 3.15, 0.8, 100, 3.6)
stmar12t <- GSMAR(p=1, M=2, params=params12t, model="StMAR")
```

```

get_regime_means(stmar12t)

# G-StMAR model (similar to the StMAR model above)
params12gs <- c(1.38, 0.88, 0.27, 3.8, 0.74, 3.15, 0.8, 3.6)
gstmar12 <- GSMAR(p=1, M=c(1, 1), params=params12gs, model="G-StMAR")
get_regime_means(gstmar12)

```

get_regime_vars Calculate regime specific variances $\gamma_{m,0}$

Description

get_regime_vars calculates the unconditional regime specific variances $\gamma_{m,0}$ for the given GMAR, StMAR, or G-StMAR model.

Usage

```
get_regime_vars(gsmar)
```

Arguments

gsmar object of class 'gsmar' created with the function fitGSMAR or GSMAR.

Value

Returns a length M vector containing the unconditional variances of the components processes: m:th element for the m:th regime.

References

- Kalliovirta L., Meitz M. and Saikkonen P. 2015. Gaussian Mixture Autoregressive model for univariate time series. *Journal of Time Series Analysis*, **36**, 247-266.
- Meitz M., Preve D., Saikkonen P. 2018. A mixture autoregressive model based on Student's t-distribution. arXiv:1805.04010 [[econ.EM](#)].
- There are currently no published references for the G-StMAR model, but it's a straightforward generalization with theoretical properties similar to the GMAR and StMAR models.
- Lutkepohl H. 2005. New Introduction to Multiple Time Series Analysis. *Springer*.

See Also

Other moment functions: [cond_moments\(\)](#), [get_regime_autocovs\(\)](#), [get_regime_means\(\)](#), [uncond_moments\(\)](#)

Examples

```
# GMAR model
params13 <- c(1.4, 0.88, 0.26, 2.46, 0.82, 0.74, 5.0, 0.68, 5.2, 0.72, 0.2)
gmar13 <- GSMAR(p=1, M=3, params=params13, model="GMAR")
get_regime_vars(gmar13)

# StMAR model
params12t <- c(1.38, 0.88, 0.27, 3.8, 0.74, 3.15, 0.8, 100, 3.6)
stmar12t <- GSMAR(p=1, M=2, params=params12t, model="StMAR")
get_regime_vars(stmar12t)

# G-StMAR model (similar to the StMAR model above)
params12gs <- c(1.38, 0.88, 0.27, 3.8, 0.74, 3.15, 0.8, 3.6)
gstmar12 <- GSMAR(p=1, M=c(1, 1), params=params12gs, model="G-StMAR")
get_regime_vars(gstmar12)
```

get_test_Omega

Generate the covariance matrix Omega for quantile residual tests

Description

get_test_Omega generates the covariance matrix Omega used in the quantile residual tests.

Usage

```
get_test_Omega(
  data,
  p,
  M,
  params,
  model = c("GMAR", "StMAR", "G-StMAR"),
  restricted = FALSE,
  constraints = NULL,
  parametrization = c("intercept", "mean"),
  g,
  dim_g
)
```

Arguments

data	a numeric vector or class 'ts' object containing the data. NA values are not supported.
p	a positive integer specifying the autoregressive order of the model.
M	For GMAR and StMAR models: a positive integer specifying the number of mixture components.

	<p>For G-StMAR models: a size (2×1) integer vector specifying the number of <i>GMAR type</i> components $M1$ in the first element and <i>StMAR type</i> components $M2$ in the second element. The total number of mixture components is $M=M1+M2$.</p>
params	<p>a real valued parameter vector specifying the model.</p> <p>For non-restricted models: For GMAR model: Size $(M(p+3) - 1 \times 1)$ vector $\theta=(v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1})$, where $v_m = (\phi_{m,0}, \phi_m, \sigma_m^2)$ and $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$, $m = 1, \dots, M$.</p> <p>For StMAR model: Size $(M(p+4) - 1 \times 1)$ vector $(\theta, \nu) = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.</p> <p>For G-StMAR model: Size $(M(p+3) + M2 - 1 \times 1)$ vector $(\theta, \nu) = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_{M1+1}, \dots, \nu_M)$.</p> <p>With linear constraints: Replace the vectors ϕ_m with vectors ψ_m and provide a list of constraint matrices C that satisfy $\phi_m = R_m \psi_m$ for all $m = 1, \dots, M$, where $\psi_m = (\psi_{m,1}, \dots, \psi_{m,q_m})$.</p> <p>For restricted models: For GMAR model: Size $(3M + p - 1 \times 1)$ vector $\theta = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1})$, where $\phi = (\phi_1, \dots, \phi_p)$.</p> <p>For StMAR model: Size $(4M + p - 1 \times 1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.</p> <p>For G-StMAR model: Size $(3M + M2 + p - 1 \times 1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1}, \nu_{M1+1}, \dots, \nu_M)$.</p> <p>With linear constraints: Replace the vector ϕ with vector ψ and provide a constraint matrix C that satisfies $\phi = R\psi$, where $\psi = (\psi_1, \dots, \psi_q)$.</p> <p>Symbol ϕ denotes an AR coefficient, σ^2 a variance, α a mixing weight, and ν a degrees of freedom parameter. If <code>parametrization=="mean"</code>, just replace each intercept term $\phi_{m,0}$ with regimewise mean $\mu_m = \phi_{m,0} / (1 - \sum \phi_{i,m})$. In the G-StMAR model, the first $M1$ components are <i>GMAR type</i> and the rest $M2$ components are <i>StMAR type</i>. Note that in the case $M=1$, the parameter α is dropped, and in the case of StMAR or G-StMAR model, the degrees of freedom parameters ν_m have to be larger than 2.</p>
model	<p>is "GMAR", "StMAR", or "G-StMAR" model considered? In the G-StMAR model, the first $M1$ components are <i>GMAR type</i> and the rest $M2$ components are <i>StMAR type</i>.</p>
restricted	<p>a logical argument stating whether the AR coefficients $\phi_{m,1}, \dots, \phi_{m,p}$ are restricted to be the same for all regimes.</p>
constraints	<p>specifies linear constraints applied to the autoregressive parameters.</p> <p>For non-restricted models: a list of size $(p \times q_m)$ constraint matrices C_m of full column rank satisfying $\phi_m = C_m \psi_m$ for all $m = 1, \dots, M$, where $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$ and $\psi_m = (\psi_{m,1}, \dots, \psi_{m,q_m})$.</p> <p>For restricted models: a size $(p \times q)$ constraint matrix C of full column rank satisfying $\phi = C\psi$, where $\phi = (\phi_1, \dots, \phi_p)$ and $\psi = (\psi_1, \dots, \psi_q)$.</p> <p>Symbol ϕ denotes an AR coefficient. Note that regardless of any constraints, the nominal autoregressive order is always p for all regimes. Ignore or set to NULL if applying linear constraints is not desired.</p>
parametrization	<p>is the model parametrized with the "intercepts" $\phi_{m,0}$ or "means" $\mu_m = \phi_{m,0} / (1 - \sum \phi_{i,m})$?</p>
g	<p>a function specifying the transformation.</p>
dim_g	<p>output dimension of the transformation g.</p>

Details

This function is used for quantile residuals tests in `quantile_residual_tests`.

Value

Returns size (`dim_gxdim_g`) covariance matrix Omega.

References

- Galbraith, R., Galbraith, J. 1974. On the inverses of some patterned matrices arising in the theory of stationary time series. *Journal of Applied Probability* **11**, 63-71.
- Kalliovirta L. (2012) Misspecification tests based on quantile residuals. *The Econometrics Journal*, **15**, 358-393.
- Kalliovirta L., Meitz M. and Saikkonen P. 2015. Gaussian Mixture Autoregressive model for univariate time series. *Journal of Time Series Analysis*, **36**, 247-266.
- Meitz M., Preve D., Saikkonen P. 2018. A mixture autoregressive model based on Student's t-distribution. arXiv:1805.04010 [[econ.EM](#)].
- Virolainen S. 2020. A mixture autoregressive model based on Gaussian and Student's t-distribution. arXiv:2003.05221 [[econ.EM](#)].

See Also

[quantile_residual_tests](#)

get_varying_h	<i>Get differences 'h' which are adjusted for overly large degrees of freedom parameters</i>
---------------	--

Description

`get_varying_h` adjusts differences for overly large degrees of freedom parameters for finite difference approximation of the derivatives of the log-likelihood function. StMAR and G-StMAR models are supported.

Usage

```
get_varying_h(p, M, params, model)
```

Arguments

- | | |
|---|---|
| p | a positive integer specifying the autoregressive order of the model. |
| M | For GMAR and StMAR models: a positive integer specifying the number of mixture components. |

	<p>For G-StMAR models: a size (2×1) integer vector specifying the number of <i>GMAR type</i> components $M1$ in the first element and <i>StMAR type</i> components $M2$ in the second element. The total number of mixture components is $M=M1+M2$.</p>
params	<p>a real valued parameter vector specifying the model.</p> <p>For non-restricted models: For GMAR model: Size $(M(p+3) - 1 \times 1)$ vector $\theta=(v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1})$, where $v_m = (\phi_{m,0}, \phi_m, \sigma_m^2)$ and $\phi_m=(\phi_{m,1}, \dots, \phi_{m,p})$, $m = 1, \dots, M$.</p> <p>For StMAR model: Size $(M(p+4) - 1 \times 1)$ vector $(\theta, \nu)=(v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.</p> <p>For G-StMAR model: Size $(M(p+3)+M2 - 1 \times 1)$ vector $(\theta, \nu)=(v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_{M1+1}, \dots, \nu_M)$.</p> <p>With linear constraints: Replace the vectors ϕ_m with vectors ψ_m and provide a list of constraint matrices \mathbf{C} that satisfy $\phi_m=R_m\psi_m$ for all $m = 1, \dots, M$, where $\psi_m = (\psi_{m,1}, \dots, \psi_{m,q_m})$.</p> <p>For restricted models: For GMAR model: Size $(3M + p - 1 \times 1)$ vector $\theta = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1})$, where $\phi=(\phi_1, \dots, \phi_p)$.</p> <p>For StMAR model: Size $(4M+p-1 \times 1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.</p> <p>For G-StMAR model: Size $(3M+M2+p-1 \times 1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1}, \nu_{M1+1}, \dots, \nu_M)$.</p> <p>With linear constraints: Replace the vector ϕ with vector ψ and provide a constraint matrix C that satisfies $\phi=R\psi$, where $\psi = (\psi_1, \dots, \psi_q)$.</p> <p>Symbol ϕ denotes an AR coefficient, σ^2 a variance, α a mixing weight, and ν a degrees of freedom parameter. If parametrization=="mean", just replace each intercept term $\phi_{m,0}$ with regimewise mean $\mu_m = \phi_{m,0}/(1 - \sum \phi_{i,m})$. In the G-StMAR model, the first $M1$ components are <i>GMAR type</i> and the rest $M2$ components are <i>StMAR type</i>. Note that in the case $\mathbf{M=1}$, the parameter α is dropped, and in the case of StMAR or G-StMAR model, the degrees of freedom parameters ν_m have to be larger than 2.</p>
model	<p>is "GMAR", "StMAR", or "G-StMAR" model considered? In the G-StMAR model, the first $M1$ components are <i>GMAR type</i> and the rest $M2$ components are <i>StMAR type</i>.</p>

Details

This function is used for approximating gradient and Hessian of a StMAR or G-StMAR model. Large degrees of freedom parameters cause significant numerical error if too small differences are used.

Value

Returns a vector with the same length as params. For other parameters than degrees of freedom parameters larger than 100, the differences will be $6e-6$. For the large degrees of freedom parameters, the difference will be `signif(df/1000, digits=2)`.

GSMAR	<i>Create object of class 'gsmar' defining a GMAR, StMAR, or G-StMAR model</i>
-------	--

Description

GSMAR creates an S3 object of class 'gsmar' that defines a GMAR, StMAR, or G-StMAR model.

Usage

```
GSMAR(
  data,
  p,
  M,
  params,
  model = c("GMAR", "StMAR", "G-StMAR"),
  restricted = FALSE,
  constraints = NULL,
  conditional = TRUE,
  parametrization = c("intercept", "mean"),
  calc_qresiduals,
  calc_cond_moments,
  calc_std_errors = FALSE,
  custom_h = NULL
)

## S3 method for class 'gsmar'
logLik(object, ...)

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

## S3 method for class 'gsmar'
summary(object, ..., digits = 2)

## S3 method for class 'gsmar'
plot(x, ..., include_dens = TRUE)

## S3 method for class 'gsmar'
print(x, ..., digits = 2, summary_print = FALSE)
```

Arguments

data	a numeric vector or class 'ts' object containing the data. NA values are not supported.
p	a positive integer specifying the autoregressive order of the model.

M	<p>For GMAR and StMAR models: a positive integer specifying the number of mixture components.</p> <p>For G-StMAR models: a size (2×1) integer vector specifying the number of <i>GMAR type</i> components M1 in the first element and <i>StMAR type</i> components M2 in the second element. The total number of mixture components is $M=M1+M2$.</p>
params	<p>a real valued parameter vector specifying the model.</p> <p>For non-restricted models:</p> <p>For GMAR model: Size $(M(p+3) - 1 \times 1)$ vector $\theta=(v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1})$, where $v_m = (\phi_{m,0}, \phi_m, \sigma_m^2)$ and $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$, $m = 1, \dots, M$.</p> <p>For StMAR model: Size $(M(p+4) - 1 \times 1)$ vector $(\theta, \nu) = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.</p> <p>For G-StMAR model: Size $(M(p+3) + M2 - 1 \times 1)$ vector $(\theta, \nu) = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_{M1+1}, \dots, \nu_M)$.</p> <p>With linear constraints: Replace the vectors ϕ_m with vectors ψ_m and provide a list of constraint matrices C that satisfy $\phi_m = R_m \psi_m$ for all $m = 1, \dots, M$, where $\psi_m = (\psi_{m,1}, \dots, \psi_{m,q_m})$.</p> <p>For restricted models:</p> <p>For GMAR model: Size $(3M + p - 1 \times 1)$ vector $\theta = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1})$, where $\phi = (\phi_1, \dots, \phi_p)$.</p> <p>For StMAR model: Size $(4M + p - 1 \times 1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.</p> <p>For G-StMAR model: Size $(3M + M2 + p - 1 \times 1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.</p> <p>With linear constraints: Replace the vector ϕ with vector ψ and provide a constraint matrix C that satisfies $\phi = R\psi$, where $\psi = (\psi_1, \dots, \psi_q)$.</p> <p>Symbol ϕ denotes an AR coefficient, σ^2 a variance, α a mixing weight, and ν a degrees of freedom parameter. If parametrization="mean", just replace each intercept term $\phi_{m,0}$ with regimewise mean $\mu_m = \phi_{m,0} / (1 - \sum \phi_{i,m})$. In the G-StMAR model, the first M1 components are <i>GMAR type</i> and the rest M2 components are <i>StMAR type</i>. Note that in the case M=1, the parameter α is dropped, and in the case of StMAR or G-StMAR model, the degrees of freedom parameters ν_m have to be larger than 2.</p>
model	is "GMAR", "StMAR", or "G-StMAR" model considered? In the G-StMAR model, the first M1 components are <i>GMAR type</i> and the rest M2 components are <i>StMAR type</i> .
restricted	a logical argument stating whether the AR coefficients $\phi_{m,1}, \dots, \phi_{m,p}$ are restricted to be the same for all regimes.
constraints	<p>specifies linear constraints applied to the autoregressive parameters.</p> <p>For non-restricted models: a list of size $(p \times q_m)$ constraint matrices C_m of full column rank satisfying $\phi_m = C_m \psi_m$ for all $m = 1, \dots, M$, where $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$ and $\psi_m = (\psi_{m,1}, \dots, \psi_{m,q_m})$.</p> <p>For restricted models: a size $(p \times q)$ constraint matrix C of full column rank satisfying $\phi = C\psi$, where $\phi = (\phi_1, \dots, \phi_p)$ and $\psi = (\psi_1, \dots, \psi_q)$.</p> <p>Symbol ϕ denotes an AR coefficient. Note that regardless of any constraints, the nominal autoregressive order is always p for all regimes. Ignore or set to NULL if applying linear constraints is not desired.</p>
conditional	a logical argument specifying whether the conditional or exact log-likelihood function should be used.

parametrization	is the model parametrized with the "intercepts" $\phi_{m,0}$ or "means" $\mu_m = \phi_{m,0}/(1 - \sum \phi_{i,m})$?
calc_qresiduals	should quantile residuals be calculated? Default is TRUE iff the model contains data.
calc_cond_moments	should conditional means and variances be calculated? Default is TRUE iff the model contains data.
calc_std_errors	should approximate standard errors be calculated?
custom_h	A numeric vector with same the length as the parameter vector: i:th element of custom_h is the difference used in central difference approximation for partial differentials of the log-likelihood function for the i:th parameter. If NULL (default), then the difference used for differentiating overly large degrees of freedom parameters is adjusted to avoid numerical problems, and the difference is $6e-6$ for the other parameters.
object	object of class 'gsmar' created with fitGSMAR or GSMAR.
...	in the plot method: arguments passed to the function density which calculates the kernel density estimate of the data.
digits	number of digits to be printed (max 20)
x	object of class 'gsmar' created with fitGSMAR or GSMAR.
include_dens	Plot also kernel density estimate of the data and model implied stationary density with regimewise densities? See the details.
summary_print	if set to TRUE then the print will include approximate standard errors for the estimates, log-likelihood, information criteria values, modulus of the roots of the characteristic AR polynomias for each regime, and several unconditional moments.

Details

Models can be built without data, e.q., in order to simulate from the process, but some things such as quantile residuals and conditional moments can't be calculated without data.

If include_dens == TRUE, the kernel density estimate of the data is calculated with the function density from the package stats. By default, the default settings of that function are used, including the usage of Gaussian kernel. Use the dot parameters to adjust the settings if desired.

By the model implied stationary density we mean the stationary one-dimensional mixture density of M regimes (see KMS 2015, Theorem 1 and the discussion following it for the Gaussian case and Theorem 2 in PMS 2018 for the Student's t case). The regimewise densities (i.e. each density 1,...,M in the stationary mixture density) are multiplied with the mixing weight parameters accordingly.

In the density plot black represents the kernel density estimate of the data, grey dashed line the model implied density, and the colored dotter lines the regime wise densities.

Value

Returns an object of class 'gsmar' defining the specified GMAR, StMAR, or G-StMAR model. If data is supplied, the returned object contains (by default) empirical mixing weights, some conditional and unconditional moments, and quantile residuals. Note that the first p observations are taken as the initial values so the mixing weights, conditional moments, and quantile residuals start from the $p+1$:th observation (interpreted as $t=1$).

Methods (by generic)

- logLik: Log-likelihood method
- residuals: residuals method to extract quantile residuals
- summary: summary method, standard errors in brackets
- plot: Plot method for class 'gsmar'
- print: print method

References

- Kalliovirta L., Meitz M. and Saikkonen P. 2015. Gaussian Mixture Autoregressive model for univariate time series. *Journal of Time Series Analysis*, **36**, 247-266.
- Meitz M., Preve D., Saikkonen P. 2018. A mixture autoregressive model based on Student's t-distribution. arXiv:1805.04010 [econ.EM].
- Virolainen S. 2020. A mixture autoregressive model based on Gaussian and Student's t-distribution. arXiv:2003.05221 [econ.EM].

See Also

[fitGSMAR](#), [iterate_more](#), [add_data](#), [stmar_to_gstmar](#), [swap_parametrization](#), [get_gradient](#), [simulateGSMAR](#), [predict.gsmar](#), [cond_moments](#), [uncond_moments](#), [LR_test](#), [Wald_test](#)

Examples

```
# GMAR model without data
params22 <- c(0.9, 0.4, 0.2, 0.5, 0.7, 0.5, -0.2, 0.7, 0.7)
gmar22 <- GSMAR(p=2, M=2, params=params22, model="GMAR")
gmar22

# StMAR model, without data
params12t <- c(1.38, 0.88, 0.27, 3.8, 0.74, 3.15, 0.8, 300, 3.6)
stmar12t <- GSMAR(p=1, M=2, params=params12t, model="StMAR")
stmar12t

# G-StMAR model with data
params42gs <- c(0.04, 1.34, -0.59, 0.54, -0.36, 0.01, 0.06, 1.28, -0.36,
              0.2, -0.15, 0.04, 0.19, 9.75)
gstmar42 <- GSMAR(data=M10Y1Y, p=4, M=c(1, 1), params=params42gs,
                  model="G-StMAR")
gstmar42
```

```
# Restricted G-StMAR model with data
params42gsr <- c(0.13, 0.03, 1.29, -0.4, 0.25, -0.2, 0.03, 0.05, 0.51, 2.76)
gstmar42r <- GSMAR(data=M10Y1Y, p=4, M=c(1, 1), params=params42gsr,
                  model="G-StMAR", restricted=TRUE)

gstmar42r
```

isStationary *DEPRECATED, USE is_stationary INSTEAD! Check the stationarity condition of specified GMAR, StMAR, or G-StMAR model.*

Description

isStationary checks the stationarity condition of the specified GMAR, StMAR, or G-StMAR model. DEPRECATED, USE is_stationary INSTEAD!

Usage

```
isStationary(
  p,
  M,
  params,
  model = c("GMAR", "StMAR", "G-StMAR"),
  restricted = FALSE,
  constraints = NULL
)
```

Arguments

- p** a positive integer specifying the autoregressive order of the model.
- M** **For GMAR and StMAR models:** a positive integer specifying the number of mixture components.
For G-StMAR models: a size (2x1) integer vector specifying the number of *GMAR type* components M1 in the first element and *StMAR type* components M2 in the second element. The total number of mixture components is $M=M1+M2$.
- params** a real valued parameter vector specifying the model.
For non-restricted models: For GMAR model: Size $(M(p+3) - 1x1)$ vector $\theta=(v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1})$, where $v_m = (\phi_{m,0}, \phi_m, \sigma_m^2)$ and $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$, $m = 1, \dots, M$.
For StMAR model: Size $(M(p+4) - 1x1)$ vector $(\theta, \nu) = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.
For G-StMAR model: Size $(M(p+3) + M2 - 1x1)$ vector $(\theta, \nu) = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_{M1+1}, \dots, \nu_M)$.
With linear constraints: Replace the vectors ϕ_m with vectors ψ_m and provide a list of constraint matrices **C** that satisfy $\phi_m = R_m \psi_m$ for all $m = 1, \dots, M$, where $\psi_m = (\psi_{m,1}, \dots, \psi_{m,q_m})$.

For restricted models: For GMAR model: Size $(3M + p - 1 \times 1)$ vector $\theta = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1})$, where $\phi = (\phi_1, \dots, \phi_p)$.

For StMAR model: Size $(4M + p - 1 \times 1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.

For G-StMAR model: Size $(3M + M2 + p - 1 \times 1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.

With linear constraints: Replace the vector ϕ with vector ψ and provide a constraint matrix C that satisfies $\phi = R\psi$, where $\psi = (\psi_1, \dots, \psi_q)$.

Symbol ϕ denotes an AR coefficient, σ^2 a variance, α a mixing weight, and ν a degrees of freedom parameter. If parametrization="mean", just replace each intercept term $\phi_{m,0}$ with regimewise mean $\mu_m = \phi_{m,0} / (1 - \sum \phi_{i,m})$. In the **G-StMAR** model, the first M1 components are *GMAR type* and the rest M2 components are *StMAR type*. Note that in the case **M=1**, the parameter α is dropped, and in the case of **StMAR** or **G-StMAR** model, the degrees of freedom parameters ν_m have to be larger than 2.

model is "GMAR", "StMAR", or "G-StMAR" model considered? In the G-StMAR model, the first M1 components are *GMAR type* and the rest M2 components are *StMAR type*.

restricted a logical argument stating whether the AR coefficients $\phi_{m,1}, \dots, \phi_{m,p}$ are restricted to be the same for all regimes.

constraints specifies linear constraints applied to the autoregressive parameters.

For non-restricted models: a list of size $(p \times q_m)$ constraint matrices C_m of full column rank satisfying $\phi_m = C_m \psi_m$ for all $m = 1, \dots, M$, where $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$ and $\psi_m = (\psi_{m,1}, \dots, \psi_{m,q_m})$.

For restricted models: a size $(p \times q)$ constraint matrix C of full column rank satisfying $\phi = C\psi$, where $\phi = (\phi_1, \dots, \phi_p)$ and $\psi = (\psi_1, \dots, \psi_q)$.

Symbol ϕ denotes an AR coefficient. Note that regardless of any constraints, the nominal autoregressive order is always p for all regimes. Ignore or set to NULL if applying linear constraints is **not** desired.

Details

DEPRECATED, USE `is_stationary` INSTEAD! This function falsely returns FALSE for stationary models when the parameter is extremely close to the boundary of the stationarity region.

Value

Returns TRUE or FALSE accordingly.

References

- Kalliovirta L., Meitz M. and Saikkonen P. 2015. Gaussian Mixture Autoregressive model for univariate time series. *Journal of Time Series Analysis*, **36**, 247-266.
- Meitz M., Preve D., Saikkonen P. 2018. A mixture autoregressive model based on Student's t-distribution. arXiv:1805.04010 [econ.EM].
- Virolainen S. 2020. A mixture autoregressive model based on Gaussian and Student's t-distribution. arXiv:2003.05221 [econ.EM].

is_stationary	Check the stationary condition of specified GMAR, StMAR, or G-StMAR model.
---------------	--

Description

is_stationary checks the stationarity condition of the specified GMAR, StMAR, or G-StMAR model.

Usage

```
is_stationary(
  p,
  M,
  params,
  model = c("GMAR", "StMAR", "G-StMAR"),
  restricted = FALSE,
  constraints = NULL
)
```

Arguments

- p** a positive integer specifying the autoregressive order of the model.
- M** **For GMAR and StMAR models:** a positive integer specifying the number of mixture components.
For G-StMAR models: a size (2×1) integer vector specifying the number of *GMAR type* components M_1 in the first element and *StMAR type* components M_2 in the second element. The total number of mixture components is $M = M_1 + M_2$.
- params** a real valued parameter vector specifying the model.
For non-restricted models: For GMAR model: Size $(M(p+3) - 1 \times 1)$ vector $\theta = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1})$, where $v_m = (\phi_{m,0}, \phi_m, \sigma_m^2)$ and $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$, $m = 1, \dots, M$.
For StMAR model: Size $(M(p+4) - 1 \times 1)$ vector $(\theta, \nu) = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.
For G-StMAR model: Size $(M(p+3) + M_2 - 1 \times 1)$ vector $(\theta, \nu) = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_{M_1+1}, \dots, \nu_M)$.
With linear constraints: Replace the vectors ϕ_m with vectors ψ_m and provide a list of constraint matrices \mathbf{C} that satisfy $\phi_m = R_m \psi_m$ for all $m = 1, \dots, M$, where $\psi_m = (\psi_{m,1}, \dots, \psi_{m,q_m})$.
- For restricted models: For GMAR model:** Size $(3M + p - 1 \times 1)$ vector $\theta = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1})$, where $\phi = (\phi_1, \dots, \phi_p)$.
For StMAR model: Size $(4M + p - 1 \times 1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.
For G-StMAR model: Size $(3M + M_2 + p - 1 \times 1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1}, \nu_{M_1+1}, \dots, \nu_M)$.
With linear constraints: Replace the vector ϕ with vector ψ and provide a constraint matrix C that satisfies $\phi = R\psi$, where $\psi = (\psi_1, \dots, \psi_q)$.

Symbol ϕ denotes an AR coefficient, σ^2 a variance, α a mixing weight, and ν a degrees of freedom parameter. If parametrization=="mean", just replace each intercept term $\phi_{m,0}$ with regimewise mean $\mu_m = \phi_{m,0}/(1 - \sum \phi_{i,m})$. In the **G-StMAR** model, the first M1 components are *GMAR type* and the rest M2 components are *StMAR type*. Note that in the case **M=1**, the parameter α is dropped, and in the case of **StMAR** or **G-StMAR** model, the degrees of freedom parameters ν_m have to be larger than 2.

model	is "GMAR", "StMAR", or "G-StMAR" model considered? In the G-StMAR model, the first M1 components are <i>GMAR type</i> and the rest M2 components are <i>StMAR type</i> .
restricted	a logical argument stating whether the AR coefficients $\phi_{m,1}, \dots, \phi_{m,p}$ are restricted to be the same for all regimes.
constraints	specifies linear constraints applied to the autoregressive parameters. For non-restricted models: a list of size (pxq_m) constraint matrices C_m of full column rank satisfying $\phi_m = C_m \psi_m$ for all $m = 1, \dots, M$, where $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$ and $\psi_m = (\psi_{m,1}, \dots, \psi_{m,q_m})$. For restricted models: a size (pxq) constraint matrix C of full column rank satisfying $\phi = C\psi$, where $\phi = (\phi_1, \dots, \phi_p)$ and $\psi = (\psi_1, \dots, \psi_q)$. Symbol ϕ denotes an AR coefficient. Note that regardless of any constraints, the nominal autoregressive order is always p for all regimes. Ignore or set to NULL if applying linear constraints is not desired.

Details

This function falsely returns FALSE for stationary models when the parameter is extremely close to the boundary of the stationarity region.

Value

Returns TRUE or FALSE accordingly.

References

- Kalliovirta L., Meitz M. and Saikkonen P. 2015. Gaussian Mixture Autoregressive model for univariate time series. *Journal of Time Series Analysis*, **36**, 247-266.
- Meitz M., Preve D., Saikkonen P. 2018. A mixture autoregressive model based on Student's t-distribution. arXiv:1805.04010 [econ.EM].
- Virolainen S. 2020. A mixture autoregressive model based on Gaussian and Student's t-distribution. arXiv:2003.05221 [econ.EM].

Examples

```
# GMAR model
params22 <- c(0.4, 0.39, 0.6, 0.3, 0.4, 0.1, 0.6, 0.3, 0.8)
is_stationary(p=2, M=2, params=params22)

# StMAR model
```

```

params12t <- c(-0.3, 1, 0.9, 0.1, 0.8, 0.6, 0.7, 10, 12)
is_stationary(p=1, M=2, params=params12t, model="StMAR")

# G-StMAR model
params12gs <- c(1, 0.1, 1, 2, 0.2, 2, 0.8, 20)
is_stationary(p=1, M=c(1, 1), params=params12gs, model="G-StMAR")

# Restricted GMAR model
params13r <- c(0.1, 0.2, 0.3, -0.99, 0.1, 0.2, 0.3, 0.5, 0.3)
is_stationary(p=1, M=3, params=params13r, restricted=TRUE)

# Such StMAR(3, 2) that the AR coefficients are restricted to be the
# same for both regimes and that the second AR coefficients are
# constrained to zero.
params32trc <- c(1, 2, 0.8, -0.3, 1, 2, 0.7, 11, 12)
is_stationary(p=3, M=2, params=params32trc, model="StMAR", restricted=TRUE,
              constraints=matrix(c(1, 0, 0, 0, 0, 1), ncol=2))

```

is_stationary_int *Check the stationarity and identification conditions of specified GMAR, StMAR, or G-StMAR model.*

Description

is_stationary_int checks the stationarity condition and is_identifiable checks the identification condition of the specified GMAR, StMAR, or G-StMAR model.

Usage

```
is_stationary_int(p, M, params, restricted = FALSE)
```

```

is_identifiable(
  p,
  M,
  params,
  model = c("GMAR", "StMAR", "G-StMAR"),
  restricted = FALSE,
  constraints = NULL
)

```

Arguments

- p a positive integer specifying the autoregressive order of the model.
- M **For GMAR and StMAR models:** a positive integer specifying the number of mixture components.
For G-StMAR models: a size (2x1) integer vector specifying the number of *GMAR type* components M1 in the first element and *StMAR type* components M2 in the second element. The total number of mixture components is $M=M1+M2$.

params	<p>a real valued parameter vector specifying the model.</p> <p>For non-restricted models: For GMAR model: Size $(M(p+3) - 1x1)$ vector $\theta=(v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1})$, where $v_m = (\phi_{m,0}, \phi_m, \sigma_m^2)$ and $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$, $m = 1, \dots, M$.</p> <p>For StMAR model: Size $(M(p+4) - 1x1)$ vector $(\theta, \nu) = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.</p> <p>For G-StMAR model: Size $(M(p+3) + M2 - 1x1)$ vector $(\theta, \nu) = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_{M1+1}, \dots, \nu_M)$.</p> <p>For restricted models: For GMAR model: Size $(3M + p - 1x1)$ vector $\theta = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1})$, where $\phi = (\phi_1, \dots, \phi_p)$.</p> <p>For StMAR model: Size $(4M + p - 1x1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.</p> <p>For G-StMAR model: Size $(3M + M2 + p - 1x1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.</p> <p>Symbol ϕ denotes an AR coefficient, σ^2 a variance, α a mixing weight, and ν a degrees of freedom parameter. In the G-StMAR model, the first M1 components are <i>GMAR type</i> and the rest M2 components are <i>StMAR type</i>. Note that in the case M=1, the parameter α is dropped, and in the case of StMAR or G-StMAR model, the degrees of freedom parameters ν_m have to be larger than 2.</p>
restricted	a logical argument stating whether the AR coefficients $\phi_{m,1}, \dots, \phi_{m,p}$ are restricted to be the same for all regimes.
model	is "GMAR", "StMAR", or "G-StMAR" model considered? In the G-StMAR model, the first M1 components are <i>GMAR type</i> and the rest M2 components are <i>StMAR type</i> .
constraints	<p>specifies linear constraints applied to the autoregressive parameters.</p> <p>For non-restricted models: a list of size (pxq_m) constraint matrices C_m of full column rank satisfying $\phi_m = C_m \psi_m$ for all $m = 1, \dots, M$, where $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$ and $\psi_m = (\psi_{m,1}, \dots, \psi_{m,q_m})$.</p> <p>For restricted models: a size (pxq) constraint matrix C of full column rank satisfying $\phi = C\psi$, where $\phi = (\phi_1, \dots, \phi_p)$ and $\psi = (\psi_1, \dots, \psi_q)$.</p> <p>Symbol ϕ denotes an AR coefficient. Note that regardless of any constraints, the nominal autoregressive order is always p for all regimes. Ignore or set to NULL if applying linear constraints is not desired.</p>

Details

is_stationary_int does not support models imposing linear constraints. In order to use it for a model imposing linear constraints, one needs to expand the constraints first to obtain a nonconstrained parameters vector.

Note that is_stationary_int returns FALSE for stationary parameter vectors if they are extremely close to the boundary of the stationarity region.

is_identifiable checks that the regimes are sorted according to the mixing weight parameters and that there are no duplicate regimes.

Value

Returns TRUE or FALSE accordingly.

Warning

These functions don't have any argument checks!

References

- Kalliovirta L., Meitz M. and Saikkonen P. 2015. Gaussian Mixture Autoregressive model for univariate time series. *Journal of Time Series Analysis*, **36**, 247-266.
- Meitz M., Preve D., Saikkonen P. 2018. A mixture autoregressive model based on Student's t-distribution. arXiv:1805.04010 [econ.EM].
- Virolainen S. 2020. A mixture autoregressive model based on Gaussian and Student's t-distribution. arXiv:2003.05221 [econ.EM].

iterate_more	<i>Maximum likelihood estimation of GMAR, StMAR, or G-StMAR model with preliminary estimates</i>
--------------	--

Description

iterate_more uses a variable metric algorithm to finalize maximum likelihood estimation of a GMAR, StMAR or G-StMAR model (object of class 'gsmar') which already has preliminary estimates.

Usage

```
iterate_more(gsmar, maxit = 100, custom_h = NULL, calc_std_errors = TRUE)
```

Arguments

gsmar	object of class 'gsmar' created with the function fitGSMAR or GSMAR.
maxit	the maximum number of iterations for the variable metric algorithm.
custom_h	A numeric vector with same the length as the parameter vector: i:th element of custom_h is the difference used in central difference approximation for partial differentials of the log-likelihood function for the i:th parameter. If NULL (default), then the difference used for differentiating overly large degrees of freedom parameters is adjusted to avoid numerical problems, and the difference is 6e-6 for the other parameters.
calc_std_errors	should approximate standard errors be calculated?

Details

The main purpose of iterate_more is to provide a simple and convenient tool to finalize the estimation when the maximum number of iterations is reached when estimating a model with the main estimation function fitGSMAR. iterate_more is essentially a wrapper for the functions optim from the package stats and GSMAR from the package uGMAR.

Value

Returns an object of class 'gsmar' defining the estimated model.

References

- Kalliovirta L., Meitz M. and Saikkonen P. 2015. Gaussian Mixture Autoregressive model for univariate time series. *Journal of Time Series Analysis*, **36**, 247-266.
- Meitz M., Preve D., Saikkonen P. 2018. A mixture autoregressive model based on Student's t-distribution. arXiv:1805.04010 [econ.EM].
- Virolainen S. 2020. A mixture autoregressive model based on Gaussian and Student's t-distribution. arXiv:2003.05221 [econ.EM].

See Also

[fitGSMAR](#), [GSMAR](#), [stmar_to_gstmar](#), [profile_logliks](#), [optim](#)

Examples

```
# Estimate GMAR model with on only 1 iteration in variable metric algorithm
fit12 <- fitGSMAR(simudata, p=1, M=2, maxit=1, ncalls=1, seeds=1)
fit12

# Iterate more since iteration limit was reached
fit12 <- iterate_more(fit12)
fit12
```

loglikelihood

Compute the log-likelihood of GMAR, StMAR, or G-StMAR model

Description

loglikelihood computes the log-likelihood of the specified GMAR, StMAR, or G-StMAR model. Exists for convenience if one wants to for example plot profile log-likelihoods or employ other estimation algorithms. Use minval to control what happens when the parameter vector is outside the parameter space.

Usage

```
loglikelihood(
  data,
  p,
  M,
  params,
  model = c("GMAR", "StMAR", "G-StMAR"),
  restricted = FALSE,
```

```

constraints = NULL,
conditional = TRUE,
parametrization = c("intercept", "mean"),
return_terms = FALSE,
minval = NA
)

```

Arguments

data a numeric vector or class 'ts' object containing the data. NA values are not supported.

p a positive integer specifying the autoregressive order of the model.

M **For GMAR and StMAR models:** a positive integer specifying the number of mixture components.

For G-StMAR models: a size (2x1) integer vector specifying the number of *GMAR type* components M1 in the first element and *StMAR type* components M2 in the second element. The total number of mixture components is $M=M1+M2$.

params a real valued parameter vector specifying the model.

For non-restricted models: For GMAR model: Size $(M(p+3) - 1x1)$ vector $\theta=(v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1})$, where $v_m = (\phi_{m,0}, \phi_m, \sigma_m^2)$ and $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$, $m = 1, \dots, M$.

For StMAR model: Size $(M(p+4) - 1x1)$ vector $(\theta, \nu) = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.

For G-StMAR model: Size $(M(p+3) + M2 - 1x1)$ vector $(\theta, \nu) = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_{M1+1}, \dots, \nu_M)$.

With linear constraints: Replace the vectors ϕ_m with vectors ψ_m and provide a list of constraint matrices **C** that satisfy $\phi_m = R_m \psi_m$ for all $m = 1, \dots, M$, where $\psi_m = (\psi_{m,1}, \dots, \psi_{m,q_m})$.

For restricted models: For GMAR model: Size $(3M + p - 1x1)$ vector $\theta = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1})$, where $\phi = (\phi_1, \dots, \phi_p)$.

For StMAR model: Size $(4M + p - 1x1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.

For G-StMAR model: Size $(3M + M2 + p - 1x1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1}, \nu_{M1+1}, \dots, \nu_M)$.

With linear constraints: Replace the vector ϕ with vector ψ and provide a constraint matrix **C** that satisfies $\phi = R\psi$, where $\psi = (\psi_1, \dots, \psi_q)$.

Symbol ϕ denotes an AR coefficient, σ^2 a variance, α a mixing weight, and ν a degrees of freedom parameter. If parametrization="mean", just replace each intercept term $\phi_{m,0}$ with regimewise mean $\mu_m = \phi_{m,0} / (1 - \sum \phi_{i,m})$. In the **G-StMAR** model, the first M1 components are *GMAR type* and the rest M2 components are *StMAR type*. Note that in the case **M=1**, the parameter α is dropped, and in the case of **StMAR** or **G-StMAR** model, the degrees of freedom parameters ν_m have to be larger than 2.

model is "GMAR", "StMAR", or "G-StMAR" model considered? In the G-StMAR model, the first M1 components are *GMAR type* and the rest M2 components are *StMAR type*.

restricted a logical argument stating whether the AR coefficients $\phi_{m,1}, \dots, \phi_{m,p}$ are restricted to be the same for all regimes.

constraints	<p>specifies linear constraints applied to the autoregressive parameters.</p> <p>For non-restricted models: a list of size (pxq_m) constraint matrices C_m of full column rank satisfying $\phi_m = C_m \psi_m$ for all $m = 1, \dots, M$, where $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$ and $\psi_m = (\psi_{m,1}, \dots, \psi_{m,q_m})$.</p> <p>For restricted models: a size (pxq) constraint matrix C of full column rank satisfying $\phi = C\psi$, where $\phi = (\phi_1, \dots, \phi_p)$ and $\psi = (\psi_1, \dots, \psi_q)$.</p> <p>Symbol ϕ denotes an AR coefficient. Note that regardless of any constraints, the nominal autoregressive order is always p for all regimes. Ignore or set to NULL if applying linear constraints is not desired.</p>
conditional	a logical argument specifying whether the conditional or exact log-likelihood function should be used.
parametrization	is the model parametrized with the "intercepts" $\phi_{m,0}$ or "means" $\mu_m = \phi_{m,0}/(1 - \sum \phi_{i,m})$?
return_terms	should the terms $l_t : t = 1, \dots, T$ in the log-likelihood function (see <i>KMS 2015, eq.(13)</i> or <i>MPS 2018, eq.(15)</i>) be returned instead of the log-likelihood value?
minval	this will be returned when the parameter vector is outside the parameter space and boundaries==TRUE.

Value

Returns the log-likelihood value or the terms described in return_terms.

References

- Galbraith, R., Galbraith, J. 1974. On the inverses of some patterned matrices arising in the theory of stationary time series. *Journal of Applied Probability* **11**, 63-71.
- Kalliovirta L. (2012) Misspecification tests based on quantile residuals. *The Econometrics Journal*, **15**, 358-393.
- Kalliovirta L., Meitz M. and Saikkonen P. 2015. Gaussian Mixture Autoregressive model for univariate time series. *Journal of Time Series Analysis*, **36**, 247-266.
- Meitz M., Preve D., Saikkonen P. 2018. A mixture autoregressive model based on Student's t-distribution. arXiv:1805.04010 [econ.EM].
- Virolainen S. 2020. A mixture autoregressive model based on Gaussian and Student's t-distribution. arXiv:2003.05221 [econ.EM].

See Also

[fitGSMAR](#), [GSMAR](#), [quantile_residuals](#), [mixing_weights](#), [calc_gradient](#)

Examples

```
# GMAR model
params12 <- c(1.70, 0.85, 0.30, 4.12, 0.73, 1.98, 0.63)
loglikelihood(simudata, p=1, M=2, params=params12, model="GMAR")

# G-StMAR-model
```



```

params42gs <- c(0.04, 1.34, -0.59, 0.54, -0.36, 0.01, 0.06, 1.28, -0.36,
               0.2, -0.15, 0.04, 0.19, 9.75)
loglikelihood(M10Y1Y, p=4, M=c(1, 1), params=params42gs, model="G-StMAR")

```

loglikelihood_int	<i>Compute the log-likelihood of GMAR, StMAR, or G-StMAR model</i>
-------------------	--

Description

loglikelihood_int computes the log-likelihood of the specified GMAR, StMAR, or G-StMAR model.

Usage

```

loglikelihood_int(
  data,
  p,
  M,
  params,
  model = c("GMAR", "StMAR", "G-StMAR"),
  restricted = FALSE,
  constraints = NULL,
  conditional = TRUE,
  parametrization = c("intercept", "mean"),
  boundaries = TRUE,
  checks = TRUE,
  to_return = c("loglik", "mw", "mw_tplus1", "loglik_and_mw", "terms", "regime_cmeans",
               "regime_cvars", "total_cmeans", "total_cvars", "qresiduals"),
  minval
)

```

Arguments

- | | |
|--------|--|
| data | a numeric vector or class 'ts' object containing the data. NA values are not supported. |
| p | a positive integer specifying the autoregressive order of the model. |
| M | <p>For GMAR and StMAR models: a positive integer specifying the number of mixture components.</p> <p>For G-StMAR models: a size (2x1) integer vector specifying the number of <i>GMAR type</i> components M1 in the first element and <i>StMAR type</i> components M2 in the second element. The total number of mixture components is $M=M1+M2$.</p> |
| params | <p>a real valued parameter vector specifying the model.</p> <p>For non-restricted models: For GMAR model: Size $(M(p+3) - 1 \times 1)$ vector $\theta=(v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1})$, where $v_m = (\phi_{m,0}, \phi_m, \sigma_m^2)$ and $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$, $m = 1, \dots, M$.</p> |

For StMAR model: Size $(M(p+4)-1 \times 1)$ vector $(\theta, \nu) = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.

For G-StMAR model: Size $(M(p+3)+M2-1 \times 1)$ vector $(\theta, \nu) = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_{M+1}, \dots, \nu_M)$.

With linear constraints: Replace the vectors ϕ_m with vectors ψ_m and provide a list of constraint matrices C that satisfy $\phi_m = R_m \psi_m$ for all $m = 1, \dots, M$, where $\psi_m = (\psi_{m,1}, \dots, \psi_{m,q_m})$.

For restricted models: For GMAR model: Size $(3M + p - 1 \times 1)$ vector $\theta = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1})$, where $\phi = (\phi_1, \dots, \phi_p)$.

For StMAR model: Size $(4M+p-1 \times 1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1})$.

For G-StMAR model: Size $(3M+M2+p-1 \times 1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1}, \nu_{M+1}, \dots, \nu_M)$.

With linear constraints: Replace the vector ϕ with vector ψ and provide a constraint matrix C that satisfies $\phi = R\psi$, where $\psi = (\psi_1, \dots, \psi_q)$.

Symbol ϕ denotes an AR coefficient, σ^2 a variance, α a mixing weight, and ν a degrees of freedom parameter. If parametrization=="mean", just replace each intercept term $\phi_{m,0}$ with regimewise mean $\mu_m = \phi_{m,0}/(1 - \sum \phi_{i,m})$. In the **G-StMAR** model, the first M1 components are *GMAR type* and the rest M2 components are *StMAR type*. Note that in the case **M=1**, the parameter α is dropped, and in the case of **StMAR** or **G-StMAR** model, the degrees of freedom parameters ν_m have to be larger than 2.

model is "GMAR", "StMAR", or "G-StMAR" model considered? In the G-StMAR model, the first M1 components are *GMAR type* and the rest M2 components are *StMAR type*.

restricted a logical argument stating whether the AR coefficients $\phi_{m,1}, \dots, \phi_{m,p}$ are restricted to be the same for all regimes.

constraints specifies linear constraints applied to the autoregressive parameters.

For non-restricted models: a list of size (pxq_m) constraint matrices C_m of full column rank satisfying $\phi_m = C_m \psi_m$ for all $m = 1, \dots, M$, where $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$ and $\psi_m = (\psi_{m,1}, \dots, \psi_{m,q_m})$.

For restricted models: a size (pxq) constraint matrix C of full column rank satisfying $\phi = C\psi$, where $\phi = (\phi_1, \dots, \phi_p)$ and $\psi = (\psi_1, \dots, \psi_q)$.

Symbol ϕ denotes an AR coefficient. Note that regardless of any constraints, the nominal autoregressive order is always p for all regimes. Ignore or set to NULL if applying linear constraints is **not** desired.

conditional a logical argument specifying whether the conditional or exact log-likelihood function should be used.

parametrization

is the model parametrized with the "intercepts" $\phi_{m,0}$ or "means" $\mu_m = \phi_{m,0}/(1 - \sum \phi_{i,m})$?

boundaries a logical argument. If TRUE, then loglikelihood returns minval if...

- some component variance is not larger than zero,
- some parametrized mixing weight $\alpha_1, \dots, \alpha_{M-1}$ is not larger than zero,
- sum of the parametrized mixing weights is not smaller than one,
- if the model is not stationary,
- or if model=="StMAR" or model=="G-StMAR" and some degrees of freedom parameter ν_m is not larger than two.

	Argument minval will be used only if boundaries==TRUE.
checks	TRUE or FALSE specifying whether argument checks, such as stationarity checks, should be done.
to_return	should the returned object be the log-likelihood value, mixing weights, mixing weights including value for $\alpha_{m,T+1}$, a list containing log-likelihood value and mixing weights, the terms $l_t : t = 1, \dots, T$ in the log-likelihood function (see <i>KMS 2015, eq.(13)</i>), regimewise conditional means, regimewise conditional variances, total conditional means, total conditional variances, or quantile residuals? Default is the log-likelihood value ("loglik").
minval	this will be returned when the parameter vector is outside the parameter space and boundaries==TRUE.

Value

Note that the first p observations are taken as the initial values so the mixing weights and conditional moments start from the $p+1$:th observation (interpreted as $t=1$).

By default: log-likelihood value of the specified model,

If to_return=="mw": a size $((n_obs-p) \times M)$ matrix containing the mixing weights: for m :th component in the m :th column.

If to_return=="mw_tplus1": a size $((n_obs-p+1) \times M)$ matrix containing the mixing weights: for m :th component in the m :th column. The last row is for $\alpha_{m,T+1}$.

If to_return=="loglik_and_mw": a list of two elements. The first element contains the log-likelihood value and the second element contains the mixing weights.

If to_return=="terms": a size $((n_obs-p) \times 1)$ numeric vector containing the terms l_t .

If to_return=="regime_cmeans": a size $((n_obs-p) \times M)$ matrix containing the regime specific conditional means.

If to_return=="regime_cvars": a size $((n_obs-p) \times M)$ matrix containing the regime specific conditional variances.

If to_return=="total_cmeans": a size $((n_obs-p) \times 1)$ vector containing the total conditional means.

If to_return=="total_cvars": a size $((n_obs-p) \times 1)$ vector containing the total conditional variances.

If to_return=="qresiduals": a size $((n_obs-p) \times 1)$ vector containing the quantile residuals.

References

- Galbraith, R., Galbraith, J. 1974. On the inverses of some patterned matrices arising in the theory of stationary time series. *Journal of Applied Probability* **11**, 63-71.
- Kalliovirta L. (2012) Misspecification tests based on quantile residuals. *The Econometrics Journal*, **15**, 358-393.
- Kalliovirta L., Meitz M. and Saikkonen P. 2015. Gaussian Mixture Autoregressive model for univariate time series. *Journal of Time Series Analysis*, **36**, 247-266.
- Meitz M., Preve D., Saikkonen P. 2018. A mixture autoregressive model based on Student's t-distribution. arXiv:1805.04010 [econ.EM].
- Virolainen S. 2020. A mixture autoregressive model based on Gaussian and Student's t-distribution. arXiv:2003.05221 [econ.EM].

LR_test	<i>Perform likelihood ratio test</i>
---------	--------------------------------------

Description

LR_test performs a likelihood ratio test for a GMAR, StMAR, or G-StMAR model.

Usage

```
LR_test(gsmar1, gsmar2)

## S3 method for class 'lr'
print(x, ..., digits = 4)
```

Arguments

gsmar1	an object of class 'gsmar' generated by fitGSMAR or GSMAR, containing the freely estimated model.
gsmar2	an object of class 'gsmar' generated by fitGSMAR or GSMAR, containing the constrained model.
x	object of class 'lr' generated by the function LR_test.
...	currently not in use.
digits	how many significant digits to print?

Details

Performs a likelihood ratio test, testing the null hypothesis that the true parameter value lies in the constrained parameter space. Under the null, the test statistic is asymptotically χ^2 -distributed with k degrees of freedom, k being the difference in the dimensions of the unconstrained and constrained parameter spaces.

Note that this function does **not** verify that the two models are actually nested.

Value

Returns an object of class 'lr' containing the test statistic and the related p-value.

Methods (by generic)

- print: print method

References

- Kalliovirta L., Meitz M. and Saikkonen P. 2015. Gaussian Mixture Autoregressive model for univariate time series. *Journal of Time Series Analysis*, **36**, 247-266.
- Meitz M., Preve D., Saikkonen P. 2018. A mixture autoregressive model based on Student's t-distribution. arXiv:1805.04010 [**econ.EM**].

- Virolainen S. 2020. A mixture autoregressive model based on Gaussian and Student's t-distribution. arXiv:2003.05221 [econ.EM].

See Also

[Wald_test](#), [fitGSMAR](#), [GSMAR](#), [diagnostic_plot](#), [profile_logliks](#), [quantile_residual_tests](#), [cond_moment_plot](#)

Examples

```
# GMAR p=1, M=2 model:
fit12 <- fitGSMAR(simudata, p=1, M=2, model="GMAR", ncalls=1, seeds=1)

# GMAR p=1, M=2 model AR parameters restricted to be the same in both
# regimes:
fit12r <- fitGSMAR(simudata, p=1, M=2, model="GMAR", restricted=TRUE,
                  ncalls=1, seeds=1)

# Test with likelihood ratio test whether the AR parameters are the same in
# both regimes:
LR_test(fit12, fit12r)
```

M10Y1Y

Spread between 10-Year and 1-Year treasury rates: M10Y1Y

Description

A dataset containing monthly U.S. interest rate spread between the 10-Year Treasury constant maturity rate and 1-Year Treasury constant maturity rate from 1982 January to 2020 December.

Usage

```
M10Y1Y
```

Format

A class 'ts' time series object containing 468 observations.

Source

<https://fred.stlouisfed.org/series/GS10> <https://fred.stlouisfed.org/series/GS1>

mixingWeights	<i>DEPRECATED, USE mixing_weights INSTEAD! Calculate mixing weights of GMAR, StMAR or G-StMAR model</i>
---------------	---

Description

mixingWeights calculates the mixing weights of the specified GMAR, StMAR or G-StMAR model and returns them as a matrix. *DEPRECATED, USE mixing_weights INSTEAD!*

Usage

```
mixingWeights(
  data,
  p,
  M,
  params,
  model = c("GMAR", "StMAR", "G-StMAR"),
  restricted = FALSE,
  constraints = NULL,
  parametrization = c("intercept", "mean")
)
```

Arguments

data	a numeric vector or class 'ts' object containing the data. NA values are not supported.
p	a positive integer specifying the autoregressive order of the model.
M	<p>For GMAR and StMAR models: a positive integer specifying the number of mixture components.</p> <p>For G-StMAR models: a size (2x1) integer vector specifying the number of <i>GMAR type</i> components M1 in the first element and <i>StMAR type</i> components M2 in the second element. The total number of mixture components is $M=M1+M2$.</p>
params	<p>a real valued parameter vector specifying the model.</p> <p>For non-restricted models:</p> <p>For GMAR model: Size $(M(p+3) - 1x1)$ vector $\theta=(v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1})$, where $v_m = (\phi_{m,0}, \phi_m, \sigma_m^2)$ and $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$, $m = 1, \dots, M$.</p> <p>For StMAR model: Size $(M(p+4) - 1x1)$ vector $(\theta, \nu) = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.</p> <p>For G-StMAR model: Size $(M(p+3) + M2 - 1x1)$ vector $(\theta, \nu) = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_{M1+1}, \dots, \nu_M)$.</p> <p>With linear constraints: Replace the vectors ϕ_m with vectors ψ_m and provide a list of constraint matrices C that satisfy $\phi_m = R_m \psi_m$ for all $m = 1, \dots, M$, where $\psi_m = (\psi_{m,1}, \dots, \psi_{m,q_m})$.</p> <p>For restricted models:</p> <p>For GMAR model: Size $(3M + p - 1x1)$ vector $\theta = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1})$, where $\phi = (\phi_1, \dots, \phi_p)$.</p>

For StMAR model: Size $(4M+p-1 \times 1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1})$

For G-StMAR model: Size $(3M+M2+p-1 \times 1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1})$

With linear constraints: Replace the vector ϕ with vector ψ and provide a constraint matrix C that satisfies $\phi = R\psi$, where $\psi = (\psi_1, \dots, \psi_q)$.

Symbol ϕ denotes an AR coefficient, σ^2 a variance, α a mixing weight, and ν a degrees of freedom parameter. If parametrization=="mean", just replace each intercept term $\phi_{m,0}$ with regimewise mean $\mu_m = \phi_{m,0} / (1 - \sum \phi_{i,m})$. In the **G-StMAR** model, the first M1 components are *GMAR type* and the rest M2 components are *StMAR type*. Note that in the case **M=1**, the parameter α is dropped, and in the case of **StMAR** or **G-StMAR** model, the degrees of freedom parameters ν_m have to be larger than 2.

model is "GMAR", "StMAR", or "G-StMAR" model considered? In the G-StMAR model, the first M1 components are *GMAR type* and the rest M2 components are *StMAR type*.

restricted a logical argument stating whether the AR coefficients $\phi_{m,1}, \dots, \phi_{m,p}$ are restricted to be the same for all regimes.

constraints specifies linear constraints applied to the autoregressive parameters.

For non-restricted models: a list of size $(p \times q_m)$ constraint matrices C_m of full column rank satisfying $\phi_m = C_m \psi_m$ for all $m = 1, \dots, M$, where $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$ and $\psi_m = (\psi_{m,1}, \dots, \psi_{m,q_m})$.

For restricted models: a size $(p \times q)$ constraint matrix C of full column rank satisfying $\phi = C\psi$, where $\phi = (\phi_1, \dots, \phi_p)$ and $\psi = (\psi_1, \dots, \psi_q)$.

Symbol ϕ denotes an AR coefficient. Note that regardless of any constraints, the nominal autoregressive order is always p for all regimes. Ignore or set to NULL if applying linear constraints is **not** desired.

parametrization is the model parametrized with the "intercepts" $\phi_{m,0}$ or "means" $\mu_m = \phi_{m,0} / (1 - \sum \phi_{i,m})$?

Details

DEPRECATED, USE mixing_weights INSTEAD!

Value

If to_return=="mw": a size $((n_obs-p) \times M)$ matrix containing the mixing weights: for m:th component in m:th column.

If to_return=="mw_tplus1": a size $((n_obs-p+1) \times M)$ matrix containing the mixing weights: for m:th component in m:th column. The last row is for $\alpha_{m,T+1}$.

References

- Galbraith, R., Galbraith, J. 1974. On the inverses of some patterned matrices arising in the theory of stationary time series. *Journal of Applied Probability* **11**, 63-71.
- Kalliovirta L. (2012) Misspecification tests based on quantile residuals. *The Econometrics Journal*, **15**, 358-393.

- Kalliovirta L., Meitz M. and Saikkonen P. 2015. Gaussian Mixture Autoregressive model for univariate time series. *Journal of Time Series Analysis*, **36**, 247-266.
- Meitz M., Preve D., Saikkonen P. 2018. A mixture autoregressive model based on Student's t-distribution. arXiv:1805.04010 [econ.EM].
- Virolainen S. 2020. A mixture autoregressive model based on Gaussian and Student's t-distribution. arXiv:2003.05221 [econ.EM].

 mixing_weights

 Calculate mixing weights of GMAR, StMAR or G-StMAR model

Description

mixing_weights calculates the mixing weights of the specified GMAR, StMAR or G-StMAR model and returns them as a matrix.

Usage

```

mixing_weights(
  data,
  p,
  M,
  params,
  model = c("GMAR", "StMAR", "G-StMAR"),
  restricted = FALSE,
  constraints = NULL,
  parametrization = c("intercept", "mean")
)

```

Arguments

- | | |
|--------|--|
| data | a numeric vector or class 'ts' object containing the data. NA values are not supported. |
| p | a positive integer specifying the autoregressive order of the model. |
| M | <p>For GMAR and StMAR models: a positive integer specifying the number of mixture components.</p> <p>For G-StMAR models: a size (2x1) integer vector specifying the number of <i>GMAR type</i> components M1 in the first element and <i>StMAR type</i> components M2 in the second element. The total number of mixture components is $M=M1+M2$.</p> |
| params | <p>a real valued parameter vector specifying the model.</p> <p>For non-restricted models: For GMAR model: Size $(M(p+3) - 1x1)$ vector $\theta=(v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1})$, where $v_m = (\phi_{m,0}, \phi_m, \sigma_m^2)$ and $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$, $m = 1, \dots, M$.</p> <p>For StMAR model: Size $(M(p+4) - 1x1)$ vector $(\theta, \nu) = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.</p> |

For G-StMAR model: Size $(M(p+3)+M2-1x1)$ vector $(\theta, \nu) = (\nu_1, \dots, \nu_M, \alpha_1, \dots, \alpha_{M-1}, \nu_{M1+1}, \dots, \nu_M)$.

With linear constraints: Replace the vectors ϕ_m with vectors ψ_m and provide a list of constraint matrices \mathbf{C} that satisfy $\phi_m = R_m \psi_m$ for all $m = 1, \dots, M$, where $\psi_m = (\psi_{m,1}, \dots, \psi_{m,q_m})$.

For restricted models: For GMAR model: Size $(3M + p - 1x1)$ vector $\theta = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1})$, where $\phi = (\phi_1, \dots, \phi_p)$.

For StMAR model: Size $(4M+p-1x1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1})$.

For G-StMAR model: Size $(3M+M2+p-1x1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1})$.

With linear constraints: Replace the vector ϕ with vector ψ and provide a constraint matrix C that satisfies $\phi = R\psi$, where $\psi = (\psi_1, \dots, \psi_q)$.

Symbol ϕ denotes an AR coefficient, σ^2 a variance, α a mixing weight, and ν a degrees of freedom parameter. If parametrization=="mean", just replace each intercept term $\phi_{m,0}$ with regimewise mean $\mu_m = \phi_{m,0}/(1 - \sum \phi_{i,m})$. In the **G-StMAR** model, the first M1 components are *GMAR type* and the rest M2 components are *StMAR type*. Note that in the case **M=1**, the parameter α is dropped, and in the case of **StMAR** or **G-StMAR** model, the degrees of freedom parameters ν_m have to be larger than 2.

model is "GMAR", "StMAR", or "G-StMAR" model considered? In the G-StMAR model, the first M1 components are *GMAR type* and the rest M2 components are *StMAR type*.

restricted a logical argument stating whether the AR coefficients $\phi_{m,1}, \dots, \phi_{m,p}$ are restricted to be the same for all regimes.

constraints specifies linear constraints applied to the autoregressive parameters.

For non-restricted models: a list of size (pxq_m) constraint matrices C_m of full column rank satisfying $\phi_m = C_m \psi_m$ for all $m = 1, \dots, M$, where $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$ and $\psi_m = (\psi_{m,1}, \dots, \psi_{m,q_m})$.

For restricted models: a size (pxq) constraint matrix C of full column rank satisfying $\phi = C\psi$, where $\phi = (\phi_1, \dots, \phi_p)$ and $\psi = (\psi_1, \dots, \psi_q)$.

Symbol ϕ denotes an AR coefficient. Note that regardless of any constraints, the nominal autoregressive order is always p for all regimes. Ignore or set to NULL if applying linear constraints is **not** desired.

parametrization is the model parametrized with the "intercepts" $\phi_{m,0}$ or "means" $\mu_m = \phi_{m,0}/(1 - \sum \phi_{i,m})$?

Details

The first p observations are taken to be the initial values.

Value

If to_return=="mw": a size $((n_obs-p) \times M)$ matrix containing the mixing weights: for m:th component in m:th column.

If to_return=="mw_tplus1": a size $((n_obs-p+1) \times M)$ matrix containing the mixing weights: for m:th component in m:th column. The last row is for $\alpha_{m,T+1}$.

References

- Galbraith, R., Galbraith, J. 1974. On the inverses of some patterned matrices arising in the theory of stationary time series. *Journal of Applied Probability* **11**, 63-71.
- Kalliovirta L. (2012) Misspecification tests based on quantile residuals. *The Econometrics Journal*, **15**, 358-393.
- Kalliovirta L., Meitz M. and Saikkonen P. 2015. Gaussian Mixture Autoregressive model for univariate time series. *Journal of Time Series Analysis*, **36**, 247-266.
- Meitz M., Preve D., Saikkonen P. 2018. A mixture autoregressive model based on Student's t-distribution. arXiv:1805.04010 [econ.EM].
- Virolainen S. 2020. A mixture autoregressive model based on Gaussian and Student's t-distribution. arXiv:2003.05221 [econ.EM].

Examples

```
# GMAR model
params12 <- c(1.70, 0.85, 0.30, 4.12, 0.73, 1.98, 0.63)
mixing_weights(simudata, p=1, M=2, params=params12, model="GMAR")

# G-StMAR-model
params42gs <- c(0.04, 1.34, -0.59, 0.54, -0.36, 0.01, 0.06, 1.28, -0.36,
               0.2, -0.15, 0.04, 0.19, 9.75)
mixing_weights(M10Y1Y, p=4, M=c(1, 1), params=params42gs, model="G-StMAR")
```

mixing_weights_int *Calculate mixing weights of a GMAR, StMAR, or G-StMAR model*

Description

mixing_weights_int calculates the mixing weights of the specified GMAR, StMAR, or G-StMAR model and returns them as a matrix.

Usage

```
mixing_weights_int(
  data,
  p,
  M,
  params,
  model = c("GMAR", "StMAR", "G-StMAR"),
  restricted = FALSE,
  constraints = NULL,
  parametrization = c("intercept", "mean"),
  checks = TRUE,
  to_return = c("mw", "mw_tplus1")
)
```

Arguments

data	a numeric vector or class 'ts' object containing the data. NA values are not supported.
p	a positive integer specifying the autoregressive order of the model.
M	<p>For GMAR and StMAR models: a positive integer specifying the number of mixture components.</p> <p>For G-StMAR models: a size (2x1) integer vector specifying the number of <i>GMAR type</i> components M1 in the first element and <i>StMAR type</i> components M2 in the second element. The total number of mixture components is $M=M1+M2$.</p>
params	<p>a real valued parameter vector specifying the model.</p> <p>For non-restricted models: For GMAR model: Size $(M(p+3) - 1x1)$ vector $\theta=(v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1})$, where $v_m = (\phi_{m,0}, \phi_m, \sigma_m^2)$ and $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$, $m = 1, \dots, M$.</p> <p>For StMAR model: Size $(M(p+4) - 1x1)$ vector $(\theta, \nu) = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.</p> <p>For G-StMAR model: Size $(M(p+3) + M2 - 1x1)$ vector $(\theta, \nu) = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_{M1+1}, \dots, \nu_M)$.</p> <p>With linear constraints: Replace the vectors ϕ_m with vectors ψ_m and provide a list of constraint matrices C that satisfy $\phi_m = R_m \psi_m$ for all $m = 1, \dots, M$, where $\psi_m = (\psi_{m,1}, \dots, \psi_{m,q_m})$.</p> <p>For restricted models: For GMAR model: Size $(3M + p - 1x1)$ vector $\theta = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1})$, where $\phi = (\phi_1, \dots, \phi_p)$.</p> <p>For StMAR model: Size $(4M + p - 1x1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.</p> <p>For G-StMAR model: Size $(3M + M2 + p - 1x1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1}, \nu_{M1+1}, \dots, \nu_M)$.</p> <p>With linear constraints: Replace the vector ϕ with vector ψ and provide a constraint matrix C that satisfies $\phi = R\psi$, where $\psi = (\psi_1, \dots, \psi_q)$.</p> <p>Symbol ϕ denotes an AR coefficient, σ^2 a variance, α a mixing weight, and ν a degrees of freedom parameter. If parametrization="mean", just replace each intercept term $\phi_{m,0}$ with regimewise mean $\mu_m = \phi_{m,0} / (1 - \sum \phi_{i,m})$. In the G-StMAR model, the first M1 components are <i>GMAR type</i> and the rest M2 components are <i>StMAR type</i>. Note that in the case M=1, the parameter α is dropped, and in the case of StMAR or G-StMAR model, the degrees of freedom parameters ν_m have to be larger than 2.</p>
model	is "GMAR", "StMAR", or "G-StMAR" model considered? In the G-StMAR model, the first M1 components are <i>GMAR type</i> and the rest M2 components are <i>StMAR type</i> .
restricted	a logical argument stating whether the AR coefficients $\phi_{m,1}, \dots, \phi_{m,p}$ are restricted to be the same for all regimes.
constraints	<p>specifies linear constraints applied to the autoregressive parameters.</p> <p>For non-restricted models: a list of size (pxq_m) constraint matrices C_m of full column rank satisfying $\phi_m = C_m \psi_m$ for all $m = 1, \dots, M$, where $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$ and $\psi_m = (\psi_{m,1}, \dots, \psi_{m,q_m})$.</p> <p>For restricted models: a size (pxq) constraint matrix C of full column rank satisfying $\phi = C\psi$, where $\phi = (\phi_1, \dots, \phi_p)$ and $\psi = (\psi_1, \dots, \psi_q)$.</p>

Symbol ϕ denotes an AR coefficient. Note that regardless of any constraints, the nominal autoregressive order is always p for all regimes. Ignore or set to NULL if applying linear constraints is **not** desired.

parametrization	is the model parametrized with the "intercepts" $\phi_{m,0}$ or "means" $\mu_m = \phi_{m,0}/(1 - \sum \phi_{i,m})$?
checks	TRUE or FALSE specifying whether argument checks, such as stationarity checks, should be done.
to_return	should the returned object contain mixing weights for $t=1,\dots,T$ ("mw") or for $t=1,\dots,T+1$ ("mw_tplus1")?

Details

The first p observations are taken to be the initial values.

Value

If to_return=="mw": a size $((n_obs-p) \times M)$ matrix containing the mixing weights: for m :th component in m :th column.

If to_return=="mw_tplus1": a size $((n_obs-p+1) \times M)$ matrix containing the mixing weights: for m :th component in m :th column. The last row is for $\alpha_{m,T+1}$.

References

- Galbraith, R., Galbraith, J. 1974. On the inverses of some patterned matrices arising in the theory of stationary time series. *Journal of Applied Probability* **11**, 63-71.
- Kalliovirta L. (2012) Misspecification tests based on quantile residuals. *The Econometrics Journal*, **15**, 358-393.
- Kalliovirta L., Meitz M. and Saikkonen P. 2015. Gaussian Mixture Autoregressive model for univariate time series. *Journal of Time Series Analysis*, **36**, 247-266.
- Meitz M., Preve D., Saikkonen P. 2018. A mixture autoregressive model based on Student's t-distribution. arXiv:1805.04010 [econ.EM].
- Virolainen S. 2020. A mixture autoregressive model based on Gaussian and Student's t-distribution. arXiv:2003.05221 [econ.EM].

n_params

Calculate the number of parameters

Description

n_params calculates the number of parameters that should be in the parameter vector.

Usage

```
n_params(
  p,
  M,
  model = c("GMAR", "StMAR", "G-StMAR"),
  restricted = FALSE,
  constraints = NULL
)
```

Arguments

- p** a positive integer specifying the autoregressive order of the model.
- M** **For GMAR and StMAR models:** a positive integer specifying the number of mixture components.
For G-StMAR models: a size (2x1) integer vector specifying the number of *GMAR type* components M1 in the first element and *StMAR type* components M2 in the second element. The total number of mixture components is $M=M1+M2$.
- model** is "GMAR", "StMAR", or "G-StMAR" model considered? In the G-StMAR model, the first M1 components are *GMAR type* and the rest M2 components are *StMAR type*.
- restricted** a logical argument stating whether the AR coefficients $\phi_{m,1}, \dots, \phi_{m,p}$ are restricted to be the same for all regimes.
- constraints** specifies linear constraints applied to the autoregressive parameters.
For non-restricted models: a list of size (pxq_m) constraint matrices C_m of full column rank satisfying $\phi_m=C_m\psi_m$ for all $m = 1, \dots, M$, where $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$ and $\psi_m = (\psi_{m,1}, \dots, \psi_{m,q_m})$.
For restricted models: a size (pxq) constraint matrix C of full column rank satisfying $\phi=C\psi$, where $\phi = (\phi_1, \dots, \phi_p)$ and $\psi = (\psi_1, \dots, \psi_q)$.
 Symbol ϕ denotes an AR coefficient. Note that regardless of any constraints, the nominal autoregressive order is always p for all regimes. Ignore or set to NULL if applying linear constraints is **not** desired.

Value

Returns the number of parameters.

parameter_checks *Check the parameter vector is specified correctly*

Description

parameter_checks checks dimension, restrictions, and stationarity of the given parameter of a GMAR, StMAR, or G-StMAR model. Throws an error if any check fails. Does NOT consider the identifiability condition!

Usage

```
parameter_checks(
  p,
  M,
  params,
  model = c("GMAR", "StMAR", "G-StMAR"),
  restricted = FALSE,
  constraints = NULL
)
```

Arguments

- p** a positive integer specifying the autoregressive order of the model.
- M** **For GMAR and StMAR models:** a positive integer specifying the number of mixture components.
For G-StMAR models: a size (2×1) integer vector specifying the number of *GMAR type* components $M1$ in the first element and *StMAR type* components $M2$ in the second element. The total number of mixture components is $M=M1+M2$.
- params** a real valued parameter vector specifying the model.
For GMAR model: Size $(M(p+3)-1 \times 1)$ vector $\theta=(v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1})$, where $v_m = (\phi_{m,0}, \phi_m, \sigma_m^2)$ and $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$, $m = 1, \dots, M$.
For StMAR model: Size $(M(p+4)-1 \times 1)$ vector $(\theta, \nu) = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.
For G-StMAR model: Size $(M(p+3) + M2 - 1 \times 1)$ vector $(\theta, \nu) = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_{M1+1}, \dots, \nu_M)$.
- model** is "GMAR", "StMAR", or "G-StMAR" model considered? In the G-StMAR model, the first $M1$ components are *GMAR type* and the rest $M2$ components are *StMAR type*.
- restricted** a logical argument stating whether the AR coefficients $\phi_{m,1}, \dots, \phi_{m,p}$ are restricted to be the same for all regimes.
- constraints** specifies linear constraints applied to the autoregressive parameters.
For non-restricted models: a list of size (pxq_m) constraint matrices C_m of full column rank satisfying $\phi_m = C_m \psi_m$ for all $m = 1, \dots, M$, where $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$ and $\psi_m = (\psi_{m,1}, \dots, \psi_{m,q_m})$.
For restricted models: a size (pxq) constraint matrix C of full column rank satisfying $\phi = C\psi$, where $\phi = (\phi_1, \dots, \phi_p)$ and $\psi = (\psi_1, \dots, \psi_q)$.
 Symbol ϕ denotes an AR coefficient. Note that regardless of any constraints, the nominal autoregressive order is always p for all regimes. Ignore or set to NULL if applying linear constraints is **not** desired.

Value

Throws an informative error if any check fails. Does not return anything.

pick_alphas	<i>Pick mixing weights parameters from parameter vector</i>
-------------	---

Description

pick_alphas picks and returns the mixing weights parameters (including the non-parametrized one for the last component) from the given parameter vector.

Usage

```
pick_alphas(
    p,
    M,
    params,
    model = c("GMAR", "StMAR", "G-StMAR"),
    restricted = FALSE,
    constraints = NULL
)
```

Arguments

- p** a positive integer specifying the autoregressive order of the model.
- M** **For GMAR and StMAR models:** a positive integer specifying the number of mixture components.
For G-StMAR models: a size (2x1) integer vector specifying the number of *GMAR type* components M1 in the first element and *StMAR type* components M2 in the second element. The total number of mixture components is $M=M1+M2$.
- params** a real valued parameter vector specifying the model.
For non-restricted models: For GMAR model: Size $(M(p+3) - 1x1)$ vector $\theta=(v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1})$, where $v_m = (\phi_{m,0}, \phi_m, \sigma_m^2)$ and $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$, $m = 1, \dots, M$.
For StMAR model: Size $(M(p+4) - 1x1)$ vector $(\theta, \nu) = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.
For G-StMAR model: Size $(M(p+3) + M2 - 1x1)$ vector $(\theta, \nu) = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_{M1+1}, \dots, \nu_M)$.
With linear constraints: Replace the vectors ϕ_m with vectors ψ_m and provide a list of constraint matrices **C** that satisfy $\phi_m = R_m \psi_m$ for all $m = 1, \dots, M$, where $\psi_m = (\psi_{m,1}, \dots, \psi_{m,q_m})$.
For restricted models: For GMAR model: Size $(3M + p - 1x1)$ vector $\theta = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1})$, where $\phi = (\phi_1, \dots, \phi_p)$.
For StMAR model: Size $(4M + p - 1x1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.
For G-StMAR model: Size $(3M + M2 + p - 1x1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1}, \nu_{M1+1}, \dots, \nu_M)$.
With linear constraints: Replace the vector ϕ with vector ψ and provide a constraint matrix **C** that satisfies $\phi = R\psi$, where $\psi = (\psi_1, \dots, \psi_q)$.

Symbol ϕ denotes an AR coefficient, σ^2 a variance, α a mixing weight, and ν a degrees of freedom parameter. If parametrization=="mean", just replace each intercept term $\phi_{m,0}$ with regimewise mean $\mu_m = \phi_{m,0}/(1 - \sum \phi_{i,m})$. In the **G-StMAR** model, the first M1 components are *GMAR type* and the rest M2 components are *StMAR type*. Note that in the case **M=1**, the parameter α is dropped, and in the case of **StMAR** or **G-StMAR** model, the degrees of freedom parameters ν_m have to be larger than 2.

model is "GMAR", "StMAR", or "G-StMAR" model considered? In the G-StMAR model, the first M1 components are *GMAR type* and the rest M2 components are *StMAR type*.

restricted a logical argument stating whether the AR coefficients $\phi_{m,1}, \dots, \phi_{m,p}$ are restricted to be the same for all regimes.

constraints specifies linear constraints applied to the autoregressive parameters.

For non-restricted models: a list of size (pxq_m) constraint matrices C_m of full column rank satisfying $\phi_m = C_m \psi_m$ for all $m = 1, \dots, M$, where $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$ and $\psi_m = (\psi_{m,1}, \dots, \psi_{m,q_m})$.

For restricted models: a size (pxq) constraint matrix C of full column rank satisfying $\phi = C\psi$, where $\phi = (\phi_1, \dots, \phi_p)$ and $\psi = (\psi_1, \dots, \psi_q)$.

Symbol ϕ denotes an AR coefficient. Note that regardless of any constraints, the nominal autoregressive order is always p for all regimes. Ignore or set to NULL if applying linear constraints is **not** desired.

Value

Returns a vector of length M containing the mixing weight parameters α_m .

pick_dfs	<i>Pick degrees of freedom parameters from a parameter vector</i>
----------	---

Description

pick_dfs picks and returns the degrees of freedom parameters from the given parameter vector.

Usage

```
pick_dfs(p, M, params, model = c("GMAR", "StMAR", "G-StMAR"))
```

Arguments

p a positive integer specifying the autoregressive order of the model.

M **For GMAR and StMAR models:** a positive integer specifying the number of mixture components.
For G-StMAR models: a size (2x1) integer vector specifying the number of *GMAR type* components M1 in the first element and *StMAR type* components M2 in the second element. The total number of mixture components is $M=M1+M2$.

params

a real valued parameter vector specifying the model.

For non-restricted models: For GMAR model: Size $(M(p+3) - 1 \times 1)$ vector $\theta = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1})$, where $v_m = (\phi_{m,0}, \phi_m, \sigma_m^2)$ and $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$, $m = 1, \dots, M$.

For StMAR model: Size $(M(p+4) - 1 \times 1)$ vector $(\theta, \nu) = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.

For G-StMAR model: Size $(M(p+3) + M2 - 1 \times 1)$ vector $(\theta, \nu) = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_{M1+1}, \dots, \nu_M)$.

With linear constraints: Replace the vectors ϕ_m with vectors ψ_m and provide a list of constraint matrices \mathbf{C} that satisfy $\phi_m = R_m \psi_m$ for all $m = 1, \dots, M$, where $\psi_m = (\psi_{m,1}, \dots, \psi_{m,q_m})$.

For restricted models: For GMAR model: Size $(3M + p - 1 \times 1)$ vector $\theta = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1})$, where $\phi = (\phi_1, \dots, \phi_p)$.

For StMAR model: Size $(4M + p - 1 \times 1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.

For G-StMAR model: Size $(3M + M2 + p - 1 \times 1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1}, \nu_{M1+1}, \dots, \nu_M)$.

With linear constraints: Replace the vector ϕ with vector ψ and provide a constraint matrix C that satisfies $\phi = R\psi$, where $\psi = (\psi_1, \dots, \psi_q)$.

Symbol ϕ denotes an AR coefficient, σ^2 a variance, α a mixing weight, and ν a degrees of freedom parameter. If parametrization="mean", just replace each intercept term $\phi_{m,0}$ with regimewise mean $\mu_m = \phi_{m,0} / (1 - \sum \phi_{i,m})$. In the **G-StMAR** model, the first M1 components are *GMAR type* and the rest M2 components are *StMAR type*. Note that in the case **M=1**, the parameter α is dropped, and in the case of **StMAR** or **G-StMAR** model, the degrees of freedom parameters ν_m have to be larger than 2.

model

is "GMAR", "StMAR", or "G-StMAR" model considered? In the G-StMAR model, the first M1 components are *GMAR type* and the rest M2 components are *StMAR type*.

Value

Returns a vector of length M or M2 containing the degrees of freedom parameters.

pick_pars

Pick ϕ_0 (or μ), AR-coefficients, and variance parameters from a parameter vector

Description

pick_pars picks ϕ_0/μ , AR-coefficients, and variance parameters from the given parameter vector.

Usage

```
pick_pars(
  p,
  M,
  params,
```

```

model = c("GMAR", "StMAR", "G-StMAR"),
restricted = FALSE,
constraints = NULL
)

```

Arguments

- p** a positive integer specifying the autoregressive order of the model.
- M** **For GMAR and StMAR models:** a positive integer specifying the number of mixture components.
For G-StMAR models: a size (2x1) integer vector specifying the number of *GMAR type* components M1 in the first element and *StMAR type* components M2 in the second element. The total number of mixture components is $M=M1+M2$.
- params** a real valued parameter vector specifying the model.
For non-restricted models: For GMAR model: Size $(M(p+3) - 1x1)$ vector $\theta=(v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1})$, where $v_m = (\phi_{m,0}, \phi_m, \sigma_m^2)$ and $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$, $m = 1, \dots, M$.
For StMAR model: Size $(M(p+4) - 1x1)$ vector $(\theta, \nu) = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.
For G-StMAR model: Size $(M(p+3) + M2 - 1x1)$ vector $(\theta, \nu) = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_{M1+1}, \dots, \nu_M)$.
With linear constraints: Replace the vectors ϕ_m with vectors ψ_m and provide a list of constraint matrices **C** that satisfy $\phi_m = R_m \psi_m$ for all $m = 1, \dots, M$, where $\psi_m = (\psi_{m,1}, \dots, \psi_{m,q_m})$.
For restricted models: For GMAR model: Size $(3M + p - 1x1)$ vector $\theta = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1})$, where $\phi = (\phi_1, \dots, \phi_p)$.
For StMAR model: Size $(4M + p - 1x1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.
For G-StMAR model: Size $(3M + M2 + p - 1x1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1}, \nu_{M1+1}, \dots, \nu_M)$.
With linear constraints: Replace the vector ϕ with vector ψ and provide a constraint matrix **C** that satisfies $\phi = R\psi$, where $\psi = (\psi_1, \dots, \psi_q)$.
Symbol ϕ denotes an AR coefficient, σ^2 a variance, α a mixing weight, and ν a degrees of freedom parameter. If parametrization=="mean", just replace each intercept term $\phi_{m,0}$ with regimewise mean $\mu_m = \phi_{m,0} / (1 - \sum \phi_{i,m})$. In the **G-StMAR** model, the first M1 components are *GMAR type* and the rest M2 components are *StMAR type*. Note that in the case **M=1**, the parameter α is dropped, and in the case of **StMAR** or **G-StMAR** model, the degrees of freedom parameters ν_m have to be larger than 2.
- model** is "GMAR", "StMAR", or "G-StMAR" model considered? In the G-StMAR model, the first M1 components are *GMAR type* and the rest M2 components are *StMAR type*.
- restricted** a logical argument stating whether the AR coefficients $\phi_{m,1}, \dots, \phi_{m,p}$ are restricted to be the same for all regimes.
- constraints** specifies linear constraints applied to the autoregressive parameters.
For non-restricted models: a list of size (pxq_m) constraint matrices C_m of full column rank satisfying $\phi_m = C_m \psi_m$ for all $m = 1, \dots, M$, where $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$ and $\psi_m = (\psi_{m,1}, \dots, \psi_{m,q_m})$.

For restricted models: a size (pxq) constraint matrix C of full column rank satisfying $\phi=C\psi$, where $\phi=(\phi_1, \dots, \phi_p)$ and $\psi=(\psi_1, \dots, \psi_q)$.

Symbol ϕ denotes an AR coefficient. Note that regardless of any constraints, the nominal autoregressive order is always p for all regimes. Ignore or set to NULL if applying linear constraints is **not** desired.

Value

Returns a $(Mx(p+2))$ matrix containing the parameters, column for each component. The first row for ϕ_0 or μ depending on the parametrization, the second row for ϕ_1, \dots , the second to last row for ϕ_p , and the last row for σ^2 .

pick_phi0	<i>Pick phi0 or mean parameters from parameter vector</i>
-----------	---

Description

pick_phi0 picks and returns the phi0 or mean parameters from parameter vector.

Usage

```
pick_phi0(
  p,
  M,
  params,
  model = c("GMAR", "StMAR", "G-StMAR"),
  restricted = FALSE,
  constraints = NULL
)
```

Arguments

- p** a positive integer specifying the autoregressive order of the model.
- M** **For GMAR and StMAR models:** a positive integer specifying the number of mixture components.
For G-StMAR models: a size $(2x1)$ integer vector specifying the number of *GMAR type* components $M1$ in the first element and *StMAR type* components $M2$ in the second element. The total number of mixture components is $M=M1+M2$.
- params** a real valued parameter vector specifying the model.
For non-restricted models: For GMAR model: Size $(M(p+3) - 1x1)$ vector $\theta=(v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1})$, where $v_m=(\phi_{m,0}, \phi_m, \sigma_m^2)$ and $\phi_m=(\phi_{m,1}, \dots, \phi_{m,p})$, $m=1, \dots, M$.
For StMAR model: Size $(M(p+4) - 1x1)$ vector $(\theta, \nu)=(v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.
For G-StMAR model: Size $(M(p+3) + M2 - 1x1)$ vector $(\theta, \nu)=(v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_{M1+1}, \dots, \nu_M)$.

With linear constraints: Replace the vectors ϕ_m with vectors ψ_m and provide a list of constraint matrices \mathbf{C} that satisfy $\phi_m = R_m \psi_m$ for all $m = 1, \dots, M$, where $\psi_m = (\psi_{m,1}, \dots, \psi_{m,q_m})$.

For restricted models: For GMAR model: Size $(3M + p - 1 \times 1)$ vector $\theta = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1})$, where $\phi = (\phi_1, \dots, \phi_p)$.

For StMAR model: Size $(4M + p - 1 \times 1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.

For G-StMAR model: Size $(3M + M2 + p - 1 \times 1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.

With linear constraints: Replace the vector ϕ with vector ψ and provide a constraint matrix C that satisfies $\phi = R\psi$, where $\psi = (\psi_1, \dots, \psi_q)$.

Symbol ϕ denotes an AR coefficient, σ^2 a variance, α a mixing weight, and ν a degrees of freedom parameter. If parametrization="mean", just replace each intercept term $\phi_{m,0}$ with regimewise mean $\mu_m = \phi_{m,0} / (1 - \sum \phi_{i,m})$. In the **G-StMAR** model, the first M1 components are *GMAR type* and the rest M2 components are *StMAR type*. Note that in the case **M=1**, the parameter α is dropped, and in the case of **StMAR** or **G-StMAR** model, the degrees of freedom parameters ν_m have to be larger than 2.

model is "GMAR", "StMAR", or "G-StMAR" model considered? In the G-StMAR model, the first M1 components are *GMAR type* and the rest M2 components are *StMAR type*.

restricted a logical argument stating whether the AR coefficients $\phi_{m,1}, \dots, \phi_{m,p}$ are restricted to be the same for all regimes.

constraints specifies linear constraints applied to the autoregressive parameters.

For non-restricted models: a list of size (pq_m) constraint matrices C_m of full column rank satisfying $\phi_m = C_m \psi_m$ for all $m = 1, \dots, M$, where $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$ and $\psi_m = (\psi_{m,1}, \dots, \psi_{m,q_m})$.

For restricted models: a size (pq) constraint matrix C of full column rank satisfying $\phi = C\psi$, where $\phi = (\phi_1, \dots, \phi_p)$ and $\psi = (\psi_1, \dots, \psi_q)$.

Symbol ϕ denotes an AR coefficient. Note that regardless of any constraints, the nominal autoregressive order is always p for all regimes. Ignore or set to NULL if applying linear constraints is **not** desired.

Value

Returns a vector of length M containing the phi0 or mean parameters depending parametrization.

plot.gsmarpred *Plot method for class 'gsmarpred' objects*

Description

plot.gsmarpred is plot method for class 'gsmarpred' objects

Usage

```
## S3 method for class 'gsmarpred'
plot(x, ..., nt, mix_weights = TRUE, add_grid = TRUE)
```

Arguments

x	object of class 'gsmarpred' created with predict.gsmar.
...	arguments passed to function grid.
nt	a positive integer specifying the number of observations to be plotted along with the prediction. Default is round(length(data)*0.15).
mix_weights	TRUE if forecasts for mixing weights should be plotted, FALSE in not.
add_grid	should grid a be added to the plots?

Details

This method is intended for plotting forecasts of GSMAR processes.

plot.qrtest *Quantile residual tests for GMAR, StMAR , and G-StMAR models*

Description

quantile_residual_tests performs quantile residual tests for GMAR, StMAR, and G-StMAR models, testing normality, autocorrelation, and conditional heteroscedasticity of the quantile residuals.

Usage

```
## S3 method for class 'qrtest'
plot(x, ...)

## S3 method for class 'qrtest'
print(x, ..., digits = 3)

quantile_residual_tests(
  gsmar,
  lags_ac = c(1, 3, 6, 12),
  lags_ch = lags_ac,
  nsimu = 1,
  print_res = TRUE
)
```

Arguments

x	object of class 'qrtest' created with the function quantile_residual_tests.
...	graphical parameters passed to segments in plot.qrtest. Currently not used in print.qrtest
digits	the number of digits to be print
gsmar	object of class 'gsmar' created with the function fitGSMAR or GSMAR.

lags_ac	a numeric vector of positive integers specifying the lags for which autocorrelation is tested.
lags_ch	a numeric vector of positive integers specifying the lags for which conditional heteroscedasticity is tested.
nsimu	a positive integer specifying to how many simulated observations the covariance matrix Omega (see Kalliovirta (2012)) should be based on. If smaller than data size, then omega will be based on the given data and not on simulated data. Having the covariance matrix omega based on a large simulated sample might improve the tests size properties.
print_res	a logical argument defining whether the results should be printed or not.

Details

For a correctly specified GSMAR model employing the maximum likelihood estimator, the quantile residuals are asymptotically independent with standard normal distribution. They can hence be used in a similar manner to conventional Pearson's residuals. For more details about quantile residual based diagnostics, and in particular, about the quantile residual tests, see the cited article by *Kalliovirta (2012)*.

Value

Returns an object of class 'qrtest' containing the test results in data frames. In the cases of autocorrelation and conditional heteroscedasticity tests, the returned object also contains the associated individual statistics and their standard errors, discussed in *Kalliovirta (2012)* at the pages 369-370.

Methods (by generic)

- plot: Plot p-values of the autocorrelation and conditional heteroskedasticity tests.
- print: Print method for class 'qrtest' objects

References

- Galbraith, R., Galbraith, J. 1974. On the inverses of some patterned matrices arising in the theory of stationary time series. *Journal of Applied Probability* **11**, 63-71.
- Kalliovirta L. (2012) Misspecification tests based on quantile residuals. *The Econometrics Journal*, **15**, 358-393.
- Kalliovirta L., Meitz M. and Saikkonen P. 2015. Gaussian Mixture Autoregressive model for univariate time series. *Journal of Time Series Analysis*, **36**, 247-266.
- Meitz M., Preve D., Saikkonen P. 2018. A mixture autoregressive model based on Student's t-distribution. arXiv:1805.04010 [econ.EM].
- Virolainen S. 2020. A mixture autoregressive model based on Gaussian and Student's t-distribution. arXiv:2003.05221 [econ.EM].

See Also

[profile_logliks](#), [fitGSMAR](#), [GSMAR](#), [diagnostic_plot](#), [predict.gsmar](#), [get_test_Omega](#),

Examples

```
## The below examples take approximately 30 seconds to run.

# G-StMAR model with one GMAR type and one StMAR type regime
fit42gs <- fitGSMAR(data=M10Y1Y, p=4, M=c(1, 1), model="G-StMAR",
                  ncalls=1, seeds=4)

# Tests based on the observed data (without simulation procedure) with the
# default lags:
qrt1 <- quantile_residual_tests(fit42gs)

# Tests based on the simulation procedure using sample size 10000 and with
# the lags specified by hand:
set.seed(1)
qrt2 <- quantile_residual_tests(fit42gs, lags_ac=c(1, 6), nsimu=10000)

# GMAR model
fit12 <- fitGSMAR(data=simudata, p=1, M=2, model="GMAR", ncalls=1, seeds=1)
qrt3 <- quantile_residual_tests(fit12, lags_ac=c(1, 5, 10, 15))
```

predict.gsmar

Forecast GMAR, StMAR, or G-StMAR process

Description

predict.gsmar forecasts the specified GMAR, StMAR, or G-StMAR process by using the given data to simulate its possible future values. For one-step forecasts using the exact formula for conditional mean is supported.

Usage

```
## S3 method for class 'gsmar'
predict(
  object,
  ...,
  n_ahead,
  nsimu = 10000,
  pi = c(0.95, 0.8),
  pred_type = c("median", "mean", "cond_mean"),
  pi_type = c("two-sided", "upper", "lower", "none"),
  plot_res = TRUE,
  mix_weights = TRUE,
  nt
)
```

Arguments

object	object of class 'gsmar' created with function fitGSMAR or GSMAR.
...	additional arguments passed to grid (ignored if plot_res==FALSE).
n_ahead	a positive integer specifying how many steps in the future should be forecasted.
nsimu	a positive integer specifying to how many simulations the forecast should be based on.
pi	a numeric vector specifying confidence levels for the prediction intervals.
pred_type	should the prediction be based on sample "median" or "mean"? Or should it be one-step-ahead forecast based on the exact conditional mean ("cond_mean")? prediction intervals won't be calculated if the exact conditional mean is used.
pi_type	should the prediction intervals be "two-sided", "upper", or "lower"?
plot_res	a logical argument defining whether the forecast should be plotted or not.
mix_weights	TRUE if forecasts for mixing weights should be plotted, FALSE in not.
nt	a positive integer specifying the number of observations to be plotted along with the prediction. Default is round(length(data)*0.15).

Details

predict.gsmar uses the last p values of the data to simulate $nsimu$ possible future values for each step-ahead. The point prediction is then obtained by calculating the sample median or mean for each step and the prediction intervals are obtained from the empirical fractiles.

The function simulateGSMAR can also be used directly for quantile based forecasting.

Value

Returns a class 'gsmarpred' object containing, among the specifications,...

\$pred Point forecasts

\$pred_ints Prediction intervals

\$mix_pred Point forecasts for mixing weights

mix_pred_ints Individual prediction intervals for mixing weights, as $[, , m]$, $m=1, \dots, M$.

References

- Galbraith, R., Galbraith, J. 1974. On the inverses of some patterned matrices arising in the theory of stationary time series. *Journal of Applied Probability* **11**, 63-71.
- Kalliovirta L. (2012) Misspecification tests based on quantile residuals. *The Econometrics Journal*, **15**, 358-393.
- Kalliovirta L., Meitz M. and Saikkonen P. 2015. Gaussian Mixture Autoregressive model for univariate time series. *Journal of Time Series Analysis*, **36**, 247-266.
- Meitz M., Preve D., Saikkonen P. 2018. A mixture autoregressive model based on Student's t-distribution. arXiv:1805.04010 [econ.EM].
- Virolainen S. 2020. A mixture autoregressive model based on Gaussian and Student's t-distribution. arXiv:2003.05221 [econ.EM].

See Also

[simulateGSMAR](#), [cond_moments](#), [fitGSMAR](#), [GSMAR](#), [quantile_residual_tests](#), [diagnostic_plot](#)

Examples

```
## These examples take approximately 30 seconds to run.

# G-StMAR model with one GMAR type and one StMAR type regime
fit42gs <- fitGSMAR(M10Y1Y, p=4, M=c(1, 1), model="G-StMAR",
                  ncalls=1, seeds=4)

# Forecast 12 steps ahead based on 10000 simulated sample paths, prediction
# interval confidence levels 0.95 and 0.8, prediction based on sample median,
# and two-sided prediction intervals:
mypred <- predict(fit42gs, n_ahead=12, nsimu=10000, pi=c(0.95, 0.8),
                 pred_type="median", pi_type="two-sided")

mypred
plot(mypred)

# Forecast 24 steps ahead based on 1000 simulated sample paths, prediction
# interval confidence level 0.99 and 0.9, prediction based on sample mean,
# and upper prediction intervals:
mypred2 <- predict(fit42gs, n_ahead=24, nsimu=1000, pi=c(0.99, 0.9),
                  pred_type="mean", pi_type="upper")

# Forecast 24 steps ahead based on 1000 simulated sample paths, prediction
# interval confidence level 0.99, 0.95, 0.9 and 0.8, prediction based on
# sample median, and lower prediction intervals:
mypred3 <- predict(fit42gs, n_ahead=24, nsimu=1000, pi=c(0.99, 0.95, 0.9, 0.8),
                  pred_type="median", pi_type="lower")

# GMAR model
params12 <- c(1.70, 0.85, 0.30, 4.12, 0.73, 1.98, 0.63)
gmar12 <- GSMAR(data=simudata, p=1, M=2, params=params12, model="GMAR")
pred12 <- predict(gmar12, n_ahead=10, nsimu=1000, pi=c(0.95, 0.9, 0.8),
                 pred_type="median", pi_type="two-sided")

pred12
plot(pred12)

# One-step prediction based on the exact conditional mean:
predict(gmar12, n_ahead=1, pred_type="cond_mean", plot_res=FALSE)
```

print.gsmarpred *Print method for class 'gsmarpred' objects*

Description

print.gsmarpred is a print method for call 'gsmarpred' objects created with predict.gsmar.

Usage

```
## S3 method for class 'gsmarpred'
print(x, ..., digits = 2)
```

Arguments

x	object of class 'gsmarpred' generated by predict.gsmar.
...	currently not in use.
digits	the number of digits to be printed

print.gsmarsum	<i>Print method from objects of class 'gsmarsum'</i>
----------------	--

Description

print.gsmarsum is a print method for objects of class 'gsmarsum' created with the summary method summary.gsmar. Approximate standard errors are printed in brackets.

Usage

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

Arguments

x	object of class 'gsmarsum' generated by summary.gsmar.
...	currently not in use.
digits	the number of digits to be printed

profile_logliks	<i>Plot profile log-likelihoods around the estimates</i>
-----------------	--

Description

profile_logliks plots profile log-likelihoods around the estimates.

Usage

```
profile_logliks(gsmar, scale = 0.02, nrows, ncols, precision = 200)
```

Arguments

gsmar	object of class 'gsmar' created with the function fitGSMAR or GSMAR.
scale	a numeric scalar specifying the interval plotted for each estimate: the estimate plus-minus $\text{abs}(\text{scale} \times \text{estimate})$.
nrows	how many rows should be in the plot-matrix? The default is $\text{max}(\text{ceiling}(\log_2(\text{nparams}) - 1), 1)$.
ncols	how many columns should be in the plot-matrix? The default is $\text{ceiling}(\text{nparams}/\text{nrows})$. Note that $\text{nrows} \times \text{ncols}$ should not be smaller than the number of parameters.
precision	at how many points should each profile log-likelihood be evaluated at?

Details

The red vertical line points the estimate.

Be aware that the profile log-likelihood function is subject to a numerical error due to limited float-point precision when considering extremely large parameter values, say, overly large degrees freedom estimates.

Value

Only plots to a graphical device and doesn't return anything.

References

- Galbraith, R., Galbraith, J. 1974. On the inverses of some patterned matrices arising in the theory of stationary time series. *Journal of Applied Probability* **11**, 63-71.
- Kalliovirta L. (2012) Misspecification tests based on quantile residuals. *The Econometrics Journal*, **15**, 358-393.
- Kalliovirta L., Meitz M. and Saikkonen P. 2015. Gaussian Mixture Autoregressive model for univariate time series. *Journal of Time Series Analysis*, **36**, 247-266.
- Meitz M., Preve D., Saikkonen P. 2018. A mixture autoregressive model based on Student's t-distribution. arXiv:1805.04010 [econ.EM].
- Virolainen S. 2020. A mixture autoregressive model based on Gaussian and Student's t-distribution. arXiv:2003.05221 [econ.EM].

See Also

[quantile_residual_plot](#), [diagnostic_plot](#), [cond_moment_plot](#), [GSMAR](#), [quantile_residual_tests](#), [simulateGSMAR](#)

Examples

```
## The below examples the approximately 15 seconds to run.

# G-StMAR model with one GMAR type and one StMAR type regime
fit42gs <- fitGSMAR(M10Y1Y, p=4, M=c(1, 1), model="G-StMAR",
                  ncalls=1, seeds=4)
```

```

profile_logliks(fit42gs)

# GMAR model, graphs zoomed in closer.
fit12 <- fitGSMAR(data=simudata, p=1, M=2, model="GMAR", ncalls=1, seeds=1)
profile_logliks(fit12, scale=0.001)

```

quantileResidualPlot *DEPRECATED, USE quantile_residual_plot INSTEAD! Plot quantile residual time series and histogram*

Description

quantileResidualsPlot plots quantile residual time series and histogram. DEPRECATED, USE quantile_residual_plot INSTEAD!

Usage

```
quantileResidualPlot(gsmar)
```

Arguments

gsmar object of class 'gsmar' created with the function fitGSMAR or GSMAR.

Details

DEPRECATED, USE quantile_residual_plot INSTEAD!

Value

Only plots to a graphical device and doesn't return anything.

References

- Galbraith, R., Galbraith, J. 1974. On the inverses of some patterned matrices arising in the theory of stationary time series. *Journal of Applied Probability* **11**, 63-71.
- Kalliovirta L. (2012) Misspecification tests based on quantile residuals. *The Econometrics Journal*, **15**, 358-393.
- Kalliovirta L., Meitz M. and Saikkonen P. 2015. Gaussian Mixture Autoregressive model for univariate time series. *Journal of Time Series Analysis*, **36**, 247-266.
- Meitz M., Preve D., Saikkonen P. 2018. A mixture autoregressive model based on Student's t-distribution. arXiv:1805.04010 [econ.EM].
- Virolainen S. 2020. A mixture autoregressive model based on Gaussian and Student's t-distribution. arXiv:2003.05221 [econ.EM].

See Also

[profile_logliks](#), [diagnostic_plot](#), [fitGSMAR](#), [GSMAR](#), [quantile_residual_tests](#), [simulateGSMAR](#)

quantileResiduals *DEPRECATED, USE quantile_residuals INSTEAD! Compute quantile residuals of GMAR, StMAR, or G-StMAR model*

Description

quantileResiduals computes the quantile residuals of the specified GMAR, StMAR, or G-StMAR model. DEPRECATED, USE quantile_residuals INSTEAD!

Usage

```
quantileResiduals(
  data,
  p,
  M,
  params,
  model = c("GMAR", "StMAR", "G-StMAR"),
  restricted = FALSE,
  constraints = NULL,
  parametrization = c("intercept", "mean")
)
```

Arguments

- data** a numeric vector or class 'ts' object containing the data. NA values are not supported.
- p** a positive integer specifying the autoregressive order of the model.
- M** **For GMAR and StMAR models:** a positive integer specifying the number of mixture components.
For G-StMAR models: a size (2x1) integer vector specifying the number of *GMAR type* components M1 in the first element and *StMAR type* components M2 in the second element. The total number of mixture components is $M=M1+M2$.
- params** a real valued parameter vector specifying the model.
For non-restricted models: For GMAR model: Size $(M(p+3) - 1x1)$ vector $\theta=(v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1})$, where $v_m = (\phi_{m,0}, \phi_m, \sigma_m^2)$ and $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$, $m = 1, \dots, M$.
For StMAR model: Size $(M(p+4) - 1x1)$ vector $(\theta, \nu) = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.
For G-StMAR model: Size $(M(p+3) + M2 - 1x1)$ vector $(\theta, \nu) = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_{M1+1}, \dots, \nu_M)$.
With linear constraints: Replace the vectors ϕ_m with vectors ψ_m and provide a list of constraint matrices **C** that satisfy $\phi_m = R_m \psi_m$ for all $m = 1, \dots, M$, where $\psi_m = (\psi_{m,1}, \dots, \psi_{m,q_m})$.
For restricted models: For GMAR model: Size $(3M + p - 1x1)$ vector $\theta = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1})$, where $\phi = (\phi_1, \dots, \phi_p)$.

For StMAR model: Size $(4M+p-1 \times 1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1})$

For G-StMAR model: Size $(3M+M2+p-1 \times 1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1})$

With linear constraints: Replace the vector ϕ with vector ψ and provide a constraint matrix C that satisfies $\phi = R\psi$, where $\psi = (\psi_1, \dots, \psi_q)$.

Symbol ϕ denotes an AR coefficient, σ^2 a variance, α a mixing weight, and ν a degrees of freedom parameter. If parametrization="mean", just replace each intercept term $\phi_{m,0}$ with regimewise mean $\mu_m = \phi_{m,0} / (1 - \sum \phi_{i,m})$. In the **G-StMAR** model, the first M1 components are *GMAR type* and the rest M2 components are *StMAR type*. Note that in the case **M=1**, the parameter α is dropped, and in the case of **StMAR** or **G-StMAR** model, the degrees of freedom parameters ν_m have to be larger than 2.

model is "GMAR", "StMAR", or "G-StMAR" model considered? In the G-StMAR model, the first M1 components are *GMAR type* and the rest M2 components are *StMAR type*.

restricted a logical argument stating whether the AR coefficients $\phi_{m,1}, \dots, \phi_{m,p}$ are restricted to be the same for all regimes.

constraints specifies linear constraints applied to the autoregressive parameters.

For non-restricted models: a list of size (pxq_m) constraint matrices C_m of full column rank satisfying $\phi_m = C_m \psi_m$ for all $m = 1, \dots, M$, where $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$ and $\psi_m = (\psi_{m,1}, \dots, \psi_{m,q_m})$.

For restricted models: a size (pxq) constraint matrix C of full column rank satisfying $\phi = C\psi$, where $\phi = (\phi_1, \dots, \phi_p)$ and $\psi = (\psi_1, \dots, \psi_q)$.

Symbol ϕ denotes an AR coefficient. Note that regardless of any constraints, the nominal autoregressive order is always p for all regimes. Ignore or set to NULL if applying linear constraints is **not** desired.

parametrization

is the model parametrized with the "intercepts" $\phi_{m,0}$ or "means" $\mu_m = \phi_{m,0} / (1 - \sum \phi_{i,m})$?

Details

DEPRECATED, USE `quantile_residuals` INSTEAD!

Value

Returns a $(Tx1)$ numeric vector containing the quantile residuals of the specified GMAR, StMAR or G-StMAR model.

Suggested packages

Install the suggested package "gsl" for faster evaluation of the quantile residuals of StMAR and G-StMAR models.

References

- Galbraith, R., Galbraith, J. 1974. On the inverses of some patterned matrices arising in the theory of stationary time series. *Journal of Applied Probability* **11**, 63-71.

- Kalliovirta L. (2012) Misspecification tests based on quantile residuals. *The Econometrics Journal*, **15**, 358-393.
- Kalliovirta L., Meitz M. and Saikkonen P. 2015. Gaussian Mixture Autoregressive model for univariate time series. *Journal of Time Series Analysis*, **36**, 247-266.
- Meitz M., Preve D., Saikkonen P. 2018. A mixture autoregressive model based on Student's t-distribution. arXiv:1805.04010 [econ.EM].
- Virolainen S. 2020. A mixture autoregressive model based on Gaussian and Student's t-distribution. arXiv:2003.05221 [econ.EM].

quantileResidualTests *DEPRECATED, USE quantile_residual_tests INSTEAD! Quantile residual tests for GMAR, StMAR, and G-StMAR models*

Description

quantileResidualTests performs quantile residual tests for GMAR, StMAR, and G-StMAR models, testing normality, autocorrelation, and conditional heteroscedasticity of the quantile residuals. **DEPRECATED, USE quantile_residual_tests INSTEAD!**

Usage

```
quantileResidualTests(
  gsmar,
  lags_ac = c(1, 3, 6, 12),
  lags_ch = lags_ac,
  nsimu = 1,
  print_res = TRUE,
  lagsAC = NULL,
  lagsCH = NULL,
  printRes = NULL
)
```

Arguments

gsmar	object of class 'gsmar' created with the function fitGSMAR or GSMAR.
lags_ac	a numeric vector of positive integers specifying the lags for which autocorrelation is tested.
lags_ch	a numeric vector of positive integers specifying the lags for which conditional heteroscedasticity is tested.
nsimu	a positive integer specifying to how many simulated observations the covariance matrix Omega (see Kalliovirta (2012)) should be based on. If smaller than data size, then omega will be based on the given data and not on simulated data. Having the covariance matrix omega based on a large simulated sample might improve the tests size properties.
print_res	a logical argument defining whether the results should be printed or not.

lagsAC	deprecated! Use lags_ac instead.
lagsCH	deprecated! Use lags_ch instead.
printRes	deprecated! Use print_res instead.

Details

DEPRECATED! USE `quantile_residual_tests` INSTEAD!

For a correctly specified GSMAR model employing the maximum likelihood estimator, the quantile residuals are asymptotically independent with standard normal distribution. They can hence be used in a similar manner to conventional Pearson's residuals. For more details about quantile residual based diagnostics, and in particular, about the quantile residual tests, see the cited article by *Kalliovirta (2012)*.

Value

Returns an object of class 'qrtest' containing the test results in data frames. In the cases of auto-correlation and conditional heteroscedasticity tests, the returned object also contains the associated individual statistics and their standard errors, discussed in *Kalliovirta (2012)* at the pages 369-370.

Suggested packages

Install the suggested package "gsl" for faster evaluations in the cases of StMAR and G-StMAR models. For large StMAR and G-StMAR models with large data, the evaluations may take significantly long time without the package "gsl".

References

- Galbraith, R., Galbraith, J. 1974. On the inverses of some patterned matrices arising in the theory of stationary time series. *Journal of Applied Probability* **11**, 63-71.
- Kalliovirta L. (2012) Misspecification tests based on quantile residuals. *The Econometrics Journal*, **15**, 358-393.
- Kalliovirta L., Meitz M. and Saikkonen P. 2015. Gaussian Mixture Autoregressive model for univariate time series. *Journal of Time Series Analysis*, **36**, 247-266.
- Meitz M., Preve D., Saikkonen P. 2018. A mixture autoregressive model based on Student's t-distribution. arXiv:1805.04010 [econ.EM].
- Virolainen S. 2020. A mixture autoregressive model based on Gaussian and Student's t-distribution. arXiv:2003.05221 [econ.EM].

See Also

[profile_logliks](#), [fitGSMAR](#), [GSMAR](#), [diagnostic_plot](#), [predict.gsmar](#), [get_test_Omega](#),

quantile_residuals *Compute quantile residuals of GMAR, StMAR, or G-StMAR model*

Description

quantile_residuals computes the quantile residuals of the specified GMAR, StMAR, or G-StMAR model.

Usage

```
quantile_residuals(
  data,
  p,
  M,
  params,
  model = c("GMAR", "StMAR", "G-StMAR"),
  restricted = FALSE,
  constraints = NULL,
  parametrization = c("intercept", "mean")
)
```

Arguments

- data a numeric vector or class 'ts' object containing the data. NA values are not supported.
- p a positive integer specifying the autoregressive order of the model.
- M **For GMAR and StMAR models:** a positive integer specifying the number of mixture components.
For G-StMAR models: a size (2x1) integer vector specifying the number of *GMAR type* components M1 in the first element and *StMAR type* components M2 in the second element. The total number of mixture components is M=M1+M2.
- params a real valued parameter vector specifying the model.
For non-restricted models: For GMAR model: Size $(M(p+3) - 1x1)$ vector $\theta=(v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1})$, where $v_m = (\phi_{m,0}, \phi_m, \sigma_m^2)$ and $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$, $m = 1, \dots, M$.
For StMAR model: Size $(M(p+4) - 1x1)$ vector $(\theta, \nu) = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.
For G-StMAR model: Size $(M(p+3) + M2 - 1x1)$ vector $(\theta, \nu) = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_{M+1}, \dots, \nu_M)$.
With linear constraints: Replace the vectors ϕ_m with vectors ψ_m and provide a list of constraint matrices **C** that satisfy $\phi_m = R_m \psi_m$ for all $m = 1, \dots, M$, where $\psi_m = (\psi_{m,1}, \dots, \psi_{m,q_m})$.
For restricted models: For GMAR model: Size $(3M + p - 1x1)$ vector $\theta = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1})$, where $\phi = (\phi_1, \dots, \phi_p)$.
For StMAR model: Size $(4M + p - 1x1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.

For G-StMAR model: Size $(3M+M2+p-1 \times 1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_M)$.

With linear constraints: Replace the vector ϕ with vector ψ and provide a constraint matrix C that satisfies $\phi = R\psi$, where $\psi = (\psi_1, \dots, \psi_q)$.

Symbol ϕ denotes an AR coefficient, σ^2 a variance, α a mixing weight, and ν a degrees of freedom parameter. If parametrization=="mean", just replace each intercept term $\phi_{m,0}$ with regimewise mean $\mu_m = \phi_{m,0}/(1 - \sum \phi_{i,m})$. In the **G-StMAR** model, the first M1 components are *GMAR type* and the rest M2 components are *StMAR type*. Note that in the case **M=1**, the parameter α is dropped, and in the case of **StMAR** or **G-StMAR** model, the degrees of freedom parameters ν_m have to be larger than 2.

model is "GMAR", "StMAR", or "G-StMAR" model considered? In the G-StMAR model, the first M1 components are *GMAR type* and the rest M2 components are *StMAR type*.

restricted a logical argument stating whether the AR coefficients $\phi_{m,1}, \dots, \phi_{m,p}$ are restricted to be the same for all regimes.

constraints specifies linear constraints applied to the autoregressive parameters.

For non-restricted models: a list of size $(p \times q_m)$ constraint matrices C_m of full column rank satisfying $\phi_m = C_m \psi_m$ for all $m = 1, \dots, M$, where $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$ and $\psi_m = (\psi_{m,1}, \dots, \psi_{m,q_m})$.

For restricted models: a size $(p \times q)$ constraint matrix C of full column rank satisfying $\phi = C\psi$, where $\phi = (\phi_1, \dots, \phi_p)$ and $\psi = (\psi_1, \dots, \psi_q)$.

Symbol ϕ denotes an AR coefficient. Note that regardless of any constraints, the nominal autoregressive order is always p for all regimes. Ignore or set to NULL if applying linear constraints is **not** desired.

parametrization is the model parametrized with the "intercepts" $\phi_{m,0}$ or "means" $\mu_m = \phi_{m,0}/(1 - \sum \phi_{i,m})$?

Details

Numerical integration is employed if the quantile residuals cannot be obtained analytically with the hypergeometric function using the package 'gsl'.

Value

Returns a $(Tx1)$ numeric vector containing the quantile residuals of the specified GMAR, StMAR or G-StMAR model.

References

- Galbraith, R., Galbraith, J. 1974. On the inverses of some patterned matrices arising in the theory of stationary time series. *Journal of Applied Probability* **11**, 63-71.
- Kalliovirta L. (2012) Misspecification tests based on quantile residuals. *The Econometrics Journal*, **15**, 358-393.
- Kalliovirta L., Meitz M. and Saikkonen P. 2015. Gaussian Mixture Autoregressive model for univariate time series. *Journal of Time Series Analysis*, **36**, 247-266.

- Meitz M., Preve D., Saikkonen P. 2018. A mixture autoregressive model based on Student's t-distribution. arXiv:1805.04010 [econ.EM].
- Virolainen S. 2020. A mixture autoregressive model based on Gaussian and Student's t-distribution. arXiv:2003.05221 [econ.EM].

Examples

```
# GMAR model
params12 <- c(1.70, 0.85, 0.30, 4.12, 0.73, 1.98, 0.63)
quantile_residuals(simudata, p=1, M=2, params=params12, model="GMAR")

# G-StMAR-model
params42gs <- c(0.04, 1.34, -0.59, 0.54, -0.36, 0.01, 0.06, 1.28, -0.36,
               0.2, -0.15, 0.04, 0.19, 9.75)
quantile_residuals(M10Y1Y, p=4, M=c(1, 1), params=params42gs, model="G-StMAR")
```

quantile_residuals_int

Compute quantile residuals of GMAR, StMAR, or G-StMAR model

Description

quantile_residuals_int computes the quantile residuals of the specified GMAR, StMAR, or G-StMAR model.

Usage

```
quantile_residuals_int(
  data,
  p,
  M,
  params,
  model = c("GMAR", "StMAR", "G-StMAR"),
  restricted = FALSE,
  constraints = NULL,
  parametrization = c("intercept", "mean")
)
```

Arguments

data	a numeric vector or class 'ts' object containing the data. NA values are not supported.
p	a positive integer specifying the autoregressive order of the model.
M	For GMAR and StMAR models: a positive integer specifying the number of mixture components.

	<p>For G-StMAR models: a size (2×1) integer vector specifying the number of <i>GMAR type</i> components $M1$ in the first element and <i>StMAR type</i> components $M2$ in the second element. The total number of mixture components is $M=M1+M2$.</p>
params	<p>a real valued parameter vector specifying the model.</p> <p>For non-restricted models: For GMAR model: Size $(M(p+3) - 1 \times 1)$ vector $\theta=(v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1})$, where $v_m = (\phi_{m,0}, \phi_m, \sigma_m^2)$ and $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$, $m = 1, \dots, M$.</p> <p>For StMAR model: Size $(M(p+4) - 1 \times 1)$ vector $(\theta, \nu) = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.</p> <p>For G-StMAR model: Size $(M(p+3) + M2 - 1 \times 1)$ vector $(\theta, \nu) = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_{M1+1}, \dots, \nu_M)$.</p> <p>With linear constraints: Replace the vectors ϕ_m with vectors ψ_m and provide a list of constraint matrices C that satisfy $\phi_m = R_m \psi_m$ for all $m = 1, \dots, M$, where $\psi_m = (\psi_{m,1}, \dots, \psi_{m,q_m})$.</p> <p>For restricted models: For GMAR model: Size $(3M + p - 1 \times 1)$ vector $\theta = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1})$, where $\phi = (\phi_1, \dots, \phi_p)$.</p> <p>For StMAR model: Size $(4M + p - 1 \times 1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.</p> <p>For G-StMAR model: Size $(3M + M2 + p - 1 \times 1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.</p> <p>With linear constraints: Replace the vector ϕ with vector ψ and provide a constraint matrix C that satisfies $\phi = R\psi$, where $\psi = (\psi_1, \dots, \psi_q)$.</p> <p>Symbol ϕ denotes an AR coefficient, σ^2 a variance, α a mixing weight, and ν a degrees of freedom parameter. If parametrization="mean", just replace each intercept term $\phi_{m,0}$ with regimewise mean $\mu_m = \phi_{m,0} / (1 - \sum \phi_{i,m})$. In the G-StMAR model, the first $M1$ components are <i>GMAR type</i> and the rest $M2$ components are <i>StMAR type</i>. Note that in the case $M=1$, the parameter α is dropped, and in the case of StMAR or G-StMAR model, the degrees of freedom parameters ν_m have to be larger than 2.</p>
model	<p>is "GMAR", "StMAR", or "G-StMAR" model considered? In the G-StMAR model, the first $M1$ components are <i>GMAR type</i> and the rest $M2$ components are <i>StMAR type</i>.</p>
restricted	<p>a logical argument stating whether the AR coefficients $\phi_{m,1}, \dots, \phi_{m,p}$ are restricted to be the same for all regimes.</p>
constraints	<p>specifies linear constraints applied to the autoregressive parameters.</p> <p>For non-restricted models: a list of size $(p \times q_m)$ constraint matrices C_m of full column rank satisfying $\phi_m = C_m \psi_m$ for all $m = 1, \dots, M$, where $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$ and $\psi_m = (\psi_{m,1}, \dots, \psi_{m,q_m})$.</p> <p>For restricted models: a size $(p \times q)$ constraint matrix C of full column rank satisfying $\phi = C\psi$, where $\phi = (\phi_1, \dots, \phi_p)$ and $\psi = (\psi_1, \dots, \psi_q)$.</p> <p>Symbol ϕ denotes an AR coefficient. Note that regardless of any constraints, the nominal autoregressive order is always p for all regimes. Ignore or set to NULL if applying linear constraints is not desired.</p>
parametrization	<p>is the model parametrized with the "intercepts" $\phi_{m,0}$ or "means" $\mu_m = \phi_{m,0} / (1 - \sum \phi_{i,m})$?</p>

Details

Numerical integration is employed if the quantile residuals cannot be obtained analytically with the hypergeometric function using the package 'gsl'.

Value

Returns a $(Tx1)$ numeric vector containing the quantile residuals of the specified GMAR, StMAR or G-StMAR model.

References

- Galbraith, R., Galbraith, J. 1974. On the inverses of some patterned matrices arising in the theory of stationary time series. *Journal of Applied Probability* **11**, 63-71.
- Kalliovirta L. (2012) Misspecification tests based on quantile residuals. *The Econometrics Journal*, **15**, 358-393.
- Kalliovirta L., Meitz M. and Saikkonen P. 2015. Gaussian Mixture Autoregressive model for univariate time series. *Journal of Time Series Analysis*, **36**, 247-266.
- Meitz M., Preve D., Saikkonen P. 2018. A mixture autoregressive model based on Student's t-distribution. arXiv:1805.04010 [econ.EM].
- Virolainen S. 2020. A mixture autoregressive model based on Gaussian and Student's t-distribution. arXiv:2003.05221 [econ.EM].

quantile_residual_plot

Plot quantile residual time series and histogram

Description

quantile_residualsPlot plots quantile residual time series and histogram.

Usage

```
quantile_residual_plot(gsmar)
```

Arguments

gsmar object of class 'gsmar' created with the function fitGSMAR or GSMAR.

Value

Only plots to a graphical device and doesn't return anything.

References

- Galbraith, R., Galbraith, J. 1974. On the inverses of some patterned matrices arising in the theory of stationary time series. *Journal of Applied Probability* **11**, 63-71.
- Kalliovirta L. (2012) Misspecification tests based on quantile residuals. *The Econometrics Journal*, **15**, 358-393.
- Kalliovirta L., Meitz M. and Saikkonen P. 2015. Gaussian Mixture Autoregressive model for univariate time series. *Journal of Time Series Analysis*, **36**, 247-266.
- Meitz M., Preve D., Saikkonen P. 2018. A mixture autoregressive model based on Student's t-distribution. arXiv:1805.04010 [econ.EM].
- Virolainen S. 2020. A mixture autoregressive model based on Gaussian and Student's t-distribution. arXiv:2003.05221 [econ.EM].

See Also

[profile_logliks](#), [diagnostic_plot](#), [fitGSMAR](#), [GSMAR](#), [quantile_residual_tests](#), [simulateGSMAR](#)

Examples

```
## The below examples the approximately 15 seconds to run.

# G-StMAR model with one GMAR type and one StMAR type regime
fit42gs <- fitGSMAR(M10Y1Y, p=4, M=c(1, 1), model="G-StMAR",
                  ncalls=1, seeds=4)
quantile_residual_plot(fit42gs)

# GMAR model
fit12 <- fitGSMAR(data=simudata, p=1, M=2, model="GMAR", ncalls=1, seeds=1)
quantile_residual_plot(fit12)
```

randomIndividual	<i>DEPRECATED, USE random_ind OR smart_ind INSTEAD! Create random GMAR, StMAR, or G-StMAR model compatible parameter vector</i>
------------------	---

Description

randomIndividual creates a random GMAR, StMAR, or G-StMAR model compatible mean-parametrized parameter vector. DEPRECATED, USE random_ind INSTEAD!

smartIndividual creates a random GMAR, StMAR, or G-StMAR model compatible parameter vector close to argument params. Sometimes returns exactly the given parameter vector. DEPRECATED, USE smart_ind INSTEAD!

Usage

```

randomIndividual(
  p,
  M,
  model = c("GMAR", "StMAR", "G-StMAR"),
  restricted = FALSE,
  constraints = NULL,
  mu_scale,
  sigma_scale,
  forcastat = FALSE,
  meanscale = NULL,
  sigmascale = NULL
)

smartIndividual(
  p,
  M,
  params,
  model = c("GMAR", "StMAR", "G-StMAR"),
  restricted = FALSE,
  constraints = NULL,
  mu_scale,
  sigma_scale,
  accuracy,
  which_random = numeric(0),
  forcastat = FALSE,
  whichRandom = NULL,
  meanscale = NULL,
  sigmascale = NULL
)

```

Arguments

p	a positive integer specifying the autoregressive order of the model.
M	For GMAR and StMAR models: a positive integer specifying the number of mixture components. For G-StMAR models: a size (2x1) integer vector specifying the number of <i>GMAR type</i> components M1 in the first element and <i>StMAR type</i> components M2 in the second element. The total number of mixture components is $M=M1+M2$.
model	is "GMAR", "StMAR", or "G-StMAR" model considered? In the G-StMAR model, the first M1 components are <i>GMAR type</i> and the rest M2 components are <i>StMAR type</i> .
restricted	a logical argument stating whether the AR coefficients $\phi_{m,1}, \dots, \phi_{m,p}$ are restricted to be the same for all regimes.
constraints	specifies linear constraints applied to the autoregressive parameters.

	<p>For non-restricted models: a list of size (pq_m) constraint matrices C_m of full column rank satisfying $\phi_m = C_m \psi_m$ for all $m = 1, \dots, M$, where $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$ and $\psi_m = (\psi_{m,1}, \dots, \psi_{m,q_m})$.</p> <p>For restricted models: a size (pq) constraint matrix C of full column rank satisfying $\phi = C\psi$, where $\phi = (\phi_1, \dots, \phi_p)$ and $\psi = (\psi_1, \dots, \psi_q)$.</p> <p>Symbol ϕ denotes an AR coefficient. Note that regardless of any constraints, the nominal autoregressive order is always p for all regimes. Ignore or set to NULL if applying linear constraints is not desired.</p>
mu_scale	a real valued vector of length two specifying the mean (the first element) and standard deviation (the second element) of the normal distribution from which the $\phi_{m,0}$ or μ_m (depending on the desired parametrization) parameters (for random regimes) should be generated.
sigma_scale	a positive real number specifying the standard deviation of the (zero mean, positive only by taking absolute value) normal distribution from which the component variance parameters (for random regimes) should be generated.
forcestat	use the algorithm by Monahan (1984) to force stationarity on the AR parameters (slower) for random regimes? Not supported for constrained models.
meanscale	deprecated! Use mu_scale instead!
sigmascale	deprecated! Use sigma_scale instead!
params	a real valued parameter vector specifying the model.

For non-restricted models: For GMAR model: Size $(M(p+3) - 1 \times 1)$ vector $\theta = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1})$, where $v_m = (\phi_{m,0}, \phi_m, \sigma_m^2)$ and $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$, $m = 1, \dots, M$.

For StMAR model: Size $(M(p+4) - 1 \times 1)$ vector $(\theta, \nu) = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.

For G-StMAR model: Size $(M(p+3) + M2 - 1 \times 1)$ vector $(\theta, \nu) = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_{M1+1}, \dots, \nu_M)$.

With linear constraints: Replace the vectors ϕ_m with vectors ψ_m and provide a list of constraint matrices C that satisfy $\phi_m = R_m \psi_m$ for all $m = 1, \dots, M$, where $\psi_m = (\psi_{m,1}, \dots, \psi_{m,q_m})$.

For restricted models: For GMAR model: Size $(3M + p - 1 \times 1)$ vector $\theta = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1})$, where $\phi = (\phi_1, \dots, \phi_p)$.

For StMAR model: Size $(4M + p - 1 \times 1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.

For G-StMAR model: Size $(3M + M2 + p - 1 \times 1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1}, \nu_{M1+1}, \dots, \nu_M)$.

With linear constraints: Replace the vector ϕ with vector ψ and provide a constraint matrix C that satisfies $\phi = R\psi$, where $\psi = (\psi_1, \dots, \psi_q)$.

Symbol ϕ denotes an AR coefficient, σ^2 a variance, α a mixing weight, and ν a degrees of freedom parameter. If parametrization=="mean", just replace each intercept term $\phi_{m,0}$ with regimewise mean $\mu_m = \phi_{m,0} / (1 - \sum \phi_{i,m})$. In the **G-StMAR** model, the first $M1$ components are *GMAR type* and the rest $M2$ components are *StMAR type*. Note that in the case **M=1**, the parameter α is dropped, and in the case of **StMAR** or **G-StMAR** model, the degrees of freedom parameters ν_m have to be larger than 2.

accuracy	a real number larger than zero specifying how close to params the generated parameter vector should be. Standard deviation of the normal distribution from which new parameter values are drawn from will be corresponding parameter value divided by accuracy.
----------	---

- which_random a numeric vector of maximum length M specifying which regimes should be random instead of "smart" when using smart_ind. Does not affect mixing weight parameters. Default in none.
- whichRandom deprecated! Use which_random instead!

Details

DEPRECATED, USE random_ind OR smart_ind INSTEAD!

These functions can be used, for example, to create initial populations for the genetic algorithm. Mean-parametrization (instead of intercept terms $\phi_{m,0}$) is assumed.

Value

Returns estimated parameter vector with the form described in ini_topop.

References

- Monahan J.F. 1984. A Note on Enforcing Stationarity in Autoregressive-Moving Average Models. *Biometrika* **71**, 403-404.

random_arcoefs	<i>Create random AR coefficients</i>
----------------	--------------------------------------

Description

random_arcoefs generates random AR coefficients.

Usage

```
random_arcoefs(p, forcestat = FALSE, sd = 0.6/p)
```

Arguments

- p a positive integer specifying the autoregressive order of the model.
- forcestat use the algorithm by Monahan (1984) to force stationarity on the AR parameters (slower)?
- sd if forcestat==FALSE, then AR parameters are drawn from zero mean normal distribution with sd given by this parameter.

Details

If forcestat==TRUE, then the AR coefficients are relatively large, otherwise they are usually relatively small.

Value

Returns $p \times 1$ vector containing random AR coefficients.

References

- Monahan J.F. 1984. A Note on Enforcing Stationarity in Autoregressive-Moving Average Models. *Biometrika* **71**, 403-404.

random_ind	<i>Create random GMAR, StMAR, or G-StMAR model compatible parameter vector</i>
------------	--

Description

random_ind creates a random GMAR, StMAR, or G-StMAR model compatible mean-parametrized parameter vector.

smart_ind creates a random GMAR, StMAR, or G-StMAR model compatible parameter vector close to argument params. Sometimes returns exactly the given parameter vector.

Usage

```
random_ind(
  p,
  M,
  model = c("GMAR", "StMAR", "G-StMAR"),
  restricted = FALSE,
  constraints = NULL,
  mu_scale,
  sigma_scale,
  forcastat = FALSE
)
```

```
smart_ind(
  p,
  M,
  params,
  model = c("GMAR", "StMAR", "G-StMAR"),
  restricted = FALSE,
  constraints = NULL,
  mu_scale,
  sigma_scale,
  accuracy,
  which_random = numeric(0),
  forcastat = FALSE
)
```

Arguments

p	a positive integer specifying the autoregressive order of the model.
M	For GMAR and StMAR models: a positive integer specifying the number of mixture components.

	<p>For G-StMAR models: a size (2×1) integer vector specifying the number of <i>GMAR type</i> components $M1$ in the first element and <i>StMAR type</i> components $M2$ in the second element. The total number of mixture components is $M=M1+M2$.</p>
model	<p>is "GMAR", "StMAR", or "G-StMAR" model considered? In the G-StMAR model, the first $M1$ components are <i>GMAR type</i> and the rest $M2$ components are <i>StMAR type</i>.</p>
restricted	<p>a logical argument stating whether the AR coefficients $\phi_{m,1}, \dots, \phi_{m,p}$ are restricted to be the same for all regimes.</p>
constraints	<p>specifies linear constraints applied to the autoregressive parameters.</p> <p>For non-restricted models: a list of size (pq_m) constraint matrices C_m of full column rank satisfying $\phi_m=C_m\psi_m$ for all $m = 1, \dots, M$, where $\phi_m=(\phi_{m,1}, \dots, \phi_{m,p})$ and $\psi_m=(\psi_{m,1}, \dots, \psi_{m,q_m})$.</p> <p>For restricted models: a size (pq) constraint matrix C of full column rank satisfying $\phi=C\psi$, where $\phi=(\phi_1, \dots, \phi_p)$ and $\psi=(\psi_1, \dots, \psi_q)$.</p> <p>Symbol ϕ denotes an AR coefficient. Note that regardless of any constraints, the nominal autoregressive order is always p for all regimes. Ignore or set to NULL if applying linear constraints is not desired.</p>
mu_scale	<p>a real valued vector of length two specifying the mean (the first element) and standard deviation (the second element) of the normal distribution from which the $\phi_{m,0}$ or μ_m (depending on the desired parametrization) parameters (for random regimes) should be generated.</p>
sigma_scale	<p>a positive real number specifying the standard deviation of the (zero mean, positive only by taking absolute value) normal distribution from which the component variance parameters (for random regimes) should be generated.</p>
forcestat	<p>use the algorithm by Monahan (1984) to force stationarity on the AR parameters (slower) for random regimes? Not supported for constrained models.</p>
params	<p>a real valued parameter vector specifying the model.</p> <p>For non-restricted models: For GMAR model: Size $(M(p+3) - 1 \times 1)$ vector $\theta=(v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1})$, where $v_m=(\phi_{m,0}, \phi_m, \sigma_m^2)$ and $\phi_m=(\phi_{m,1}, \dots, \phi_{m,p})$, $m = 1, \dots, M$.</p> <p>For StMAR model: Size $(M(p+4) - 1 \times 1)$ vector $(\theta, \nu)=(v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.</p> <p>For G-StMAR model: Size $(M(p+3) + M2 - 1 \times 1)$ vector $(\theta, \nu)=(v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_{M1+1}, \dots, \nu_M)$.</p> <p>With linear constraints: Replace the vectors ϕ_m with vectors ψ_m and provide a list of constraint matrices C that satisfy $\phi_m=C\psi_m$ for all $m = 1, \dots, M$, where $\psi_m=(\psi_{m,1}, \dots, \psi_{m,q_m})$.</p> <p>For restricted models: For GMAR model: Size $(3M + p - 1 \times 1)$ vector $\theta=(\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1})$, where $\phi=(\phi_1, \dots, \phi_p)$.</p> <p>For StMAR model: Size $(4M + p - 1 \times 1)$ vector $(\theta, \nu)=(\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.</p> <p>For G-StMAR model: Size $(3M + M2 + p - 1 \times 1)$ vector $(\theta, \nu)=(\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1}, \nu_{M1+1}, \dots, \nu_M)$.</p> <p>With linear constraints: Replace the vector ϕ with vector ψ and provide a constraint matrix C that satisfies $\phi=C\psi$, where $\psi=(\psi_1, \dots, \psi_q)$.</p>

Symbol ϕ denotes an AR coefficient, σ^2 a variance, α a mixing weight, and ν a degrees of freedom parameter. If parametrization=="mean", just replace each intercept term $\phi_{m,0}$ with regimewise mean $\mu_m = \phi_{m,0}/(1 - \sum \phi_{i,m})$. In the **G-StMAR** model, the first M1 components are *GMAR type* and the rest M2 components are *StMAR type*. Note that in the case **M=1**, the parameter α is dropped, and in the case of **StMAR** or **G-StMAR** model, the degrees of freedom parameters ν_m have to be larger than 2.

accuracy	a real number larger than zero specifying how close to params the generated parameter vector should be. Standard deviation of the normal distribution from which new parameter values are drawn from will be corresponding parameter value divided by accuracy.
which_random	a numeric vector of maximum length M specifying which regimes should be random instead of "smart" when using smart_ind. Does not affect mixing weight parameters. Default in none.

Details

These functions can be used, for example, to create initial populations for the genetic algorithm. Mean-parametrization (instead of intercept terms $\phi_{m,0}$) is assumed.

Value

Returns estimated parameter vector with the form described in initpop.

References

- Monahan J.F. 1984. A Note on Enforcing Stationarity in Autoregressive-Moving Average Models. *Biometrika* **71**, 403-404.

Examples

```
set.seed(1)

# GMAR model parameter vector
params22 <- random_ind(p=2, M=2, mu_scale=c(0, 1), sigma_scale=1)
smart22 <- smart_ind(p=2, M=2, params22, accuracy=10)
cbind(params22, smart22)

# Restricted GMAR parameter vector
params12r <- random_ind(p=1, M=2, restricted=TRUE, mu_scale=c(-2, 2), sigma_scale=2)
smart12r <- smart_ind(p=1, M=2, params12r, restricted=TRUE, accuracy=20)
cbind(params12r, smart12r)

# StMAR parameter vector: first regime is random in the "smart individual"
params13t <- random_ind(p=1, M=3, model="StMAR", mu_scale=c(3, 1), sigma_scale=3)
smart13t <- smart_ind(p=1, M=3, params13t, model="StMAR", accuracy=15,
                     mu_scale=c(3, 3), sigma_scale=3, which_random=1)
cbind(params13t, smart13t)

# Restricted StMAR parameter vector
```

```

params22tr <- random_ind(p=2, M=2, model="StMAR", restricted=TRUE,
                        mu_scale=c(3, 2), sigma_scale=0.5)
smart22tr <- smart_ind(p=2, M=2, params22tr, model="StMAR", restricted=TRUE,
                      accuracy=30)
cbind(params22tr, smart22tr)

# G-StMAR parameter vector
params12gs <- random_ind(p=1, M=c(1, 1), model="G-StMAR", mu_scale=c(0, 1),
                        sigma_scale=1)
smart12gs <- smart_ind(p=1, M=c(1, 1), params12gs, model="G-StMAR",
                      accuracy=20)
cbind(params12gs, smart12gs)

# Such StMAR(3,2) that the AR coefficients are restricted to be
# the same for both regimes and that the second AR coefficients are
# constrained to zero. Second regime is random in the "smart individual".
params32trc <- random_ind(p=3, M=2, model="StMAR", restricted=TRUE,
                          constraints=matrix(c(1, 0, 0, 0, 0, 1), ncol=2),
                          mu_scale=c(-2, 0.5), sigma_scale=4)
smart32trc <- smart_ind(p=3, M=2, params32trc, model="StMAR", restricted=TRUE,
                       constraints=matrix(c(1, 0, 0, 0, 0, 1), ncol=2),
                       mu_scale=c(0, 0.1), sigma_scale=0.1, which_random=2,
                       accuracy=20)
cbind(params32trc, smart32trc)

```

random_ind_int	<i>Create random GMAR, StMAR, or G-StMAR model compatible parameter vector</i>
----------------	--

Description

random_ind_int creates a random GMAR, StMAR, or G-StMAR model compatible parameter vector.

smart_ind_int creates a random GMAR, StMAR, or G-StMAR model compatible parameter vector close to argument params.

Usage

```

random_ind_int(
  p,
  M,
  model = c("GMAR", "StMAR", "G-StMAR"),
  restricted = FALSE,
  constraints = NULL,
  mu_scale,
  sigma_scale,
  forcastat = FALSE
)

```

```

smart_ind_int(
  p,
  M,
  params,
  model = c("GMAR", "StMAR", "G-StMAR"),
  restricted = FALSE,
  constraints = NULL,
  mu_scale,
  sigma_scale,
  accuracy,
  which_random,
  forcastat = FALSE
)

```

Arguments

p	a positive integer specifying the autoregressive order of the model.
M	<p>For GMAR and StMAR models: a positive integer specifying the number of mixture components.</p> <p>For G-StMAR models: a size (2x1) integer vector specifying the number of <i>GMAR type</i> components M1 in the first element and <i>StMAR type</i> components M2 in the second element. The total number of mixture components is $M=M1+M2$.</p>
model	is "GMAR", "StMAR", or "G-StMAR" model considered? In the G-StMAR model, the first M1 components are <i>GMAR type</i> and the rest M2 components are <i>StMAR type</i> .
restricted	a logical argument stating whether the AR coefficients $\phi_{m,1}, \dots, \phi_{m,p}$ are restricted to be the same for all regimes.
constraints	<p>specifies linear constraints applied to the autoregressive parameters.</p> <p>For non-restricted models: a list of size (pxq_m) constraint matrices C_m of full column rank satisfying $\phi_m = C_m \psi_m$ for all $m = 1, \dots, M$, where $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$ and $\psi_m = (\psi_{m,1}, \dots, \psi_{m,q_m})$.</p> <p>For restricted models: a size (pxq) constraint matrix C of full column rank satisfying $\phi = C\psi$, where $\phi = (\phi_1, \dots, \phi_p)$ and $\psi = (\psi_1, \dots, \psi_q)$.</p> <p>Symbol ϕ denotes an AR coefficient. Note that regardless of any constraints, the nominal autoregressive order is always p for all regimes. Ignore or set to NULL if applying linear constraints is not desired.</p>
mu_scale	a real valued vector of length two specifying the mean (the first element) and standard deviation (the second element) of the normal distribution from which the $\phi_{m,0}$ or μ_m (depending on the desired parametrization) parameters (for random regimes) should be generated.
sigma_scale	a positive real number specifying the standard deviation of the (zero mean, positive only by taking absolute value) normal distribution from which the component variance parameters (for random regimes) should be generated.
forcastat	use the algorithm by Monahan (1984) to force stationarity on the AR parameters (slower) for random regimes? Not supported for constrained models.

params

a real valued parameter vector specifying the model.

For non-restricted models: For GMAR model: Size $(M(p+3) - 1x1)$ vector $\theta=(v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1})$, where $v_m = (\phi_{m,0}, \phi_m, \sigma_m^2)$ and $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$, $m = 1, \dots, M$.

For StMAR model: Size $(M(p+4) - 1x1)$ vector $(\theta, \nu) = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.

For G-StMAR model: Size $(M(p+3) + M2 - 1x1)$ vector $(\theta, \nu) = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_{M1+1}, \dots, \nu_M)$.

With linear constraints: Replace the vectors ϕ_m with vectors ψ_m and provide a list of constraint matrices **C** that satisfy $\phi_m = R_m \psi_m$ for all $m = 1, \dots, M$, where $\psi_m = (\psi_{m,1}, \dots, \psi_{m,q_m})$.

For restricted models: For GMAR model: Size $(3M + p - 1x1)$ vector $\theta = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1})$, where $\phi = (\phi_1, \dots, \phi_p)$.

For StMAR model: Size $(4M + p - 1x1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.

For G-StMAR model: Size $(3M + M2 + p - 1x1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1}, \nu_{M1+1}, \dots, \nu_M)$.

With linear constraints: Replace the vector ϕ with vector ψ and provide a constraint matrix **C** that satisfies $\phi = R\psi$, where $\psi = (\psi_1, \dots, \psi_q)$.

Symbol ϕ denotes an AR coefficient, σ^2 a variance, α a mixing weight, and ν a degrees of freedom parameter. If parametrization="mean", just replace each intercept term $\phi_{m,0}$ with regimewise mean $\mu_m = \phi_{m,0} / (1 - \sum \phi_{i,m})$. In the **G-StMAR** model, the first M1 components are *GMAR type* and the rest M2 components are *StMAR type*. Note that in the case **M=1**, the parameter α is dropped, and in the case of **StMAR** or **G-StMAR** model, the degrees of freedom parameters ν_m have to be larger than 2.

accuracy

a real number larger than zero specifying how close to params the generated parameter vector should be. Standard deviation of the normal distribution from which new parameter values are drawn from will be corresponding parameter value divided by accuracy.

which_random

a numeric vector of maximum length M specifying which regimes should be random instead of "smart" when using smart_ind. Does not affect mixing weight parameters. Default in none.

Value

Returns estimated parameter vector with the form described in initpop.

References

- Monahan J.F. 1984. A Note on Enforcing Stationarity in Autoregressive-Moving Average Models. *Biometrika* 71, 403-404.

random_regime	<i>Create random regime parameters</i>
---------------	--

Description

random_regime generates random regime parameters.

Usage

```
random_regime(
  p,
  mu_scale,
  sigma_scale,
  restricted = FALSE,
  constraints = NULL,
  m,
  forcastat = FALSE
)
```

Arguments

p	a positive integer specifying the autoregressive order of the model.
mu_scale	a real valued vector of length two specifying the mean (the first element) and standard deviation (the second element) of the normal distribution from which the μ_m mean-parameters are generated in random mutations in the genetic algorithm. Default is <code>c(mean(data), sd(data))</code> . Note that the genetic algorithm optimizes with mean-parametrization even when <code>parametrization="intercept"</code> , but input (in <code>initpop</code>) and output (return value) parameter vectors may be intercept-parametrized.
sigma_scale	a positive real number specifying the standard deviation of the (zero mean, positive only by taking absolute value) normal distribution from which the component variance parameters are generated in the random mutations in the genetic algorithm. Default is <code>var(stats::ar(data, order.max=10)\$resid, na.rm=TRUE)</code> .
restricted	a logical argument stating whether the AR coefficients $\phi_{m,1}, \dots, \phi_{m,p}$ are restricted to be the same for all regimes.
constraints	specifies linear constraints applied to the autoregressive parameters.

For non-restricted models: a list of size (pxq_m) constraint matrices C_m of full column rank satisfying $\phi_m = C_m \psi_m$ for all $m = 1, \dots, M$, where $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$ and $\psi_m = (\psi_{m,1}, \dots, \psi_{m,q_m})$.

For restricted models: a size (pxq) constraint matrix C of full column rank satisfying $\phi = C\psi$, where $\phi = (\phi_1, \dots, \phi_p)$ and $\psi = (\psi_1, \dots, \psi_q)$.

Symbol ϕ denotes an AR coefficient. Note that regardless of any constraints, the nominal autoregressive order is always p for all regimes. Ignore or set to NULL if applying linear constraints is **not** desired.

m	which regime? This is required for models with constraints for which a list of possibly differing constraint matrices is provided.
forcestat	use the algorithm by Monahan (1984) to force stationarity on the AR parameters (slower)? Not supported for constrained models.

Details

If forcestat==TRUE, then the AR coefficients are relatively large, otherwise they are usually relatively small.

Value

Regular models: $v_m = (\phi_{m,0}, \phi_m, \sigma_m^2)$ where $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$.

Restricted models: Not supported!

Constrained models: Replace the vectors ϕ_m with vectors ψ_m .

References

- Monahan J.F. 1984. A Note on Enforcing Stationarity in Autoregressive-Moving Average Models. *Biometrika* **71**, 403-404.

reform_constrained_pars

Reform parameter vector with linear constraints to correspond non-constrained parameter vector.

Description

reform_constrained_pars reforms the parameter vector of a model with linear constraints to the "standard form" so that it's comparable with non-constrained models.

Usage

```
reform_constrained_pars(
  p,
  M,
  params,
  model = c("GMAR", "StMAR", "G-StMAR"),
  restricted = FALSE,
  constraints = NULL
)
```

Arguments

p	a positive integer specifying the autoregressive order of the model.
M	<p>For GMAR and StMAR models: a positive integer specifying the number of mixture components.</p> <p>For G-StMAR models: a size (2x1) integer vector specifying the number of <i>GMAR type</i> components M1 in the first element and <i>StMAR type</i> components M2 in the second element. The total number of mixture components is $M=M1+M2$.</p>
params	<p>a real valued parameter vector specifying the model.</p> <p>For non-restricted models: For GMAR model: Size $(M(p+3) - 1x1)$ vector $\theta=(v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1})$, where $v_m = (\phi_{m,0}, \phi_m, \sigma_m^2)$ and $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$, $m = 1, \dots, M$.</p> <p>For StMAR model: Size $(M(p+4) - 1x1)$ vector $(\theta, \nu) = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.</p> <p>For G-StMAR model: Size $(M(p+3) + M2 - 1x1)$ vector $(\theta, \nu) = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_{M1+1}, \dots, \nu_M)$.</p> <p>With linear constraints: Replace the vectors ϕ_m with vectors ψ_m and provide a list of constraint matrices C that satisfy $\phi_m = R_m \psi_m$ for all $m = 1, \dots, M$, where $\psi_m = (\psi_{m,1}, \dots, \psi_{m,q_m})$.</p> <p>For restricted models: For GMAR model: Size $(3M + p - 1x1)$ vector $\theta = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1})$, where $\phi = (\phi_1, \dots, \phi_p)$.</p> <p>For StMAR model: Size $(4M + p - 1x1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.</p> <p>For G-StMAR model: Size $(3M + M2 + p - 1x1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1}, \nu_{M1+1}, \dots, \nu_M)$.</p> <p>With linear constraints: Replace the vector ϕ with vector ψ and provide a constraint matrix C that satisfies $\phi = R\psi$, where $\psi = (\psi_1, \dots, \psi_q)$.</p> <p>Symbol ϕ denotes an AR coefficient, σ^2 a variance, α a mixing weight, and ν a degrees of freedom parameter. If parametrization="mean", just replace each intercept term $\phi_{m,0}$ with regimewise mean $\mu_m = \phi_{m,0} / (1 - \sum \phi_{i,m})$. In the G-StMAR model, the first M1 components are <i>GMAR type</i> and the rest M2 components are <i>StMAR type</i>. Note that in the case M=1, the parameter α is dropped, and in the case of StMAR or G-StMAR model, the degrees of freedom parameters ν_m have to be larger than 2.</p>
model	is "GMAR", "StMAR", or "G-StMAR" model considered? In the G-StMAR model, the first M1 components are <i>GMAR type</i> and the rest M2 components are <i>StMAR type</i> .
restricted	a logical argument stating whether the AR coefficients $\phi_{m,1}, \dots, \phi_{m,p}$ are restricted to be the same for all regimes.
constraints	<p>specifies linear constraints applied to the autoregressive parameters.</p> <p>For non-restricted models: a list of size (pxq_m) constraint matrices C_m of full column rank satisfying $\phi_m = C_m \psi_m$ for all $m = 1, \dots, M$, where $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$ and $\psi_m = (\psi_{m,1}, \dots, \psi_{m,q_m})$.</p> <p>For restricted models: a size (pxq) constraint matrix C of full column rank satisfying $\phi = C\psi$, where $\phi = (\phi_1, \dots, \phi_p)$ and $\psi = (\psi_1, \dots, \psi_q)$.</p> <p>Symbol ϕ denotes an AR coefficient. Note that regardless of any constraints, the nominal autoregressive order is always p for all regimes. Ignore or set to NULL if applying linear constraints is not desired.</p>

Value

Returns such parameter vector corresponding to the input vector that is the form described in params for non-restricted or restricted models (for non-constrained models), and can hence be used just as the parameter vectors of non-constrained models.

reform_parameters	<i>Reform any parameter vector into standard form.</i>
-------------------	--

Description

reform_parameters takes a parameter vector of any (non-constrained) GMAR, StMAR, or G-StMAR model and returns a list with the parameter vector in the standard form, parameter matrix containing AR coefficients and component variances, mixing weights alphas, and in case of StMAR or G-StMAR model also degrees of freedom parameters.

Usage

```
reform_parameters(
  p,
  M,
  params,
  model = c("GMAR", "StMAR", "G-StMAR"),
  restricted = FALSE
)
```

Arguments

p a positive integer specifying the autoregressive order of the model.

M **For GMAR and StMAR models:** a positive integer specifying the number of mixture components.
For G-StMAR models: a size (2x1) integer vector specifying the number of *GMAR type* components M1 in the first element and *StMAR type* components M2 in the second element. The total number of mixture components is $M=M1+M2$.

params a real valued parameter vector specifying the model.
For non-restricted models: For GMAR model: Size $(M(p+3) - 1x1)$ vector $\theta=(v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1})$, where $v_m = (\phi_{m,0}, \phi_m, \sigma_m^2)$ and $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$, $m = 1, \dots, M$.
For StMAR model: Size $(M(p+4) - 1x1)$ vector $(\theta, \nu) = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.
For G-StMAR model: Size $(M(p+3) + M2 - 1x1)$ vector $(\theta, \nu) = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_{M1+1}, \dots, \nu_M)$.

For restricted models: For GMAR model: Size $(3M + p - 1x1)$ vector $\theta = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1})$, where $\phi = (\phi_1, \dots, \phi_p)$.
For StMAR model: Size $(4M + p - 1x1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.
For G-StMAR model: Size $(3M + M2 + p - 1x1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1}, \nu_{M1+1}, \dots, \nu_M)$.

Symbol ϕ denotes an AR coefficient, σ^2 a variance, α a mixing weight, and ν a degrees of freedom parameter. In the **G-StMAR** model, the first M1 components are *GMAR type* and the rest M2 components are *StMAR type*. Note that in the case **M=1**, the parameter α is dropped, and in the case of **StMAR** or **G-StMAR** model, the degrees of freedom parameters ν_m have to be larger than 2.

model is "GMAR", "StMAR", or "G-StMAR" model considered? In the G-StMAR model, the first M1 components are *GMAR type* and the rest M2 components are *StMAR type*.

restricted a logical argument stating whether the AR coefficients $\phi_{m,1}, \dots, \phi_{m,p}$ are restricted to be the same for all regimes.

Details

This function does not support models imposing linear constraints. No argument checks in this function.

Value

Returns a list with...

\$params parameter vector in the standard form.

\$pars corresponding parameter matrix containing AR coefficients and component variances. First row for phi0 or means depending on the parametrization. Column for each component.

\$alphas numeric vector containing mixing weight parameters for all of the components (also for the last one).

\$dfs numeric vector containing degrees of freedom parameters for all of components. Returned only if `model == "StMAR"` or `model == "G-StMAR"`.

reform_restricted_pars

Reform parameter vector with restricted autoregressive parameters to correspond non-restricted parameter vector.

Description

reform_restricted_pars reforms parameter vector with restricted autoregressive parameters to correspond non-restricted parameter vector.

Usage

```
reform_restricted_pars(
  p,
  M,
  params,
  model = c("GMAR", "StMAR", "G-StMAR"),
  restricted = FALSE
)
```

Arguments

p	a positive integer specifying the autoregressive order of the model.
M	For GMAR and StMAR models: a positive integer specifying the number of mixture components. For G-StMAR models: a size (2x1) integer vector specifying the number of <i>GMAR type</i> components M1 in the first element and <i>StMAR type</i> components M2 in the second element. The total number of mixture components is $M=M1+M2$.
params	a real valued parameter vector specifying the model. For non-restricted models: For GMAR model: Size $(M(p+3)-1 \times 1)$ vector $\theta=(v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1})$, where $v_m = (\phi_{m,0}, \phi_m, \sigma_m^2)$ and $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$, $m = 1, \dots, M$. For StMAR model: Size $(M(p+4)-1 \times 1)$ vector $(\theta, \nu) = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$. For G-StMAR model: Size $(M(p+3)+M2-1 \times 1)$ vector $(\theta, \nu) = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_{M1+1}, \dots, \nu_M)$. With linear constraints: Replace the vectors ϕ_m with vectors ψ_m and provide a list of constraint matrices C that satisfy $\phi_m = R_m \psi_m$ for all $m = 1, \dots, M$, where $\psi_m = (\psi_{m,1}, \dots, \psi_{m,q_m})$. For restricted models: For GMAR model: Size $(3M+p-1 \times 1)$ vector $\theta = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1})$, where $\phi = (\phi_1, \dots, \phi_p)$. For StMAR model: Size $(4M+p-1 \times 1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$. For G-StMAR model: Size $(3M+M2+p-1 \times 1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1}, \nu_{M1+1}, \dots, \nu_M)$. With linear constraints: Replace the vector ϕ with vector ψ and provide a constraint matrix C that satisfies $\phi = R\psi$, where $\psi = (\psi_1, \dots, \psi_q)$. Symbol ϕ denotes an AR coefficient, σ^2 a variance, α a mixing weight, and ν a degrees of freedom parameter. If parametrization="mean", just replace each intercept term $\phi_{m,0}$ with regimewise mean $\mu_m = \phi_{m,0} / (1 - \sum \phi_{i,m})$. In the G-StMAR model, the first M1 components are <i>GMAR type</i> and the rest M2 components are <i>StMAR type</i> . Note that in the case M=1 , the parameter α is dropped, and in the case of StMAR or G-StMAR model, the degrees of freedom parameters ν_m have to be larger than 2.
model	is "GMAR", "StMAR", or "G-StMAR" model considered? In the G-StMAR model, the first M1 components are <i>GMAR type</i> and the rest M2 components are <i>StMAR type</i> .
restricted	a logical argument stating whether the AR coefficients $\phi_{m,1}, \dots, \phi_{m,p}$ are restricted to be the same for all regimes.

Value

Returns such parameter vector corresponding to the input vector that is the form described in params for non-restricted models (for non-constrained models). Linear constraints are not supported.

regime_distance	<i>Calculate "distance" between two regimes</i>
-----------------	---

Description

regime_distance scales each regime parameter to the same magnitude and then calculates distance between scaled regime_pars1 and regime_pars2.

Usage

```
regime_distance(regime_pars1, regime_pars2)
```

Arguments

regime_pars1 a numeric vector representing a regime.
 regime_pars2 a numeric vector representing another regime, same length as regime_pars1

Value

Returns "distance" between regime_pars1 and regime_pars2. Values are scaled to the same magnitude before calculating the "distance". Read the source code for details.

remove_all_constraints	<i>Transform constrained and restricted parameter vector into the regular form</i>
------------------------	--

Description

remove_all_constraints transforms constrained and restricted parameter vector into the regular form.

Usage

```
remove_all_constraints(  
  p,  
  M,  
  params,  
  model = c("GMAR", "StMAR", "G-StMAR"),  
  restricted = FALSE,  
  constraints = NULL  
)
```

Arguments

p	a positive integer specifying the autoregressive order of the model.
M	<p>For GMAR and StMAR models: a positive integer specifying the number of mixture components.</p> <p>For G-StMAR models: a size (2×1) integer vector specifying the number of <i>GMAR type</i> components M1 in the first element and <i>StMAR type</i> components M2 in the second element. The total number of mixture components is $M=M1+M2$.</p>
params	<p>a real valued parameter vector specifying the model.</p> <p>For non-restricted models: For GMAR model: Size $(M(p+3) - 1 \times 1)$ vector $\theta=(v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1})$, where $v_m = (\phi_{m,0}, \phi_m, \sigma_m^2)$ and $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$, $m = 1, \dots, M$.</p> <p>For StMAR model: Size $(M(p+4) - 1 \times 1)$ vector $(\theta, \nu) = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.</p> <p>For G-StMAR model: Size $(M(p+3) + M2 - 1 \times 1)$ vector $(\theta, \nu) = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_{M1+1}, \dots, \nu_M)$.</p> <p>With linear constraints: Replace the vectors ϕ_m with vectors ψ_m and provide a list of constraint matrices C that satisfy $\phi_m = R_m \psi_m$ for all $m = 1, \dots, M$, where $\psi_m = (\psi_{m,1}, \dots, \psi_{m,q_m})$.</p> <p>For restricted models: For GMAR model: Size $(3M + p - 1 \times 1)$ vector $\theta = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1})$, where $\phi = (\phi_1, \dots, \phi_p)$.</p> <p>For StMAR model: Size $(4M + p - 1 \times 1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.</p> <p>For G-StMAR model: Size $(3M + M2 + p - 1 \times 1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.</p> <p>With linear constraints: Replace the vector ϕ with vector ψ and provide a constraint matrix C that satisfies $\phi = R\psi$, where $\psi = (\psi_1, \dots, \psi_q)$.</p> <p>Symbol ϕ denotes an AR coefficient, σ^2 a variance, α a mixing weight, and ν a degrees of freedom parameter. If parametrization="mean", just replace each intercept term $\phi_{m,0}$ with regimewise mean $\mu_m = \phi_{m,0} / (1 - \sum \phi_{i,m})$. In the G-StMAR model, the first M1 components are <i>GMAR type</i> and the rest M2 components are <i>StMAR type</i>. Note that in the case M=1, the parameter α is dropped, and in the case of StMAR or G-StMAR model, the degrees of freedom parameters ν_m have to be larger than 2.</p>
model	is "GMAR", "StMAR", or "G-StMAR" model considered? In the G-StMAR model, the first M1 components are <i>GMAR type</i> and the rest M2 components are <i>StMAR type</i> .
restricted	a logical argument stating whether the AR coefficients $\phi_{m,1}, \dots, \phi_{m,p}$ are restricted to be the same for all regimes.
constraints	<p>specifies linear constraints applied to the autoregressive parameters.</p> <p>For non-restricted models: a list of size $(p \times q_m)$ constraint matrices C_m of full column rank satisfying $\phi_m = C_m \psi_m$ for all $m = 1, \dots, M$, where $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$ and $\psi_m = (\psi_{m,1}, \dots, \psi_{m,q_m})$.</p> <p>For restricted models: a size $(p \times q)$ constraint matrix C of full column rank satisfying $\phi = C\psi$, where $\phi = (\phi_1, \dots, \phi_p)$ and $\psi = (\psi_1, \dots, \psi_q)$.</p> <p>Symbol ϕ denotes an AR coefficient. Note that regardless of any constraints, the nominal autoregressive order is always p for all regimes. Ignore or set to NULL if applying linear constraints is not desired.</p>

Value

Returns such parameter vector corresponding to the input vector that is the form described in `params` for non-restricted and non-constrained models.

<code>simudata</code>	<i>Simulated data</i>
-----------------------	-----------------------

Description

A dataset containing 200 observations simulated from a GMAR $p=1$, $M=2$ process.

Usage

`simudata`

Format

A numeric vector of length 200.

Source

Simulated

<code>simulateGSMAR</code>	<i>Simulate values from GMAR, StMAR, and G-StMAR processes</i>
----------------------------	--

Description

`simulateGSMAR` simulates values from the specified GMAR, StMAR, or G-StMAR process. Can be utilized for forecasting future values of the process.

Usage

`simulateGSMAR(gsmar, nsimu, init_values, ntimes = 1, drop = TRUE)`

Arguments

<code>gsmar</code>	object of class 'gsmar' created with the function <code>fitGSMAR</code> or <code>GSMAR</code> .
<code>nsimu</code>	a positive integer specifying how many values (ahead from <code>init_values</code>) will be simulated.
<code>init_values</code>	a numeric vector with length $\geq p$ specifying the initial values for the simulation. The last element will be used as the initial value for the first lag, the second last element will be initial value for the second lag, etc. If not specified, initial values will be simulated from the process's stationary distribution.
<code>ntimes</code>	a positive integer specifying how many sets of simulations should be performed.
<code>drop</code>	if TRUE (default) then the components of the returned list are coerced to lower dimension if <code>ntimes==1</code> , i.e., <code>\$sample</code> and <code>\$component</code> will be vectors and <code>\$mixing_weights</code> will be matrix.

Details

The argument `ntimes` is intended for forecasting: a GSMAR process can be forecasted by simulating its possible future values. One can perform a large number of sets of simulations and calculate the sample quantiles from the simulated values to obtain prediction intervals. See the forecasting example below for a hand-on demonstration.

Value

If `drop==TRUE` and `ntimes==1` (default): `$sample` and `$component` are vectors and `$mixing_weights` is a (`nsimuxM`) matrix. Otherwise, returns a list with...

`$sample` a size (`nsimuxntimes`) matrix containing the simulated values.

`$component` a size (`nsimuxntimes`) matrix containing the information from which mixture component each value was generated from.

`$mixing_weights` a size (`nsimuxMxntimes`) array containing the mixing weights corresponding to the sample: the dimension `[i, ,]` is the time index, the dimension `[, i,]` indicates the regime, and the dimension `[, , i]` indicates the `i`:th set of simulations.

References

- Galbraith, R., Galbraith, J. 1974. On the inverses of some patterned matrices arising in the theory of stationary time series. *Journal of Applied Probability* **11**, 63-71.
- Kalliovirta L. (2012) Misspecification tests based on quantile residuals. *The Econometrics Journal*, **15**, 358-393.
- Kalliovirta L., Meitz M. and Saikkonen P. 2015. Gaussian Mixture Autoregressive model for univariate time series. *Journal of Time Series Analysis*, **36**, 247-266.
- Meitz M., Preve D., Saikkonen P. 2018. A mixture autoregressive model based on Student's t-distribution. arXiv:1805.04010 [econ.EM].
- Virolainen S. 2020. A mixture autoregressive model based on Gaussian and Student's t-distribution. arXiv:2003.05221 [econ.EM].

See Also

[fitGSMAR](#), [GSMAR](#), [predict.gsmar](#), [add_data](#), [cond_moments](#), [mixing_weights](#)

Examples

```
set.seed(1)

# GMAR model:
params22 <- c(0.9, 0.4, 0.2, 0.5, 0.7, 0.5, -0.2, 0.7, 0.7)
mod22 <- GSMAR(p=2, M=2, params=params22, model="GMAR")
mysim <- simulateGSMAR(mod22, nsimu=500)
ts.plot(mysim$sample)
ts.plot(mysim$component)
ts.plot(mysim$mixing_weights, col=rainbow(2), lty=2)
```

```

# G-StMAR model, with initial values:
params42gs <- c(0.04, 1.34, -0.59, 0.54, -0.36, 0.01, 0.06, 1.28, -0.36,
               0.2, -0.15, 0.04, 0.19, 9.75)
gstmar42 <- GSMAR(data=M10Y1Y, p=4, M=c(1, 1), params=params42gs,
                 model="G-StMAR")
sim42gs <- simulateGSMAR(gstmar42, nsimu=500, init_values=1:4)
ts.plot(sim42gs$sample)
ts.plot(sim42gs$component)
ts.plot(sim42gs$mixing_weights, col=rainbow(2), lty=2)

# FORECASTING EXAMPLE:
# GMAR model, 1000 sets of simulations with initial values from the data:
params12 <- c(1.70, 0.85, 0.30, 4.12, 0.73, 1.98, 0.63)
gmar12 <- GSMAR(data=simdata, p=1, M=2, params=params12, model="GMAR")
sim12 <- simulateGSMAR(gmar12, nsimu=5, init_val=gmar12$data, ntimes=1000)
apply(sim12$sample, MARGIN=1, FUN=median) # Point prediction
apply(sim12$sample, MARGIN=1, FUN=quantile, probs=c(0.025, 0.975)) # 95% pi
apply(sim12$mixing_weights, MARGIN=1:2, FUN=median) # mix.weight point pred
apply(sim12$mixing_weights, MARGIN=1:2, FUN=quantile,
      probs=c(0.025, 0.975)) # mix.weight 95% prediction intervals

```

sort_components

Sort the mixture components of a GMAR, StMAR, or G-StMAR model

Description

sort_components sorts mixture components of the specified GMAR, StMAR, or G-StMAR model according to the mixing weight parameters when the parameter vector has the "standard/regular form" for restricted or non-restricted models.

Usage

```

sort_components(
  p,
  M,
  params,
  model = c("GMAR", "StMAR", "G-StMAR"),
  restricted = FALSE
)

```

Arguments

p a positive integer specifying the autoregressive order of the model.

M **For GMAR and StMAR models:** a positive integer specifying the number of mixture components.

For G-StMAR models: a size (2×1) integer vector specifying the number of *GMAR type* components $M1$ in the first element and *StMAR type* components $M2$ in the second element. The total number of mixture components is $M=M1+M2$.

params

a real valued parameter vector specifying the model.

For non-restricted models: For GMAR model: Size $(M(p+3) - 1 \times 1)$ vector $\theta=(v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1})$, where $v_m = (\phi_{m,0}, \phi_m, \sigma_m^2)$ and $\phi_m=(\phi_{m,1}, \dots, \phi_{m,p})$, $m = 1, \dots, M$.

For StMAR model: Size $(M(p+4) - 1 \times 1)$ vector $(\theta, \nu)=(v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.

For G-StMAR model: Size $(M(p+3)+M2 - 1 \times 1)$ vector $(\theta, \nu)=(v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_{M1+1}, \dots, \nu_M)$.

With linear constraints: Replace the vectors ϕ_m with vectors ψ_m and provide a list of constraint matrices C that satisfy $\phi_m=R_m\psi_m$ for all $m = 1, \dots, M$, where $\psi_m = (\psi_{m,1}, \dots, \psi_{m,q_m})$.

For restricted models: For GMAR model: Size $(3M + p - 1 \times 1)$ vector $\theta=(\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1})$, where $\phi=(\phi_1, \dots, \phi_p)$.

For StMAR model: Size $(4M+p-1 \times 1)$ vector $(\theta, \nu)=(\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.

For G-StMAR model: Size $(3M+M2+p-1 \times 1)$ vector $(\theta, \nu)=(\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1}, \nu_{M1+1}, \dots, \nu_M)$.

With linear constraints: Replace the vector ϕ with vector ψ and provide a constraint matrix C that satisfies $\phi=R\psi$, where $\psi = (\psi_1, \dots, \psi_q)$.

Symbol ϕ denotes an AR coefficient, σ^2 a variance, α a mixing weight, and ν a degrees of freedom parameter. If parametrization=="mean", just replace each intercept term $\phi_{m,0}$ with regimewise mean $\mu_m = \phi_{m,0}/(1 - \sum \phi_{i,m})$. In the **G-StMAR** model, the first $M1$ components are *GMAR type* and the rest $M2$ components are *StMAR type*. Note that in the case $M=1$, the parameter α is dropped, and in the case of **StMAR** or **G-StMAR** model, the degrees of freedom parameters ν_m have to be larger than 2.

model

is "GMAR", "StMAR", or "G-StMAR" model considered? In the G-StMAR model, the first $M1$ components are *GMAR type* and the rest $M2$ components are *StMAR type*.

restricted

a logical argument stating whether the AR coefficients $\phi_{m,1}, \dots, \phi_{m,p}$ are restricted to be the same for all regimes.

Details

This function does not support models imposing linear constraints.

Value

Returns a parameter vector sorted according to its mixing weight parameters, described in params.

standard_errors	Calculate standard errors for estimates of a GMAR, StMAR, or GStMAR model
-----------------	---

Description

standard_errors numerically approximates standard errors for the given estimates of GMAR, StMAR, or GStMAR model.

Usage

```
standard_errors(
  data,
  p,
  M,
  params,
  model = c("GMAR", "StMAR", "G-StMAR"),
  restricted = FALSE,
  constraints = NULL,
  conditional = TRUE,
  parametrization = c("intercept", "mean"),
  custom_h = NULL,
  minval
)
```

Arguments

data	a numeric vector or class 'ts' object containing the data. NA values are not supported.
p	a positive integer specifying the autoregressive order of the model.
M	<p>For GMAR and StMAR models: a positive integer specifying the number of mixture components.</p> <p>For G-StMAR models: a size (2x1) integer vector specifying the number of <i>GMAR type</i> components M1 in the first element and <i>StMAR type</i> components M2 in the second element. The total number of mixture components is $M=M1+M2$.</p>
params	<p>a real valued parameter vector specifying the model.</p> <p>For non-restricted models: For GMAR model: Size $(M(p+3) - 1x1)$ vector $\theta=(v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1})$, where $v_m = (\phi_{m,0}, \phi_m, \sigma_m^2)$ and $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$, $m = 1, \dots, M$.</p> <p>For StMAR model: Size $(M(p+4) - 1x1)$ vector $(\theta, \nu) = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.</p> <p>For G-StMAR model: Size $(M(p+3) + M2 - 1x1)$ vector $(\theta, \nu) = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_{M1+1}, \dots, \nu_M)$.</p> <p>With linear constraints: Replace the vectors ϕ_m with vectors ψ_m and provide a list of constraint matrices C that satisfy $\phi_m = R_m \psi_m$ for all $m = 1, \dots, M$, where $\psi_m = (\psi_{m,1}, \dots, \psi_{m,q_m})$.</p>

For restricted models: For GMAR model: Size $(3M + p - 1 \times 1)$ vector $\theta = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1})$, where $\phi = (\phi_1, \dots, \phi_p)$.

For StMAR model: Size $(4M + p - 1 \times 1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.

For G-StMAR model: Size $(3M + M2 + p - 1 \times 1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.

With linear constraints: Replace the vector ϕ with vector ψ and provide a constraint matrix C that satisfies $\phi = R\psi$, where $\psi = (\psi_1, \dots, \psi_q)$.

Symbol ϕ denotes an AR coefficient, σ^2 a variance, α a mixing weight, and ν a degrees of freedom parameter. If parametrization=="mean", just replace each intercept term $\phi_{m,0}$ with regimewise mean $\mu_m = \phi_{m,0} / (1 - \sum \phi_{i,m})$. In the **G-StMAR** model, the first M1 components are *GMAR type* and the rest M2 components are *StMAR type*. Note that in the case **M=1**, the parameter α is dropped, and in the case of **StMAR** or **G-StMAR** model, the degrees of freedom parameters ν_m have to be larger than 2.

model	is "GMAR", "StMAR", or "G-StMAR" model considered? In the G-StMAR model, the first M1 components are <i>GMAR type</i> and the rest M2 components are <i>StMAR type</i> .
restricted	a logical argument stating whether the AR coefficients $\phi_{m,1}, \dots, \phi_{m,p}$ are restricted to be the same for all regimes.
constraints	specifies linear constraints applied to the autoregressive parameters. For non-restricted models: a list of size (pxq_m) constraint matrices C_m of full column rank satisfying $\phi_m = C_m \psi_m$ for all $m = 1, \dots, M$, where $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$ and $\psi_m = (\psi_{m,1}, \dots, \psi_{m,q_m})$. For restricted models: a size (pxq) constraint matrix C of full column rank satisfying $\phi = C\psi$, where $\phi = (\phi_1, \dots, \phi_p)$ and $\psi = (\psi_1, \dots, \psi_q)$. Symbol ϕ denotes an AR coefficient. Note that regardless of any constraints, the nominal autoregressive order is always p for all regimes. Ignore or set to NULL if applying linear constraints is not desired.
conditional	a logical argument specifying whether the conditional or exact log-likelihood function should be used.
parametrization	is the model parametrized with the "intercepts" $\phi_{m,0}$ or "means" $\mu_m = \phi_{m,0} / (1 - \sum \phi_{i,m})$?
custom_h	a numeric vector with the same length as params specifying the difference 'h' used in finite difference approximation for each parameter separately. If NULL (default), then the difference used for differentiating overly large degrees of freedom parameters is adjusted to avoid numerical problems, and the difference is 6e-6 for the other parameters.
minval	this will be returned when the parameter vector is outside the parameter space and boundaries==TRUE.

Value

Returns approximate standard errors of the parameter values in a numeric vector.

stmarpars_to_gstmar	<i>Transform a StMAR or G-StMAR model parameter vector to a corresponding G-StMAR model parameter vector with large dfs parameters reduced.</i>
---------------------	---

Description

stmarpars_to_gstmar transforms a StMAR model parameter vector to a corresponding G-StMAR model parameter vector with large dfs parameters reduced by switching the related regimes to be GMAR type.

Usage

```
stmarpars_to_gstmar(
  p,
  M,
  params,
  model = c("GMAR", "StMAR", "G-StMAR"),
  restricted = FALSE,
  constraints = NULL,
  maxdf = 100
)
```

Arguments

p a positive integer specifying the autoregressive order of the model.

M **For GMAR and StMAR models:** a positive integer specifying the number of mixture components.
For G-StMAR models: a size (2x1) integer vector specifying the number of *GMAR type* components M1 in the first element and *StMAR type* components M2 in the second element. The total number of mixture components is $M=M1+M2$.

params a real valued parameter vector specifying the model.
For non-restricted models: For GMAR model: Size $(M(p+3) - 1x1)$ vector $\theta=(v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1})$, where $v_m = (\phi_{m,0}, \phi_m, \sigma_m^2)$ and $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$, $m = 1, \dots, M$.
For StMAR model: Size $(M(p+4) - 1x1)$ vector $(\theta, \nu) = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.
For G-StMAR model: Size $(M(p+3) + M2 - 1x1)$ vector $(\theta, \nu) = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_{M1+1}, \dots, \nu_M)$.
With linear constraints: Replace the vectors ϕ_m with vectors ψ_m and provide a list of constraint matrices **C** that satisfy $\phi_m = R_m \psi_m$ for all $m = 1, \dots, M$, where $\psi_m = (\psi_{m,1}, \dots, \psi_{m,q_m})$.
For restricted models: For GMAR model: Size $(3M + p - 1x1)$ vector $\theta = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1})$, where $\phi = (\phi_1, \dots, \phi_p)$.
For StMAR model: Size $(4M + p - 1x1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.

For G-StMAR model: Size $(3M+M2+p-1x1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots)$.

With linear constraints: Replace the vector ϕ with vector ψ and provide a constraint matrix C that satisfies $\phi = R\psi$, where $\psi = (\psi_1, \dots, \psi_q)$.

Symbol ϕ denotes an AR coefficient, σ^2 a variance, α a mixing weight, and ν a degrees of freedom parameter. If parametrization=="mean", just replace each intercept term $\phi_{m,0}$ with regimewise mean $\mu_m = \phi_{m,0} / (1 - \sum \phi_{i,m})$. In the **G-StMAR** model, the first M1 components are *GMAR type* and the rest M2 components are *StMAR type*. Note that in the case **M=1**, the parameter α is dropped, and in the case of **StMAR** or **G-StMAR** model, the degrees of freedom parameters ν_m have to be larger than 2.

model	is "GMAR", "StMAR", or "G-StMAR" model considered? In the G-StMAR model, the first M1 components are <i>GMAR type</i> and the rest M2 components are <i>StMAR type</i> .
restricted	a logical argument stating whether the AR coefficients $\phi_{m,1}, \dots, \phi_{m,p}$ are restricted to be the same for all regimes.
constraints	specifies linear constraints applied to the autoregressive parameters. For non-restricted models: a list of size (pxq_m) constraint matrices C_m of full column rank satisfying $\phi_m = C_m\psi_m$ for all $m = 1, \dots, M$, where $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$ and $\psi_m = (\psi_{m,1}, \dots, \psi_{m,q_m})$. For restricted models: a size (pxq) constraint matrix C of full column rank satisfying $\phi = C\psi$, where $\phi = (\phi_1, \dots, \phi_p)$ and $\psi = (\psi_1, \dots, \psi_q)$. Symbol ϕ denotes an AR coefficient. Note that regardless of any constraints, the nominal autoregressive order is always p for all regimes. Ignore or set to NULL if applying linear constraints is not desired.
maxdf	regimes with degrees of freedom parameter value larger than this will be turned into GMAR type.

Value

Returns a list with three elements: \$params contains the corresponding G-StMAR model parameter vector, \$reg_order contains the permutation that was applied to the regimes (GMAR type components first, and decreasing ordering by mixing weight parameters), and \$M a vector of length two containing the number of GMAR type regimes in the first element and the number of StMAR type regimes in the second.

Examples

```
params12 <- c(2, 0.9, 0.1, 0.8, 0.5, 0.5, 0.4, 12, 300)
stmarpars_to_gstmar(p=1, M=2, params=params12, model="StMAR", maxdf=100)
```

stmar_to_gstmar	<i>Estimate a G-StMAR model based on a StMAR model with large degrees of freedom parameters</i>
-----------------	---

Description

stmar_to_gstmar estimates a G-StMAR model based on a StMAR model with large degree of freedom parameters.

Usage

```
stmar_to_gstmar(
  gsmar,
  maxdf = 100,
  estimate,
  calc_std_errors,
  maxit = 100,
  custom_h = NULL
)
```

Arguments

gsmar	object of class 'gsmar' created with the function fitGSMAR or GSMAR.
maxdf	regimes with degrees of freedom parameter value larger than this will be turned into GMAR type.
estimate	set TRUE if the new model should be estimated with a variable metric algorithm using the StMAR model parameter value as the initial value. By default TRUE iff the model contains data.
calc_std_errors	set TRUE if the approximate standard errors should be calculated. By default TRUE iff the model contains data.
maxit	the maximum number of iterations for the variable metric algorithm. Ignored if estimate==FALSE.
custom_h	A numeric vector with same the length as the parameter vector: i:th element of custom_h is the difference used in central difference approximation for partial differentials of the log-likelihood function for the i:th parameter. If NULL (default), then the difference used for differentiating overly large degrees of freedom parameters is adjusted to avoid numerical problems, and the difference is 6e-6 for the other parameters.

Details

If a StMAR model contains large estimates for the degrees of freedom parameters, one should consider switching to the corresponding G-StMAR model that lets the corresponding regimes to be GMAR type. stmar_to_gstmar does this switch conveniently.

Value

Returns an object of class 'gsmar' defining the specified GMAR, StMAR, or G-StMAR model. If data is supplied, the returned object contains (by default) empirical mixing weights, some conditional and unconditional moments, and quantile residuals. Note that the first p observations are taken as the initial values so the mixing weights, conditional moments, and quantile residuals start from the $p+1$:th observation (interpreted as $t=1$).

References

- Kalliovirta L., Meitz M. and Saikkonen P. 2015. Gaussian Mixture Autoregressive model for univariate time series. *Journal of Time Series Analysis*, **36**, 247-266.
- Meitz M., Preve D., Saikkonen P. 2018. A mixture autoregressive model based on Student's t-distribution. arXiv:1805.04010 [econ.EM].
- Virolainen S. 2020. A mixture autoregressive model based on Gaussian and Student's t-distribution. arXiv:2003.05221 [econ.EM].

See Also

[fitGSMAR](#), [GSMAR](#), [iterate_more](#), [get_gradient](#), [get_regime_means](#), [swap_parametrization](#), [stmar_to_gstmar](#)

Examples

```
# These are long running example that take approximately 15 seconds to run.
fit42t <- fitGSMAR(data=M10Y1Y, p=4, M=2, model="StMAR", ncalls=1, seeds=6)
fit42t # Overly large degrees of freedom estimate!

# Switch to the appropriate G-StMAR model:
fit42gs <- stmar_to_gstmar(fit42t)
fit42gs
```

swap_parametrization	<i>Swap the parametrization of object of class 'gsmar' defining a GMAR, StMAR, or G-StMAR model</i>
----------------------	---

Description

swap_parametrization swaps the parametrization of object of class 'gsmar' to "mean" if the current parametrization is "intercept", and vice versa.

Usage

```
swap_parametrization(gsmar, calc_std_errors = TRUE, custom_h = NULL)
```

Arguments

gsmar	object of class 'gsmar' created with the function <code>fitGSMAR</code> or <code>GSMAR</code> .
calc_std_errors	should approximate standard errors be calculated?
custom_h	A numeric vector with same the length as the parameter vector: <i>i</i> :th element of <code>custom_h</code> is the difference used in central difference approximation for partial differentials of the log-likelihood function for the <i>i</i> :th parameter. If NULL (default), then the difference used for differentiating overly large degrees of freedom parameters is adjusted to avoid numerical problems, and the difference is $6e-6$ for the other parameters.

Details

`swap_parametrization` is a convenient tool if you have estimated the model in "intercept"-parametrization but wish to work with "mean"-parametrization in the future, or vice versa. For example, approximate standard errors are readily available for parametrized parameters only.

Value

Returns an object of class 'gsmar' defining the specified GMAR, StMAR, or G-StMAR model. If data is supplied, the returned object contains (by default) empirical mixing weights, some conditional and unconditional moments, and quantile residuals. Note that the first *p* observations are taken as the initial values so the mixing weights, conditional moments, and quantile residuals start from the *p*+1:th observation (interpreted as *t*=1).

References

- Kalliovirta L., Meitz M. and Saikkonen P. 2015. Gaussian Mixture Autoregressive model for univariate time series. *Journal of Time Series Analysis*, **36**, 247-266.
- Meitz M., Preve D., Saikkonen P. 2018. A mixture autoregressive model based on Student's t-distribution. arXiv:1805.04010 [econ.EM].
- Virolainen S. 2020. A mixture autoregressive model based on Gaussian and Student's t-distribution. arXiv:2003.05221 [econ.EM].

See Also

[fitGSMAR](#), [GSMAR](#), [iterate_more](#), [get_gradient](#), [get_regime_means](#), [swap_parametrization](#), [stmar_to_gstmar](#)

Examples

```
# G-StMAR model with intercept parametrization
params42gs <- c(0.04, 1.34, -0.59, 0.54, -0.36, 0.01, 0.06, 1.28, -0.36,
              0.2, -0.15, 0.04, 0.19, 9.75)
gstmar42 <- GSMAR(data=M10Y1Y, p=4, M=c(1, 1), params=params42gs,
                 model="G-StMAR")
summary(gstmar42)

# Swap to mean parametrization
```

```
gstmar42 <- swap_parametrization(gstmar42)
summary(gstmar42)
```

T10Y1Y

Spread between 10-Year and 1-Year treasury rates: T10Y1Y

Description

A dataset containing monthly U.S. interest rate spread between the 10-Year Treasury constant maturity rate and 1-Year Treasury constant maturity rate from 1953IV to 2020II.

Usage

```
T10Y1Y
```

Format

A class 'ts' time series object containing 803 observations.

Source

<https://fred.stlouisfed.org/series/GS10> <https://fred.stlouisfed.org/series/GS1>

uGMAR

uGMAR: Estimate Univariate Gaussian and Student's t Mixture Autoregressive Models

Description

uGMAR is a package for estimating univariate Gaussian Mixture Autoregressive (GMAR), Student's t Mixture Autoregressive (StMAR), and Gaussian and Student's t Mixture Autoregressive (G-StMAR) models. In addition to unconstrained and constrained estimation, it provides tools for quantile residuals based model diagnostics, forecasting, and simulation, to name a few.

Many of the functions documented are not exported but for intended internal use only. The readme file is a good place to start.

uncond_moments	<i>Calculate unconditional mean, variance, first p autocovariances and autocorrelations of the GSMAR process.</i>
----------------	---

Description

uncond_moments calculates the unconditional mean, variance, and the first p autocovariances and autocorrelations of the GSMAR process.

Usage

```
uncond_moments(gsmar)
```

Arguments

gsmar object of class 'gsmar' created with the function fitGSMAR or GSMAR.

Value

Returns a list containing the unconditional mean, variance, and the first p autocovariances and autocorrelations. Note that the lag-zero autocovariance/correlation is not included in the "first p" but is given in the uncond_variance component separately.

References

- Kalliovirta L., Meitz M. and Saikkonen P. 2015. Gaussian Mixture Autoregressive model for univariate time series. *Journal of Time Series Analysis*, **36**, 247-266.
- Meitz M., Preve D., Saikkonen P. 2018. A mixture autoregressive model based on Student's t-distribution. arXiv:1805.04010 [[econ.EM](#)].
- There are currently no published references for the G-StMAR model, but it's a straightforward generalization with theoretical properties similar to the GMAR and StMAR models.
- Lutkepohl H. 2005. New Introduction to Multiple Time Series Analysis. *Springer*.

See Also

Other moment functions: [cond_moments\(\)](#), [get_regime_autocovs\(\)](#), [get_regime_means\(\)](#), [get_regime_vars\(\)](#)

Examples

```
# GMAR model
params13 <- c(1.4, 0.88, 0.26, 2.46, 0.82, 0.74, 5.0, 0.68, 5.2, 0.72, 0.2)
gmar13 <- GSMAR(p=1, M=3, params=params13, model="GMAR")
uncond_moments(gmar13)

# StMAR model
params12t <- c(1.38, 0.88, 0.27, 3.8, 0.74, 3.15, 0.8, 100, 3.6)
stmar12t <- GSMAR(p=1, M=2, params=params12t, model="StMAR")
uncond_moments(stmar12t)
```

```
# G-StMAR model (similar to the StMAR model above)
params12gs <- c(1.38, 0.88, 0.27, 3.8, 0.74, 3.15, 0.8, 3.6)
gstmar12 <- GSMAR(p=1, M=c(1, 1), params=params12gs, model="G-StMAR")
uncond_moments(gstmar12)
```

uncond_moments_int *Calculate unconditional mean, variance, and the first p autocovariances and autocorrelations of a GSMAR process.*

Description

uncond_moments_int calculates the unconditional mean, variance, and the first p autocovariances and autocorrelations of the specified GSMAR process.

Usage

```
uncond_moments_int(
  p,
  M,
  params,
  model = c("GMAR", "StMAR", "G-StMAR"),
  restricted = FALSE,
  constraints = NULL,
  parametrization = c("intercept", "mean")
)
```

Arguments

- p** a positive integer specifying the autoregressive order of the model.
- M** **For GMAR and StMAR models:** a positive integer specifying the number of mixture components.
For G-StMAR models: a size (2x1) integer vector specifying the number of *GMAR type* components M1 in the first element and *StMAR type* components M2 in the second element. The total number of mixture components is $M=M1+M2$.
- params** a real valued parameter vector specifying the model.
For non-restricted models: For GMAR model: Size $(M(p+3) - 1x1)$ vector $\theta=(v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1})$, where $v_m = (\phi_{m,0}, \phi_m, \sigma_m^2)$ and $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$, $m = 1, \dots, M$.
For StMAR model: Size $(M(p+4) - 1x1)$ vector $(\theta, \nu) = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.
For G-StMAR model: Size $(M(p+3) + M2 - 1x1)$ vector $(\theta, \nu) = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_{M1+1}, \dots, \nu_M)$.
With linear constraints: Replace the vectors ϕ_m with vectors ψ_m and provide a list of constraint matrices **C** that satisfy $\phi_m = R_m \psi_m$ for all $m = 1, \dots, M$, where $\psi_m = (\psi_{m,1}, \dots, \psi_{m,q_m})$.

For restricted models: For GMAR model: Size $(3M + p - 1 \times 1)$ vector $\theta = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1})$, where $\phi = (\phi_1, \dots, \phi_p)$.

For StMAR model: Size $(4M + p - 1 \times 1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.

For G-StMAR model: Size $(3M + M2 + p - 1 \times 1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.

With linear constraints: Replace the vector ϕ with vector ψ and provide a constraint matrix C that satisfies $\phi = R\psi$, where $\psi = (\psi_1, \dots, \psi_q)$.

Symbol ϕ denotes an AR coefficient, σ^2 a variance, α a mixing weight, and ν a degrees of freedom parameter. If parametrization="mean", just replace each intercept term $\phi_{m,0}$ with regimewise mean $\mu_m = \phi_{m,0} / (1 - \sum \phi_{i,m})$. In the **G-StMAR** model, the first M1 components are *GMAR type* and the rest M2 components are *StMAR type*. Note that in the case **M=1**, the parameter α is dropped, and in the case of **StMAR** or **G-StMAR** model, the degrees of freedom parameters ν_m have to be larger than 2.

model is "GMAR", "StMAR", or "G-StMAR" model considered? In the G-StMAR model, the first M1 components are *GMAR type* and the rest M2 components are *StMAR type*.

restricted a logical argument stating whether the AR coefficients $\phi_{m,1}, \dots, \phi_{m,p}$ are restricted to be the same for all regimes.

constraints specifies linear constraints applied to the autoregressive parameters.

For non-restricted models: a list of size $(p \times q_m)$ constraint matrices C_m of full column rank satisfying $\phi_m = C_m \psi_m$ for all $m = 1, \dots, M$, where $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$ and $\psi_m = (\psi_{m,1}, \dots, \psi_{m,q_m})$.

For restricted models: a size $(p \times q)$ constraint matrix C of full column rank satisfying $\phi = C\psi$, where $\phi = (\phi_1, \dots, \phi_p)$ and $\psi = (\psi_1, \dots, \psi_q)$.

Symbol ϕ denotes an AR coefficient. Note that regardless of any constraints, the nominal autoregressive order is always p for all regimes. Ignore or set to NULL if applying linear constraints is **not** desired.

parametrization is the model parametrized with the "intercepts" $\phi_{m,0}$ or "means" $\mu_m = \phi_{m,0} / (1 - \sum \phi_{i,m})$?

Details

Differs from the function `uncond_moments` in arguments. This function exists for technical reasons only.

Value

Returns a list containing the unconditional mean, variance, and the first p autocovariances and autocorrelations. Note that the lag-zero autocovariance/correlation is not included in the "first p " but is given in the `uncond_variance` component separately.

References

- Kalliovirta L., Meitz M. and Saikkonen P. 2015. Gaussian Mixture Autoregressive model for univariate time series. *Journal of Time Series Analysis*, **36**, 247-266.

- Meitz M., Preve D., Saikkonen P. 2018. A mixture autoregressive model based on Student's t-distribution. arXiv:1805.04010 [[econ.EM](#)].
- There are currently no published references for the G-StMAR model, but it's a straightforward generalization with theoretical properties similar to the GMAR and StMAR models.
- Lutkepohl H. 2005. New Introduction to Multiple Time Series Analysis. *Springer*.

Wald_test	<i>Perform Wald test</i>
-----------	--------------------------

Description

Wald_test performs a Wald test for a GMAR, StMAR, or G-StMAR model.

Usage

```
Wald_test(gsmar, A, c, h = 6e-06)

## S3 method for class 'wald'
print(x, ..., digits = 4)
```

Arguments

gsmar	object of class 'gsmar' created with the function fitGSMAR or GSMAR.
A	a size $(k \times n_{params})$ matrix with full row rank specifying part of the null hypothesis where n_{params} is the number of parameters in the (unconstrained) model. See details for more information.
c	a length k vector specifying part of the null hypothesis. See details for more information.
h	the difference used to approximate the derivatives.
x	object of class 'wald' generated by the function Wald_test.
...	other arguments passed to fn.
digits	how many significant digits to print?

Details

Denoting the true parameter value by θ_0 , we test the null hypothesis $A\theta_0 = c$. Under the null, the test statistic is asymptotically χ^2 -distributed with k ($=\text{nrow}(A)$) degrees of freedom. The parameter θ_0 is assumed to have the same form as in the model supplied in the argument gsmar and it is presented in the documentation of the argument params in the function GSMAR (see ?GSMAR).

Finally, note that this function does **not** check whether the specified constraints are feasible (e.g. whether the implied constrained model would be stationary or have positive definite error term covariance matrices).

Value

Returns an object of class 'wald' containing the test statistic and the related p-value.

Methods (by generic)

- print: print method

References

- Kalliovirta L., Meitz M. and Saikkonen P. 2015. Gaussian Mixture Autoregressive model for univariate time series. *Journal of Time Series Analysis*, **36**, 247-266.
- Meitz M., Preve D., Saikkonen P. 2018. A mixture autoregressive model based on Student's t-distribution. arXiv:1805.04010 [econ.EM].
- Virolainen S. 2020. A mixture autoregressive model based on Gaussian and Student's t-distribution. arXiv:2003.05221 [econ.EM].

See Also

[LR_test](#), [fitGSMAR](#), [GSMAR](#), [diagnostic_plot](#), [profile_logliks](#), [quantile_residual_tests](#), [cond_moment_plot](#)

Examples

```
# GMAR p=1, M=2 model:
fit12 <- fitGSMAR(simudata, p=1, M=2, model="GMAR", ncalls=1, seeds=1)

# Test with Wald test whether the AR coefficients are the same in both
# regimes:
# There are 7 parameters in the model and the AR coefficient of the
# first regime is the 2nd element, whereas the AR coefficient of the second
# regime is in the 5th element.
A <- matrix(c(0, 1, 0, 0, -1, 0, 0), nrow=1, ncol=7)
c <- 0
Wald_test(fit12, A=A, c=c)
```

warn_dfs

Warn about large degrees of freedom parameter values

Description

warn_dfs warns if the model contains large degrees of freedom parameter values.

Usage

```
warn_dfs(
  object,
  p,
  M,
  params,
```



```

model = c("GMAR", "StMAR", "G-StMAR"),
warn_about = c("derivs", "errors")
)

```

Arguments

object	an object to be tested
p	a positive integer specifying the autoregressive order of the model.
M	<p>For GMAR and StMAR models: a positive integer specifying the number of mixture components.</p> <p>For G-StMAR models: a size (2x1) integer vector specifying the number of <i>GMAR type</i> components M1 in the first element and <i>StMAR type</i> components M2 in the second element. The total number of mixture components is $M=M1+M2$.</p>
params	<p>a real valued parameter vector specifying the model.</p> <p>For non-restricted models: For GMAR model: Size $(M(p+3) - 1x1)$ vector $\theta=(v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1})$, where $v_m = (\phi_{m,0}, \phi_m, \sigma_m^2)$ and $\phi_m = (\phi_{m,1}, \dots, \phi_{m,p})$, $m = 1, \dots, M$.</p> <p>For StMAR model: Size $(M(p+4) - 1x1)$ vector $(\theta, \nu) = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.</p> <p>For G-StMAR model: Size $(M(p+3) + M2 - 1x1)$ vector $(\theta, \nu) = (v_1, \dots, v_M, \alpha_1, \dots, \alpha_{M-1}, \nu_{M1+1}, \dots, \nu_M)$.</p> <p>With linear constraints: Replace the vectors ϕ_m with vectors ψ_m and provide a list of constraint matrices C that satisfy $\phi_m = R_m \psi_m$ for all $m = 1, \dots, M$, where $\psi_m = (\psi_{m,1}, \dots, \psi_{m,q_m})$.</p> <p>For restricted models: For GMAR model: Size $(3M + p - 1x1)$ vector $\theta = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1})$, where $\phi = (\phi_1, \dots, \phi_p)$.</p> <p>For StMAR model: Size $(4M + p - 1x1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1}, \nu_1, \dots, \nu_M)$.</p> <p>For G-StMAR model: Size $(3M + M2 + p - 1x1)$ vector $(\theta, \nu) = (\phi_{1,0}, \dots, \phi_{M,0}, \phi, \sigma_1^2, \dots, \sigma_M^2, \alpha_1, \dots, \alpha_{M-1}, \nu_{M1+1}, \dots, \nu_M)$.</p> <p>With linear constraints: Replace the vector ϕ with vector ψ and provide a constraint matrix C that satisfies $\phi = R\psi$, where $\psi = (\psi_1, \dots, \psi_q)$.</p> <p>Symbol ϕ denotes an AR coefficient, σ^2 a variance, α a mixing weight, and ν a degrees of freedom parameter. If parametrization=="mean", just replace each intercept term $\phi_{m,0}$ with regimewise mean $\mu_m = \phi_{m,0} / (1 - \sum \phi_{i,m})$. In the G-StMAR model, the first M1 components are <i>GMAR type</i> and the rest M2 components are <i>StMAR type</i>. Note that in the case M=1, the parameter α is dropped, and in the case of StMAR or G-StMAR model, the degrees of freedom parameters ν_m have to be larger than 2.</p>
model	is "GMAR", "StMAR", or "G-StMAR" model considered? In the G-StMAR model, the first M1 components are <i>GMAR type</i> and the rest M2 components are <i>StMAR type</i> .
warn_about	warn about inaccurate derivatives or standard errors?

Details

Either provide a class 'gsmar' object or specify the model by hand.

Value

Doesn't return anything but throws a warning if any degrees of freedom parameters have value larger than 100.

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