

Package ‘HMB’

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Type Package

Title Hierarchical Model-Based Estimation Approach

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Description For estimation of a variable of interest using two sources of auxiliary information available in a nested structure. For reference see Saarela et al. (2016)<[doi:10.1007/s13595-016-0590-1](https://doi.org/10.1007/s13595-016-0590-1)> and Saarela et al. (2018) <[doi:10.3390/rs10111832](https://doi.org/10.3390/rs10111832)>.

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getSpec	<i>Method getSpec</i>
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Description

Get model specifications of HMB-class object

Usage

```
getSpec(obj)

## S4 method for signature 'HMB'
getSpec(obj)
```

Arguments

obj Object of class HMB

Value

A list containing the estimated parameters, together with model arguments

Examples

```
pop_U = sample(nrow(HMB_data), 20000)
pop_Sa = sample(pop_U, 5000)
pop_S = sample(pop_U, 300)

y_S = HMB_data[pop_S, "GSV"]
X_S = HMB_data[pop_S, c("hMAX", "h80", "CRR", "pVeg")]
X_Sa = HMB_data[pop_Sa, c("hMAX", "h80", "CRR", "pVeg")]
Z_Sa = HMB_data[pop_Sa, c("B20", "B30", "B50")]
Z_U = HMB_data[pop_U, c("B20", "B30", "B50")]

hmb_model = hmb(y_S, X_S, X_Sa, Z_Sa, Z_U)
getSpec(hmb_model)
```

ghmb

*Generalized Hierarchical Model-Based estimation method***Description**

Generalized Hierarchical Model-Based estimation method

Usage`ghmb(y_S, X_S, X_Sa, Z_Sa, Z_U, Omega_S, Sigma_Sa)`**Arguments**

<code>y_S</code>	Response object that can be coerced into a column vector. The <code>_S</code> denotes that <code>y</code> is part of the sample S , with $N_S \leq N_{Sa} \leq N_U$.
<code>X_S</code>	Object of predictors variables that can be coerced into a matrix. The rows of <code>X_S</code> correspond to the rows of <code>y_S</code> .
<code>X_Sa</code>	Object of predictor variables that can be coerced into a matrix. The set Sa is the intermediate sample.
<code>Z_Sa</code>	Object of predictor variables that can be coerced into a matrix. The set Sa is the intermediate sample, and the Z -variables often some sort of auxiliary, inexpensive data. The rows of <code>Z_Sa</code> correspond to the rows of <code>X_Sa</code> .
<code>Z_U</code>	Object of predictor variables that can be coerced into a matrix. The set U is the universal population sample.
<code>Omega_S</code>	The covariance structure of ϵ_S , up to a constant.
<code>Sigma_Sa</code>	The covariance structure of u_{Sa} , up to a constant.

Details

The GHMB assumes two models

$$y = \mathbf{x}\boldsymbol{\beta} + \epsilon$$

$$\mathbf{x}\boldsymbol{\beta} = \mathbf{z}\boldsymbol{\alpha} + \mathbf{u}$$

$$\epsilon \perp u$$

For a sample from the superpopulation, the GHMB assumes

$$E(\epsilon) = \mathbf{0}, E(\epsilon\epsilon^T) = \omega^2\boldsymbol{\Omega}$$

$$E(\mathbf{u}) = \mathbf{0}, E(\mathbf{u}\mathbf{u}^T) = \sigma^2\boldsymbol{\Sigma}$$

Value

A fitted object of class HMB.

References

Saarela, S., Holm, S., Healey, S.P., Andersen, H.-E., Petersson, H., Prentius, W., Patterson, P.L., Næsset, E., Gregoire, T.G. & Ståhl, G. (2018). Generalized Hierarchical Model-Based Estimation for Aboveground Biomass Assessment Using GEDI and Landsat Data, *Remote Sensing*, 10(11), 1832.

See Also

[summary](#), [getSpec](#).

Examples

```
pop_U    = sample(nrow(HMB_data), 20000)
pop_Sa   = sample(pop_U, 2500)
pop_S    = sample(pop_U, 300)

y_S      = HMB_data[pop_S, "GSV"]
X_S      = HMB_data[pop_S, c("hMAX", "h80", "CRR", "pVeg")]
X_Sa     = HMB_data[pop_Sa, c("hMAX", "h80", "CRR", "pVeg")]
Z_Sa     = HMB_data[pop_Sa, c("B20", "B30", "B50")]
Z_U      = HMB_data[pop_U, c("B20", "B30", "B50")]

Omega_S  = diag(1, nrow(X_S))
Sigma_Sa = diag(1, nrow(Z_Sa))

ghmb_model = ghmb(
  y_S, X_S, X_Sa, Z_Sa, Z_U, Omega_S, Sigma_Sa)
ghmb_model
```

gtsmb

Generalized Two-Staged Model-Based estimation

Description

Generalized Two-Staged Model-Based estimation

Usage

```
gtsmb(y_S, X_S, X_Sa, Z_Sa, Z_U, Omega_S, Phis_Sa)
```

Arguments

y_S	Response object that can be coerced into a column vector. The <code>_S</code> denotes that <code>y</code> is part of the sample <code>S</code> , with $N_S \leq N_{Sa} \leq N_U$.
X_S	Object of predictors variables that can be coerced into a matrix. The rows of <code>X_S</code> correspond to the rows of <code>y_S</code> .
X_Sa	Object of predictor variables that can be coerced into a matrix. The set <code>Sa</code> is the intermediate sample.

Z_Sa	Object of predictor variables that can be coresed into a matrix. The set Sa is the intermediate sample, and the Z-variables often some sort of auxilairy, inexpensive data. The rows of Z_Sa correspond to the rows of X_Sa
Z_U	Object of predictor variables that can be coresed into a matrix. The set U is the universal population sample.
Omega_S	The covariance structure of ϵ_S , up to a constant.
Phis_Sa	A 3D array, where the third dimension corresponds to the covariance structure of $E(\xi_{k,Sa}\xi_{j,Sa}^T)$, in the order $k = 1, \dots, p, j = 1, \dots, k$. For $p = 3$, the order (k,j) will thus be (1,1), (2,1), (2,2), (3,1), (3,2), (3,3).

Details

The GTSMB assumes the superpopulations

$$y = \mathbf{x}\boldsymbol{\beta} + \epsilon$$

$$x_k = \mathbf{z}\boldsymbol{\gamma}_k + \xi_k$$

$$\epsilon \perp \xi_k$$

For a sample from the superpopulation, the GTSMB assumes

$$E(\epsilon) = \mathbf{0}, E(\epsilon\epsilon^T) = \omega^2\boldsymbol{\Omega}$$

$$E(\xi_k) = \mathbf{0}, E(\xi_k\xi_j^T) = \theta_{\Phi,k,j}^2\boldsymbol{\Phi}_{k,j}, \theta_{\Phi,k,j}^2\boldsymbol{\Phi}_{k,j} = \theta_{\Phi,j,k}^2\boldsymbol{\Phi}_{j,k}$$

Value

A fitted object of class HMB.

References

Holm, S., Nelson, R. & Ståhl, G. (2017) Hybrid three-phase estimators for large-area forest inventory using ground plots, airborne lidar, and space lidar. *Remote Sensing of Environment*, 197, 85–97.

Saarela, S., Holm, S., Healey, S.P., Andersen, H.-E., Petersson, H., Prentius, W., Patterson, P.L., Næsset, E., Gregoire, T.G. & Ståhl, G. (2018). Generalized Hierarchical Model-Based Estimation for Aboveground Biomass Assessment Using GEDI and Landsat Data, *Remote Sensing*, 10(11), 1832.

See Also

[summary](#), [getSpec](#).

Examples

```

pop_U = sample(nrow(HMB_data), 20000)
pop_Sa = sample(pop_U, 500)
pop_S = sample(pop_U, 100)

y_S = HMB_data[pop_S, "GSV"]
X_S = HMB_data[pop_S, c("hMAX", "h80", "CRR")]
X_Sa = HMB_data[pop_Sa, c("hMAX", "h80", "CRR")]
Z_Sa = HMB_data[pop_Sa, c("B20", "B30", "B50")]
Z_U = HMB_data[pop_U, c("B20", "B30", "B50")]

Omega_S = diag(1, nrow(X_S))
Phis_Sa = array(0, c(nrow(X_Sa), nrow(X_Sa), ncol(X_Sa) * (ncol(X_Sa) + 1) / 2))
Phis_Sa[, , 1] = diag(1, nrow(X_Sa)) # Phi(1,1)
Phis_Sa[, , 2] = diag(1, nrow(X_Sa)) # Phi(2,1)
Phis_Sa[, , 3] = diag(1, nrow(X_Sa)) # Phi(2,2)
Phis_Sa[, , 4] = diag(1, nrow(X_Sa)) # Phi(3,1)
Phis_Sa[, , 5] = diag(1, nrow(X_Sa)) # Phi(3,2)
Phis_Sa[, , 6] = diag(1, nrow(X_Sa)) # Phi(3,3)

gtsmb_model = gtsmb(y_S, X_S, X_Sa, Z_Sa, Z_U, Omega_S, Phis_Sa)
gtsmb_model

```

hmb

Hierarchical Model-Based estimation

Description

Hierarchical Model-Based estimation

Usage

```
hmb(y_S, X_S, X_Sa, Z_Sa, Z_U)
```

Arguments

y_S	Response object that can be coerced into a column vector. The $_S$ denotes that y is part of the sample S , with $N_S \leq N_{Sa} \leq N_U$.
X_S	Object of predictors variables that can be coerced into a matrix. The rows of X_S correspond to the rows of y_S .
X_Sa	Object of predictor variables that can be coerced into a matrix. The set Sa is the intermediate sample.
Z_Sa	Object of predictor variables that can be coerced into a matrix. The set Sa is the intermediate sample, and the Z-variables often some sort of auxiliary, inexpensive data. The rows of Z_Sa correspond to the rows of X_Sa .
Z_U	Object of predictor variables that can be coerced into a matrix. The set U is the universal population sample.

Details

The HMB assumes two models

$$y = \mathbf{x}\boldsymbol{\beta} + \epsilon$$

$$\mathbf{x}\boldsymbol{\beta} = \mathbf{z}\boldsymbol{\alpha} + u$$

$$\epsilon \perp u$$

For a sample from the superpopulation, the HMB assumes

$$E(\boldsymbol{\epsilon}) = \mathbf{0}, E(\boldsymbol{\epsilon}\boldsymbol{\epsilon}^T) = \omega^2\mathbf{I}$$

$$E(\mathbf{u}) = \mathbf{0}, E(\mathbf{u}\mathbf{u}^T) = \sigma^2\mathbf{I}$$

Value

A fitted object of class HMB.

References

Saarela, S., Holm, S., Grafström, A., Schnell, S., Næsset, E., Gregoire, T.G., Nelson, R.F. & Ståhl, G. (2016). Hierarchical model-based inference for forest inventory utilizing three sources of information, *Annals of Forest Science*, 73(4), 895-910.

Saarela, S., Holm, S., Healey, S.P., Andersen, H.-E., Petersson, H., Prentius, W., Patterson, P.L., Næsset, E., Gregoire, T.G. & Ståhl, G. (2018). Generalized Hierarchical Model-Based Estimation for Aboveground Biomass Assessment Using GEDI and Landsat Data, *Remote Sensing*, 10(11), 1832.

See Also

[summary](#), [getSpec](#).

Examples

```
pop_U = sample(nrow(HMB_data), 20000)
pop_Sa = sample(pop_U, 5000)
pop_S = sample(pop_U, 300)

y_S = HMB_data[pop_S, "GSV"]
X_S = HMB_data[pop_S, c("hMAX", "h80", "CRR", "pVeg")]
X_Sa = HMB_data[pop_Sa, c("hMAX", "h80", "CRR", "pVeg")]
Z_Sa = HMB_data[pop_Sa, c("B20", "B30", "B50")]
Z_U = HMB_data[pop_U, c("B20", "B30", "B50")]

hmb_model = hmb(y_S, X_S, X_Sa, Z_Sa, Z_U)
hmb_model
```

HMB-class	<i>Class HMB</i>
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Description

Class HMB is the base class for the HMB-package

See Also

[hmb](#), [ghmb](#), [tsmb](#), [gtsmb](#)

HMB_data	<i>Sample Data for HMB package</i>
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Description

A data frame with 100000 records.
Names are GSV: hMAX: h80: CRR: pVeg: B20: B30: B50:

show	<i>Method show</i>
------	--------------------

Description

Display model outputs
Display model summary properties

Usage

```
## S4 method for signature 'HMB'  
show(object)  
  
## S4 method for signature 'SummaryHMB'  
show(object)
```

Arguments

object Object of class HMB

Examples

```
pop_U = sample(nrow(HMB_data), 20000)
pop_Sa = sample(pop_U, 5000)
pop_S = sample(pop_U, 300)

y_S = HMB_data[pop_S, "GSV"]
X_S = HMB_data[pop_S, c("hMAX", "h80", "CRR", "pVeg")]
X_Sa = HMB_data[pop_Sa, c("hMAX", "h80", "CRR", "pVeg")]
Z_Sa = HMB_data[pop_Sa, c("B20", "B30", "B50")]
Z_U = HMB_data[pop_U, c("B20", "B30", "B50")]

hmb_model = hmb(y_S, X_S, X_Sa, Z_Sa, Z_U)
show(hmb_model)
pop_U = sample(nrow(HMB_data), 20000)
pop_Sa = sample(pop_U, 5000)
pop_S = sample(pop_U, 300)

y_S = HMB_data[pop_S, "GSV"]
X_S = HMB_data[pop_S, c("hMAX", "h80", "CRR", "pVeg")]
X_Sa = HMB_data[pop_Sa, c("hMAX", "h80", "CRR", "pVeg")]
Z_Sa = HMB_data[pop_Sa, c("B20", "B30", "B50")]
Z_U = HMB_data[pop_U, c("B20", "B30", "B50")]

hmb_model = hmb(y_S, X_S, X_Sa, Z_Sa, Z_U)
show(summary(hmb_model))
```

summary	<i>Method summary</i>
---------	-----------------------

Description

Summary of HMB model

Usage

```
summary(obj)

## S4 method for signature 'HMB'
summary(obj)
```

Arguments

obj Object of class HMB

Value

Summary of HMB model.

Examples

```
pop_U = sample(nrow(HMB_data), 20000)
pop_Sa = sample(pop_U, 5000)
pop_S = sample(pop_U, 300)

y_S = HMB_data[pop_S, "GSV"]
X_S = HMB_data[pop_S, c("hMAX", "h80", "CRR", "pVeg")]
X_Sa = HMB_data[pop_Sa, c("hMAX", "h80", "CRR", "pVeg")]
Z_Sa = HMB_data[pop_Sa, c("B20", "B30", "B50")]
Z_U = HMB_data[pop_U, c("B20", "B30", "B50")]

S_Sa_map = matrix(pop_S, nrow = nrow(X_S), ncol = nrow(X_Sa))
S_Sa_map = t(apply(S_Sa_map, 1, function(x) {
  return(x == pop_Sa)
})) * 1

hmb_model = hmb(y_S, X_S, X_Sa, Z_Sa, Z_U)
summary(hmb_model)
```

SummaryHMB-class	<i>Class SummaryHMB</i>
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Description

Class SummaryHMB defines summary information for HMB object.

tsmb	<i>Two-staged Model-Based estimation</i>
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Description

Two-staged Model-Based estimation

Usage

```
tsmb(y_S, X_S, X_Sa, Z_Sa, Z_U)
```

Arguments

y_S	Response object that can be coerced into a column vector. The _S denotes that y is part of the sample S, with $N_S \leq N_{Sa} \leq N_U$.
X_S	Object of predictors variables that can be coerced into a matrix. The rows of X_S correspond to the rows of y_S.
X_Sa	Object of predictor variables that can be coerced into a matrix. The set Sa is the intermediate sample.

Z_Sa	Object of predictor variables that can be coresed into a matrix. The set <i>Sa</i> is the intermediate sample, and the Z-variables often some sort of auxilairy, inexpensive data. The rows of Z_Sa correspond to the rows of X_Sa
Z_U	Object of predictor variables that can be coresed into a matrix. The set <i>U</i> is the universal population sample.

Details

The TSMB assumes the superpopulations

$$y = \mathbf{x}^T \boldsymbol{\beta} + \epsilon$$

$$x_k = \mathbf{z}^T \boldsymbol{\gamma}_k + \xi_k$$

$$\epsilon \perp \xi_k$$

For a sample from the superpopulation, the TSMB assumes

$$E(\boldsymbol{\epsilon}) = \mathbf{0}, E(\boldsymbol{\epsilon} \boldsymbol{\epsilon}^T) = \omega^2 \mathbf{I}$$

$$E(\boldsymbol{\xi}_k) = \mathbf{0}, E(\boldsymbol{\xi}_k \boldsymbol{\xi}_j^T) = \phi_{k,j}^2 \mathbf{I}$$

Value

A fitted object of class HMB.

References

Saarela, S., Holm, S., Grafström, A., Schnell, S., Næsset, E., Gregoire, T.G., Nelson, R.F. & Ståhl, G. (2016). Hierarchical model-based inference for forest inventory utilizing three sources of information. *Annals of Forest Science*, 73(4), 895-910.

See Also

[summary](#), [getSpec](#).

Examples

```
pop_U = sample(nrow(HMB_data), 20000)
pop_Sa = sample(pop_U, 5000)
pop_S = sample(pop_U, 300)

y_S = HMB_data[pop_S, "GSV"]
X_S = HMB_data[pop_S, c("hMAX", "h80", "CRR", "pVeg")]
X_Sa = HMB_data[pop_Sa, c("hMAX", "h80", "CRR", "pVeg")]
Z_Sa = HMB_data[pop_Sa, c("B20", "B30", "B50")]
Z_U = HMB_data[pop_U, c("B20", "B30", "B50")]

tsmb_model = tsmb(y_S, X_S, X_Sa, Z_Sa, Z_U)
tsmb_model
```

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