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> and Saarela et al. (2018) <doi:10.3390/rs10111832>.

License GPL (>= 2)

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LazyData TRUE

Imports Rcpp (>= 0.12.16)

Depends methods, stats, R (>= 3.5)

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Collate RcppExports.R helper_functions.R HMB-class.R SummaryHMB-class.R ghmb.R gtsmb.R hmb.R tsmb.R

RoxygenNote 6.1.0

NeedsCompilation yes

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R topics documented:

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getSpec   *Method getSpec*

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

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 auxilairy, 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.
Omega_S	The covariance structure of ϵ_S, up to a constant.
Sigma_Sa	The covariance structure of $\boldsymbol{u}_{Sa}$, up to a constant.

Details

The GHMB assumes two models

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

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

$$\epsilon \perp u$$

For a sample from the superpopulation, the GHMB assumes

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

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

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 estmation*

Description

Generalized Two-Staged Model-Based estmation

Usage

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

Arguments

y_S	Response object that can be coersed 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 coersed into a matrix. The rows of X_S correspond to the rows of y_S.
X_Sa	Object of predictor variables that can be coresed 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 *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 $E(\boldsymbol{\xi}_{k,Sa}\boldsymbol{\xi}_{j,Sa}^T)$, in the order $k = 1, \ldots, p, j = 1, \ldots k$. 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

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

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

$$\epsilon \perp \xi_k$$

For a sample from the superpopulation, the GTSMB assumes

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

$$E(\boldsymbol{\xi}_k) = \boldsymbol{0}, E(\boldsymbol{\xi}_k\boldsymbol{\xi}_j^T) = \theta_{\Phi,k,j}^2\boldsymbol{\Phi}_{k,j}, \theta_{\Phi,k,j}^2\boldsymbol{\Phi}_{k,j} = \theta_{\Phi,j,k}^2\boldsymbol{\Phi}_{j,k}$$

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 estmation*

Description

Hierarchical Model-Based estmation

Usage

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

Arguments

y_S	Response object that can be coersed 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 coersed into a matrix. The rows of X_S correspond to the rows of y_S.
X_Sa	Object of predictor variables that can be coresed 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 *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.

Details

The HMB assumes two models

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

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

$$\epsilon \perp u$$

For a sample from the superpopulation, the HMB assumes

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

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

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   *Class HMB*

Description

Class HMB is the base class for the HMB-package

See Also

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

HMB_data   *Sample Data for HMB package*

Description

A data frame with 100000 records.

Names are GSV: hMAX: h80: CRR: pVeg: B20: B30: B50:

show   *Method show*

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 *Method summary*

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   *Class SummaryHMB*

Description

Class SummaryHMB defines summary information for HMB object.

---

tsmb   *Two-staged Model-Based estmation*

Description

Two-staged Model-Based estmation

Usage

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

Arguments

y_S	Response object that can be coersed 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 coersed into a matrix. The rows of X_S correspond to the rows of y_S.
X_Sa	Object of predictor variables that can be coresed 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 *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.

Details

The TSMB assumes the superpopulations

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

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

$$\epsilon \perp \xi_k$$

For a sample from the superpopulation, the TSMB assumes

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

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

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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