

# Package: HMB (via r-universe)

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**Type** Package

**Title** Hierarchical Model-Based Estimation Approach

**Version** 1.1

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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)>.

**License** GPL (>= 2)

**Encoding** UTF-8

**LazyData** TRUE

**Imports** Rcpp (>= 0.12.16)

**Depends** methods, stats, R (>= 3.5)

**LinkingTo** Rcpp, RcppArmadillo

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SummaryHMB-class.R ghmb.R gtsmb.R hmb.R tsmb.R

**RoxygenNote** 6.1.0

**NeedsCompilation** yes

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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**

y_S	Response object that can be coerced into a column vector. The <i>_S</i> denotes that <i>y</i> is part of the sample <i>S</i> , 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 <i>Sa</i> is the intermediate sample.
Z_Sa	Object of predictor variables that can be coerced into a matrix. The set <i>Sa</i> is the intermediate sample, and the <i>Z</i> -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 <i>U</i> is the universal population sample.
Omega_S	The covariance structure of $\epsilon_S$ , up to a constant.
Sigma_Sa	The covariance structure of $u_{Sa}$ , up to a constant.

**Details**

The GHMB assumes two models

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

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

$$\epsilon \perp \mathbf{u}$$

For a sample from the superpopulation, the GHMB assumes

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

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

**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-Stage Model-Based estimation*

---

## Description

Generalized Two-Stage Model-Based estimation

## Usage

```
gtsmb(y_S, X_S, X_Sa, Z_Sa, Z_U, Omega_S, Phis_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 <code>S</code> , 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 <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 $\chi_{Sa}$
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 $\epsilon_S$ , 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

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

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

## 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

*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	<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>
------	--

---

**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 <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 <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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