

# Package ‘BIOMASS’

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**Type** Package

**Title** Estimating Above-Ground Biomass and Its Uncertainty in Tropical Forests

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**Description** Contains data analysis functions to estimate above-ground biomass and its uncertainty in tropical forests. BIOMASS functions allow to (1) retrieve and to correct taxonomy, (2) estimate wood density and its uncertainty, (3) construct height-diameter models, (4) estimate the above-ground biomass at the stand level with associated uncertainty.

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## R topics documented:

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**Description**

Contains data analysis functions to estimate above-ground biomass and its uncertainty in tropical forests. BIOMASS functions allow to (1) retrieve and to correct taxonomy, (2) estimate wood density and its uncertainty, (3) construct height-diameter models, (4) estimate the above-ground biomass at the stand level with associated uncertainty.

**Author(s)**

Maxime REJOU-MECHAIN, Ariane TANGUY, Camille PIPONIOT, Jerome CHAVE, Bruno HERAULT

Maintainer: Maxime REJOU-MECHAIN <maxime.rejou@gmail.com>

**References**

Rejou-Mechain M., Tanguy A., Piponiot C., Chave J., Herault B. (2016). BIOMASS : An R Package for estimating above-ground biomass and its uncertainty in tropical forests. R package version 1.0.

**Examples**

```
## Not run:
library(BIOMASS)

data(KarnatakaForest)
str(KarnatakaForest)

# Dataset containing height and diameter measurements from two 1-ha plots
# established in the lowland rainforest of French Guiana, at the Nouragues
# Ecological Research Station
data(NouraguesHD)
str(NouraguesHD)

#####
# WOOD DENSITY

# 1-RETRIEVE AND CORRECT TAXONOMY

# Checking typos in taxonomy
Taxo <- correctTaxo(genus = KarnatakaForest$genus, species = KarnatakaForest$species)
KarnatakaForest$genusCorr <- Taxo$genusCorrected
KarnatakaForest$speciesCorr <- Taxo$speciesCorrected

# Retrieving APG III Families and Orders from Genus names
```

```

APG <- getTaxonomy(KarnatakaForest$genusCorr, findOrder = T)
KarnatakaForest$familyAPG <- APG$family
KarnatakaForest$orderAPG <- APG$order

# 2-RETRIEVE WOOD DENSITY
dataWD <- getWoodDensity(genus = KarnatakaForest$genusCorr,
                        species = KarnatakaForest$speciesCorr,
                        stand = KarnatakaForest$plotID)

#####
# TREE HEIGHT

# Compare different local H-D models
HDmodel <- modelHD(D = NouraguesHD$D, H = NouraguesHD$H,
                  drawGraph = TRUE, useWeight = TRUE)

# Compute the local H-D model with the lowest RSE
HDmodel <- modelHD(D = NouraguesHD$D, H = NouraguesHD$H,
                  method = "log2", useWeight = TRUE)

# Compute models specific to given stands
HDmodelPerPlot <- by(NouraguesHD, NouraguesHD$plotId,
                    function(x) modelHD(D = x$D, H = x$H, method = "weibull", useWeight = T),
                    simplify = FALSE)
RSEmodels <- sapply(HDmodelPerPlot, function(x) x$RSE)
Coeffmodels <- lapply(HDmodelPerPlot, function(x) x$coefficients)

# Retrieve height data from a local HD model
dataHlocal <- retrieveH(D = KarnatakaForest$D, model = HDmodel)

# Retrieve height data from a Feldpaush et al. (2012) averaged model
dataHfeld <- retrieveH(D = KarnatakaForest$D, region = "SEAsia")

# Retrieve height data from Chave et al. (2012) equation 6
dataHchave <- retrieveH(D = KarnatakaForest$D,
                      coord = cbind(KarnatakaForest$long, KarnatakaForest$lat))

#####
# AGB CALCULATION

KarnatakaForest$WD = dataWD$meanWD
KarnatakaForest$H = dataHlocal$H
KarnatakaForest$Hfeld = dataHfeld$H

# Compute AGB(Mg) per tree
AGBtree <- computeAGB(D = KarnatakaForest$D, WD = KarnatakaForest$WD,
                    H = KarnatakaForest$H)

# Compute AGB(Mg) per plot
AGBPlotList <- by(KarnatakaForest, KarnatakaForest$plotId,
                  function(x) computeAGB(D = x$D, WD = x$WD, H = x$H),
                  simplify = F)
AGBplot <- sapply(AGBPlotList, sum)

```

```

# Compute AGB(Mg) per tree without height information (Eq. 7 from Chave et al. (2014))
AGBPlotListChave <- by(KarnatakaForest, KarnatakaForest$plotId,
  function(x) computeAGB(D = x$D, WD = x$WD, coord = cbind(x$long, x$lat)),
  simplify = F)
AGBplotChave <- sapply(AGBPlotListChave, sum)

# Compute AGB(Mg) per tree with Feldpausch et al. (2012) regional H-D model
AGBPlotListFeld <- by(KarnatakaForest, KarnatakaForest$plotId,
  function(x) computeAGB(D = x$D, WD = x$WD, H = x$Hfeld),
  simplify = F)
AGBplotFeld <- sapply(AGBPlotListFeld, sum)

#####
# PROPAGATING ERRORS

KarnatakaForest$sdWD = dataWD$sdWD
KarnatakaForest$HfeldRSE = dataHfeld$RSE

# Per plot using the local HD model constructed above (modelHD)
resultMC <- by(KarnatakaForest, KarnatakaForest$plotId,
  function(x) AGBmonteCarlo(D = x$D, WD = x$WD, H = x$H, errWD = x$sdWD,
    HDmodel = HDmodel, Dpropag = "chave2004"),
  simplify = F)
meanAGBperplot <- unlist(sapply(resultMC, "[", 1))
credperplot <- sapply(resultMC, "[", 4)

# Per plot using the Feldpaush regional HD averaged model
resultMC <- by(KarnatakaForest, KarnatakaForest$plotId,
  function(x) AGBmonteCarlo(D = x$D, WD = x$WD, errWD = x$sdWD, H = x$Hfeld,
    errH = x$HfeldRSE, Dpropag = "chave2004"),
  simplify = F)
meanAGBperplotFeld <- unlist(sapply(resultMC, "[", 1))
credperplotFeld <- sapply(resultMC, "[", 4)

# Per plot using Chave et al. (2014) Equation 7
resultMC <- by(KarnatakaForest, KarnatakaForest$plotId,
  function(x) AGBmonteCarlo(D = x$D, WD = x$WD, errWD = x$sdWD,
    coord = cbind(x$long, x$lat),
    Dpropag = "chave2004"),
  simplify = F)
meanAGBperplotChave <- unlist(sapply(resultMC, "[", 1))
credperplotChave <- sapply(resultMC, "[", 4)

## End(Not run)

```

**Description**

Propagation of the errors throughout the steps needed to compute AGB.

**Usage**

```
AGBmonteCarlo(D, WD = NULL, errWD = NULL, H = NULL, errH = NULL, HDmodel = NULL,
coord = NULL, Dpropag = NULL, n = 1000)
```

**Arguments**

D	Vector of tree diameters (in cm)
WD	Vector of wood density estimates (in g/cm <sup>3</sup> )
errWD	Vector of error associated to the wood density estimates (should be of the same size as WD)
H	(option 1) Vector of tree heights (in m). If set, errH must be set too.
errH	(if H) Residual standard error (RSE) of a model or vector of errors (sd values) associated to tree height values (in the latter case the vector should be of the same length as H).
HDmodel	(option 2) Model used to estimate tree height from tree diameter (output from <a href="#">modelHD</a> , see example)
coord	(option 3) Coordinates of the site(s), either a vector giving a single site (e.g. c(longitude, latitude)) or a matrix/dataframe with two columns (e.g. cbind(longitude, latitude)). The coordinates are used to predict height-diameter allometry with bioclimatic variables.
Dpropag	This variable can take three kind of values, indicating how to propagate the errors on diameter measurements : a single numerical value or a vector of the same size as D, both representing the standard deviation associated with the diameter measurements or "chave2004" (an important error on 5 percent of the measures, a smaller error on 95 percent of the trees).
n	Number of iteration. Cannot be smaller than 50 or larger than 1000. By default n = 1000

**Details**

See Rejou-Mechain et al. (in prep) for all details on the error propagation procedure.

**Value**

Returns a list with:

meanAGB	Mean stand AGB value following the error propagation
medAGB	Median stand AGB value following the error propagation
sdAGB	Standard deviation of the stand AGB value following the error propagation
credibilityAGB	Credibility interval at 95% of the stand AGB value following the error propagation
AGB_simu	Matrix with the AGB of the trees (rows) times the n iterations (columns)

**Author(s)**

Bruno HERAULT, Camille PIPONOT, Ariane TANGUY, Maxime REJOU-MECHAIN

**References**

Chave, J. et al. (2004). *Error propagation and scaling for tropical forest biomass estimates*. Philosophical Transactions of the Royal Society B: Biological Sciences, 359(1443), 409-420.

Rejou-Mechain et al. (in prep). *BIOMASS: An R Package for estimating above-ground biomass and its uncertainty in tropical forests*.

**Examples**

```
# Load a database
data(NouraguesHD)
data(KarnatakaForest)

# Modelling height-diameter relationship
HDmodel <- modelHD(D = NouraguesHD$D, H = NouraguesHD$H, method = "log2")

# Retrieving wood density values
KarnatakaWD <- getWoodDensity(KarnatakaForest$genus, KarnatakaForest$species,
stand = KarnatakaForest$plotId)

# Propagating errors with a standard error in wood density in one plot
filt <- KarnatakaForest$plotId=="BSP20"
resultMC <- AGBmonteCarlo(D = KarnatakaForest$D[filt], WD = KarnatakaWD$meanWD[filt],
errWD = KarnatakaWD$sdWD[filt], HDmodel = HDmodel)

str(resultMC)

# If only the coordinates are available
lat <- KarnatakaForest$lat[filt]
long <- KarnatakaForest$long[filt]
coord <- cbind(long, lat)
## Not run:
resultMC <- AGBmonteCarlo(D = KarnatakaForest$D[filt], WD = KarnatakaWD$meanWD[filt],
errWD = KarnatakaWD$sdWD[filt], coord = coord)

str(resultMC)
## End(Not run)

# Propagating errors with a standard error in wood density in all plots at once
KarnatakaForest$meanWD = KarnatakaWD$meanWD
KarnatakaForest$sdWD = KarnatakaWD$sdWD

## Not run:
resultMC <- by(KarnatakaForest, KarnatakaForest$plotId,
function(x) AGBmonteCarlo(D = x$D, WD = x$meanWD, errWD = x$sdWD,
HDmodel = HDmodel, Dpropag = "chave2004"))

meanAGBperplot <- unlist(sapply(resultMC, "[", 1))
credperplot <- sapply(resultMC, "[", 4)
## End(Not run)
```

computeAGB

*Computing tree above-ground biomass (AGB)***Description**

This function uses the Chave's pantropical models to estimate the above-ground biomass of tropical trees.

**Usage**

```
computeAGB(D, WD, H = NULL, coord = NULL)
```

**Arguments**

D	Tree diameter (in cm), either a vector or a single value
WD	Wood density (in g/cm <sup>3</sup> ), either a vector or a single value. If not available, see <a href="#">getWoodDensity</a> .
H	(optional) Tree height (H in m), either a vector or a single value. If not available, see <a href="#">retrieveH</a> and <a href="#">modelHD</a> . Compulsory if the coordinates coord are not given.
coord	(optional) Coordinates of the site(s), either a vector giving a single site (e.g. c(longitude, latitude)) or a matrix/dataframe with two columns (e.g. cbind(longitude, latitude)). The coordinates are used to account for variation in height-diameter relationship thanks to an environmental proxy (parameter E in Chave et al. 2014). Compulsory if tree heights H are not given.

**Details**

This function uses two different ways of computing the above-ground biomass of a tree:

1) If height data are available, the AGB is computed thanks to the following equation (Eq. 5 in Chave et al., 2014):

$$AGB = 0.0673 * (WD * H * D^2)^{0.976}$$

2) If no height data is available, the AGB is computed thanks to the site coordinates with the following equation, slightly modified from Eq. 7 in Chave et al., 2014:

$$AGB = \exp(-2.024 - 0.896 * E + 0.920 * \log(WD) + 2.795 * \log(D) - 0.0461 * (\log(D)^2))$$

where E is a measure of environmental stress estimated from the site coordinates (coord).

**Value**

The function returns the ABG in Mg (or ton).

**Author(s)**

Maxime REJOU-MECHAIN, Ariane TANGUY

## References

Chave et al. (2014) *Improved allometric models to estimate the above-ground biomass of tropical trees*, *Global Change Biology*, 20 (10), 3177-3190

## See Also

[computeE](#)

## Examples

```
# Create variables
D <- 10:99
WD <- runif(length(D), min = 0.1, max = 1)
H <- D^(2/3)

# If you have height data
AGB <- computeAGB(D,WD,H)

# If you don't have height data and a single site
lat <- 4.08
long <- -52.68
coord <- cbind(long, lat)
## Not run: AGB <- computeAGB(D, WD, coord = coord)

# If you don't have height data and several sites (here three)
lat <- c(rep(4.08, 30), rep(3.98, 30), rep(4.12, 30))
long <- c(rep(-52.68, 30), rep(-53.12, 30), rep(-53.29, 30))
coord <- cbind(long, lat)
## Not run: AGB <- computeAGB(D, WD, coord = coord)
```

---

correctTaxo

*Checking typos in names*

---

## Description

This function corrects typos for a given taxonomic name using the Taxonomic Name Resolution Service (TNRS) via the Taxosaurus interface. This function has been adapted from the `tnrs` function from the `taxize` package ([tnrs](#)).

## Usage

```
correctTaxo(genus, species, score = 0.5)
```

## Arguments

<code>genus</code>	Vector of genus to be checked.
<code>species</code>	Vector of species to be checked (same size as the genus vector).
<code>score</code>	Score of the matching (see <a href="http://tnrs.iplantcollaborative.org/instructions.html#match">http://tnrs.iplantcollaborative.org/instructions.html#match</a> ).



**Value**

The function returns a dataframe with the corrected (or not) genera and species.

**Author(s)**

Ariane TANGUY, Maxime REJOU-MECHAIN

**References**

Boyle, B. et al. (2013). *The taxonomic name resolution service: An online tool for automated standardization of plant names*. BMC bioinformatics, 14, 1.

Chamberlain, S. A. and Szocs, E. (2013). *taxize: taxonomic search and retrieval in R*. F1000Research, 2.

**Examples**

```
## Not run: correctTaxo(genus = "Astrocarium standleanum")
```

---

getTaxonomy	<i>Retrieving the taxonomy</i>
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---

**Description**

From a genus, the function getTaxonomy finds the APG III family, and optionally the order, from the Genus Family database (see [genusFamily](#)) and the APGIII dataset (see [apgFamilies](#))

**Usage**

```
getTaxonomy(genus, findOrder = FALSE)
```

**Arguments**

genus	Vector of genus names
findOrder	Boolean. If TRUE, the output will contain the taxonomical orders of the families.

**Value**

Data frame with the order (if findOrder is TRUE), family and genus.

**Author(s)**

Ariane TANGUY, Maxime REJOU-MECHAIN

**Examples**

```
# Find the Family of the Aphelandra genus
getTaxonomy("Aphelandra")
# ... and the order
getTaxonomy("Aphelandra", findOrder = TRUE)
```

---

getWoodDensity	<i>Estimating wood density</i>
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### Description

The function estimates the wood density (WD) of the trees from their taxonomy or from their congeners using the global wood density database (Chave et al. 2009, Zanne et al. 2009) or any additional dataset. The WD can either be attributed to an individual at a species, genus, family or stand level.

### Usage

```
getWoodDensity(genus, species, stand = NULL, family = NULL, region = "World",
addWoodDensityData = NULL)
```

### Arguments

genus	Vector of genus names
species	Vector of species names
stand	(optional) Vector with the corresponding stands of your data. If set, the missing wood densities at the genus level will be attributed at stand level. If not, the value attributed will be the mean of the whole tree dataset.
family	(optional) Vector of families. If set, the missing wood densities at the genus level will be attributed at family level if available.
region	Region of interest of your sample. By default, Region is set to 'World', but you can restrict the WD estimates to a single region : <ul style="list-style-type: none"> <li>• AfricaExtraTrop: Africa (extra tropical)</li> <li>• AfricaTrop: Africa (tropical)</li> <li>• Australia: Australia</li> <li>• AustraliaTrop: Australia (tropical)</li> <li>• CentralAmericaTrop: Central America (tropical)</li> <li>• China: China</li> <li>• Europe: Europe</li> <li>• India: India</li> <li>• Madagascar: Madagascar</li> <li>• Mexico: Mexico</li> <li>• NorthAmerica: North America</li> <li>• Oceania: Oceania</li> <li>• SouthEastAsia: South-East Asia</li> <li>• SouthEastAsiaTrop: South-East Asia (tropical)</li> <li>• SouthAmericaExtraTrop: South America (extra tropical)</li> <li>• SouthAmericaTrop: South America (tropical)</li> <li>• World: World</li> </ul>

**addWoodDensityData**

A dataframe containing additional wood density data to be combined with the global wood density database. The dataframe should be organized in a dataframe with four columns: "family", "genus", "species", "wd" (column order and names should be respected).

**Details**

The function assigns to each taxon a species- or genus- level average if at least one wood density value at the genus level is available for that taxon in the reference database. If not, the mean wood density of the family (if set) or of the stand (if set) is given.

The function also provides an estimate of the error associated with the wood density estimate (i.e. a standard deviation): a mean standard deviation value is given to the tree at the appropriate taxonomic level using the `sd_10` dataset (see [sd\\_10](#)).

**Value**

Returns a dataframe containing the following information:

family	(if set) Family
genus	Genus
species	Species
meanWD	Mean wood density
sdWD	Standard deviation of the wood density that can be used in error propagation (see <a href="#">sd_10</a> and <a href="#">AGBmonteCarlo</a> )
levelWD	Level at which wood density has been calculated. Can be species, genus, family, Dataset (mean of the entire dataset) or, if stand is set, the name of the stand (mean of the current stand)
nInd	Number of individuals taken into account to compute the mean wood density

**Author(s)**

Maxime REJOU-MECHAIN, Ariane TANGUY

**References**

Chave, Jerome, et al. *Towards a worldwide wood economics spectrum*. Ecology letters 12.4 (2009): 351-366.

Zanne, A. E., et al. *Global wood density database*. Dryad. Identifier: <http://hdl.handle.net/10255/dryad.235> (2009).

**See Also**

[wdData](#), [sd\\_10](#)

## Examples

```
# Load a data set
data(KarnatakaForest)

# Compute the Wood Density up to the genus level and give the mean wood density of the dataset
WD <- getWoodDensity(genus = KarnatakaForest$genus,
species = KarnatakaForest$species)

# Compute the Wood Density up to the genus level and then give the mean wood density per stand
WD <- getWoodDensity(genus = KarnatakaForest$genus,
species = KarnatakaForest$species,
stand = KarnatakaForest$plotId)

# Compute the Wood Density up to the family level and then give the mean wood density per stand
WD <- getWoodDensity(family = KarnatakaForest$family,
genus = KarnatakaForest$genus,
species = KarnatakaForest$species,
stand = KarnatakaForest$plotId)
str(WD)
```

---

KarnatakaForest	<i>Karnataka forest dataset</i>
-----------------	---------------------------------

---

## Description

Dataset from 96 forest plots (1 ha) established in the central Western Ghats of India by Ramesh et al. (2010).

## Usage

```
data("KarnatakaForest")
```

## Format

A data frame with 65965 observations on the following 8 variables :

plotId Names of the plots  
treeId Tree Id, contains a letter (A, B, C...) when an individual has multiple stems  
family Family  
genus Genus  
species Species  
D Diameter  
lat Latitude  
long Longitude

## References

Ramesh, B. R. et al. (2010). *Forest stand structure and composition in 96 sites along environmental gradients in the central Western Ghats of India* Ecological Archives E091-216. Ecology, 91(10), 3118-3118.

## Examples

```
data(KarnatakaForest)
str(KarnatakaForest)
```

---

modelHD	<i>Fitting height-diameter model</i>
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---

## Description

This function fits and compares (optional) height-diameter models.

## Usage

```
modelHD(D, H, method = NULL, useWeight = FALSE, drawGraph = FALSE)
```

## Arguments

D	Vector with diameter measurements (in cm). NA values are accepted but a minimum of 10 valid entries (i.e. having a corresponding height in H) is required.
H	Vector with total height measurements (in m). NA values are accepted but a minimum of 10 valid entries (i.e. having a corresponding diameter in D) is required.
method	Method used to fit the relationship. To be chosen between: <ul style="list-style-type: none"> <li>• log1, log2, log3 <ul style="list-style-type: none"> <li>– log 1: <math>(\log(H) = a + b * \log(D))</math> (equivalent to a power model)</li> <li>– log 2: <math>(\log(H) = a + b * \log(D) + c * \log(D)^2)</math></li> <li>– log 3: <math>(\log(H) = a + b * \log(D) + c * \log(D)^2 + d * \log(D)^3)</math></li> </ul> </li> <li>• weibull: <math>H = a * (1 - \exp(-(D/b)^c))</math></li> <li>• michaelis: <math>H = (A * D)/(B + D)</math></li> </ul> If NULL, all the methods will be compared.
useWeight	If weight is TRUE, model weights will be $(D^2) * H$ (i.e. weights are proportional to tree volume, so that larger trees have a stronger influence during the construction of the model).
drawGraph	If TRUE, a graphic will illustrate the relationship between H and D.

## Details

All the back transformations in loglog are done using the Baskerville correction  $(0.5 * RSE^2)$ , where RSE is the Residual Standard Error).

**Value**

Returns a list with:

input	list of the data used to construct the model (list(H, D))
model	outputs of the model (same outputs as given by <a href="#">lm</a> , <a href="#">nls</a> )
RSE	Residual Standard Error of the model
RSElog	Residual Standard Error of the log model (NULL if other model)
residuals	Residuals of the model
coefficients	Coefficients of the model
R.squared	$R^2$ of the model
formula	Formula of the model
method	Name of the method used to construct the model
predicted	Predicted height values

**Author(s)**

Maxime REJOU-MECHAIN, Ariane TANGUY

**See Also**

[retrieveH](#), [predictHeight](#)

**Examples**

```
# Load a data set
data(NouraguesHD)

# To model the height from a dataset
## Not run: HDmodel <- modelHD(D = NouraguesHD$D, H = NouraguesHD$H, drawGraph = TRUE)

# If the method needed is known
HDmodel <- modelHD(D = NouraguesHD$D, H = NouraguesHD$H, method = "weibull", drawGraph = TRUE)
HDmodel <- modelHD(D = NouraguesHD$D, H = NouraguesHD$H, method = "log1", drawGraph = TRUE)

# Using weights
HDmodel <- modelHD(D = NouraguesHD$D, H = NouraguesHD$H, method = "weibull", useWeight = TRUE,
drawGraph = TRUE)
```

---

NouraguesHD	<i>Height-Diameter data</i>
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---

**Description**

Dataset from two 1-ha plots from the Nouragues forest (French Guiana)

**Usage**

```
data("NouraguesHD")
```

**Format**

A data frame with 1033 observations on the following 3 variables :

plotId Names of the plots

D Diameter

H Height

**Examples**

```
data(NouraguesHD)
str(NouraguesHD)
```

---

retrieveH	<i>Retrieving tree height from models</i>
-----------	---

---

**Description**

From the diameter and either i) a model, ii) the coordinates of the plot or iii) the region, this function gives an estimation of the total tree height.

**Usage**

```
retrieveH(D, model = NULL, coord = NULL, region = NULL)
```

**Arguments**

D	Vector of diameters.
model	A model output by the function <a href="#">modelHD</a> .
coord	Coordinates of the site(s), either a vector (e.g. c(longitude, latitude)) or a matrix/dataframe with two columns (e.g. cbind(longitude, latitude)).
region	Area of your dataset to estimate tree height thanks to Weibull-H region-, continent-specific and pantropical models proposed by Feldpausch et al. (2012). To be chosen between:

- Africa: Africa
- CAfrica: Central Africa
- EAfrica: Eastern Africa
- WAfrica: Western Africa
- SAmerica: Southern America
- BrazilianShield: Brazilian Shield
- ECAmazonia: East-Central Amazonia
- GuianaShield: Guiana Shield
- WAmazonia: Western Amazonia
- SEAsia: South-Eastern Asia
- NAustralia: Northern Australia
- Pantropical: Pantropical

### Value

Returns a list with:

H	H predicted by the model
RSE	Residual Standard Error of the model

### Author(s)

Ariane TANGUY, Maxime REJOU-MECHAIN

### References

Feldpausch et al. *Tree height integrated into pantropical forest biomass estimates*. Biogeosciences (2012): 3381-3403.

Chave et al. *Improved allometric models to estimate the above-ground biomass of tropical trees*. Global change biology 20.10 (2014): 3177-3190.

### See Also

[modelHD](#)

### Examples

```
# Load a database
data(NouraguesHD)
model <- modelHD(D = NouraguesHD$D, H = NouraguesHD$H, method = "log2")

# If any height model is available
H <- retrieveH(D = NouraguesHD$D, model = model)

# If the only data available are the coordinates of your spot
lat <- 4.08
long <- -52.68
coord <- cbind(long, lat)
## Not run: H <- retrieveH(D = NouraguesHD$D, coord = coord)
```



```
# If the only data available is the region of your spot  
H <- retrieveH(D = NouraguesHD$D, region = "GuianaShield")
```

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