

# Package ‘sitreeE’

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**Title** Sitree Extensions

**Author** Clara Anton Fernandez [aut, cre]

**Maintainer** Clara Anton Fernandez <caf@nibio.no>

**Depends** R (>= 3.1.0)

**Imports** data.table, sitree

**Description** Provides extensions for package 'sitree' for allometric variables, growth, mortality, recruitment, management, tree removal and external modifiers functions.

**License** GPL (>= 2)

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**LazyLoad** yes

**NeedsCompilation** no

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 AM2016ClimateSensitiveSINorway

*Climate-sensitive site index models for Norway*


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### Description

Implementation of models for climate-sensitive site index models for Norway as described in Antón-Fernández et al. (2016).

### Usage

```
AM2016ClimateSensitiveSINorway(soilquality, t.early.summer, waterbal, SI.spp)
```

### Arguments

soilquality	A factor with levels 1 to 5 indicating the soilquality category. 1 being the poorest soils and 5 the best soils
t.early.summer	A vector with sum temperatures (in C) in spring and early summer (april, june and july)
waterbal	A vector with the montly moisture surplus in June (difference between the 30-year mean precipitation in June and mean potential evapotranspiration in June.).
SI.spp	SI species, that is, the species for which SI should be calculated. 1 = spruce, 2 = pine, 3 = birch.

### Value

Returns a vector with the estimated SI.

### Author(s)

Clara Anton-Fernandez

### References

Anton-Fernandez, Clara, Blas Mola-Yudego, Lise Dalsgaard, and Rasmus Astrup. 2016. "Climate-Sensitive Site Index Models for Norway." *Canadian Journal of Forest Research* 46 (6)

### Examples

```
AM2016ClimateSensitiveSINorway (soilquality = as.factor(c(1,2,3,4)),
                                t.early.summer = c(10,20,30,10),
                                waterbal = c(-40, 20,10,10),
                                SI.spp = c(1,2,2,3))
```

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biomass.birch.M1988    *Marklund's biomass equations*

---

## Description

Implements Marklund's (1988) biomass equations for above-ground biomass and Petersson and Ståhl (2006) for below-ground biomass.

## Usage

```
biomass.spruce.M1988(dbh.cm, H.m)
biomass.pine.M1988(dbh.cm, H.m)
biomass.birch.M1988(dbh.cm, H.m)
```

## Arguments

dbh.cm	A vector with the dbh (diameter at breast height) of the trees, in cm.
H.m	A vector with the heights of the trees, in meters.

## Value

It returns a data.frame with the following biomass components in kg: living.branches, dead.branches, stem.wood, stump.roots, bark, usoil, rot1, rot2, and foliage.

## Author(s)

Clara Anton Fernandez <caf@nibio.no>

## References

Marklund, L. G. 1988. "Biomassfunktioner för tall, gran och björk i Sverige [Biomass functions for pine, spruce and birch in Sweden]." Report 45. Umeå, Sweden: Swedish University of Agricultural Sciences. Department of Forest Survey. Petersson, Hans, and Göran Ståhl. 2006. "Functions for Below-Ground Biomass of Pinus Sylvestris, Picea Abies, Betula Pendula and Betula Pubescens in Sweden." Scandinavian Journal of Forest Research 21 (S7): 84–93.

## Examples

```
biomass.spruce.M1988(dbh.cm = c(10, 20), H.m = c(8, 12))
```

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biomass.birch.S2014    *Implements biomass functions for birch for Norway from Smith et al (2014, 2016)*

---

### Description

Implements biomass functions for birch for Norway from Smith et al (2014, 2016). Total biomass aboveground does include stump calculated using biomass.birch.M1988. Total biomass belowground does not include stump.

### Usage

```
biomass.birch.S2014(dbh.cm, H.m)
```

### Arguments

dbh.cm

H.m

### Details

It uses stump.roots from biomass.birch.M1988 to calculate aboveground biomass (in kg) and belowground biomass (in kg). Aboveground biomass is calculated as Smith's aboveground biomass (2014) + stump.roots. Belowground biomass is calculated as Smith's belowground biomass (2016) - stump.roots.

### Value

Returns a data.frame with the following biomass components: biomass.total.kg, biomass.aboveground.kg.S2014, biomass.belowground.kg.S2014, biomass.belowground.kg, biomass.aboveground.kg, living.branches, dead.branches, stem.wood, stump.roots, bark, usoil, rot1, rot2, foliage)

### Author(s)

Clara Anton Fernandez (caf@nibio.no)

### References

Smith, Aaron, Aksel Granhus, and Rasmus Astrup. 2016. "Functions for Estimating Belowground and Whole Tree Biomass of Birch in Norway." *Scandinavian Journal of Forest Research* 31 (6): 568–82. Smith, Aaron, Aksel Granhus, Rasmus Astrup, Ole Martin Bollandsås, and Hans Petersson. 2014. "Functions for Estimating Aboveground Biomass of Birch in Norway." *Scandinavian Journal of Forest Research* 29 (6): 565–78.

### See Also

[biomass.birch.M1988](#)

## Examples

```
biomass.birch.S2014(dbh.cm = c(10, 20), H.m = c(12, 16))
```

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biomass.norway.sitree *Calculates biomass for trees using the Norwegian biomass equations*

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## Description

Calculates biomass

## Usage

```
biomass.norway.sitree(dbh.mm, height.dm, tree.sp)
```

## Arguments

dbh.mm	Diameter at breast height in mm.
height.dm	Tree height in dm.
tree.sp	Tree species according to the Norwegian NFI. It will use <a href="#">biomass.spruce.M1988</a> when tree.sp is 1, 2, 3, 21, or 29, <a href="#">biomass.pine.M1988</a> when tree.sp is 10, 11, or 20, and <a href="#">biomass.birch.S2014</a> otherwise.

## Value

Returns a data.table containing the 12 columns resulting from applying the biomass functions.

## See Also

[biomass.birch.S2014](#), [biomass.pine.M1988](#), [biomass.spruce.M1988](#)

## Examples

```
bio.nor <- biomass.norway.sitree (dbh.mm = c(50, 60, 100 ), height.dm = c(40, 60,  
80),  
tree.sp = c(1, 10, 30))
```

---

biomass.sitree	<i>Biomass for live, dead, or removed trees using Norwegian biomass functions</i>
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### Description

Calculates biomass for trees using the Norwegian biomass equations.

### Usage

```
biomass.sitree(tr, plot.data)
```

### Arguments

tr	A trList or trListDead object.
plot.data	A data.frame or list with plot information. It should have at least plot.id and tree2ha.

### Value

Returns a data.table containing the 12 columns resulting from applying the biomass functions.

### Author(s)

Clara Anton Fernandez <caf@nibio.no>

### See Also

[biomass.birch.S2014](#), [biomass.birch.M1988](#), [biomass.pine.M1988](#), [biomass.spruce.M1988](#), [biomass.norway.sitree](#)

### Examples

```
##---- Should be DIRECTLY executable !! ----
##-- ==> Define data, use random,
##--or do help(data=index) for the standard data sets.
library(sitree)
## result.sitree <- sitree (tree.df = stand.west.tr,
##                          stand.df = stand.west.st,
##                          functions = list(
##                            fn.growth = 'grow.dbhinc.hgtinc',
##                            fn.mort = 'mort.B2007',
##                            fn.recr = 'recr.BBG2008',
##                            fn.management = NULL,
##                            fn.tree.removal = NULL,
##                            fn.modif = NULL,
##                            fn.prep.common.vars = 'prep.common.vars.fun'
##                          ),
##                          n.periods = 20,
```

```
##           period.length = 5,  
##           mng.options = NA,  
##           print.comments = FALSE,  
##           fn.dbh.inc = "dbh.BN2009",  
##           fn.hgt.inc = "height.korf"  
##         )  
## ## The function is currently defined as  
## biom <- biomass.sitree(tr = result.sitree$live, plot.data = result.sitree$plot.data)  
## biom
```

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height.of.X.tallest.trees

*Mean height of X tallest trees*

---

### Description

It calculates the mean height of the X tallest trees by grouping variable (e.g. the plot ID)

### Usage

```
height.of.X.tallest.trees(height, uplotID, num.trees)
```

### Arguments

height	A vector with heights
uplotID	A vector with the grouping variable, most often this would be the plot ID.
num.trees	Number of trees used to calculate the mean height.

### Value

It returns a data.frame with two columns containing the uplotID and the mean height of the X tallest trees.

### Note

This function can be used to calculate the average of the X largest values of any variable grouped by a grouping variable. It is mostly a wrapper for aggregate.

### Author(s)

Clara Antón Fernández (caf@nibio.no)

### See Also

[lore.height](#)

**Examples**

```
library(sitree)
height.of.X.tallest.trees(height = tr$height,
                           uplotID = tr$plot.id, 5)
```

---

lorey.height	<i>Lorey's height</i>
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**Description**

Calculates Lorey's height (mean height weighted by basal area). If group.id is not NULL, it will calculate Lorey's height for each group.

**Usage**

```
lorey.height(BA, height, group.id = NULL)
```

**Arguments**

BA	A vector with the basal areas of the trees
height	A vector with the height of the trees
group.id	An optional vector with a grouping variable.

**Value**

If a grouping variable is provided it returns a data frame with two columns (group.id, and lorey.height).  
If a grouping variable is not provided it will return the Lorey's height.

**Author(s)**

Clara Anton Fernandez (caf@nibio.no)

**See Also**

[height.of.X.tallest.trees](#)

**Examples**

```
library(sitree)
BA <- pi*(tr$dbh/2)^2
lorey.height(BA, tr$height)
lorey.height(BA, tr$height, tr$plot.id)
```



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PBAL	<i>Basal area of larger trees</i>
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**Description**

It calculates the basal area of larger trees for a plot.

**Usage**

PBAL(BA)

**Arguments**

BA	A vector of trees basal area
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**Value**

It returns a vector with the sum of the basal areas of larger trees. Trees with similar BA are not considered larger.

**Examples**

PBAL(c(1, 2, 3, 4, 4))

---

PBAL.dbh.greater	<i>Basal area of larger trees which are at least X cm larger than the tree of interest</i>
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**Description**

Calculates the basal area (in cm<sup>2</sup> if dbh is in mm) of trees that are at least X (in the same units as dbh) larger than the tree of interest for a list of trees.

**Usage**

PBAL.dbh.greater(dbh.mm, dbh.mm.diff)

**Arguments**

dbh.mm	a vector of dbh in mm
dbh.mm.diff	minimum dbh difference between the tree and the tree of interest to be considered

**Details**

It estimates the basal area (in cm<sup>2</sup>) of trees that are at least dbh.mm.diff mm larger than the tree of interest.

**Value**

It returns a list with the basal area of larger trees.

**Author(s)**

Cara Antón-Fernández (email: caf@nibio.no)

**See Also**

[PBAL](#)

**Examples**

```
library(sitree)
PBAL.dbh.greater(c(100,89,51,74,4), 3)

aggregate(dbh ~ plot.id, data = tr, FUN = PBAL.dbh.greater, dbh.mm.diff = 2)
```

---

PlotDataToLong	<i>Convert Plot data to a data.frame/data.table format</i>
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**Description**

It attempts to convert the plot level information to a data.frame/data.list format. For example, if management is an element of the plot list (pd) it will melt it to a long format.

**Usage**

```
PlotDataToLong(pd)
```

**Arguments**

pd	A list with plot information. It specifically looks for two elements 'stand.age.years' and 'management'.
----	--

**Value**

It returns a data.table with all vector from pd as columns, and dataframes melted.

**Examples**

```
library(sitree)

##result.sitree <- sitree (tree.df = tr,stand.df = fl,
## functions = list(fn.growth = 'grow.dbhinc.hgtinc',
## fn.mort = 'mort.B2007',
## fn.recr = 'recr.BBG2008',
## fn.management = 'management.prob',
```

```

## fn.tree.removal = 'mng.tree.removal',
## fn.modif       = NULL,
## fn.prep.common.vars = 'prep.common.vars.fun'),
## n.periods = 5,
## period.length = 5,mng.options = NA,
## print.comments = FALSE,
## fn.dbh.inc = "dbh.BN2009",
## fn.hgt.inc = "height.korf",
## species.spruce = c(1, 2, 3),
## species.pine = c(10, 11, 20, 21, 29),species.harw = c(30, 31),
## fun.final.felling = "harv.prob",
## fun.thinning     = "thin.prob",per.vol.harv = 0.83)

## PlotDataToLong(result.sitree$plot.data)

```

---

top.height

*Top height of the n thickest trees*


---

### Description

Average height of the n thickest trees per ha

### Usage

```
top.height(thickness, height, num.trees.per.ha, plot.id, plot.size.m2)
```

### Arguments

thickness	A vector with the thickness for every tree. Other variables can be used instead to thickness. This is only used to order the trees.
height	Height of the trees.
num.trees.per.ha	Number of trees per ha that the top height should correspond to. E.g. 100 trees per ha.
plot.id	Vector with the plot.id to which every tree corresponds to.
plot.size.m2	Plot size in square meters. It can be either a single number if all plots have the same size of a vector of equal length as thickness, height, and plot.id with the corresponding plot size for each tree.

### Details

thickness, height, and plot.id should have the same length, that is, one value per tree.

### Value

It returns a data.frame with two columns: top.heights in the same units as height, and plot.id.

**Examples**

```
top.height(thickness = runif(100, 10,40), height = runif(100, 12, 45),
  num.trees.per.ha = 100, plot.id = 1, plot.size.m2 = 250)
```

---

tree.age	<i>EStimation of individual tree age</i>
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**Description**

Estimates individual tree age of trees within a plot based on basal area, site index, species, and development class.

**Usage**

```
tree.age(stand.age.years, plot.id, tree.BA.m2, dbh.mm,
  SI.spp, SI.m, spp, dev.class, apply.correction = TRUE)
```

**Arguments**

stand.age.years	The age of the stand in years.
plot.id	The unique ID of the stand
tree.BA.m2	A vector with the basal areas of each tree in m2.
dbh.mm	A vector with the DBH in mm of each tree.
SI.spp	Species for which SI has been calculated (1, 2, 3).
SI.m	Site index (SI) in m.
spp	Species group classification.
dev.class	Development class.
apply.correction	TRUE/FALSE. If a correction to age should be applied

**Value**

A vector with the estimated ages of trees

**Author(s)**

Clara Anton Fernandez <caf@nibio.no>

**Examples**

```
tree.age(stand.age.years = 40,
  plot.id = c(1,1), tree.BA.m2 = c(0.05, 0.5), dbh.mm
  = c(50,150), SI.spp = 2,
  SI.m = 11, spp = c(1,1), dev.class = 3, apply.correction = TRUE)
```

---

volume.sitree	<i>Volume for sitree output for Norwegian conditions</i>
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---

## Description

It calculates volume following the Norwegian national forest inventory equations for a `trList` or `trListDead` object

## Usage

```
volume.sitree(tr, plot.data)
```

## Arguments

<code>tr</code>	a <code>trListDead</code> or <code>trList</code> object
<code>plot.data</code>	a list or <code>data.frame</code> containing at least a 'kom' and 'tree2ha' column/element. kom is the kommune (municipality) code, and tree2ha should be the expansion factor to go from tree to per ha basis.

## Details

It uses the `volume.norway` function to estimate the volume for all trees with `dbh.mm` greater than 0. It returns NA when `dbh.mm` is 0 or lower. `tree2ha` is included to facilitate the calculation of per ha values.

## Value

It returns a `data.table` with columns for `treeid`, `plot.id`, `dbh.mm`, `height.dm`, `kom`, `tree2ha`, `tree.sp`, `vol.w.tr.m3` (volume with bark in m3 per tree), and `vol.wo.tr.m3` (volume without bark in m3 per tree)

## Author(s)

Clara Anton Fernandez

## Examples

```
library(sitree)
#res <- sitree (tree.df = tr,
#              stand.df = fl,
#              functions = list(
#                fn.growth = 'grow.dbhinc.hgtinc',
#                fn.mort = 'mort.B2007',
#                fn.recr = 'recr.BBG2008',
##                fn.management = 'management.prob',
##                fn.tree.removal = 'mng.tree.removal',
##                fn.modif = NULL,
##                fn.prep.common.vars = 'prep.common.vars.fun'
```

```
##           ),
##           n.periods = 5,
##           period.length = 5,
##           mng.options = NA,
##           print.comments = FALSE,
##           fn.dbh.inc = "dbh.BN2009",
##           fn.hgt.inc = "height.korf",
##           species.spruce = c(1, 2, 3),
##           species.pine = c(10, 11, 20, 21, 29),
##           species.harw = c(30, 31),
##           fun.final.felling = "harv.prob",
##           fun.thinning      = "thin.prob",
##           per.vol.harv = 0.83
##         )
## volume.sitree(tr = res$live, plot.data = res$plot.data)
```

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