

Package: sitreeE (via r-universe)

May 14, 2026

Version 0.0-10

Date 2026-01-14

Title Sitree Extensions

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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)

Encoding UTF-8

LazyLoad yes

NeedsCompilation no

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Repository <https://inasevmon.r-universe.dev>

Date/Publication 2026-01-14 10:30:02 UTC

RemoteUrl <https://github.com/cran/sitreeE>

RemoteRef HEAD

RemoteSha dccdbe61d064f2525759d100268df77a81d7c599

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AM2016ClimateSensitiveSINorway

Climate-sensitive site index models for Norway

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). doi: 10.1139/cjfr-2015-0155

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))
```

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))
```

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	dbh (diameter at breast height) in cm.
H.m	Tree height in meters.

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. <https://doi.org/10.1080/02827581.2016.1141232> 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. <http://dx.doi.org/10.1080/02827581.2014.951389>

See Also

[biomass.birch.M1988](#)

Examples

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

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

Description

Calculates biomass for trees using the Norwegian biomass equations.

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 biomass.spruce.M1988 when tree.sp is 1, 2, 3, 21, or 29, biomass.pine.M1988 when tree.sp is 10, 11, or 20, and biomass.birch.S2014 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

```
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"
    )

    biom <- biomass.sitree(tr = result.sitree$live, plot.data = result.sitree$plot.data)
```

`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

<code>height</code>	A vector with heights
<code>uplotID</code>	A vector with the grouping variable, most often this would be the plot ID.
<code>num.trees</code>	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

[lorey.height](#)

Examples

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

lorey.height	<i>Lorey's height</i>
--------------	-----------------------

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)
```

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 tree's basal area.

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>
------------------	--

Description

Calculates the basal area (in cm² 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 cm²) of trees that are at least dbh.mm.diff mm larger than the tree of interest.


```

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	<i>Top height of the n thickest trees</i>
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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 or 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

tr	a trListDead or trList object
plot.data	a list or data.frame 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 Antón-Fernández (email: caf@nibio.no)

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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