Package: PEcAn.allometry (via r-universe)

September 18, 2024

Type Package

Title PEcAn Allometry Functions

Version 1.7.3.9000

Description Synthesize allometric equations or fit allometries to data.

Imports coda (>= 0.18), grDevices, graphics, methods, stats, utils, MCMCpack, mvtnorm, tools, PEcAn.DB

Suggests knitr (>= 1.42), markdown, rmarkdown (>= 2.19), testthat (>= 1.0.2), withr

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LazyLoad yes

LazyData FALSE

Encoding UTF-8

RoxygenNote 7.3.2

VignetteBuilder knitr

Repository https://pecanproject.r-universe.dev

RemoteUrl https://github.com/PecanProject/pecan

RemoteRef HEAD

RemoteSha f22a7c4bbc532e4551f7bc9624cef649da317ac1

Contents

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 allom.BayesFit *allom.BayesFit*

Description

Module to fit a common power-law allometric model to a mixture of raw data and allometric equations in a Heirarchical Bayes framework with multiple imputation of the allometric data

Usage

```
allom.BayesFit(allom, nrep = 10000, form = "power", dmin = 0.1, dmax = 500)
```

Arguments

allom   - object (usually generated by query.allom.data) which needs to be a list with two entries: 'field' - contains a list, each entry for which is a data frame with 'x' and 'y'. Can be NULL 'parm' - a single data frame with the following components:

    n sample size

    a eqn coefficient

    b eqn coefficient

    c eqn coefficient

    d eqn coefficient

    e eqn coefficient

    se standard error

    eqn sample size

    Xmin smallest tree sampled (cm)

    Xmax largest tree sampled (cm)

    Xcor units correction on X

    Ycor units correction on Y

    Xtype type of measurement on the X

    spp - USFS species code

nrep   - number of MCMC replicates

form   functional form of the allometry: 'power' vs 'exp'

dmin   minimum dbh of interest

dmax   maximum dbh of interest

Details

dependencies: requires MCMCpack and mvtnorm

note: runs 1 chain, but multiple chains can be simulated by multiple function calls

Value

returns MCMC chain and ONE instance of 'data' note: in many cases the estimates are multiply imputed

Author(s)

Michael Dietze

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allom.predict *allom.predict*

Description

Function for making tree-level Monte Carlo predictions from allometric equations estimated from the PEcAn allometry module

Usage

```
allom.predict(
  object,
  dbh,
  pft = NULL,
  component = NULL,
  n = NULL,
  use = "Bg",
  interval = "prediction",
  single.tree = FALSE
)
```

Arguments

object	Allometry model object. Option includes
	'list of mcmc' - mcmc outputs in a list by PFT then component
	'vector of file paths' - path(s) to AllomAve RData files
	'directory where files are located -
dbh	Diameter at Breast Height (cm)
pft	Plant Functional Type. Needs to match the name used in AllomAve. Can be NULL if only one PFT/species exists, otherwise needs to the same length as dbh
component	Which component to predict. Can be NULL if only one component was analysed in AllomAve.
n	Number of Monte Carlo samples. Defaults to the same number as in the MCMC object
use	c('Bg','mu','best')
interval	c('none','confidence','prediction') default is prediction
single.tree	logical: Is this a DBH time series from one individual tree? If TRUE, will use a fixed error for all draws.

Value

matrix of Monte Carlo predictions that has n rows and one column per DBH

Author(s)

Michael Dietze, Christy Rollinson

Examples

```
## Not run:
  object = '~/Dropbox//HF C Synthesis/Allometry Papers & Analysis/'
  dbh = seq(10,50,by=5)
  mass = allom.predict(object,dbh,n=100)


## End(Not run)
```

AllomAve   *AllomAve*

Description

Allometry wrapper function that handles loading and subsetting the data, fitting the Bayesian models, and generating diagnostic figures. Set up to loop over multiple PFTs and components. Writes raw MCMC and PDF of diagnositcs to file and returns table of summary stats.

There are two usages of this function. When running 'online' (connected to the PEcAn database), pass the database connection, con, and the pfts subsection of the PEcAn settings. When running 'stand alone' pass the pft list mapping species to species codes and the file paths to the allometry table and field data (optional)

Usage

```
AllomAve(
  pfts,
  components = 6,
  outdir = NULL,
  con = NULL,
  field = NULL,
 parm = system.file("data/Table3_GTR-NE-319.v2.csv", package = "PEcAn.allometry"),
  ngibbs = 5000,
  nchain = 3,
  dmin = 0.1,
  dmax = 500
)
```

Arguments

`pfts`	pft list from PEcAn settings (if con) OR list of pft spcd's If the latter, the names within the list are used to identify PFTs

> **'acronym'** - USDA species acronyms (see plants.usda.gov), used with FIELD data (vector)
>
> **'spcd'** - USFS species codes, use with PARM data (vector)

`components`	IDs for allometry components from Jenkins et al 2004 Table 5. Default is stem biomass (6). See data(allom.components)
`outdir`	output directory files are written to. Default is getwd()
`con`	database connection
`field`	path(s) to raw data files
`parm`	path to allometry equation file (NULL default loads Jenkins Table 3)
`ngibbs`	number of MCMC iterations (per chain) to run
`nchain`	number of MCMC chains
`dmin`	minimum dbh of interest
`dmax`	maximum dbh of interest

Value

nested list of parameter summary statistics

Author(s)

Michael Dietze

Examples

```
if(FALSE){
  pfts = list(FAGR = data.frame(spcd=531,acronym='FAGR'))
  allom.stats = AllomAve(pfts,ngibbs=500)

  ## example of a PFT with multiple species (late hardwood)
  ## note that if you're just using Jenkins the acronym column is optional
  pfts = list(LH = data.frame(spcd = c(531,318),acronym=c('FAGR','ACSA3')))
}
```

AllomUnitCoef	*AllomUnitCoef*

Description

converts length units FROM cm TO specified units converts mass units TO kg FROM specificed units

Usage

```
AllomUnitCoef(x, tp = NULL)
```

Arguments

x	units: mm, cm, cm2, m, in, g, kg, lb, Mg
tp	diameter type, leave NULL if DBH. Options: 'd.b.h.^2','cbh','crc'

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load.allom	*load.allom*

Description

loads allom files

Usage

```
load.allom(object)
```

Arguments

object	Allometry model object. Option includes

'vector of file paths' - path(s) to AllomAve RData files
'directory where files are located -

Value

mcmc outputs in a list by PFT then component

Author(s)

Michael Dietze

Examples

```
## Not run:
  object = '~/Dropbox//HF C Synthesis/Allometry Papers & Analysis/'
  allom.mcmc = load.allom(object)


## End(Not run)
```

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nu   *nu*

Description

converts factors to numeric

Usage

```
nu(x)
```

Arguments

x   data

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query.allom.data   *query.allom.data*

Description

Module to grab allometric information from the raw data table Will grab both original field data and tallied equations

Usage

```
query.allom.data(pft_name, variable, con, nsim = 10000)
```

Arguments

pft_name   name of Plant Functional Type to be queried

variable   name of response variable

con   open database connection

nsim   number of pseudo-data simulations for estimating SE

Details

Tallied equation format based on Jenkins et al 2004 USFS General Technical Report NE-319 database is assumed to conform to the PEcAn Schema

Author(s)

Michael Dietze

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read.allom.data   *read.allom.data*

Description

Extracts PFT- and component-specific data and allometeric equations from the specified files.

Usage

```
read.allom.data(pft.data, component, field, parm, nsim = 10000)
```

Arguments

pft.data	PFT dataframe
	acronym USDA species acronyms, used with FIELD data (vector)
	spcd USFS species codes, use with TALLY data (vector)
component	allometry ID, Jenkins table 5
field	raw field data
parm	allometry equation file, Jenkins table 3
nsim	number of Monte Carlo draws in numerical transforms

Details

This code also estimates the standard error from R-squared, which is required to simulate pseudo-data from the allometric eqns.

Value

field	PFT-filtered field Data
parm	Component- and PFT-filtered Allometric Equations

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