Package ‘forestHES’

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Title Forest Health Evaluation System at the Forest Stand Level in China
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Description Assessing forest ecosystem health is an effective way for forest resource management. The national forest health evaluation system at the forest stand level using analytic hierarchy process, has a high application value and practical significance. The package can effectively and easily realize the total assessment process, and help foresters to further assess and management forest resources.
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Description

Assessing forest ecosystem health is an effective way for forest resource management. Zhang & Lei (2014) proposed and developed a national forest health evaluation system at the forest stand level using analytic hierarchy process (AHP), has a high application value and practical significance. The R package concentrates on to realize the calculation of the national forest health evaluation system.

Author(s)

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References


Examples

```r
# Forest health evaluation for single sample plot
tree.singlefhes<-fhes(c1=0.67, c2=1.89, c3=2.04, c4=4, c5=2.04, c6=1, c7=0.3, c8=3.4839, c9=0.75, c10=0.15, c11=0, c12=0.75, c13=0.35, c14=2500, c15=53, c16=1.56, c17=5.49, c18=34.03, c19=2.05, c20=21.38, c21=91.67)
tree.singlefhes

# Assigned the threshold of some variables, according to specific realistic condition or research contents

tree.spefhes<-fhes(c1=0.67, c2=1.89, c3=2.04, c4=4, c5=2.04, c6=1, c7=0.3, c8=3.4839, c9=0.75, c10=0.15, c11=0, c12=0.75, c13=0.35, c14=2500, c15=53, c16=1.56, c17=5.49, c18=34.03, c19=2.05, c20=21.38, c21=91.67, L_18=15, U_18=90, L_19=2, U_19=14, L_20=8, U_20=40, L_21=60, U_21=120)
tree.spefhes

# Forest health evaluation for multiple sample plot

tree.multiplefhes<-fhes(c1=c(0.67,0,0,0.68), c2=c(1.89,1.33,1.79), c3=c(2.04,1.91,2.19), c4=c(4,3,4), c5=c(2.04,1.47,2.19), c6=c(1,0,1), c7=c(0.3,0.95,0.9), c8=c(3.4839,3.1579,5.9231), c9=c(0.75,0,0.3), c10=c(0.15,0,0.09)
```
envdata

Survey data of Environmental factors for pine-oak mixed forests

Description

Environmental factors of pine-oak codominant mixed forests in the Qinling Mountains

Usage

data("envdata")

Format

A data frame with 20 observations on the following 16 variables.

plot.id  Identification number of sample plots
Ele  Elevation
SLP  Slope position
Asp  Slope aspect
SLG  Slope gradient
TN  Total nitrogen
TP  Total phosphorus
TK  Total potassium
OM  Organic matter
pH  pH value
AN  Available nitrogen
AP  Available phosphorus
AK  Available potassium
BA  Base area
AD  Average tree DBH
AH  Average tree height
Details

Twenty 20*20 m plots were established for the pine-oak codominant mixed forests within the Qinling National Forest Ecosystem Research Station (Huoditang forest)

References


Examples

data(envdata)
envdata

fhes

The national forest health evaluation system

Description

Zhang & Lei (2014) proposed and developed a national forest health evaluation system at the forest stand level using analytic hierarchy process (AHP), has a high application value and practical significance.

Usage

fhes(c1, c2, c3, c4, c5, c6, c7, c8, c9, c10, c11, c12, c13, c14, c15, c16, c17, c18, c19, c20, c21, L_8 = 3.2, U_8 = 6.4, L_15 = 30, U_15 = 60, L_16 = 0.8, U_16 = 1.3, O1_16 = 1.15, O2_16 = 1.25, L_17 = 5, U_17 = 8.5, O1_17 = 6.5, O2_17 = 7, L_18 = 10, U_18 = 80, L_19 = 1.49, U_19 = 13.19, L_20 = 5, U_20 = 30, L_21 = 80, U_21 = 200)

Arguments

c1 Tree diversity index

c2 Shrub diversity index

c3 Herb diversity index

c4 Storey quantity

c5 Tree size diversity index

c6 Age structure

c7 Canopy closure

c8 Average volume increment per hectare

c9 Bio-disaster ratio
c10  Non bio-disaster ratio

c11  Crown length ratio

c12  Crown fade ratio

c13  Foliage falling ratio

c14  Regeneration density

c15  Soil depth

c16  Soil density

c17  Soil pH

c18  Soil organic matter

c19  Soil total nitrogen

c20  Soil available phosphorus

c21  Soil available potassium

L_8  Lower limit of Average volume increment per hectare
U_8  Upper limit of average volume increment per hectare
L_15 Lower limit of average volume increment per hectare
U_15 Upper limit of average volume increment per hectare
L_16 Lower limit of soil density
U_16 Upper limit of soil density
O1_16 Effective range of soil density
O2_16 Effective range of soil density
L_17 Lower limit of soil pH
U_17 Upper limit of soil pH
O1_17 Effective range of soil pH
O2_17 Effective range of soil pH
L_18 Lower limit of soil organic matter
U_18 Upper limit of soil organic matter
L_19 Lower limit of soil total nitrogen
U_19 Upper limit of soil total nitrogen
L_20 Lower limit of soil available phosphorus
U_20 Upper limit of soil available phosphorus
L_21 Lower limit of soil available potassium
U_21 Upper limit of soil available potassium

Details

None
Value

- indexSystem
- legend
- index
- coverted.Index
- weighted.Index
- unweighted.Criterion
- weighted.Criterion
- evaluation

Note

None

Author(s)

Zongzheng Chai

References


See Also

None

Examples

```r
# forest health evaluation for singel sample plot
tree.singlefhes<-fhes(c1=0.67,c2=1.89,c3=2.04,c4=4,c5=2.04,c6=1,c7=0.3,
c8=3.4839,c9=0.75,c10=0.15,c11=0,c12=0.75,c13=0.35,
c14=2500,c15=53,c16=1.56,c17=34.03,c19=2.05,
c20=21.38,c21=91.67)
tree.singlefhes
```

```
# Assigned the threshold of some variables, according to specific realistic condition or research contents
tree.spefhes<-fhes(c1=0.67,c2=1.89,c3=2.04,c4=4,c5=2.04,c6=1,c7=0.3,
c8=3.4839,c9=0.75,c10=0.15,c11=0,c12=0.75,c13=0.35,
c14=2500,c15=53,c16=1.56,c17=34.03,c19=2.05,
c20=21.38,c21=91.67,
L_18=15,U_18=90,L_19=2,U_19=14,
L_20=8,U_20=40,L_21=60,U_21=120)
```
herbdata

Survey data of undergrowth herb cluster for pine-oak mixed forests

Description

Undergrowth herb data of pine-oak codominant mixed forests in the Qinling Mountains

Usage

data("herbdata")

Format

A data frame with 229 observations on the following 4 variables.

- plot.id  Identification number of sample plots
- spe.id  Identification number of tree species
- coverage  Coverage of herb species
- abundance  Abundance of herb species

Details

Twenty 20*20 m plots were established for the pine–oak codominant mixed forests within the Qinling National Forest Ecosystem Research Station (Huoditang forest)
References


Examples

data(herbdata)
herbdata

indexSystem | The national forest health evaluation system

Description

The national forest health evaluation system

Usage

data("indexSystem")

Format

A data frame with 21 observations on the following 9 variables.

Criterion | a factor with levels b1 b2 b3 b4 b5 b6 b7
WeightB | a numeric vector
Index | a factor with levels c1 c10 c11 c12 c13 c14 c15* c16* c17* c18* c19* c2 c20* c21* c3 c4 c5 c6 c7 c8* c9
WeightC | a numeric vector
Mode | a factor with levels down mid up
L | a numeric vector
U | a numeric vector
O1 | a numeric vector
O2 | a numeric vector

Details

ID see legend

Source

longtowide

References


Examples

data(indexSystem)

longtowide

A R function for converting to long data to wide data

Description

Converting regular survey data (long data, similar to the treedata and herbdata in the package) to species matrix, and attributes matrix (wide data).

Usage

longtowide(longdata, left, up, inner = NULL, fun = rep("sum", length(inner)), freq = FALSE)

Arguments

longdata
Regular survey data (long data, similar to the treedata and herbdata in the package)
left
Row names of matrix data after converted
up
Column names of matrix data after converted
inner
Attributes data need to converted
fun
Functions need to applied in the converting process
freq
Frequency of attributes

Value

Wide data, such species matrix, and attributes matrix, etc.

Author(s)

Zongzheng Chai
Examples

####Example####

Following two example data with different subject, pineoakTree and herb data is for the base data of individual trees, and the herb data is for the base data of cluster.

data(treedata)
data(herbdata)

####Merge a species matrix from base data

Note: following calculation only for the base data of individual not cluster

```
pineoak$spematrix<-longtowide(longdata=treedata,left="plot.id",up="spe.id")
pineoak$spematrix
```

```
treedata$abundance<-1
head(treedata)
tree$spematrix<-longtowide(longdata=treedata,left="plot.id",up="spe.id",inner="abundance")
tree$spematrix
herb$spematrix<-longtowide(longdata=herbdata,left="plot.id",up="spe.id",inner="abundance")
herb$spematrix
```

####Compute the frequency of species in the multiple plots

```
tree$freq<-longtowide(longdata=treedata,left="plot.id",up="spe.id",freq=TRUE)
tree$freq
herb$freq<-longtowide(longdata=herbdata,left="plot.id",up="spe.id",freq=TRUE)
herb$freq
```

####Compute the attribute matrix from base data

```
tree$dbh<-longtowide(longdata=treedata,left="plot.id",up="spe.id",inner="dbh.cm")
tree$dbh
herb$cover<-longtowide(longdata=herbdata,left="plot.id",up="spe.id",inner="coverage")
herb$cover
```

```
tree$multattr<-longtowide(longdata=treedata,left="plot.id",up="spe.id",inner=c("dbh.cm","ht.m"))
tree$multattr
herb$multattr<-longtowide(longdata=herbdata,left="plot.id",up="spe.id",inner=c("coverage","abundance"))
herb$multattr
```

####Calculation of Importance value (IV) for species####

```
tree$freq<-longtowide(longdata=treedata,left="plot.id",up="spe.id",freq=TRUE)$frequency
treedata$base<-pi*(treedata$dbh.cm)^2/10000
tree$dominance<-longtowide(longdata=treedata,left="plot.id",up="spe.id",inner="base")/(20*400)
```

```
tree$refreq<-tree$freq/rowSums(tree.freq)*100
```
mcIntosh

Calculation of mcIntosh diversity index

Description
Calculation of mcIntosh diversity index

Usage
mcIntosh(x, MARGIN = 1)

Arguments
x The species matrix
MARGIN Compute the mcIntosh diversity index by row, MARGIN can be set 1; compute the mcIntosh diversity index by column, MARGIN can be set 2;

Value
The mcIntosh diversity index
Author(s)
Zongzheng Chai

References

Examples
There are three R codes provided as examples.

```r
# Example 1: Calculating membership diversity index for multiple plots

# Convert raw data to species matrix
data(herbdata)
herb.spematrix <- longtowide(longdata = herbdata, left = "plot.id", up = "spe.id", inner = "abundance")

# Compute species McIntosh diversity index for each plot
herb.mcIntosh <- mcIntosh(herb.spematrix)
herb.mcIntosh

# Example 2: Standardizing indices using membership functional models

# Standardize the indices by membership functional models

 membership

Description
Obtained indices always cannot be used to evaluate the forest health because the indices with different dimension. And three membership functional models were thus used to standardize these indices.

Usage

```r
membership(mode = c("up", "down", "mid"), X, L, U, O1, O2)
```

Arguments

- **mode**: Three membership functional models were thus used to standardize these indices, which are up mode, down mode, and middle mode, respectively. For the up mode, a higher value is better; for the down mode, lower is better; for the middle mode, which have an effective range.
- **X**: The actual observed value of indices
- **L**: Lower limit of the indices
- **U**: Upper limit of the indices
- **O1** and **O2**: O1 and O2 are the effective range of the indices

Value

Standardized the indices by membership functional models
**preabs**

**Author(s)**

Zongzheng Chai

**References**


**Examples**

```
up.index<-membership(mode="up",X=0.67,L=0,U=2.173)
up.index
down.index<-membership(mode="down",X=0.8,L=0,U=2.73)
down.index
mid.index<-membership(mode="mid",X=c(0.1,0.3,0.4,0.6,0.9),L=0.2,U=1.0,0.1=0.5,0.2=0.7)
mid.index
```

```
preabs A R function for converting species matrix (wide data) to present-absent matrix
```

**Description**

Converting species matrix (wide data) to present-absent matrix

**Usage**

```
preabs(widedata)
```

**Arguments**

- `widedata` A species matrix

**Value**

A present-absent matrix

**Examples**

```
herb.spematrix<-longtowide(longdata=herbdata,left="plot.id",up="spe.id",
inner="abundance")
herb.preabs<-preabs(herb.spematrix)
herb.preabs
```
### Description

Example data of test Indices for forest health evaluation system

### Usage

```r
data("testIndex")
```

### Format

A data frame with 30 observations on the following 21 variables.

- `c1` Tree diversity index
- `c2` Shrub diversity index
- `c3` Herb diversity index
- `c4` Storey quantity
- `c5` Tree size diversity index
- `c6` Age structure
- `c7` Canopy closure
- `c8` Average volume increment per hectare
- `c9` Bio-disaster ratio
- `c10` Non bio-disaster ratio
- `c11` Crown length ratio
- `c12` Crown fade ratio
- `c13` Foliage falling ratio
- `c14` Regeneration density
- `c15` Soil depth
- `c16` Soil density
- `c17` Soil pH
- `c18` Soil organic matter
- `c19` Soil total nitrogen
- `c20` Soil available phosphorus
- `c21` Soil available potassium

### Examples

```r
data(testIndex)
testIndex
```
Survey data of individual trees for pine-oak mixed forests

Description

Tree data of pine-oak codominant mixed forests in the Qinling Mountains

Usage

data("treedata")

Format

A data frame with 1054 observations on the following 5 variables.

plot.id  Identification number of sample plots
tree.id  Identification number of trees
spe.id  Identification number of tree species
dbh.cm  Diameter at breast height of trees
ht.m  Tree height of trees

Details

Twenty 20*20 m plots were established for the pine-oak codominant mixed forests within the Qinling National Forest Ecosystem Research Station (Huoditang forest)

References


Examples

data(treedata)
treedata
Description

To show the distribution of species attributes (such as DBH, tree height) in the sample plots

Usage

vardis(data, varcat = "numeric", plot.id, var, breaks, include.lowest = FALSE, right = TRUE)

Arguments

data 
Data class should be a dataframe, the colnames with plot.id, species name, and some attributes (such as DBH, tree height), see data (treedata)

varcat 
Category of species attributes, numeric and character, respectively.

plot.id 
Identification number of sample plots

var 
Attributes of species in the sample plot

breaks 
Either a numeric vector of two or more unique cut points or a single number (greater than or equal to 2) giving the number of intervals into which x is to be cut. See the explanation of breaks of cut function

include.lowest 
Labels for the levels of the resulting category. By default, labels are constructed using "(a,b]" interval notation. If labels = FALSE, simple integer codes are returned instead of a factor. See the explanation of include.lowest of cut function

right 
Logical, indicating if the intervals should be closed on the right (and open on the left) or vice versa. See the explanation of right of cut function

Value

Distribution of species attributes (such as DBH, tree height) in the sample plots

Author(s)

Zongzheng Chai

Examples

when variable category is numeric

Variable distribution according to the actual range of variable and sizeclass=1
data(treedata)
numericVar.actualsize1 <- vardis(treedata, plot.id="plot.id", var="ht.m",
breaks=seq(min(treedata$ht.m),max(treedata$ht.m),1))
numericVar.actualsize1

Variable distribution according to the actual range of variable and sizeclass=2
numericVar.actualsize2 <- vardis(treedata, plot.id="plot.id", var="ht.m", 
breaks=seq(min(treedata$ht.m),max(treedata$ht.m),1))
numericVar.actualsize2


A R function for converting to wide data to long data

Description
Converting wide data, such as species matrix, and attributes matrix to long data, such as the treedata and herbdata.

Usage
widetolong(widedata, leftlab = "left", uplab = "up", innerlab = "inner")

Arguments
widedata: Data similar to the species matrix, and attributes matrix, etc.
leftlab: Row labels of wide data
uplab: Column labels of wide data
innerlab: Attributes labels of inner data of wide data

Value
Long data, such as treedata, herbdata, etc.
Author(s)
Zongzheng Chai

Examples
herb.spematrix<-longtowide(longdata=herbdata,left="plot.id",up="spe.id",inner="abundance")
herb.spedata<-widetolong(herb.spematrix,
    leftlab="plot.id",uplab="spe.id",innerlab="abundance")
herb.spedata
##After removed zero in inner data
rd0herb.spedata<-herb.spedata[which(herb.spedata$abundance==0),]
rd0herb.spedata
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