

Package ‘forestHES’

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Type Package

Title Forest Health Evaluation System at the Forest Stand Level

Version 2.0.1

Depends R (>= 3.5.0)

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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forestHES-package	<i>Forest health evaluation system at the forest stand level</i>
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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)

Zongzheng Chai, chaizz@126.com

References

Zhang HR, and Lei XD. 2014. Health management techniques for typical forest types. Beijing: Publishing house of forestry, China.

Examples

```
##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=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(0.67,0,0.68),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),
                       c11=c(0,0,0),c12=c(0.75,0.07,0.84),c13=c(0.35,0.11,0.84),
                       c14=c(833.33,833.33,2500),c15=c(53,59,43),c16=c(1.28,1.56,1.33),
                       c17=c(5.49,5.91,5.27),c18=c(38.32,34.03,25.37),c19=c(2.05,1.04,1.27),
```

```

c20=c(21.38,34.66,14.19),c21=c(86.67,80,91.67))
tree.multiplefhes

##More regular method of forest health evaluation for multiple sample plot
data(testIndex)
tree.fhes<-fhes(c1=testIndex$C1,c2=testIndex$C2,c3=testIndex$C3,c4=testIndex$C4,
  c5=testIndex$C5,c6=testIndex$C6,c7=testIndex$C7,c8=testIndex$C8,
  c9=testIndex$C9,c10=testIndex$C10,c11=testIndex$C11,c12=testIndex$C12,
  c13=testIndex$C13,c14=testIndex$C14,c15=testIndex$C15,c16=testIndex$C16,
  c17=testIndex$C17,c18=testIndex$C18,c19=testIndex$C19,c20=testIndex$C20,
  c21=testIndex$C21)
tree.fhes
pie(table(tree.fhes$evaluation$grade))

```

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

Chai ZZ, Wang DX. 2016. Environmental influences on the successful regeneration of pine-oak mixed forests in the Qinling Mountains, China. Scandinavian Journal of Forest Research,31(4):368-381.DOI:10.1080/02827581.2015.1062912

Examples

```
data(envdata)
envdata
```

fhes	<i>Forest health evaluation system</i>
------	--

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
01_16	Effective range of soil density
02_16	Effective range of soil density
L_17	Lower limit of soil pH
U_17	Upper limit of soil pH
01_17	Effective range of soil pH
02_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	index system
legend	legend
index	index
coverted.Index	coverted.Index
weighted.Index	weighted.Index
unweighted.Criterion	unweighted.Criterion
weighted.Criterion	weighted.Criterion
evaluation	evaluation results

Note

None

Author(s)

Zongzheng Chai

References

Zhang HR, and Lei XD. 2014. Health management techniques for typical forest types. Beijing: Publishing house of forestry, China

See Also

None

Examples

```
##forest health evaluation for singel sample plot
tree.singlefhcs<-fhcs(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.singlefhcs

##Assigned the threshold of some variables, according to specific
##realistic condition or research contents
tree.spefhcs<-fhcs(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.spefhcs

##forest health evaluation for multiple sample plot
```

```

tree.multiplefhes<-fhes(c1=c(0.67,0,0.68),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),
                        c11=c(0,0,0),c12=c(0.75,0.07,0.84),c13=c(0.35,0.11,0.84),
                        c14=c(833.33,833.33,2500),c15=c(53,59,43),c16=c(1.28,1.56,1.33),
                        c17=c(5.49,5.91,5.27),c18=c(38.32,34.03,25.37),c19=c(2.05,1.04,1.27),
                        c20=c(21.38,34.66,14.19),c21=c(86.67,80,91.67))
tree.multiplefhes

##More regular method of forest health evaluation for multiple sample plot
data(testIndex)
tree.fhes<-fhes(c1=testIndex$C1,c2=testIndex$C2,c3=testIndex$C3,c4=testIndex$C4,
                c5=testIndex$C5,c6=testIndex$C6,c7=testIndex$C7,c8=testIndex$C8,
                c9=testIndex$C9,c10=testIndex$C10,c11=testIndex$C11,c12=testIndex$C12,
                c13=testIndex$C13,c14=testIndex$C14,c15=testIndex$C15,c16=testIndex$C16,
                c17=testIndex$C17,c18=testIndex$C18,c19=testIndex$C19,c20=testIndex$C20,
                c21=testIndex$C21)
tree.fhes
pie(table(tree.fhes$evaluation$grade))

```

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

Chai ZZ, Wang DX. 2016. Environmental influences on the successful regeneration of pine-oak mixed forests in the Qinling Mountains, China. *Scandinavian Journal of Forest Research*,31(4):368-381.DOI:10.1080/02827581.2015.1062912

Examples

```
data(herbdata)
herbdata
```

indexSystem	<i>The national forest health evaluation system</i>
-------------	---

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

Zhang HR, and Lei XD. 2014. Health management techniques for typical forest types. Beijing: Publishing house of forestry, China.

References

Zhang HR, and Lei XD. 2014. Health management techniques for typical forest types. Beijing: Publishing house of forestry, China

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
##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

##Equivalent method to merge species matrix from base data
treedata$abundance<-1
```

```

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

####Compute the frequency of species in the multiple plots
##Merge a frequency matrix from base data
tree.freq<-longtowitz(longdata=treedata,left="plot.id",up="spe.id",freq=TRUE)
tree.freq
herb.freq<-longtowitz(longdata=herbdata,left="plot.id",up="spe.id",freq=TRUE)
herb.freq

####Compute the attribute matrix from base data
##Single attribute matrix
tree.dbh<-longtowitz(longdata=treedata,left="plot.id",up="spe.id",inner="dbh.cm")
tree.dbh
herb.cover<-longtowitz(longdata=herbdata,left="plot.id",up="spe.id",inner="coverage")
herb.cover

##Multiple attribute matrix
tree.multattr<-longtowitz(longdata=treedata,left="plot.id",up="spe.id",
inner=c("dbh.cm","ht.m"))
tree.multattr
herb.multattr<-longtowitz(longdata=herbdata,left="plot.id",up="spe.id",
inner=c("coverage","abundance"))
herb.multattr

#####Calculation of Importance value (IV) for species#####
####Calculation of Importance value (IV) for individual tree data
##Covert long data to wide data
tree.freq<-longtowitz(longdata=treedata,left="plot.id",up="spe.id",freq=TRUE)$frequency
tree.density<-longtowitz(longdata=treedata,left="plot.id",up="spe.id")/(20*400)
treedata$base<-pi*(treedata$dbh.cm)^2/10000
tree.dominance<-longtowitz(longdata=treedata,left="plot.id",up="spe.id",inner="base")/(20*400)
##Compute the relative value
tree.refreq<-tree.freq/rowSums(tree.freq)*100
tree.redensity<-tree.density/rowSums(tree.density)*100
tree.redominance<-tree.dominance/rowSums(tree.dominance)*100
##Compute the importance value matrix
treeIVmatirx<-(tree.refreq+tree.redensity+tree.redominance)/3
##Compute the total importance value for species
treeTIV<-colSums(treeIVmatirx)/20
##Order the total importance value for species
sortedtreeTIV<-sort(treeTIV,decreasing=TRUE)
sortedtreeTIV

####Calculation of Importance value (IV) for clust herb data
##Covert long data to wide data
herb.freq<-longtowitz(longdata=herbdata,left="plot.id",up="spe.id",freq=TRUE)$frequency
herb.dencover<-longtowitz(longdata=herbdata,left="plot.id",up="spe.id",
inner=c("abundance","coverage"))
herb.density<-herb.dencover$abundance/100

```

```

herb.coverage<-herb.dencover$coverage/100
##Compute the relative value
herb.refreq<-herb.freq/rowSums(herb.freq)*100
herb.redensity<-herb.density/rowSums(herb.density)*100
herb.recoverage<-herb.coverage/rowSums(herb.coverage)*100
##Compute the importance value matrix
herbIVmatirx<-(herb.refreq+herb.redensity+herb.recoverage)/3
##Compute the total importance value for species
herbTIV<-colSums(herbIVmatirx)/20
##Order the total importance value for species
sortedherbTIV<-sort(herbTIV,decreasing=TRUE)
sortedtreeTIV

```

mcIntosh	<i>Calculation of mcIntosh diversity index</i>
----------	--

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

McIntosh RP.1967. An index of diversity and the relation of certain concepts to diversity. Ecol.Soc.Am. 48:329-404.

Examples

```
#####Calculation based on multiple plots
####convert raw data to species matrix
##raw data of multiple plots
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
```

membership	<i>Standardize the indices by membership functional models</i>
------------	--

Description

Obtained indices always can not 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

```
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	O1 and O2 are the effective range of the indices
O2	O1 and O2 are the effective range of the indices.

Value

Standardized the indices by membership functional models

Author(s)

Zongzheng Chai

References

Zhang HR, and Lei XD. 2014. Health management techniques for typical forest types. Beijing: Publishing house of forestry, China.

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,O1=0.5,O2=0.7)
mid.index

```

preabs	<i>A R function for converting species matrix (wide data) to present-absent matrix</i>
--------	--

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

```

testIndex	<i>Test Indices for forest health evaluation system</i>
-----------	---

Description

Example data of test Indices for forest health evaluation system

Usage

```
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

```
data(testIndex)
testIndex
```

treedata

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.

References

Chai ZZ, Wang DX. 2016. Environmental influences on the successful regeneration of pine-oak mixed forests in the Qinling Mountains, China. *Scandinavian Journal of Forest Research*,31(4):368-381.DOI:10.1080/02827581.2015.1062912

Examples

```
data(treedata)
treedata
```

`vardis`

Distribution of species attributes in the sample plots

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

<code>data</code>	Data class should be a dataframe, the colnames with <code>plot.id</code> , species name, and some attributes (such as DBH, tree height), see <code>data(treedata)</code>
<code>varcat</code>	Category of species attributes, numeric and character, respectively.
<code>plot.id</code>	Identification number of sample plots
<code>var</code>	Attributes of species in the sample plot
<code>breaks</code>	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 <code>x</code> is to be cut. See the explanation of <code>breaks</code> of <code>cut</code> 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 variabel catogory 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),2))
numericVar.actualsize2
##when the lower value of actual range of variable included,include.lowest can set TRUE
numericVar.actualInlower<-vardis(treedata,plot.id="plot.id",var="ht.m",
                                 breaks=seq(min(treedata$ht.m),max(treedata$ht.m),1),
                                 include.lowest=TRUE)
numericVar.actualInlower
##when the upper value of actual range of variable excluded,include.lowest can be set FALSE
numericVar.actualExupper<-vardis(treedata,plot.id="plot.id",var="ht.m",
                                 breaks=seq(min(treedata$ht.m),max(treedata$ht.m),1),
                                 right=FALSE)
numericVar.actualExupper

####Variable distribution according to the specific range of variable
range(treedata$ht.m)
##[1] 2.6 32.2
##specific range can be set between 2 and 34, sizeclass is 2
numericVar.specific<-vardis(treedata,plot.id="plot.id",var="ht.m",
                            breaks=2*1:17)
numericVar.specific

#####when variabel catogory is character#####
characterVar<-vardis(treedata,varcat="character",plot.id="plot.id",var="spe.id")
characterVar
```

widetolong*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)

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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 innerdata
rd0herb.spedata<-herb.spedata[-which(herb.spedata$abundance==0),]
rd0herb.spedata
```

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