Package ‘forestHES’

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Type Package

Title Forest Health Evaluation System at the Forest Stand Level

Version 2.0.1

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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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Author Zongzheng Chai [aut, cre] (<`https://orcid.org/0000-0002-0530-0040`>)

Maintainer Zongzheng Chai <`chaizz@126.com`>

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Contents

`forestHES-package` *Forest health evaluation system at the forest stand level*

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 packge concentrates on to relize 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 regulare 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` *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`	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.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 regulare 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` *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

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<-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
##Merge a frequency matrix from base data
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
##Single attribute matrix
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

##Multiple attribute matrix
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######
####Calculation of Importance value (IV) for individual tree data
##Covert long data to wide data
tree.freq<-longtowide(longdata=treedata,left="plot.id",up="spe.id",freq=TRUE)$frequency
tree.density<-longtowide(longdata=treedata,left="plot.id",up="spe.id")/(20*400)
treedata$base<-pi*(treedata$dbh.cm)^2/10000
tree.dominance<-longtowide(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<-longtowide(longdata=herbdata,left="plot.id",up="spe.id",freq=TRUE)$frequency
herb.dencover<-longtowide(longdata=herbdata,left="plot.id",up="spe.id",
inner=c("abundance","coverage"))
herb.density<-herb.dencover$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` *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

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` *Standardize the indices by membership functional models*

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` *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
```

`testIndex` *Test Indices for forest health evaluation system*

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 od 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 (sucha as DBH,tree height), see data (treedata)
`varcat`	Catory 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 od 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)

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

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