Package ‘ahpsurvey’

November 24, 2019

Type Package

Title Analytic Hierarchy Process for Survey Data

Version 0.4.1

Description The Analytic Hierarchy Process is a versatile multi-criteria decision-making tool introduced by Saaty (1987) <doi:10.1016/0270-0255(87)90473-8> that allows decision-makers to weigh attributes and evaluate alternatives presented to them. This package provides a consistent methodology for researchers to reformat data and run analytic hierarchy process in R on data that are formatted using the survey data entry mode. It is optimized for performing the analytic hierarchy process with many decision-makers, and provides tools and options for researchers to aggregate individual preferences and test multiple options. It also allows researchers to quantify, visualize and correct for inconsistency in the decision-maker's comparisons.

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Encoding UTF-8

LazyData true

RoxygenNote 7.0.1

Imports Rdpack, stats, magrittr, knitr, tidyr, dplyr, randomNames

Suggests ggplot2, scales

RdMacros Rdpack


VignetteBuilder knitr

NeedsCompilation no

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Repository CRAN

Date/Publication 2019-11-24 16:10:02 UTC
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| ahp | Canned routine for AHP |

**Description**

ahp is a canned routine that returns a data.frame of individuals’ priorities (based on ahp.indpref), number of missing values, consistency ratios, and top three pairs of inconsistent pairwise comparisons. An optional argument `agg` allows the user to generate a data.frame of aggregated priorities alongside individual priorities.

**Usage**

```r
ahp(
  df,
  atts,
  negconvert = FALSE,
  reciprocal = TRUE,
  method = "eigen",
  aggmeth = "geometric",
  qt = 0,
  censorcr = Inf,
  agg = FALSE,
  ID = NULL,
  col = NULL,
  suppress = "none"
)
```
Arguments

df  a dataframe, each row corresponding to one decision-maker, with columns ordered according to atts.
atts  a list of attributes in the correct order
negconvert  logical, whether to convert all positive values to negative. In the pairwise comparison A_B, if -6 denotes A is more important than B by 6 units, set negconvert = TRUE.
reciprocal  logical, whether to convert negative values (after negconvert) to its reciprocal. If the comparison A_B where B is more important than A was already entered in its reciprocal (e.g. 1/6), choose reciprocal = FALSE. When reciprocal = FALSE, do not set negconvert = TRUE.
method  if method = "eigen", the individual priority weights are computed using the Dominant Eigenvalues method described in Saaty (2003). Otherwise, then the priorities are computed based on the averages of normalized values. Basically it normalizes the matrices so that all of the columns add up to 1, and then computes the averages of the row as the priority weights of each attribute. Three modes of finding the averages are available: arithmetic: the arithmetic mean; geometric: the geometric mean (the default); rootmean: the square root of the sum of the squared value.
aggmethod  how to aggregate the individual priorities. By default aggmethod = method. Apart from the methods offered in method, aggmethod also permits three other options: tmean computes the trimmed arithmetic mean, tgmean computes the trimmed geometric mean (both with quantiles trimmed based on qt), and sd computes the standard deviation from the arithmetic mean. If method = "eigen" and aggmethod is not specified, aggmethod defaults to "geometric".
qt  specifies the quantile which the top and bottom priority weights are trimmed. Used only if aggmethod = 'tmean' or aggmethod = 'tgmean'. For example, qt = 0.25 specifies that the aggregation is the arithmetic mean of the values from the 25 to 75 percentile. By default qt = 0.
censorcr  the threshold of censoring observations. All observations with a consistency ratio higher than the specified CR will be dropped from the routine. By default, censorcr = Inf, i.e. drops no observations.
agg  by default, agg = FALSE, which suppresses the output of Aggregated priorities. If agg = TRUE, the output will be a list where $AggPref contains the Aggregated priorities and Standard Deviations.
ID  the column name, or a vector of column names, of variables in df, which are used to indicate specific observations. For example, if a survey dataset comes with an identifier/ multiple identified for each observation, use this so that the output dataframe would contain this identifier.
col  a list of column names which contains the columns for the pairwise comparison matrix in chronological order, as specified in atts. For example, if atts is c("A","B","C"), then col would be c("A_B","A_C","B_C"), with "A_B" being a pairwise comparison of attribute A and B. col = NULL by default, indicating that the dataframe specified already contained the pairwise comparisons in correct order and nothing else except of what is inside ID.
ahp.aggjudge

**suppress**
Suppresses the supplementary indices. Can take the values of "all" (suppresses all indices), "pwerror" (suppresses pwerror), or "cr" (supplements consistency ratio).

**Value**
If `agg = TRUE`, returns a list of the results with two elements, `indpref` and `aggpref`. `$indpref` contains individual preference weight (same as `ahp.indpref`), consistency ratios, and the top three most inconsistent pairwise comparisons (same as `ahp.pwerror`). `$aggpref` contains the Aggregated Priorities and Standard Deviations. Otherwise (i.e. default setting), outputs a `data.frame` with only `$indpref`.

**Author(s)**
Frankie Cho

**References**

**Examples**
```r
data(city200)
ahp(df = city200, atts = c("cult", "fam", "house", "jobs", "trans"), negconvert = TRUE)
```

### Description
Aggregate individual judgments from pairwise comparison matrices

### Usage
```r
ahp.aggjudge(ahpmat, atts, aggmethod = "geometric", qt = 0)
```

### Arguments
- **ahpmat**
  A list of pairwise comparison matrices of each decision maker generated by `ahp.mat`.
- **atts**
  A list of attributes in the correct order
The method of aggregating the judgments by all decision-makers. Five modes aggregation are available: arithmetic: the arithmetic mean; geometric: the geometric mean (the default); rootmean: the square root of the sum of the squared value, tmean: the trimmed mean, tgmean: trimmed geometric mean. The quantiles trimmed are based on qt. It can also be set to sd, where it reports the standard deviation from the arithmetic mean.

qt specifies the quantile which the top and bottom priority weights are trimmed. Used only if aggmethod = 'tmean' or aggmethod = 'tgmean'. For example, qt = 0.25 specifies that the aggregation is the arithmetic mean of the values from the 25 to 75 percentile. By default qt = 0.

Value

A data.frame of the aggregated pairwise judgments of all the decision-makers.

Author(s)

Frankie Cho

Examples

```r
## Computes individual judgments with geometric mean and aggregates them
## with a trimmed arithmetic mean

data(city200)
atts <- c('cult', 'fam', 'house', 'jobs', 'trans')
cityahp <- ahp.mat(df = city200, atts = atts, negconvert = TRUE)
ahp.aggjudge(cityahp, atts, aggmethod = 'tmean', qt = 0.1)
```

---

**ahp.aggpref**

**Aggregate priority weights**

**Description**

Compute and aggregate individual priority weights from pairwise comparison matrices

**Usage**

```r
ahp.aggpref(ahpmat, atts, method = "geometric", aggmethod = method, qt = 0)
```
Arguments

ahpmat A list of pairwise comparison matrices of each decision maker generated by ahp.mat.
atts a list of attributes in the correct order
method if method = "eigen", the individual priority weights are computed using the Dominant Eigenvalues method described in Saaty (2003). Otherwise, then the priorities are computed based on the averages of normalized values. Basically it normalizes the matrices so that all of the columns add up to 1, and then computes the averages of the row as the priority weights of each attribute. Three modes of finding the averages are available: arithmetic: the arithmetic mean; geometric: the geometric mean (the default); rootmean: the square root of the sum of the squared value.
aggmethod how to aggregate the individual priorities. By default aggmethod = method. Apart from the methods offered in method, aggmethod also permits three other options: tmean computes the trimmed arithmetic mean, tgmean computes the trimmed geometric mean (both with quantiles trimmed based on qt), and sd computes the standard deviation from the arithmetic mean. If method = "eigen" and aggmethod is not specified, aggmethod defaults to "geometric".
qt specifies the quantile which the top and bottom priority weights are trimmed. Used only if aggmethod = 'tmean' or aggmethod = 'tgmean'. For example, qt = 0.25 specifies that the aggregation is the arithmetic mean of the values from the 25 to 75 percentile. By default qt = 0.

Value

A data.frame of the aggregated priorities of all the decision-makers.

Author(s)

Frankie Cho

References


Examples

## Computes individual priorities with geometric mean and aggregates them
## with a trimmed arithmetic mean
library(magrittr)
data(city200)
atts <- c('cult', 'fam', 'house', 'jobs', 'trans')
```r
cityahp <- ahp.mat(df = city200, atts = atts, negconvert = TRUE)
ahp.aggpref(cityahp, atts, method = 'geometric', aggmethod = 'tmean', qt = 0.1)
```

### ahp.cr

**Calculates the consistency ratio of each decision-maker**

**Description**

The `ahp.cr` function calculates the consistency ratio of each decision-maker, defined by the following equation:

\[
CR = \frac{(\lambda - n)}{(n - 1)(RI)}
\]

Where \(\lambda\) is the maximum eigenvalue of the pairwise comparison matrix, \(n\) is the number of attributes, and \(RI\) is the random index. Following Saaty and Tran (2007), the \(RI\) is a function of \(n\) and is the consistency ratio of randomly generated pairwise comparison matrices.

**Usage**

```r
ahp.cr(ahpmat, atts, ri = NULL)
```

**Arguments**

- `ahpmat`: A list of pairwise comparison matrices of each decision maker generated by `ahp.mat`.
- `atts`: a list of attributes in the correct order. The RI is asymptotic as it approaches \(n=15\), thus it is set to be equal to 1.6 if the number of attributes exceeds 16.
- `ri`: A user-supplied random index value, probably user generated using `ahp.ri`.

**Value**

A list of consistency ratios of each decision-maker.

**Author(s)**

Frankie Cho

**References**

Examples

data(city200)
atts <- c('cult', 'fam', 'house', 'jobs', 'trans')

cityahp <- ahp.mat(df = city200, atts = atts, negconvert = TRUE)
ahp.cr(cityahp, atts)

ahp.error

Matrix of the product between the pairwise comparison value and pj/pi

Description

Consider the comparison matrix where element $a_{ij}$ contains the pairwise comparison between the attributes i and j. The weights of the matrix was constructed as in agg.indpref using the Perron eigenvector where $p_i$ and $p_j$ are the weights of the $i^{th}$ and the $j^{th}$ element respectively. ahp.error constructs a matrix $\epsilon_{ij} = a_{ij}p_j/p_i$.

Usage

ahp.error(ahpmat, atts, reciprocal = FALSE)

Arguments

- **ahpmat**: A list of pairwise comparison matrices of each decision maker generated by ahp.mat.
- **atts**: a list of attributes in the correct order
- **reciprocal**: whether to remove all numbers lower than 1 and put all numbers above 1 in the upper triangular matrix. Useful for visualizing the inconsistency rapidly.

Value

A list of matrices containing $\epsilon_{ij} = a_{ij}p_j/p_i$ for each decision-maker, with elements from the lower triangle set as NA automatically (since it is essentially equal to the element in the upper triangle).

Author(s)

Frankie Cho

References

Examples

```r
atts <- c('cult', 'fam', 'house', 'jobs', 'trans')
data(city200)

cityahp <- ahp.mat(city200, atts, negconvert = TRUE)
ahp.error(cityahp, atts)
```

---

**ahp.harker**

*Replace inconsistent pairwise comparisons*

**Description**

Based on the matrix derived from `ahp.error`, replaces the top \( n \) number of inconsistent pairwise comparisons with a value calculated by from the method in Harker (1987). While there are strong arguments against replacing inconsistent values without the decision-maker’s consent for the sake of satisfying the consistency ratio criterion of consistency ratio < 0.1 (see Saaty and Tran (2007)), it is often not possible for enumerators to ask respondents to change their answers based on consistency, whereas truncating inconsistent decisions may make the dataset unrepresentative of the population. Researchers should think carefully and explain fully the methods used to process AHP data, and whenever possible, use a lower number of iterations.

**Usage**

```r
ahp.harker(
  ahpmat, atts,
  round = FALSE, limit = FALSE,
  iterations = 1, stopcr = 0, printiter = TRUE
)
```

**Arguments**

- **ahpmat** A list of pairwise comparison matrices of each decision maker generated by `ahp.mat`.
- **atts** A list of attributes in the correct order
- **round** Rounds the imputation values of the matrix to the nearest integer if TRUE. Defaults to FALSE.
- **limit** If set to TRUE, if the imputation value is larger than 9 or smaller than 1/9, the value is converted to 9 and 1/9 respectively. Defaults to FALSE.
iterations  The number of comparisons with the highest inconsistency to be changed. For example, if iterations = 3, ahp.harker changes the first, second, and third most inconsistent pairwise comparisons using that method. Defaults to 1.

stopcr  The stopping Consistency Ratio, which was calculated by ahp.cr. Complements iter by giving iterations a criteria to stop when a matrix is sufficiently consistent. The function will continue looping and replacing more elements of the pairwise comparison matrices until the consistency ratio of the new matrix is lower than stopcr, or the maximum number of iterations is reached, and will stop and move onto the next individual. When stopcr is set, the number of replaced elements will differ among each decision-maker. Defaults to 0 (i.e. the loop will not be stopped unless iterations is reached).

printiter  Whether the number of iterations taken for each pairwise matrix is reported or not. If printiter = TRUE, it prints out the final number of iterations that each individual decision-maker took to reach a value lower than stopcr. Generally it is not needed if stopcr is not specified. When stopcr is specified, this is a good way of identifying how many pairwise comparisons are actually replaced by the algorithm for each decision maker. Defaults to TRUE.

Value  A list of matrices with values replaced with consistent values.

Author(s)  Frankie Cho

References  


See Also  ahp.error ahp.cr

Examples  
atts <- c('cult', 'fam', 'house', 'jobs', 'trans')
data(city200)

cityahp <- ahp.mat(city200, atts, negconvert = TRUE)
ahp.harker(cityahp, atts)
Description

ahp.indpref computes the individual priorities of the decision-makers, and returns a data.frame containing the priority weights of the decision-makers.

Usage

ahp.indpref(ahpmat, atts, method = "geometric")

Arguments

- **ahpmat**: A list of pairwise comparison matrices of each decision maker generated by ahp.mat.
- **atts**: a list of attributes in the correct order
- **method**: if method = "eigen", the individual priority weights are computed using the Dominant Eigenvalues method described in Saaty (2003). Otherwise, then the priorities are computed based on the averages of normalized values. Basically it normalizes the matrices so that all of the columns add up to 1, and then computes the averages of the row as the priority weights of each attribute. Three other modes of finding the averages are available: arithmetic: the arithmetic mean; geometric: the geometric mean (the default); rootmean: the square root of the sum of the squared value.

Value

A data.frame of the individual priorities of all the decision-makers.

Author(s)

Frankie Cho

References

ahp.mat

Generate AHP pairwise matrices from survey data

Description

ahp.mat takes in paired comparisons from survey data with questions using the analytic hierarchy process and converts it into pairwise comparison matrices for each individual decision-maker. Examples based on Saaty (2004).

Usage

ahp.mat(df, atts, negconvert = FALSE, reciprocal = TRUE)

Arguments

df a dataframe, each row corresponding to one decision-maker, with columns ordered according to atts.
atts a list of attributes in the correct order
negconvert logical, whether to convert all positive values to negative. In the pairwise comparison A_B, if -6 denotes A is more important than B by 6 units, set negconvert = TRUE.
reciprocal logical, whether to convert negative values (after negconvert) to its reciprocal. If the comparison A_B where B is more important than A was already entered in its reciprocal (e.g. 1/6), choose reciprocal = FALSE. When reciprocal = FALSE, do not set negconvert = TRUE.

Value

A list of pairwise comparison matrices of each decision-maker.

Author(s)

Frankie Cho

References

Examples

```r
data(city200)
atts <- c('cult', 'fam', 'house', 'jobs', 'trans')
ahp.mat(df = city200, atts = atts, negconvert = TRUE)
```

Description

Imputes the missing values of a list of matrices produced by `ahp.mat` using the methods and assumptions made in Harker (1987). Missing values must be coded as `NA`. As suggested in Harker (1987), a minimum of n-1 comparisons must be made, where n is the number of attributes (assuming that the decision-maker is perfectly consistent). Note that the algorithm assumes that the NA values will be imputed under perfect consistency with the other pairwise comparisons made.

Usage

```r
ahp.missing(ahpmat, atts, round = FALSE, limit = FALSE)
```

Arguments

- `ahpmat`: A list of pairwise comparison matrices of each decision maker generated by `ahp.mat`.
- `atts`: A list of attributes in the correct order.
- `round`: Rounds the imputation values of the matrix to the nearest integer if `TRUE`. Defaults to `FALSE`.
- `limit`: If set to `TRUE`, if the imputation value is larger than 9 or smaller than 1/9, the value is converted to 9 and 1/9 respectively. Defaults to `FALSE`.

Value

A list of matrices with all `NA` values imputed.

Author(s)

Frankie Cho

References

Examples

library(magrittr)

atts <- c('cult', 'fam', 'house', 'jobs', 'trans')
data(city200)

set.seed(42)
## Make a dataframe that is missing at random
missing.df <- city200[1:10,]
for (i in 1:10){
  missing.df[i, round(stats::runif(1,1,10))] <- NA
}
missingahp <- ahp.mat(missing.df, atts, negconvert = TRUE)
ahp.missing(missingahp, atts)

ahp.pwerror  
Finds the pairwise comparisons with the maximum amount of inconsistency

Description

After constructing a list of matrices with $\epsilon_{ij} = a_{ij} w_j / w_i$ (following ahp.error), this algorithm extracts the top $n$ numbers of pairwise comparison matrices with the highest $\epsilon_{ij}$ for each decision-maker.

Usage

ahp.pwerror(ahpmat, atts, npw = 3)

Arguments

ahpmat A list of pairwise comparison matrices of each decision maker generated by ahp.mat.
atts a list of attributes in the correct order
npw Number of pairwise comparisons

Value

A list of matrices containing $\epsilon_{ij} = a_{ij} w_j / w_i$ for each decision-maker, with elements from the lower triangle set as NA automatically (since it is essentially equal to the element in the upper triangle).

Author(s)

Frankie Cho
References


Examples

```r
library(magrittr)
atts <- c('cult', 'fam', 'house', 'jobs', 'trans')
data(city200)
cityahp <- ahp.mat(city200, atts, negconvert = TRUE)
ahp.error(cityahp, atts)
```

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<thead>
<tr>
<th>ahp.ri</th>
<th>Generate random indices</th>
</tr>
</thead>
</table>

### Description

The `ahp.ri` function calculates the mean consistency indices of a specific numbers of random number pairwise comparison matrices.

The random index of one pairwise comparison matrix is given as below, where \( \lambda \) is the maximum eigenvalue and \( n \) is the number of attributes.

\[
RI = \frac{\lambda - n}{(n - 1)}
\]

`ahp.ri` creates `nsims` number of pairwise comparison matrices with number of dimensions=`dim`, and returns its average.

### Usage

```r
ahp.ri(nsims, dim, seed = 42)
```

### Arguments

- **nsims**: Number of random pairwise comparison matrices to be generated. Processing time increases substantially with higher `nsims`.
- **dim**: Number of dimensions of the matrix.
- **seed**: The random number generator seed for reproducibility, which is same as `set.seed`. By default, seed = 42.
Value

The generated random index, which is numeric.

Author(s)

Frankie Cho

Examples

`ahp.ri(nsims = 10000, dim = 5, seed = 42)`

Description

The `ahpsurvey` package provides a workflow for researchers to reformat data and run analytic hierarchy process on data that are originally formatted using the survey data entry mode. A diversified toolbox is available for researchers to explore ways to impute missing pairwise comparisons or to adjust comparisons based on consistency, and to conveniently customize the methods which weights derived from surveys are extracted and aggregated.

Author(s)

Frankie Cho <htcho@connnect.hku.hk>

Description

A data.frame of one decision-maker with weights the same as Saaty (2004), with the pairwise comparisons of atts: `c('cult','fam','house','jobs','trans')`, about a choosing the best city to live in based on five attributes: Culture, Family, House, Jobs, and Transportation. Negative values in the data denote that the attribute on the left is more important than the right, thus if used with `ahp.mat`, `negconvert` must be set to `TRUE`.

Usage

`data(city1)`
Format

A data frame with 1 row and 10 variables, which are pairwise comparisons of `atts`.

Source

Saaty (2004)

data(city200)

Description

A data.frame of one decision-maker with weights the same as Saaty (2004), with the pairwise comparisons of `atts`: `c('cult', 'fam', 'house', 'jobs', 'trans')`, about choosing the best city to live in based on five attributes: Culture, Family, House, Jobs, and Transportation. The choices of 200 decision-makers are simulated based on the underlying weights and randomness generated by a normal random distribution. The true weights are stored in `data(city1)`. The normal random distribution was set with a mean at the true weight value and a standard deviation of 2,1,2,1,5,2,1,5,2,5,0,5,0,5,1 in chronological order of the columns in `city200`.

Usage

data(city200)

Format

A data.frame with 200 row and 10 variables, which are pairwise comparisons of `atts`.

Source

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