Package 'Prize'

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Type Package

Title Prize: an R package for prioritization estimation based on analytic hierarchy process

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Description The high throughput studies often produce large amounts of numerous genes and proteins of interest. While it is difficult to study and validate all of them. Analytic Hierarchy Process (AHP) offers a novel approach to narrowing down long lists of candidates by prioritizing them based on how well they meet the research goal. AHP is a mathematical technique for organizing and analyzing complex decisions where multiple criteria are involved. The technique structures problems into a hierarchy of elements, and helps to specify numerical weights representing the relative importance of each element. Numerical weight or priority derived from each element allows users to find alternatives that best suit their goal and their understanding of the problem.

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Imports diagram, stringr, ggplot2, reshape2, grDevices, matrixcalc, stats, gplots, methods, utils, graphics

Suggests RUnit, BiocGenerics

biocViews Software, MultipleComparison, GeneExpression, CellBiology, RNASeq

NeedsCompilation no

R topics documented:

Prize-package	*Prize: an R package for prioritization estimation based on analytic hierarchy process*

Description

The Prize package is a decision analysis tool based on Analytic Hierarchy Process (AHP), which provides a logical framework to rank and prioritize a group of alternatives. Once the decision makers have their list of available options (alternatives) and defined their criteria for prioritization, the Prize package allows aggregation of individual judgements against each criterion into a group judgement, then use these judgements to calculate final ahp weight for ranking. The Prize package also provides visualizarion tools to illustrate the problem hierarchy, the criteria weights and final ranking.

Author(s)

Daryanaz Dargahi <daryanazdargahi@gmail.com>

References

Saaty, T. L. (1977) A scaling methods for priorities in hierarchical structure. Journal of Mathematical Psychology, 15, 234-281.

T.L. Saaty. The Analytic Hierarchy Process, Planning, Piority Setting, Re- source Allocation. McGraw-Hill, New york, 1980.

E. Forman and K. Peniwati. Aggregating individual judgments and priorities with the analytic hierarchy process. European Journal of Operational Research, 108(1):165-169, 1998.

J.C. Gower. Some distance properties of latent root and vector methods used in multivariate analysis. Biometrika, 53(3/4):pp. 325-338, 1966.

Examples

```
##########################################
## aggregation of individual opinions
##########################################
mat = matrix(nrow = 4, ncol = 1, data = NA)
mat[,1] = c(system.file('extdata','ind1.tsv',package = 'Prize'),
            system.file('extdata','ind2.tsv',package = 'Prize'),
            system.file('extdata','ind3.tsv',package = 'Prize'),
            system.file('extdata','ind4.tsv',package = 'Prize'))
rownames(mat) = c('ind1','ind2','ind3', 'ind4')
colnames(mat) = c('individual_judgement')

# non-weighted AIJ
res = gaggregate(srcfile = mat, method = 'geometric', simulation = 500)
```

```
########################################
## Estimating idealised prioritise
## Rating AHP
########################################
category_pcm = read.delim(system.file('extdata','number.tsv', package = 'Prize')
                            , sep = '\t', header = TRUE, row.names = 1)
alt_mat = read.delim(system.file('extdata','numEpitope_alternative_category.tsv',
                     package = 'Prize'), sep = '\t', header = FALSE)
rate = rating(category_pcm, alt_mat, simulation = 500)


########################################
## Prioritization estimation using AHP
########################################
mat <- matrix(nrow = 7, ncol = 3, data = NA)
mat[,1] <- c('0', '1','2','3','4','4.1','4.2')
mat[,2] <- c('Prioritization_of_DE_genes','Tumor_expression','Normal_expression',
             'Frequency', 'Epitopes', 'Number_of_epitopes', 'Size_of_epitopes')
mat[,3] <- c(system.file('extdata','aggreg.judgement.tsv',package = 'Prize'),
             system.file('extdata','tumor.PCM.tsv',package = 'Prize'),
             system.file('extdata','normal.PCM.tsv',package = 'Prize'),
             system.file('extdata','freq.PCM.tsv',package = 'Prize'),
             system.file('extdata','epitope.PCM.tsv',package = 'Prize'),
             system.file('extdata','epitopeNum.PCM.tsv',package = 'Prize'),
             system.file('extdata','epitopeLength.PCM.tsv',package = 'Prize'))

# prioritization pipeline
prioritization <- pipeline(mat, model = 'relative', simulation = 500)


########################################
## visualizaion
########################################
# visualizing individal opinion consistency ratio
crplot(ICR(res), angle = 45)

# visualizing the distance among individual opinion and aggregated group judgment
dplot(IP(res))

# visualizing problem hierarchy
ahplot(ahp_plot(prioritization), fontsize = 0.7, cradx = 0.11 ,sradx = 0.12,
       cirx= 0.18, ciry = 0.07, dist = 0.06)

# visualizing prioritized alternatives
rainbowplot(rainbow_plot(prioritization)$criteria_rainbowplot, xcex = 3)
rainbowplot(rainbow_plot(prioritization)$subcriteria_rainbowplot, xcex = 3)

# visualizing criteria/subcriteria score
wplot(weight_plot(prioritization)$criteria_wplot, type = 'pie',
      fontsize = 7, pcex = 3)
wplot(weight_plot(prioritization)$criteria_wplot, type = 'bar',
      fontsize = 7, pcex = 3, xlab = 'Weight', ylab = 'Criteria')
```

---

aggreg.judgement-data *A pairwise comparison matrix (PCM)*

Description

Aggreg.judgement includes a PCM computed from aggregation of decision makers opinions. The PCM includes 4 criteria to prioritize a set of genes of interest according to their potential to serve as a tumor marker/therapeutic target. The criteria include: Tumor_expression, Normal_expression, Frequency, and Epitopes.

Author(s)

Daryanaz Dargahi

References

T.L. Saaty. The Analytic Hierarchy Process, Planning, Piority Setting, Re- source Allocation. McGraw-Hill, New york, 1980. E. Forman and K. Peniwati. Aggregating individual judgments and priorities with the analytic hierarchy process. European Journal of Operational Research, 1998.

---

ahmatrix *ahmatrix*

Description

Converting a triangular matrix into a square pairwise comparison matrix (PCM) where the diagonal values are equal to 1 and a[i,j] = 1/a[j,i].

Usage

```
ahmatrix(x)
```

Arguments

x a numeric triangular matrix, where empty elements are specified with NA.

Value

An S4 object including a PCM.

Author(s)

Daryanaz Dargahi

Examples

```
mat <- matrix(nrow = 3, ncol = 3, data = NA)
mat[1,2] <- 5
mat[1,3] <- 2
mat[2,3] <- 7

res <- ahmatrix(mat)
```

---

ahmatrixObj-class   *Class* ahmatrixObj

Description

An object that stores a pairwise comparison matrix.

Objects from the Class

Objects can be created by calls of the form new("ahmatrixObj", ...).

Slots

ahp_matrix: A pairwise comparison matrix.

Author(s)

Daryanaz Dargahi <daryanazdargahi@gmail.com>

---

ahp   *ahp*

Description

Computing AHP weights as well as Satty's inconsistency.

Usage

```
ahp(x, simulation = 500)
```

Arguments

x	a pairwise comparison matrix (PCM) with diagonal values equal 1 and a[i,j] = 1/a[j,i].
simulation	the simulation size in order to compute Satty's inconsistency. The default value is 500.

Value

An S4 object including a numeric vector of AHP weights and Satty's inconsistency.

Author(s)

Daryanaz Dargahi

References

T.L. Saaty. A scaling method for priorities in hierarchical structures. Journal of Mathematical Psychology, 15(3):234-281, 1977.

T.L. Saaty. The Analytic Hierarchy Process, Planning, Piority Setting, Re- source Allocation. McGraw-Hill, New york, 1980.

Examples

```
mat <- matrix(c(1,2,5, 1/2,1,3, 1/5,1/3,1), nrow = 3, ncol = 3, byrow = TRUE)
res <- ahp(mat, simulation = 500)
```

---

ahplot	*ahplot*

Description

Plotting the problem hierarchy, showing the relationships between goal, criteria, and subcriteria.

Usage

```
ahplot(srcfile, fontsize = 0.5, cradx = 0.07, crady = 0.05,
  sradx = 0.05, srady = 0.05, cirx = 0.1, ciry = 0.05, gcol = "green",
  ccol = "yellow", scol = "orange", lcol = "black", dist = 0.05,
  digit = 3, main = NULL)
```

Arguments

srcfile	a character matrix, where the first column specifies the hierarchy order. The second and third columns include the ID of decisison elements and ahp weights (optional), respectively (See the example below).
fontsize	the font size of characters.
cradx,crady	the horizontal and vertical radius of the criteria box, respectively.
sradx,srady	the horizontal and vertical radius of the subcriteria box, respectively.
cirx,ciry	the horizontal and vertical radius of the goal
gcol,ccol,scol	the filling color of the goal, criteria, and subcriteria boxes, respectively.
lcol	the line color surrounding the goal, criteria, and subcriteria boxes.
dist	the distance between the weights and the tree edges.
digit	the number of digits after decimal point to be shown on the arrows.
main	a character string as the plot title

Value

An object created by 'diagram'.

Author(s)

Daryanaz Dargahi

Examples

```
mat <- matrix(nrow = 7, ncol = 2, data = NA)
mat[,1] <- c('0', '1','2','3','4','4.1','4.2')
mat[,2] <- c('Prioritization_of_DE_genes','Tumor_expression','Normal_expression',
'Frequency', 'Epitopes', 'Number_of_epitopes', 'Size_of_epitopes')

# plotting a problem hierarchy
ahplot(mat, fontsize = 0.7, cradx = 0.11 ,sradx = 0.12, cirx= 0.18, ciry = 0.07)

# plotting a problem hierarchy with AHP weights shown on the edges of the graph
mat <- cbind(mat, c(1, 0.470, 0.341, 0.117, 0.073, 0.009, 0.064))
ahplot(mat, fontsize = 0.7, cradx = 0.11 ,sradx = 0.12, cirx= 0.18, ciry = 0.07)
```

---

ahpObj-class   *Class* ahpObj

Description

An object that stores AHP priorities and consistency ratio.

Objects from the Class

Objects can be created by calls of the form new("ahpObj", ...).

Slots

weight: A vector of AHP priorities.

saaty_inconsistency: The consistency ratio.

Author(s)

Daryanaz Dargahi <daryanazdargahi@gmail.com>

---

ahp_matrix   *AHP matrix slot*

Description

ahp_matrix is a slot of ahmatrixObj class. It consists of a square pairwise comparison matrix.

Author(s)

Daryanaz Dargahi <daryanazdargahi@gmail.com>

Examples

```
mat <- matrix(nrow = 3, ncol = 3, data = NA)
mat[1,2] <- 5
mat[1,3] <- 2
mat[2,3] <- 7
res <- ahmatrix(mat)
ahp_matrix(res)
```

---

ahp_plot   *AHP plot slot*

Description

ahp_plot is a slot of pipelineObj class. It consists of a matrix of problem hierarchy.

Author(s)

Daryanaz Dargahi <daryanazdargahi@gmail.com>

Examples

```
mat <- matrix(nrow = 7, ncol = 3, data = NA)
mat[,1] <- c('0', '1','2','3','4','4.1','4.2')
mat[,2] <- c('Prioritization_of_DE_genes','Tumor_expression','Normal_expression',
             'Frequency', 'Epitopes', 'Number_of_epitopes', 'Size_of_epitopes')
mat[,3] <- c(system.file('extdata','aggreg.judgement.tsv',package = 'Prize'),
             system.file('extdata','tumor.PCM.tsv',package = 'Prize'),
             system.file('extdata','normal.PCM.tsv',package = 'Prize'),
             system.file('extdata','freq.PCM.tsv',package = 'Prize'),
             system.file('extdata','epitope.PCM.tsv',package = 'Prize'),
             system.file('extdata','epitopeNum.PCM.tsv',package = 'Prize'),
             system.file('extdata','epitopeLength.PCM.tsv',package = 'Prize'))

result <- pipeline(mat, model = 'relative', simulation = 500)
ahp_plot(result)
```

---

ahp_weights   *AHP weights slot*

Description

ahp_weights is a slot of pipelineObj class. It consists of a list of matrices representing AHP priorities for all decision elements

Author(s)

Daryanaz Dargahi <daryanazdargahi@gmail.com>

Examples

```
mat <- matrix(nrow = 7, ncol = 3, data = NA)
mat[,1] <- c('0', '1','2','3','4','4.1','4.2')
mat[,2] <- c('Prioritization_of_DE_genes','Tumor_expression','Normal_expression',
             'Frequency', 'Epitopes', 'Number_of_epitopes', 'Size_of_epitopes')
mat[,3] <- c(system.file('extdata','aggreg.judgement.tsv',package = 'Prize'),
             system.file('extdata','tumor.PCM.tsv',package = 'Prize'),
             system.file('extdata','normal.PCM.tsv',package = 'Prize'),
             system.file('extdata','freq.PCM.tsv',package = 'Prize'),
             system.file('extdata','epitope.PCM.tsv',package = 'Prize'),
             system.file('extdata','epitopeNum.PCM.tsv',package = 'Prize'),
             system.file('extdata','epitopeLength.PCM.tsv',package = 'Prize'))

result <- pipeline(mat, model = 'relative', simulation = 500)
ahp_weights(result)
```

AIJ   *Aggregated individual judgements (AIJ) slot*

Description

AIJ (Aggregated individual judgements) is a slot of geoAggreg class. It consists of a matrix of aggregated group judgements (a pairwise comparison matrix).

Author(s)

Daryanaz Dargahi <daryanazdargahi@gmail.com>

Examples

```
mat <- matrix(nrow = 4, ncol = 1, data = NA)
mat[,1] <- c(system.file('extdata','ind1.tsv',package = 'Prize'),
             system.file('extdata','ind2.tsv',package = 'Prize'),
             system.file('extdata','ind3.tsv',package = 'Prize'),
             system.file('extdata','ind4.tsv',package = 'Prize'))
rownames(mat) <- c('ind1','ind2','ind3', 'ind4')
colnames(mat) <- c('individual_judgement')

# non-weighted aggregation
res <- gaggregate(srcfile = mat, method = 'geometric', simulation = 500)
AIJ(res)
```

AIP   *Aggregated individual priorities (AIP) slot*

Description

AIP (Aggregated individual priorities) is a slot of ariAggreg class. It consists of a vector of aggregated group priorities.

Author(s)

Daryanaz Dargahi <daryanazdargahi@gmail.com>

Examples

```
mat <- matrix(nrow = 4, ncol = 1, data = NA)
mat[,1] <- c(system.file('extdata','ind1.tsv',package = 'Prize'),
             system.file('extdata','ind2.tsv',package = 'Prize'),
             system.file('extdata','ind3.tsv',package = 'Prize'),
             system.file('extdata','ind4.tsv',package = 'Prize'))
rownames(mat) <- c('ind1','ind2','ind3', 'ind4')
colnames(mat) <- c('individual_judgement')

# non-weighted aggregation
res <- gaggregate(srcfile = mat, method = 'arithmetic', simulation = 500)
AIP(res)
```

---

ariAggreg-class   *Class* ariAggreg

Description

An object that stores the aggregated group priorities as well as consistency ratio of the individual judgements.

Objects from the Class

Objects can be created by calls of the form new("ariAggreg", ...).

Slots

AIP: A vector of aggregated group priorities.

ICR: A vector of individals judgements consistency ratio.

IP: A matrix of individual and aggregated group AHP priorities.

Author(s)

Daryanaz Dargahi <daryanazdargahi@gmail.com>

CI   *Consistency index (CI) slot*

Description

CI (Consistency index) is a slot of geoAggreg class. It consists of a vector of the individuals consistency index.

Author(s)

Daryanaz Dargahi <daryanazdargahi@gmail.com>

Examples

```
mat <- matrix(nrow = 4, ncol = 1, data = NA)
mat[,1] <- c(system.file('extdata','ind1.tsv',package = 'Prize'),
             system.file('extdata','ind2.tsv',package = 'Prize'),
             system.file('extdata','ind3.tsv',package = 'Prize'),
             system.file('extdata','ind4.tsv',package = 'Prize'))
rownames(mat) <- c('ind1','ind2','ind3', 'ind4')
colnames(mat) <- c('individual_judgement')

# non-weighted aggregation
res <- gaggregate(srcfile = mat, method = 'geometric', simulation = 500)
CI(res)
```

---

crplot   *crplot*

Description

Plotting the consistency ratio (CR) of individual judgements. According to Satty, a pairwise comparison matrix is considered to be consistent if CR is equal or less than 0.1. Therefore, CRs equal to or less than 0.1 are colored in green (Pass) and CRs greater than 0.1 are colored in red (Failed).

Usage

```
crplot(srcfile, fontsize = 15, xcex = 10, ycex = 10, angle = 90,
  xlab = "ID", ylab = "ICR", main = NULL)
```

Arguments

srcfile   a numeric vector of individual CR

fontsize   the font size of plot title, x and y axis labels. The default value is 15.

xcex,ycex   the font size of x and y axis, respectively. The default values is 10.

angle   the angle of the labels on x axis

xlab,ylab   the label to be shown on the x and y axis, respectively.

main   the plot title

Value

An object created by 'ggplot'.

Author(s)

Daryanaz Dargahi

Examples

```
data <- c(0.1132, 0.0142, 0.0324, 0.10075, 0.0883)
names(data) <- c('individual_1','individual_2','individual_3','individual_4','individual_5')
crplot(data, fontsize = 15, xcex = 10, ycex = 10, xlab = 'ID', ylab = 'ICR', main = 'Individuals consistency ratio
```

---

dplot   *dplot*

Description

Computing and plotting the distance between individuals and group judgement. Distances are computed using classical multidimensional scaling (MDS) approach.

Usage

```
dplot(srcfile, fontsize = 15, xcex = 10, ycex = 10, lcex = 5,
  hjust = 0.5, vjust = 1, xlab = "Coordinate 1", ylab = "Coordinate 2",
  main = NULL)
```

Arguments

srcfile	a numeric matrix of individual and group priorities.
fontsize	the font size of the plot title, and x and y axis labels. The default value is 15.
xcex,ycex	the font size of the x and y axis, respectively. The default values is 10.
lcex	the font size of point labels in dplot
hjust,vjust	the horizontal and vertical justification of point labels, respectively.
xlab,ylab	the label of the x and y axis, respectively.
main	the plot title

Value

An object created by 'ggplot'.

Author(s)

Daryanaz Dargahi

References

J.C. Gower. Some distance properties of latent root and vector methods used in multivariate analysis. Biometrika, 53(3/4):pp. 325-338, 1966.

Examples

```
mat <- matrix(nrow = 5, ncol = 4, data = NA)
rownames(mat) <- c('Ind1','Ind2','Ind3', 'Ind4' ,'Group judgement')
colnames(mat) <- c('Tumor_expression','Normal_expression','Frequency','Epitopes')
mat[1,] <- c(0.4915181, 0.3058879, 0.12487821, 0.07771583)
mat[2,] <- c(0.3060687, 0.4949012, 0.12868606, 0.07034399)
mat[3,] <- c(0.4627138, 0.3271881, 0.13574662, 0.07435149)
mat[4,] <- c(0.6208484, 0.2414021, 0.07368481, 0.06406465)
mat[5,] <- c(0.4697298, 0.3406738, 0.11600194, 0.07359445)
```

```
dplot(mat, xlab = 'Coordinate 1', ylab = 'Coordinate 2', main = 'Distance plot')
```

---

epitope.PCM-data | *A pairwise comparison matrix (PCM)*

Description

epitope.PCM is a criteria with two subcriteria in the prioritization of a set of genes of interest. This file includes a PCM of the two subcriteria including number of epitopes and size of epitopes. The pairwise comparisons are performed according to the Saaty's fundamental scale.

Author(s)

Daryanaz Dargahi

---

epitopeLength.PCM-data
A pairwise comparison matrix (PCM)

Description

EpitopeLength.PCM is a subcriteria (of the Epitope criterion) in the prioritization of a set of genes of interest. This file includes a PCM of the genes with respect to size (length) of epitopes according to the UniProt annotation (uniprot.org). The pairwise comparisons are performed according to the Saaty's fundamental scale.

Author(s)

Daryanaz Dargahi

References

T.L. Saaty. The Analytic Hierarchy Process, Planning, Piority Setting, Re- source Allocation. McGraw-Hill, New york, 1980.

---

epitopeNum.PCM-data   *A pairwise comparison matrix (PCM)*

Description

EpitopeNum.PCM is a subcriteria (of the Epitope criterion) in the prioritization of a set of genes of interest. This file includes a PCM of the genes with respect to the number of epitopes according to the UniProt annotation (uniprot.org). The pairwise comparisons are performed according to the Saaty's fundamental scale.

Author(s)

Daryanaz Dargahi

References

T.L. Saaty. The Analytic Hierarchy Process, Planning, Piority Setting, Re- source Allocation. McGraw-Hill, New york, 1980.

---

epitope_num_rating-data

Rating categories and idealised priorities

Description

The rating categories and computed idealised priorities of alternatives (genes) with respect to their number of epitopes. This matrix is computed by the rating() function.

Author(s)

Daryanaz Dargahi

---

epitope_size_rating-data

Rating categories and idealised priorities

Description

The rating categories and computed idealised priorities of alternatives (genes) with respect to their epitope size. This matrix is computed by the rating() function.

Author(s)

Daryanaz Dargahi

`freq.PCM-data`   *A pairwise comparison matrix (PCM)*

Description

Freq.PCM is a criteria (with no subcriteria) in the prioritization of a set of genes of interest. This file includes a PCM of the genes with respect to their expression frquency in tumor tissue. The pairwise comparisons are performed according to the Saaty's fundamental scale.

Author(s)

Daryanaz Dargahi

References

T.L. Saaty. The Analytic Hierarchy Process, Planning, Piority Setting, Re- source Allocation. McGraw-Hill, New york, 1980.

`freq_exp_rating-data`   *Rating categories and idealised priorities*

Description

The rating categories and computed idealised priorities of alternatives (genes) with respect to their expression frequency in tumor tissue. This matrix is computed by the rating() function.

Author(s)

Daryanaz Dargahi

`gaggregate`   *gaggregate*

Description

Aggregating individual judgments (pairwise comparison matrices - PCMs) into a group judgement or group priority.

Usage

```
gaggregate(srcfile, method = "geometric", simulation = 500)
```

Arguments

srcfile   a matrix with one or two columns. Column one (required) includes the path
                (location) to each individual pairwise comparison matrix and column two (op-
                tional) includes the individual weights. The matrix rowname is individuals iden-
                tifier.

method   two methods are available for aggregation of individual opinions, (1) arith-
                metic, which compute the arithmetic mean of individual priorities, (2) geomet-
                ric, which computes the geometric mean of individual PCMs. If individuals are
                assigned with a weight, the weighted arithmetic/geometric mean will be com-
                puted. The default method is 'geometric'.

simulation   simulation size for computation of Satty's inconsistency. The default value is
                500.

Value

An S4 object including group PCM/prioritise;

If geometric mean is used, the returning object includes: aggregated group PCM (AIJ), group con-
sistency ratio (GCR), individual consistency ratios (ICR), consensus index (CI), and priority matrix
(IP).

If aritmetic mean is used, the returning object includes: agrregated group priority (AIP), individual
consistency ratios (ICR), and priority matrix (IP).

Author(s)

Daryanaz Dargahi

References

E. Forman and K. Peniwati. Aggregating individual judgments and priorities with the analytic
hierarchy process. European Journal of Operational Research, 108(1):165-169, 1998.

Examples

```
mat <- matrix(nrow = 4, ncol = 1, data = NA)
mat[,1] <- c(system.file('extdata','ind1.tsv',package = 'Prize'),
             system.file('extdata','ind2.tsv',package = 'Prize'),
             system.file('extdata','ind3.tsv',package = 'Prize'),
             system.file('extdata','ind4.tsv',package = 'Prize'))
rownames(mat) <- c('ind1','ind2','ind3', 'ind4')
colnames(mat) <- c('individual_judgement')

# non-weighted aggregation
res <- gaggregate(srcfile = mat, method = 'geometric', simulation = 500)

# weighted aggregation
# Decision makers are assigned with a priority value based on their specialization and perspectives.
mat <- cbind(mat, c(0.35,0.25,0.15,0.25))
colnames(mat)[2] <- 'individual_weight'
```

```
res <- gaggregate(srcfile = mat, method = 'geometric', simulation = 500)
```

GCR *Group consistency ratio (GCR) slot*

Description

GCR (Group consistency ratio) is a slot of geoAggreg class. It consists of the consistency ratio of the aggregated group judgement.

Author(s)

Daryanaz Dargahi <daryanazdargahi@gmail.com>

Examples

```
mat <- matrix(nrow = 4, ncol = 1, data = NA)
mat[,1] <- c(system.file('extdata','ind1.tsv',package = 'Prize'),
             system.file('extdata','ind2.tsv',package = 'Prize'),
             system.file('extdata','ind3.tsv',package = 'Prize'),
             system.file('extdata','ind4.tsv',package = 'Prize'))
rownames(mat) <- c('ind1','ind2','ind3', 'ind4')
colnames(mat) <- c('individual_judgement')

# non-weighted aggregation
res <- gaggregate(srcfile = mat, method = 'geometric', simulation = 500)
GCR(res)
```

---

genes.list-data *A pairwise comparison matrix (PCM)*

Description

A matrix of genes to prioritize based on their tumor and normal expression, frequency of expression in tumor tissue, and number and size of epitopes.

Author(s)

Daryanaz Dargahi

---

geoAggreg-class   *Class* geoAggreg

Description

An object that stores the aggregated group judgements as well as consistency ratio of the individuals and group judgements.

Objects from the Class

Objects can be created by calls of the form new("geoAggreg", ...).

Slots

AIJ: A matrix of aggregated group judgements (a pairwise comparison matrix).

GCR: The consistency ratio of the aggregated group judgement.

CI: A vector of the individuals consistency index.

ICR: A vector of individals judgements consistency ratio.

IP: A matrix of individual and aggregated group AHP priorities.

Author(s)

Daryanaz Dargahi <daryanazdargahi@gmail.com>

ICR   *Individual consistency ratio (ICR) slot*

Description

Individual consistency ratio (ICR) is a slot of geoAggreg and ariAggreg classes. It consists of a vector of individals judgements consistency ratio.

Author(s)

Daryanaz Dargahi <daryanazdargahi@gmail.com>

Examples

```
mat <- matrix(nrow = 4, ncol = 1, data = NA)
mat[,1] <- c(system.file('extdata','ind1.tsv',package = 'Prize'),
             system.file('extdata','ind2.tsv',package = 'Prize'),
             system.file('extdata','ind3.tsv',package = 'Prize'),
             system.file('extdata','ind4.tsv',package = 'Prize'))
rownames(mat) <- c('ind1','ind2','ind3', 'ind4')
colnames(mat) <- c('individual_judgement')

# Aggregation of individual judgements
res <- gaggregate(srcfile = mat, method = 'geometric', simulation = 500)
ICR(res)

# Aggregation of individual priorities
res <- gaggregate(srcfile = mat, method = 'arithmetic', simulation = 500)
ICR(res)
```

---

ind1-data   *An individual judgement matrix*

Description

A numeric square matrix generated based on Saaty's fundamental scale. This matrix includes judgements of a decision maker.

Author(s)

Daryanaz Dargahi

References

T.L. Saaty. The Analytic Hierarchy Process, Planning, Piority Setting, Re- source Allocation. McGraw-Hill, New york, 1980.

---

ind2-data   *An individual judgement matrix*

Description

A numeric square matrix generated based on Saaty's fundamental scale. This matrix includes judgements of a decision maker.

Author(s)

Daryanaz Dargahi

References

T.L. Saaty. The Analytic Hierarchy Process, Planning, Piority Setting, Re- source Allocation. McGraw-Hill, New york, 1980.

---

ind3-data   *An individual judgement matrix*

Description

A numeric square matrix generated based on Saaty's fundamental scale. This matrix includes judgements of a decision maker.

Author(s)

Daryanaz Dargahi

References

T.L. Saaty. The Analytic Hierarchy Process, Planning, Piority Setting, Re- source Allocation. McGraw-Hill, New york, 1980.

---

ind4-data   *An individual judgement matrix*

Description

A numeric square matrix generated based on Saaty's fundamental scale. This matrix includes judgements of a decision maker.

Author(s)

Daryanaz Dargahi

References

T.L. Saaty. The Analytic Hierarchy Process, Planning, Piority Setting, Re- source Allocation. McGraw-Hill, New york, 1980.

IP   *Individual priority (IP) slot*

Description

IP (Individual priority) is a slot of geoAggreg and ariAggreg classes. It consists of a matrix of individual and aggregated group AHP priorities.

Author(s)

Daryanaz Dargahi <daryanazdargahi@gmail.com>

Examples

```
mat <- matrix(nrow = 4, ncol = 1, data = NA)
mat[,1] <- c(system.file('extdata','ind1.tsv',package = 'Prize'),
             system.file('extdata','ind2.tsv',package = 'Prize'),
             system.file('extdata','ind3.tsv',package = 'Prize'),
             system.file('extdata','ind4.tsv',package = 'Prize'))
rownames(mat) <- c('ind1','ind2','ind3', 'ind4')
colnames(mat) <- c('individual_judgement')

# Aggregation of individual judgements
res <- gaggregate(srcfile = mat, method = 'geometric', simulation = 500)
IP(res)

# Aggregation of individual priorities
res <- gaggregate(srcfile = mat, method = 'arithmetic', simulation = 500)
IP(res)
```

---

normal.PCM-data   *A pairwise comparison matrix (PCM)*

Description

Normal.PCM is a criteria (with no subcriteria) in the prioritization of a set of genes of interest. This file includes a PCM of the genes with respect to their expression level in healthy (normal) tissues. The pairwise comparisons are performed according to the Saaty's fundamental scale.

Author(s)

Daryanaz Dargahi

References

T.L. Saaty. The Analytic Hierarchy Process, Planning, Piority Setting, Re- source Allocation. McGraw-Hill, New york, 1980.

`normal_exp_rating-data`

Rating categories and idealised priorities

Description

The rating categories and computed idealised priorities of alternatives (genes) with respect to their expression in healthy (normal) tissues. This matrix is computed by the rating() function.

Author(s)

Daryanaz Dargahi

`number-data`   *A pairwise comparison matrix (PCM)*

Description

Number is a PCM of the categories defined for the number of epitopes subcriteria. The categories include: Single and Multiple. The pairwise comparisons are performed according to the Saaty's fundamental scale.

Author(s)

Daryanaz Dargahi

References

T.L. Saaty. The Analytic Hierarchy Process, Planning, Piority Setting, Re- source Allocation. McGraw-Hill, New york, 1980.

`numEpitope_alternative_category-data`

A pairwise comparison matrix (PCM)

Description

A matrix assigning each alternative (gene) to a category with respect to their number of epitopes. The categories include: Single and Multiple.

Author(s)

Daryanaz Dargahi

---

pipeline	*pipeline*

Description

a pipeline for prioritization estimation using analytic hierarchy process (AHP), which supports both relative and rating AHP models.

Usage

```
pipeline(srcfile, model, simulation = 500)
```

Arguments

srcfile	a character matrix, where the first column specifies the hierarchy order, the second column includes elements IDs, and the third column includes the path to the PCM/priority matrices (See the example below).
model	the AHP computation model. Choose from relative and rating models. If using the relative model pairwise comparison matrices must be provided for the evaluation of alternatives. However, if using the raing model, rating matrices must be provided for the evaluation of alternatives.
simulation	simulation size for computation of Saaty's inconsistency

Value

An S4 object including the ahp wight and consistancy measures, and data structures to visualize with ahplot(), rainbowplot(), and wplot().

Author(s)

Daryanaz Dargahi

Examples

```
mat <- matrix(nrow = 7, ncol = 3, data = NA)
mat[,1] <- c('0', '1','2','3','4','4.1','4.2')
mat[,2] <- c('Prioritization_of_DE_genes','Tumor_expression','Normal_expression',
             'Frequency', 'Epitopes', 'Number_of_epitopes', 'Size_of_epitopes')
mat[,3] <- c(system.file('extdata','aggreg.judgement.tsv',package = 'Prize'),
             system.file('extdata','tumor.PCM.tsv',package = 'Prize'),
             system.file('extdata','normal.PCM.tsv',package = 'Prize'),
             system.file('extdata','freq.PCM.tsv',package = 'Prize'),
             system.file('extdata','epitope.PCM.tsv',package = 'Prize'),
             system.file('extdata','epitopeNum.PCM.tsv',package = 'Prize'),
             system.file('extdata','epitopeLength.PCM.tsv',package = 'Prize'))

result <- pipeline(mat, model = 'relative', simulation = 500)
```

---

pipelineObj-class   *Class* pipelineObj

Description

An object that stores the problem hierarchy as well as AHP priorities.

Objects from the Class

Objects can be created by calls of the form new("pipelineObj", ...).

Slots

ahp_plot: A matrix of problem hierarchy.

weight_plot: A list of matrices representing AHP priorities at the criteria and subcriteria level.

rainbow_plot: A list of matrices representing final AHP ranking of alternatives at the criteria and subcriteria level.

ahp_weights: A list of matrices representing AHP priorities for all decision elements.

simulation: A numeric value of the simulation size.

saaty_inconsistency: A list of Saaty inconsistency ratios.

Author(s)

Daryanaz Dargahi <daryanazdargahi@gmail.com>

---

rainbowplot   *rainbowplot*

Description

Plotting prioritized alternatives in a color-coded barplot, where a color is assigned to each criteria/subcriteria.

Usage

```
rainbowplot(srcfile, range = NULL, fontsize = 10, xcex = 4, ycex = 8,
  color = "rainbow", xlab = "Total priority score", ylab = "Alternative",
  digit = 3, dist = 0.02, main = NULL)
```

Arguments

srcfile	a numeric matrix with alternatives on the rows and criteria/subcriteria on the columns. alternative's AHP weights for each criteria, and the sum of each row on the last column (see example below).
range	specifies which alternatives to plot. Either provide a range (e.g. 1:5) or a vector of numbers (e.g. c(2,5,12,20)). if range is NULL then all alternatives will be plotted. The default value is NULL.
fontsize	the font size of the plot title, x and y axis labels, and legend. The default value is 10.
xcex	the font size of the labels on the bars. The default values is 4.
ycex	the font size of the y axis. The default values is 8.
color	the color palette to fill bars. Either provide a vector of n colors, where n is the number of criteria/subcriteria, or choose from the following palettes 'rainbow, heat, terrain, topo, cm'. The default value is rainbow.
xlab,ylab	the label of the x and y axis, respectively.
digit	the number of digits after decimal point to be shown on the bars. The default value is 3.
dist	the distance between the bar and its lable. The default value is 0.02.
main	the plot title

Value

An object created by 'ggplot'.

Author(s)

Daryanaz Dargahi

Examples

```
mat <- matrix(c(0.007,0.289,0.033,0.118,0.447, 0.015,0.155,0.015,0.088,0.275, 0.048,0.078,0.007,0.044,0.177, 0.
                nrow = 4, ncol = 5, byrow = TRUE, dimnames = list(c('CA9','MUC16','CD70','MUC1'), c('Tumor_expressio
rainbowplot(mat, range = NULL, xlab = 'Total priority score' , ylab = 'Alternative', dist = 0.04)
```

---

rainbow_plot	*Rainbow plot slot*

Description

rainbow_plot is a slot of pipelineObj class. It consists of a list of matrices representing final AHP ranking of alternatives at the criteria and subcriteria level.

Author(s)

Daryanaz Dargahi <daryanazdargahi@gmail.com>

Examples

```
mat <- matrix(nrow = 7, ncol = 3, data = NA)
mat[,1] <- c('0', '1','2','3','4','4.1','4.2')
mat[,2] <- c('Prioritization_of_DE_genes','Tumor_expression','Normal_expression',
             'Frequency', 'Epitopes', 'Number_of_epitopes', 'Size_of_epitopes')
mat[,3] <- c(system.file('extdata','aggreg.judgement.tsv',package = 'Prize'),
             system.file('extdata','tumor.PCM.tsv',package = 'Prize'),
             system.file('extdata','normal.PCM.tsv',package = 'Prize'),
             system.file('extdata','freq.PCM.tsv',package = 'Prize'),
             system.file('extdata','epitope.PCM.tsv',package = 'Prize'),
             system.file('extdata','epitopeNum.PCM.tsv',package = 'Prize'),
             system.file('extdata','epitopeLength.PCM.tsv',package = 'Prize'))

result <- pipeline(mat, model = 'relative', simulation = 500)
rainbow_plot(result)
```

---

rating	*rating*

Description

Estimates idealised priorities of alternatives (the rating AHP model).

Usage

```
rating(scale, alternative, NA_category = NULL, simulation = 500)
```

Arguments

scale	a pairwise comparison matrix (PCM) of rating categories.
alternative	a N by 2 character matrix, where N is the number of alternatives. The matrix includes alternatives on column #1 and the rating category they belong to on column #2.
NA_category	a character string or vector which specifies categories with the value of zero. Since zero is not achievable by PCM matrix.
simulation	simulation size for computation of Saaty's inconsistency

Value

An S4 object including the raw and normalized ahp priorities, Satty's inconsistency, and rating matrix.

Author(s)

Daryanaz Dargahi

References

T.L. Saaty. Rank from comparisons and from ratings in the analytic hierarchy/network processes. European Journal of Operational Research, 168(2):557-570, January 2006.

T.L. Saaty. The Analytic Hierarchy Process, Planning, Piority Setting, Resource Allocation. McGraw-Hill, New york, 1980.

Examples

```
mat <- matrix(nrow = 4, ncol = 4, data = NA)

# The category PCM matrix
rownames(mat) <- c('excellent','good','fair','poor')
colnames(mat) <- c('excellent','good','fair','poor')
mat[1,] <- c(1,2,4,6)
mat[2,] <- c(NA,1,2,4)
mat[3,] <- c(NA,NA,1,2)
mat[4,] <- c(NA,NA,NA,1)

# The alternative matrix
alt <- matrix(nrow = 5, ncol = 2, data = NA)
alt[,1] <- c("Andy", "Emily", "Nina", "Alex", "Jack")
alt[,2] <- c("good", "poor", "good", "fair", "excellent")

result <- rating(mat, alt, simulation = 500)

# Specifying a category with value of zero
alt <- rbind(alt, c('shannon', 'Not_available'))

result <- rating(mat, alt, NA_category = 'Not_available', simulation = 500)
```

---

ratingObj-class   *Class* ratingObj

Description

An object that stores the idealised priorities of alternatives (The rating AHP model).

Objects from the Class

Objects can be created by calls of the form new("ratingObj", ...).

Slots

weight: A matrix of rating categoris and their AHP and idealised prioritise.

saaty_inconsistency: The consistency ratio of the categories pairwise comparison matrix.

RM: A matrix of alternatives with their scale category and idealised prioritise.

Author(s)

Daryanaz Dargahi <daryanazdargahi@gmail.com>

RM   *Rating matrix (RM) slot*

Description

RM (Rating matrix) is a slot of ratingObj class. It consists of a matrix of alternatives with their scale category and idealised prioritise.

Author(s)

Daryanaz Dargahi <daryanazdargahi@gmail.com>

Examples

```
mat <- matrix(nrow = 4, ncol = 4, data = NA)

# Category PCM matrix
rownames(mat) <- c('excellent','good','fair','poor')
colnames(mat) <- c('excellent','good','fair','poor')
mat[1,] <- c(1,2,4,6)
mat[2,] <- c(NA,1,2,4)
mat[3,] <- c(NA,NA,1,2)
mat[4,] <- c(NA,NA,NA,1)

# Alternative matrix
alt <- matrix(nrow = 5, ncol = 2, data = NA)
alt[,1] <- c("Andy", "Emily", "Nina", "Alex", "Jack")
alt[,2] <- c("good", "poor", "good", "fair", "excellent")

result <- rating(mat, alt, simulation = 500)
RM(result)
```

---

saaty_inconsistency   *Saaty inconsistency slot*

Description

saaty_inconsistency is a slot of ahpObj, pipelineObj, and ratingObj classes. It consists of Saarty's consistency ratio of a pairwise comparison matrix.

Author(s)

Daryanaz Dargahi <daryanazdargahi@gmail.com>

Examples

```
# ahp()
mat <- matrix(c(1,2,5, 1/2,1,3, 1/5,1/3,1), nrow = 3, ncol = 3, byrow = TRUE)
res <- ahp(mat, simulation = 500)
saaty_inconsistency(res)

# pipeline()
mat <- matrix(nrow = 7, ncol = 3, data = NA)
mat[,1] <- c('0', '1','2','3','4','4.1','4.2')
mat[,2] <- c('Prioritization_of_DE_genes','Tumor_expression','Normal_expression',
             'Frequency', 'Epitopes', 'Number_of_epitopes', 'Size_of_epitopes')
mat[,3] <- c(system.file('extdata','aggreg.judgement.tsv',package = 'Prize'),
             system.file('extdata','tumor.PCM.tsv',package = 'Prize'),
             system.file('extdata','normal.PCM.tsv',package = 'Prize'),
             system.file('extdata','freq.PCM.tsv',package = 'Prize'),
             system.file('extdata','epitope.PCM.tsv',package = 'Prize'),
             system.file('extdata','epitopeNum.PCM.tsv',package = 'Prize'),
             system.file('extdata','epitopeLength.PCM.tsv',package = 'Prize'))

result <- pipeline(mat, model = 'relative', simulation = 500)
saaty_inconsistency(result)

# rating()
mat <- matrix(nrow = 4, ncol = 4, data = NA)
## Category PCM matrix
rownames(mat) <- c('excellent','good','fair','poor')
colnames(mat) <- c('excellent','good','fair','poor')
mat[1,] <- c(1,2,4,6)
mat[2,] <- c(NA,1,2,4)
mat[3,] <- c(NA,NA,1,2)
mat[4,] <- c(NA,NA,NA,1)
## Alternative matrix
alt <- matrix(nrow = 5, ncol = 2, data = NA)
alt[,1] <- c("Andy", "Emily", "Nina", "Alex", "Jack")
alt[,2] <- c("good", "poor", "good", "fair", "excellent")

result <- rating(mat, alt, simulation = 500)
saaty_inconsistency(result)
```

---

simulation	*Simulation slot*

Description

simulation is a slot of pipelineObj class. It consists of a numeric value of the simulation size (used in order to estimate Saaty's consistency ratio).

Author(s)

Daryanaz Dargahi <daryanazdargahi@gmail.com>

Examples

```
mat <- matrix(nrow = 7, ncol = 3, data = NA)
mat[,1] <- c('0', '1','2','3','4','4.1','4.2')
mat[,2] <- c('Prioritization_of_DE_genes','Tumor_expression','Normal_expression',
             'Frequency', 'Epitopes', 'Number_of_epitopes', 'Size_of_epitopes')
mat[,3] <- c(system.file('extdata','aggreg.judgement.tsv',package = 'Prize'),
             system.file('extdata','tumor.PCM.tsv',package = 'Prize'),
             system.file('extdata','normal.PCM.tsv',package = 'Prize'),
             system.file('extdata','freq.PCM.tsv',package = 'Prize'),
             system.file('extdata','epitope.PCM.tsv',package = 'Prize'),
             system.file('extdata','epitopeNum.PCM.tsv',package = 'Prize'),
             system.file('extdata','epitopeLength.PCM.tsv',package = 'Prize'))

result <- pipeline(mat, model = 'relative', simulation = 500)
simulation(result)
```

---

tumor.PCM-data   *A pairwise comparison matrix (PCM)*

Description

Tumor.PCM is a criteria (with no subcriteria) in the prioritization of a set of genes of interest. This file includes a PCM of the genes with respect to their expression level in tumor tissue. The pairwise comparisons are performed according to the Saaty's fundamental scale.

Author(s)

Daryanaz Dargahi

References

T.L. Saaty. The Analytic Hierarchy Process, Planning, Piority Setting, Re- source Allocation. McGraw-Hill, New york, 1980.

---

tumor_exp_rating-data   *Rating categories and idealised priorities*

Description

The rating categories and computed idealised priorities of alternatives (genes) with respect to their expression in tumor tissue. This matrix is computed by the rating() function.

Author(s)

Daryanaz Dargahi

---

weight   *Weight slot*

Description

weight is a slot of ahpObj and ratingObj classes. It consists of computed AHP weights from a pairwise comparison matrix.

Author(s)

Daryanaz Dargahi <daryanazdargahi@gmail.com>

Examples

```
# ahp()
mat <- matrix(c(1,2,5, 1/2,1,3, 1/5,1/3,1), nrow = 3, ncol = 3, byrow = TRUE)
res <- ahp(mat, simulation = 500)
weight(res)

# rating()
mat <- matrix(nrow = 4, ncol = 4, data = NA)

## Category PCM matrix
rownames(mat) <- c('excellent','good','fair','poor')
colnames(mat) <- c('excellent','good','fair','poor')
mat[1,] <- c(1,2,4,6)
mat[2,] <- c(NA,1,2,4)
mat[3,] <- c(NA,NA,1,2)
mat[4,] <- c(NA,NA,NA,1)
## Alternative matrix
alt <- matrix(nrow = 5, ncol = 2, data = NA)
alt[,1] <- c("Andy", "Emily", "Nina", "Alex", "Jack")
alt[,2] <- c("good", "poor", "good", "fair", "excellent")

result <- rating(mat, alt, simulation = 500)
weight(result)
```

---

weight_plot   *Weight plot slot*

Description

weight_plot is a slot of pipelineObj class. It consists of a list of matrices representing AHP priorities at the criteria and subcriteria level.

Author(s)

Daryanaz Dargahi <daryanazdargahi@gmail.com>

Examples

```
mat <- matrix(nrow = 7, ncol = 3, data = NA)
mat[,1] <- c('0', '1','2','3','4','4.1','4.2')
mat[,2] <- c('Prioritization_of_DE_genes','Tumor_expression','Normal_expression',
             'Frequency', 'Epitopes', 'Number_of_epitopes', 'Size_of_epitopes')
mat[,3] <- c(system.file('extdata','aggreg.judgement.tsv',package = 'Prize'),
             system.file('extdata','tumor.PCM.tsv',package = 'Prize'),
             system.file('extdata','normal.PCM.tsv',package = 'Prize'),
             system.file('extdata','freq.PCM.tsv',package = 'Prize'),
             system.file('extdata','epitope.PCM.tsv',package = 'Prize'),
             system.file('extdata','epitopeNum.PCM.tsv',package = 'Prize'),
             system.file('extdata','epitopeLength.PCM.tsv',package = 'Prize'))

result <- pipeline(mat, model = 'relative', simulation = 500)
weight_plot(result)
```

---

wplot	*Wplot*

Description

Plotting the criteria/subcriteria ahp weights in a bar/pie plot.

Usage

```
wplot(srcfile, color = "rainbow", fontsize = 15, xcex = 10, ycex = 10,
  pcex = 5, digit = 2, xlab = NULL, ylab = NULL, type = "bar",
  main = NULL)
```

Arguments

srcfile	a matrix, where the first column includes criteria/subcriteria ID and the second includes the ahp weights.
color	the color palette to fill bars. Either provide a vector of n colors, where n is the number of criteria, or choose from the following palettes 'rainbow, heat, terrain, topo, cm'. The default value is rainbow.
fontsize	the font size of the plot title, and x and y axis labels. The default value is 15.
xcex,ycex	the font size of the x and y axis, respectively. The default values is 10.
pcex	the font size of the labels inside pie chart
digit	the number of digits after decimal point to be shown on the x axis.
xlab,ylab	the label of the x and y axis, respectively.
type	wplot offers two plot types; bar and pie plots. Default value is bar.
main	the plot title

Value

An object created by 'ggplot'.

Author(s)

Daryanaz Dargahi

Examples

```
mat <- matrix(nrow = 4, ncol = 2, data = NA)
mat[,1] <- c('Tumor_expression','Normal_expression','Frequency','Epitope')
mat[,2] <- c(0.470, 0.341, 0.116, 0.073)

wplot(mat, xlab = 'Weight', ylab = 'Criteria', type = 'bar')
wplot(mat, type = 'pie')
```

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