Package 'RMallow'

October 12, 2022

Type Package

Title Fit Multi-Modal Mallows' Models to Ranking Data

Version 1.1

Date 2020-01-23

Depends combinat

Description An EM algorithm to fit Mallows' Models to full or partial rankings, with or without ties. Based on Adkins and Flinger (1998) <doi:10.1080/03610929808832223>.

License GPL (>= 2)

Repository CRAN

Date/Publication 2020-02-07 01:10:16 UTC

NeedsCompilation no

Author Erik Gregory [aut, cre]

Maintainer Erik Gregory <egregory2011@gmail.com>

R topics documented:

RMallow-package 2
AllKendall 3
AllSeqDists 3
BestFit 4
ConstructSeqs 5
C_lam 5
datas 6
DistanceDistribution 6
elect 7
EStep 7
FormatOut 8
hello 9
KendallInfo 9
Lambda 10
Likelihood 11
Mallows 11

NextTable 12
Rgen 13
SeqDistribution 13
SimplifySequences 14
three.mode 14
two.mode 15
two.seq 16
UpdateLambda 16
UpdateP 17
UpdateR 18

Index **19**

`RMallow-package` *Fit Multi-modal Mallows' models to ranking data.*

Description

Fits the Mallows' model to ranking data. Data can be partially or fully-ranked.

Details

Package:	RMallow
Type:	Package
Version:	1.0
Date:	2012-02-18
License:	GPL (>= 2)

Author(s)

Erik Gregory Maintainer: <egregory2007@yahoo.com>

References

"Mixtures of distance-based models for ranking data". Thomas Brendan Murphy & Donal Martin. 1 April 2002. Computational Statistics & Data Analysis 41 (2003) 645-655.

"Estimating a Population Distribution of Sequences of k Items from Cross- Sectional Data". Laurel A. Smith (Beckett) and Denis A. Evans. Journal of the Royal Statistical Society. Series C (Applied Statistics). Vol. 40, No. 1 (1991), pp.31-42. Blackwell Publishing for the Royal Statistical Society. Accessed 16/08/2010. http://www.jstor.org/stable/2347903 .

"A Non-iterative procedure for maximum likelihood estimation of the parameters of Mallows' Model Based on Partial Rankings". Laura Adkins and Michael Flinger. Communication in Statistics - Theory and Methods, 27:9, 2199-2220. 1998, Marchel Dekker, Inc. http://dx.doi.org/10.1080/03610929808832223 .

`AllKendall` *All Kendall's distances between two sets of rankings.*

Description

Calculates all of the Kendall's distances between two different sets of rankings.

Usage

```
AllKendall(r, seqs, data.info = NULL)
```

Arguments

`r`	One set of sequences.
`seqs`	Another set of sequences.
`data.info`	Optional argument, a 0/1/NA matrix specifying all of the relevant information to calculate Kendall's difference for "r". Used for efficiency in "Solve".

Value

Matrix where output[i, j] represents the distance from sequence "i" in "r" to sequence "j" in "seqs".

Author(s)

Erik Gregory

Examples

```
data1 <- do.call("rbind", list(1:5, 5:1, c(3, 2, 1, 4, 5)))
data2 <- do.call("rbind", list(1:5, 5:1))
# AllKendall(data1, data2)
```

`AllSeqDists` *Calculate all distances between a set of sequences and a fixed sequence.*

Description

Used to calculate the sequence Kendall distance distribution in N! space.

Usage

```
AllSeqDists(seqs)
```

Arguments

seqs	Matrix or data frame of sequences.

Value

Vector of the distances from the sequences to 1:N.

Author(s)

Erik Gregory

BestFit *Fit Mallows model N times and select most likely model. The EM algorithm to fit Multi-Modal Mallows' models is prone to getting stuck in local maxima, so we run it several times and selec the best one.*

Description

Fit Mallows model N times and select most likely model. The EM algorithm to fit Multi-Modal Mallows' models is prone to getting stuck in local maxima, so we run it several times and selec the best one.

Usage

```
BestFit(datas, N, iter, G)
```

Arguments

N	number of times to run the model
iter	maximum number of iterations for each run
G	Number of cluster centers
datas	data set to fit

Value

best fitting model.

`ConstructSeqs` *Constructs sequences from Kendall Information matricies.*

Description

Sequences in a fully-ordered sequence space have a unique Kendall Information vector associated with them. This function creates the sequence from the Kendall information vector.

Usage

```
ConstructSeqs(prefs, n.abils)
```

Arguments

`prefs`	Ordering preference between columns in the data. 1 cooresponds to an increase, 0 to a decrease.
`n.abils`	Number of columns in the original data set.

Value

List of fully-ordered sequences, one for each row of prefs.

Author(s)

Erik Gregory

Examples

```
ConstructSeqs(matrix(c(1, 1, 1, 0, 0, 0), nrow = 1), 4)
# Should output (4, 1, 2, 3)
```

`C_lam` *Calculate the normalizing coefficient for Mallow's model in a sequence space.*

Description

Calculate the normalizing coefficient, as a function of the lambda parameter, and the size of the sequence space.

Usage

```
C_lam(lambda, dists = NULL, dists.table = NULL)
```

Arguments

lambda	Spread parameter for Mallows' model.
dists	Vector of all distances from each sequence to 1:N
dists.table	Table version of "dists" above.

Value

Normalizing coefficient of Mallows' model in N! space with lambda = lambda.

Author(s)

Erik Gregory

---

datas *Sample data set.*

Description

Simple synthetic data set containing 3 modal sequences in 15! space, with some noise added.

Format

The format is: num [1:1700, 1:15] 1 15 1 15 15 12 10 4 1 15 ...

Examples

```
data(datas)
head(datas)
```

DistanceDistribution *Calculate the Kendall distance distribution in N! space.*

Description

This function counts the number of fully-ordered vectors at each distance in N! space.

Usage

```
DistanceDistribution(N = 3)
```

Arguments

N	Integer value, greater than or equal to 3.

Value

Table-like structure, where the names represent the distance from the modal sequence of each sequence in N! space, and the values represent the number of sequences at that distance in the sequence space.

Author(s)

Erik Gregory

---

elect *1980 APA Presidential Candidate ranking data.*

Description

This data is a pre-processed version of the 1980 American Psychological Association Presidential candidate ranking data. It has uninformative rankings removed, and values pre-simplified into partial rankings.

Format

The format is: int [1:1378, 1:3] 1 1 1 1 2 2 1 1 2 2 ... - attr(*, "dimnames")=List of 2 ..$: chr [1:1378] "1" "2" "3" "6" ... ..$: chr [1:3] "Carter" "Reagan" "Anderson"

Source

The American Psychological Association, http://www.electionstudies.org/studypages/1980prepost/1980prepost.htm

Examples

```
data(elect)
head(elect)
```

EStep *The Expectation step of the EM algorithm.*

Description

Assigns each ranking the probability that it belongs to each cluster, given current parameters.

Usage

```
EStep(R, r, p, lambda, G, N, C, all.dists = NULL)
```

Arguments

R	Current cluster modal sequences.
r	The data of partial or full rankings.
p	The proportion of the data currently assigned to each cluster.
lambda	The lambda parameters from Mallow's model for each cluster.
G	Number of clusters, length(R).
N	Number of rows in the data.
C	Vector of normalizing coefficients for the clusters.
all.dists	For efficiency, provide all of the Kendall distances between each sequence and each cluster mode.

Value

Matrix where output[i, j] represents the current probability that subject "i" belongs to cluster "j".

Author(s)

Erik Gregory

References

"Mixtures of distance-based models for ranking data". Thomas Brendan Murphy & Donal Martin. 1 April 2002. Computational Statistics & Data Analysis 41 (2003) 645-655.

FormatOut *Formats the data in the "Solve" function for output.*

Description

Data formatting function.

Usage

```
FormatOut(R, p, lambda, z, datas, likelihood)
```

Arguments

R	The modal sequences.
p	Proportion of data in each cluster.
lambda	Mallows' spread parameters for each cluster.
z	Probability of cluster membership for each individual.
datas	Matrix of partial sequences.
likelihood	Vector of the log-likelihood of the model at each iteration.

Value

R	The modal sequences
p	Proportion in each cluster
lambda	Spread parameters for each cluster
datas	Rankings merged with their cluster membership, distance from each cluster center, and probability of each cluster membership
min.like	Likelihood at each iteration

Author(s)

Erik Gregory

---

hello *Hello, World!*

Description

Prints 'Hello, world!'.

Usage

```
hello()
```

Examples

```
hello()
```

KendallInfo *All information used to calculate Kendall's distance.*

Description

Performs each column-wise comparison on a matrix of sequences. A 0 value denotes that there is an increase between the two columns, 1 a decrease, and NA indicates that the column values are identical in the row.

Usage

```
KendallInfo(r, inds = NULL)
```

Arguments

r	Matrix of sequences.
inds	Possibly efficiency increase when doing repeated calculations, currently not used.

Value

Matrix of 0s, 1s, and NAs representing pairwise comparisons of vector values.

Author(s)

Erik Gregory

References

http://en.wikipedia.org/wiki/Kendall_tau_distance

`Lambda` *Objective function to determine lambda.*

Description

Objective function to find the root of in calculating the lambda parameters for each cluster.

Usage

```
Lambda(lambda, rhs, dists, dists.table = NULL)
```

Arguments

`lambda`	lambda value to calculate the function output at.
`rhs`	Right-hand side of the equation in the referenced paper.
`dists`	Not used.
`dists.table`	Table of distances between each sequence and the modal sequence in N! space.

Value

Output of the objective function to determine the root of. Goal is zero.

Author(s)

Erik Gregory

References

"Mixtures of distance-based models for ranking data". Thomas Brendan Murphy & Donal Martin. 1 April 2002. Computational Statistics & Data Analysis 41 (2003) 645-655.

Likelihood *Likelihood of the data and parameters.*

Description

Calculates the log-likelihood of the data with the current parameters and Kendall's distance.

Usage

```
Likelihood(z, p, C.lam, lambda, all.dists.data)
```

Arguments

z	Probability of each cluster membership.
p	Proportion in each cluster.
C.lam	Vector of normalizing coefficients for Mallows' model.
lambda	Current spread parameters
all.dists.data	All distances from the data to the modal sequences.

Value

Current log-likelihood of the data with the current parameters.

Author(s)

Erik Gregory

References

"Mixtures of distance-based models for ranking data". Thomas Brendan Murphy & Donal Martin. 1 April 2002. Computational Statistics & Data Analysis 41 (2003) 645-655.

Mallows *Fits a Multi-Modal Mallows' model to ranking data.*

Description

Fits the Multi-Modal Mallows' model to partial or full ranking data, using Kendall's metric and an EM algorithm. This is essentially metric sequence clustering.

Usage

```
Mallows(datas, G, iter = 10, hyp = NULL,
  plot.like = FALSE)
```

Arguments

datas	Matrix of partial or fully-ranked data.
G	Number of modes, 2 or greater.
iter	Maximum number of iterations.
hyp	Hypothesis sequence vector, to initialize one of the cluster centers at.
plot.like	Should the likelihood be printed at each iteration?

Value

See output of FormatOut

Author(s)

Erik Gregory

References

"Mixtures of distance-based models for ranking data". Thomas Brendan Murphy & Donal Martin. 1 April 2002. Computational Statistics & Data Analysis 41 (2003) 645-655.

NextTable — *Calculates the table of Kendall distances in (N+1)! space, given those in N! space.*

Description

This is identical to counting the number of fully-ordered vectors at each bubble sort distance in (N+1)! space.

Usage

```
NextTable(last.table, N.last)
```

Arguments

last.table	Table of distances in N! space.
N.last	N

Value

Table of distances in (N+1)! space.

Author(s)

Erik Gregory

Rgen — *Initialize sequence modes for the clustering process.*

Description

Initialize sequence modes for the clustering process.

Usage

```
Rgen(G, hyp = NULL, abils)
```

Arguments

G	number of cluster centers, including the hypothesis if provided
hyp	a single sequence of length abils to initialize one of the cluster centers
abils	number of items being ranked

Value

A list of G cluster centers, each of length abils

Author(s)

Erik Gregory

Examples

```
Rgen(3, 1:5, 5)
```

SeqDistribution — *Calculates distances in N! space.*

Description

Calculates Kendall's distances of each sequence in N! space. This is VERY Inefficient for N >= 8. See DistanceDistribution for an astronomical improvement (possibly on the order of 10^10).

Usage

```
SeqDistribution(N)
```

Arguments

N	Length of the ranking. Preferrably less than 9.

Value

Vector of Kendall distances from 1:N to each sequence in N! space.

Author(s)

Erik Gregory

`SimplifySequences` *Change the form of ordered sequences.*

Description

Simplifies sequences so that each tie group is only of distance 1 to the next tie group. For example, we would simplify (1, 1, 2, 4, 4, 5) to (1, 1, 2, 3, 3, 4).

Usage

```
SimplifySequences(loss.time)
```

Arguments

`loss.time`	Matrix of sequences to be simplified.

Value

Simplified sequences, as described in Description.

Author(s)

Erik Gregory

`three.mode` *Fitted version of the toy datas data set, with three modal sequences.*

Description

The data has 3 modal sequences, and we can compare this to the two.mode data set.

Format

The format is: List of 5 $ R :List of 3 ..$: int [1:15] 1 2 3 4 5 6 7 8 9 10 ... ..$: int [1:15] 1 3 5 7 9 2 4 6 8 10 ... ..$: int [1:15] 15 14 13 12 11 10 9 8 7 6 ... $ p : num [1:3] 0.447 0.118 0.435 $ lambda : num [1:3] 2.01 1000 2.04 $ datas :'data.frame': 1700 obs. of 23 variables: ..$ X1 : num [1:1700] 1 15 1 15 15 12 10 4 1 15 ... ..$ X2 : num [1:1700] 2 14 2 14 14 13 13 12 2 14 ... ..$ X3 : num [1:1700] 3 13 3 13 13 2 4 6 3 13 ... ..$ X4 : num [1:1700] 4 12 4 12 12 8 7 1 4 12 ... ..$ X5 : num [1:1700] 5 11 5 11 11 9 14 5 5 11 ... ..$ X6 : num [1:1700] 6 10 6 10 10 1 8 10 6 10 ... ..$ X7 : num [1:1700] 7 9 7 9 9 15 1 13 7 9 ... ..$ X8 : num [1:1700] 8 8 8 8 8 10 9 9 8 8 ... ..$ X9 : num [1:1700] 9 7 9 7 7 6 5 14 9 7 ... ..$ X10 : num [1:1700] 10 6 10 6 6 11 11 8 10 6 ... ..$ X11 : num [1:1700] 11 5 11 5 5 3 15 2 11 5 ... ..$ X12 : num [1:1700] 12 4 12 4 4 14 12 11 12 4 ... ..$ X13 : num [1:1700] 13 3 13 3 3 7 2 7 13 3 ... ..$ X14 : num [1:1700] 14 2 14 2 2 5 3 15 14 2 ... ..$ X15 : num [1:1700] 15 1 15 1 1 4 6 3 15 1 ... ..$ clust : int [1:1700] 1 3 1 3 3 3 3 1 1 3 ... ..$ pvals.1: num [1:1700] 1.00 1.03e-91 1.00 2.04e-93 1.03e-91 ... ..$ pvals.2: num [1:1700] 0 0 0 0 0 0 0 0 0 0 ... ..$ pvals.3: num [1:1700] 1.02e-92 1.00 1.34e-93 1.00 1.00 ... ..$ seq : Factor w/ 3 levels "1 2 3 4 5 6 7 8 9 10 11 12 13 14 15",..: 1 3 1 3 3 3 3 1 1 3 ... ..$ dists.1: num [1:1700] 0 105 0 105 105 61 58 46 0 105 ... ..$ dists.2: num [1:1700] 10 95 10 95 95 61 54 54 10 95 ... ..$ dists.3: num [1:1700] 105 0 105 0 0 44 47 59 105 0 ... $ min.like: num [1:100] -122710 -51439 -50310 -49976 -49718 ...

Examples

```
data(three.mode)
head(three.mode[[4]])
```

---

two.mode *Two-mode Mallows' model fit to toy data set "datas"*

Description

"datas" has 3 modes, but we observe here what happens when we try to fit it with 2 modal sequences. The most prominent modal sequences are 1:15, 15:1

Format

The format is: List of 5 $ R :List of 2 ..$: int [1:15] 1 2 3 4 5 6 7 8 9 10 ... ..$: int [1:15] 15 14 13 12 11 10 9 8 7 6 ... $ p : num [1:2] 0.557 0.443 $ lambda : num [1:2] 2.05 2.02 $ datas :'data.frame': 1700 obs. of 21 variables: ..$ X1 : num [1:1700] 1 15 1 15 15 12 10 4 1 15 ... ..$ X2 : num [1:1700] 2 14 2 14 14 13 13 12 2 14 ... ..$ X3 : num [1:1700] 3 13 3 13 13 2 4 6 3 13 ... ..$ X4 : num [1:1700] 4 12 4 12 12 8 7 1 4 12 ... ..$ X5 : num [1:1700] 5 11 5 11 11 9 14 5 5 11 ... ..$ X6 : num [1:1700] 6 10 6 10 10 1 8 10 6 10 ... ..$ X7 : num [1:1700] 7 9 7 9 9 15 1 13 7 9 ... ..$ X8 : num [1:1700] 8 8 8 8 8 10 9 9 8 8 ... ..$ X9 : num [1:1700] 9 7 9 7 7 6 5 14 9 7 ... ..$ X10 : num [1:1700] 10 6 10 6 6 11 11 8 10 6 ... ..$ X11 : num [1:1700] 11 5 11 5 5 3 15 2 11 5 ... ..$ X12 : num [1:1700] 12 4 12 4 4 14 12 11 12 4 ... ..$ X13 : num [1:1700] 13 3 13 3 3 7 2 7 13 3 ... ..$ X14 : num [1:1700] 14 2 14 2 2 5 3 15 14 2 ... ..$ X15 : num [1:1700] 15 1 15 1 1 4 6 3 15 1 ... ..$ clust : int [1:1700] 1 2 1 2 2 2 2 1 1 2 ... ..$ pvals.1: num [1:1700] 1.00 4.15e-94 1.00 4.15e-94 4.15e-94 ... ..$ pvals.2: num [1:1700] 5.4e-93 1.0 5.4e-93 1.0 1.0 ... ..$ seq : Factor w/ 2 levels "1 2 3 4 5 6 7 8 9 10 11 12 13 14 15",..: 1 2 1 2 2 2 2 1 1 2 ... ..$ dists.1: num [1:1700] 0 105 0 105 105 61 58 46 0 105 ... ..$ dists.2: num [1:1700] 105 0 105 0 0 44 47 59 105 0 ... $ min.like: num [1:100] -178063 -139298 -58290 -54074 -53902 ...

Examples

```
data(two.mode)
head(two.mode[[4]])
```

`two.seq` *Bi-modal Mallow's model fit to the APA data set.*

Description

The two-modes seem to divide well between Democrats and Republicans...

Format

The format is: List of 5 $ R :List of 2 ..$: int [1:3] 1 3 2 ..$: int [1:3] 3 1 2 $ p : num [1:2] 0.541 0.459 $ lambda : num [1:2] 2.19 2.32 $ datas :'data.frame': 1378 obs. of 9 variables: ..$ Carter : int [1:1378] 1 1 1 1 2 2 1 1 2 2 ... ..$ Reagan : int [1:1378] 1 2 2 2 1 1 2 3 1 1 ... ..$ Anderson: int [1:1378] 1 2 2 3 3 3 3 2 3 3 ... ..$ clust : int [1:1378] 1 1 1 1 2 2 1 1 2 2 ... ..$ pvals.1 : num [1:1378] 0.541 0.992 0.992 0.932 0.131 ... ..$ pvals.2 : num [1:1378] 0.45893 0.00809 0.00809 0.06802 0.86945 ... ..$ seq : Factor w/ 2 levels "1 3 2","3 1 2": 1 1 1 1 2 2 1 1 2 2 ... ..$ dists.1 : num [1:1378] 0 0 0 1 2 2 1 0 2 2 ... ..$ dists.2 : num [1:1378] 0 2 2 2 1 1 2 3 1 1 ... $ min.like: num [1:100] -6421 -3386 -2916 -2811 -2799 ...

Source

American Psychological Association http://www.electionstudies.org/studypages/anes_mergedfile_1980/anes_mergedfile_19

Examples

```
data(two.seq)
head(two.seq[[4]])
```

`UpdateLambda` *Update the Lambda parameters of clusters.*

Description

Updates the Lambda parameters to maximize the likelihood of the data under Mallows' model.

Usage

```
UpdateLambda(r, R, z, G, dists.to.Rg, dists.table,
  top.bound = 1000)
```

Arguments

r	Matrix of partial rankings.
R	Current modal sequences.
z	Current probabilities of memberships in each cluster.
G	Number of modal sequences.
dists.to.Rg	Matrix of the distances between the data and the current modal sequences.
dists.table	Table of the distance distribution in N! space, under Kendall's metric.
top.bound	The maximum value for the lambda parameter.

Value

Vector of new lambda parameters for the clusters.

Author(s)

Erik Gregory

References

"Mixtures of distance-based models for ranking data". Thomas Brendan Murphy & Donal Martin. 1 April 2002. Computational Statistics & Data Analysis 41 (2003) 645-655.

UpdateP *Update Proportion in each cluster.*

Description

Updates the proportion of data assigned to each cluster.

Usage

```
UpdateP(z)
```

Arguments

z	Probabilities that each sequence is in each cluster.

Value

Proportion of data in each cluster.

Author(s)

Erik Gregory

References

"Mixtures of distance-based models for ranking data". Thomas Brendan Murphy & Donal Martin. 1 April 2002. Computational Statistics & Data Analysis 41 (2003) 645-655.

`UpdateR` *Update modal sequences in each cluster.*

Description

Maximizes the likelihood of the data by updating the cluster centers of the model.

Usage

```
UpdateR(r, z, infos = NULL)
```

Arguments

`r`	Matrix of sequences being clustered.
`z`	Probability of cluster membership for each sequence and each cluster.
`infos`	The KendallInfo matrix for "r".

Value

New cluster centers for each cluster.

Author(s)

Erik Gregory

References

"Mixtures of distance-based models for ranking data". Thomas Brendan Murphy & Donal Martin. 1 April 2002. Computational Statistics & Data Analysis 41 (2003) 645-655.

Index

∗ **BubbleSort**
FormatOut, 8
∗ **DistanceDistribution(10)**
DistanceDistribution, 6
∗ **Distance**
AllSeqDists, 3
KendallInfo, 9
∗ **Kendall**
AllKendall, 3
AllSeqDists, 3
DistanceDistribution, 6
FormatOut, 8
KendallInfo, 9
NextTable, 12
∗ **Mallow**
Lambda, 10
Likelihood, 11
Mallows, 11
∗ **Sequences**
ConstructSeqs, 5
∗ **#**
DistanceDistribution, 6
∗ **bubblesort**
DistanceDistribution, 6
NextTable, 12
SeqDistribution, 13
∗ **center**
UpdateR, 18
∗ **cluster**
Mallows, 11
UpdateR, 18
∗ **datasets**
datas, 6
elect, 7
three.mode, 14
two.mode, 15
two.seq, 16
∗ **dataset**
two.seq, 16
∗ **distance**
AllKendall, 3
SeqDistribution, 13
∗ **expectation**
EStep, 7
∗ **lambda**
Lambda, 10
UpdateLambda, 16
∗ **likelihood**
Likelihood, 11
∗ **maximization**
EStep, 7
UpdateLambda, 16
∗ **normalize**
C_lam, 5
∗ **proportion**
UpdateP, 17
∗ **ranking**
RMallow-package, 2
∗ **sequence**
SimplifySequences, 14
∗ **simplify**
SimplifySequences, 14

AllKendall, 3
AllSeqDists, 3

BestFit, 4

C_lam, 5
ConstructSeqs, 5

datas, 6
DistanceDistribution, 6

elect, 7
EStep, 7

FormatOut, 8

hello, 9

KendallInfo, 9

Lambda, 10
Likelihood, 11

Mallows, 11

NextTable, 12

Rgen, 13
RMallow *(*RMallow-package*)*, 2
RMallow-package, 2

SeqDistribution, 13
SimplifySequences, 14

three.mode, 14
two.mode, 15
two.seq, 16

UpdateLambda, 16
UpdateP, 17
UpdateR, 18