

# Package ‘RMallow’

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**Type** Package

**Title** Fit Multi-Modal Mallows' Models to Ranking Data

**Version** 1.1

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**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](https://doi.org/10.1080/03610929808832223)>.

**License** GPL (>= 2)

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RMallow-package	<i>Fit Multi-modal Mallows' models to ranking data.</i>
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## 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	<i>All Kendall's distances between two sets of rankings.</i>
------------	--

---

**Description**

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

**Usage**

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

**Arguments**

<code>r</code>	One set of sequences.
<code>seqs</code>	Another set of sequences.
<code>data.info</code>	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	<i>Calculate all distances between a set of sequences and a fixed sequence.</i>
-------------	---

---

**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 select 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 select 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	<i>Constructs sequences from Kendall Information matrices.</i>
---------------	--

---

**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 corresponds 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	<i>Calculate the normalizing coefficient for Mallow's model in a sequence space.</i>
-------	--

---

**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	<i>Sample data set.</i>
-------	-------------------------

---

**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	<i>Calculate the Kendall distance distribution in <math>N!</math> space.</i>
----------------------	--

---

**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	<i>1980 APA Presidential Candidate ranking data.</i>
-------	--

---

**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	<i>The Expectation step of the EM algorithm.</i>
-------	--

---

**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	<i>Hello, World!</i>
-------	----------------------

---

**Description**

Prints 'Hello, world!'.

**Usage**

```
hello()
```

**Examples**

```
hello()
```

---

KendallInfo	<i>All information used to calculate Kendall's distance.</i>
-------------	--

---

**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](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	<i>Likelihood of the data and parameters.</i>
------------	---

---

**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.

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Mallows	<i>Fits a Multi-Modal Mallows' model to ranking data.</i>
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---

**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**

<code>datas</code>	Matrix of partial or fully-ranked data.
<code>G</code>	Number of modes, 2 or greater.
<code>iter</code>	Maximum number of iterations.
<code>hyp</code>	Hypothesis sequence vector, to initialize one of the cluster centers at.
<code>plot.like</code>	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	<i>Calculates the table of Kendall distances in <math>(N+1)!</math> space, given those in <math>N!</math> space.</i>
-----------	--

---

**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**

<code>last.table</code>	Table of distances in $N!$ space.
<code>N.last</code>	$N$

**Value**

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

**Author(s)**

Erik Gregory

---

Rgen	<i>Initialize sequence modes for the clustering process.</i>
------	--

---

**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	<i>Calculates distances in N! space.</i>
-----------------	--

---

**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	<i>Bi-modal Mallow's model fit to the APA data set.</i>
---------	---

---

**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\\_1980/](http://www.electionstudies.org/studypages/anes_mergedfile_1980/anes_mergedfile_1980/)

**Examples**

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

---

UpdateLambda	<i>Update the Lambda parameters of clusters.</i>
--------------	--

---

**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.

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