Package ‘clickstream’

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Type Package
Title Analyzes Clickstreams based on Markov Chains
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Author Michael Scholz
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Description A set of tools to read, analyze and write lists of click sequences on websites (i.e. clickstream). A click can be represented by a number, character or string. Clickstreams can be modeled as zero- (only computes occurrence probabilities), first- or higher-order Markov chains.
License GPL-2
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Description

This package allows modeling clickstreams with Markov chains. It supports to model clickstreams as zero-order, first-order or higher-order Markov chains.

Details

- Package: clickstream
- Type: Package
- Version: 1.1.3
- Date: 2015-01-06
- License: GPL-2
- Depends: R (>= 3.0), methods

Author(s)

Michael Scholz <michael.scholz@uni-passau.de>

References


Examples

```r
# fitting a simple Markov chain and predicting the next click
clickstreams <- c("User1,h,c,c,p,c,h,c,p,c,p,p,o",
                  "User2,i,c,i,c,c,c,d",
                  "User3,h,i,c,i,c,p,c,c,p,c,i,d",
                  "User4,c,p,c,d",
```
absorbingStates-methods

```r
csf <- tempfile()
writelines(clickstreams, csf)
cls <- readClickstreams(csf, header=TRUE)
mc <- fitMarkovChain(cls)
startPattern <- new("Pattern", sequence=c("h", "c"))
predict(mc, startPattern)
plot(mc)
```

absorbingStates-methods

*Returns all absorbing states*

Description

Returns all absorbing states

Usage

```r
absorbingStates(object)
```

Arguments

- `object`  
  An instance of the MarkovChain-class

Methods

- `list("signature(object = "MarkovChain")")`  
  Returns the names of all states that never have a successor in a clickstream (i.e. that are absorbing).

Author(s)

Michael Scholz `michael.scholz@uni-passau.de`

clusterClickstreams

*Perform k-means clustering on a list of clickstreams*

Description

Perform k-means clustering on a list of clickstreams. For each clickstream a transition matrix of a given order is computed. These transition matrices are used as input for performing k-means clustering.

Usage

```r
clusterClickstreams(clickstreamList, order = 0, centers, ...)
```
Arguments

**clickstreamList**

A list of clickstreams for which the cluster analysis is performed.

**order**

The order of the transition matrices used as input for clustering (default is 0).

**centers**

The number of clusters.

... Additional parameters for k-means clustering (see `kmeans`).

Value

This method returns a `ClickstreamClusters` object (S3-class). It is a list with the following components:

- **clusters** A list of `Clickstream` objects representing the resulting clusters.
- **centers** A matrix of cluster centres.
- **states** Vector of states.
- **totss** The total sum of squares.
- **withinss** Vector of within-cluster sum of squares, one component per cluster.
- **tot.withinss** Total within-cluster sum of squares, i.e., \( \text{sum(withinss)} \).
- **betweenss** The between-cluster sum of squares, i.e., \( \text{totss} - \text{tot.withinss} \).

Author(s)

Michael Scholz <michael.scholz@uni-passau.de>

See Also

- `print.ClickstreamClusters`
- `summary.ClickstreamClusters`

Examples

```r
clickstreams <- c("User1,h,c,c,p,c,h,c,p,c,p,c,p,o",
                   "User2,i,c,i,c,c,c,d",
                   "User3,h,i,c,i,c,p,c,c,p,c,i,d",
                   "User4,c,c,p,c,d",
                   "User5,h,c,c,p,c,p,p,i,p,o",
                   "User6,i,h,c,c,p,c,p,c,d")
csf <- tempfile()
writelines(clickstreams, csf)
cls <- readClickstreams(csf, header=TRUE)
clusters <- clusterClickstreams(cls, order=0, centers=2)
print(clusters)
```
fitMarkovChain

Fits a list of clickstreams to a Markov chain

Description
This function fits a list of clickstreams to a Markov chain. Zero-order, first-order as well as higher-order Markov chains are supported. For estimating higher-order Markov chains this function solves the following quadratic programming problem:

\[
\min \left\| \sum_{i=1}^{k} X - \lambda_i Q_i X \right\|
\]

s.t.
\[
\sum_{i=1}^{k} \lambda_i = 1
\]
\[
\lambda_i \geq 0
\]

The distribution of states is given as \(X\). \(\lambda_i\) is the lag parameter for lag \(i\) and \(Q_i\) the transition matrix.

Usage
fitMarkovChain(clickstreamList, order = 1)

Arguments
- clickstreamList: A list of clickstreams for which a Markov chain is fitted.
- order: (Optional) The order of the Markov chain that is fitted from the clickstreams. Per default, Markov chains with \(\text{order}=1\) are fitted. It is also possible to fit zero-order Markov chains (\(\text{order}=0\)) and higher-order Markov chains.

Details
For solving the quadratic programming problem of higher-order Markov chains, an augmented Lagrange multiplier method from the package Rsolnp is used.

Value
Returns a MarkovChain object.

Note
At least half of the clickstreams need to consist of as many clicks as the order of the Markov chain that should be fitted.

Author(s)
Michael Scholz <michael.scholz@uni-passau.de>
MarkovChain-class

References


See Also

MarkovChain, Rsolnp

Examples

# fitting a simple Markov chain
clickstreams<-c("User1,h,c,c,p,c,h,c,p,p,c,p,p,o",
"User2,i,c,i,c,c,d",
"User3,h,i,c,i,c,p,c,c,i,d",
"User4,c,c,p,c,d",
"User5,h,c,c,p,c,p,p,i,p,o",
"User6,i,h,c,c,p,c,p,c,d")

csf< tempfile()
writeLines(clickstreams, csf)
cls< readClickstreams(csf, header=TRUE)
mc< fitMarkovChain(cls)
show(mc)

Description

Class "MarkovChain"

Objects from the Class

Objects can be created by calls of the form new("MarkovChain", ...). This S4 class describes MarkovChain objects.

Author(s)

Michael Scholz <michael.scholz@uni-passau.de>

See Also

fitMarkovChain
Pattern-class

Examples

```r
# show MarkovChain definition
showClass("MarkovChain")

# fit a simple Markov chain from a list of click streams
clickstreams <- c("User1,h,c,c,p,c,h,c,p,p,c,p,p,o",
                   "User2,i,c,i,c,c,c,d",
                   "User3,h,i,c,i,c,p,c,c,p,c,c,i,d",
                   "User4,c,c,p,c,d",
                   "User5,h,c,c,p,p,c,p,p,i,p,o",
                   "User6,i,h,c,c,p,p,c,p,c,d")

csf <- tempfile()
writeLines(clickstreams, csf)
cls <- readClickstreams(csf, header=TRUE)
mc <- fitMarkovChain(cls)
show(mc)
```

<table>
<thead>
<tr>
<th>Pattern-class</th>
<th>Class &quot;Pattern&quot;</th>
</tr>
</thead>
</table>

Description

This S4 class describes a click pattern consisting of a sequence of clicks and a probability of occurrence.

Objects from the Class

Objects can be created by calls of the form `new("Pattern", sequence, probability, ...)`. This S4 class describes a click pattern consisting of a sequence of clicks and a probability of occurrence.

Author(s)

Michael Scholz <michael.scholz@uni-passau.de>

See Also

randomClicks

Examples

```r
# show Pattern definition
showClass("Pattern")

# create simple Pattern objects
pattern1 <- new("Pattern", sequence=c("h", "c", "p"))
pattern2 <- new("Pattern", sequence=c("c", "p", "p"), probability=0.2)
pattern3 <- new("Pattern", sequence=c("h", "p", "p"), probability=0.35, absorbingProbabilities=data.frame(d=0.6, o=0.4))
```
predict-methods

Predicts the next click(s) of a user

Description

Predicts the next click(s) of a user

Usage

```r
## S4 method for signature 'MarkovChain'
predict(object, startPattern, dist = 1, ties = "random")
```

Arguments

- `object`: A MarkovChain object used for predicting the next click(s)
- `startPattern`: The first clicks of a user as Pattern object. A Pattern object with an empty sequence is also possible.
- `dist`: (Optional) The number of clicks that should be predicted (default is 1).
- `ties`: (Optional) The strategy for handling ties in predicting the next click. Possible strategies are `random` (default) and `first`.

Methods

- `list("signature(object = "MarkovChain")")` This method predicts the next click(s) of a user. The first clicks of a user are given as Pattern object. The next click(s) are predicted based on the transition probabilities in the MarkovChain object. The probability distribution of the next click (n) is estimated as follows:

  \[
  X^{(n)} = B \cdot \sum_{i=1}^{k} \lambda_i Q_i X^{(n-i)}
  \]

  The distribution of states at time n is given as \(X^n\). The transition matrix for lag i is given as \(Q_i\). \(\lambda_i\) specifies the lag parameter and \(B\) the absorbing probability matrix.

Author(s)

Michael Scholz <michael.scholz@uni-passau.de>

See Also

fitMarkovChain
Examples

```r
# fitting a simple Markov chain and predicting the next click

clickstreams <- c("User1,h,c,c,p,c,h,c,p,c,p,c,p,o",
                  "User2,i,c,i,c,c,d",
                  "User3,h,i,c,i,c,p,c,p,c,i,d",
                  "User4,c,c,i,c,d",
                  "User5,h,c,c,p,p,c,p,i,p,o",
                  "User6,i,h,c,c,p,c,p,c,d")

csf <- tempfile()
writeLines(clickstreams, csf)
cls <- readClickstreams(csf, header = TRUE)
mc <- fitMarkovChain(cls)
startPattern <- new("Pattern", sequence = c("h", "c"))
predict(mc, startPattern)

# predict with predefined absorbing probabilities

startPattern <- new("Pattern", sequence = c("h", "c"),
                      absorbingProbabilities = data.frame(d = 0.2, o = 0.8))
predict(mc, startPattern)
```

predict.ClickstreamClusters

*Predicts the cluster for a given Pattern object*

Description

Predicts the cluster for a given Pattern object. Potential clusters need to be identified with the method `clusterClickstreams` before predicting the cluster.

Usage

```r
## S3 method for class 'ClickstreamClusters'
predict(object, pattern, ...)
```

Arguments

- **object**: A `ClickstreamClusters` object containing the potential clusters. A `ClickstreamClusters` object represents the result of a cluster analysis on a list of clickstreams (see `clusterClickstreams`).
- **pattern**: The first clicks of a user as `Pattern` object.
- **...**: Ignored parameters.

Value

Returns the index of the clusters to which the given `Pattern` object most probably belongs to.
Author(s)
Michael Scholz <michael.scholz@uni-passau.de>

See Also
clusterClickstreams, print.ClickstreamClusters

Examples

```r
# Create clickstream data
clickstreams <- c("User1,h,c,c,p,c,h,c,p,p,c,p,o", 
                  "User2,i,c,i,c,c,d", 
                  "User3,h,i,c,i,c,p,c,p,c,c,i,d", 
                  "User4,c,c,p,c,d", 
                  "User5,h,c,c,p,p,c,p,p,i,o", 
                  "User6,i,h,c,c,p,p,c,p,c,d")

csf <- tempfile()
writeLines(clickstreams, csf)
cls <- readClickstreams(csf, header=TRUE)
clusters <- clusterClickstreams(cls, order=0, centers=2)
pattern <- new("Pattern", sequence=c("h", "c"))
predict(clusters, pattern)
```

print.ClickstreamClusters

*Prints a ClickstreamClusters object*

Description

Prints a ClickstreamClusters object. A ClickstreamClusters object represents the result of a cluster analysis on a list of clickstreams (see `clusterClickstreams`).

Usage

```r
## S3 method for class 'ClickstreamClusters'
print(x, ...)
```

Arguments

- `x` A ClickstreamClusters object returned by `clusterClickstreams`.
- `...` Ignored parameters.

Author(s)
Michael Scholz <michael.scholz@uni-passau.de>

See Also
clusterClickstreams, summary.ClickstreamClusters
print.Clickstreams

Examples

```r
clickstreams <- c("User1,h,c,c,p,c,h,c,p,p,c,p,p,o",
                  "User2,i,c,i,c,c,c,d",
                  "User3,h,i,c,i,c,p,c,c,p,c,c,i,d",
                  "User4,c,c,p,c,d",
                  "User5,h,c,c,p,p,c,p,p,i,p,o",
                  "User6,i,h,c,c,p,p,c,p,c,d")
csf <- tempfile()
writelines(clickstreams, csf)
cls <- readClickstreams(csf, header=TRUE)
clusters <- clusterClickstreams(cls, order=0, centers=2)
print(clusters)
```

Description

Prints a list of clickstreams.

Usage

```r
## S3 method for class 'Clickstreams'
print(x, ...)
```

Arguments

- `x`: A list of clickstreams.
- `...`: Ignored parameters.

Author(s)

Michael Scholz <michael.scholz@uni-passau.de>

See Also

`readClickstreams`, `randomClickstreams`

Examples

```r
clickstreams <- c("User1,h,c,c,p,c,h,c,p,p,c,p,p,o",
                  "User2,i,c,i,c,c,c,d",
                  "User3,h,i,c,i,c,p,c,c,p,c,c,i,d",
                  "User4,c,c,p,c,d",
                  "User5,h,c,c,p,p,c,p,p,i,p,o",
                  "User6,i,h,c,c,p,p,c,p,c,d")
csf <- tempfile()
writelines(clickstreams, csf)
cls <- readClickstreams(csf, header=TRUE)
print(cls)
```
print.MarkovChainSummary

Prints the summary of a MarkovChain object

Description

Prints the summary of a MarkovChain object.

Usage

```r
## S3 method for class 'MarkovChainSummary'
print(x, ...)
```

Arguments

- `x` A MarkovChainSummary object generated with `summary`
- `...` Ignored parameters.

Author(s)

Michael Scholz <michael.scholz@uni-passau.de>

See Also

`summary`

Examples

```r
clickstreams <- c("User1,h,c,c,p,c,h,c,p,p,c,p,p,o",
                  "User2,i,c,i,c,c,d",
                  "User3,h,i,c,i,c,p,c,c,p,c,i,d",
                  "User4,c,c,p,c,d",
                  "User5,h,c,c,p,p,c,p,p,i,p,o",
                  "User6,i,h,c,c,p,p,c,p,c,d")

csf <- tempfile()
writeLines(clickstreams, csf)
cls <- readClickstreams(csf, header = TRUE)
mc <- fitMarkovChain(cls)
print(summary(mc))
```
randomClicks-methods

Generates a sequence of clicks

Description

Generates a sequence of clicks

Usage

randomClicks(object, startPattern, dist)

Arguments

object A MarkovChain object used for generating the next click(s)
startPattern The first clicks of a user as Pattern object. A Pattern object with an empty sequence is also possible.
dist (Optional) The number of clicks that should be generated (default is 1).

Methods

list("signature(object = "MarkovChain")") Generates a sequence of clicks by randomly walking through the transition graph of a given MarkovChain object.

Author(s)

Michael Scholz <michael.scholz@uni-passau.de>

See Also

fitMarkovChain

Examples

# fitting a simple Markov chain and predicting the next click
clickstreams<-c("User1,h,c,c,p,c,h,c,p,c,p,c,p,o",
    "User2,i,c,i,c,c,c,d",
    "User3,h,i,c,i,c,p,c,c,p,c,i,d",
    "User4,c,c,p,c,d",
    "User5,h,c,c,p,c,p,p,i,p,o",
    "User6,i,h,c,c,p,c,p,c,d")
csf<-tempfile()
writelines(clickstreams, csf)
cls<-readClickstreams(csf, header=TRUE)
mc<-fitMarkovChain(cls)
startPattern<-new("Pattern", sequence=c("h", "c"))
predict(mc, startPattern)
randomClickstreams  Generates a list of clickstreams

Description
Generates a list of clickstreams by randomly walking through a given transition matrix.

Usage
randomClickstreams(states, startProbabilities, transitionMatrix, meanLength, n = 100)

Arguments
- states: Names of all possible states.
- startProbabilities: Start probabilities for all states.
- transitionMatrix: Matrix of transition probabilities.
- meanLength: Average length of the click streams.
- n: Number of click streams to be generated.

Value
Returns a list of clickstreams.

Author(s)
Michael Scholz <michael.scholz@uni-passau.de>

See Also
fitMarkovChain, readClickstreams, print.Clickstreams

Examples
# generate a simple list of click streams
states<-c("a", "b", "c")
startProbabilities<-c(0.2, 0.5, 0.3)
transitionMatrix<-matrix(c(0.4, 0.6, 0.3, 0.1, 0.6, 0.2, 0.8, 0), nrow=3)
cls<-randomClickstreams(states, startProbabilities, transitionMatrix, meanLength=5, n=10)
print(cls)
**readClickstreams**  
Reads a list of clickstreams from a file

**Description**
Reads a list of clickstream from a csv-file.

**Usage**
```
readClickstreams(file, sep = ",", header = FALSE)
```

**Arguments**
- **file**: The name of the file which the clickstreams are to be read from. Each line of the file appears as one click stream. If it does not contain an absolute path, the file name is relative to the current working directory, `getwd`.
- **sep**: The character used to separate clicks (default is ",").
- **header**: A logical flag indicating whether the first entry of each line in the file is the name of the clickstream user.

**Value**
A list of clickstreams. Each element is a vector of characters representing the clicks. The name of each list element is either the header of a clickstream file or a unique number.

**Author(s)**
Michael Scholz <michael.scholz@uni-passau.de>

**See Also**
`print.Clickstreams, randomClickstreams`

**Examples**
```
clickstreams <- c("User1,h,c,c,p,c,h,c,p,p,c,p,p,o",
                  "User2,i,c,i,c,c,d",
                  "User3,h,i,c,i,c,p,c,c,p,c,i,d",
                  "User4,c,c,p,c,d",
                  "User5,h,c,c,p,c,p,p,p,i,p,o",
                  "User6,i,h,c,c,p,c,p,c,d")

csf <- tempfile()
writeLines(clickstreams, csf)
cls <- readClickstreams(csf, header=TRUE)
print(cls)
```
**states-methods**

*Returns all states*

---

**Description**

Returns all states

**Usage**

```r
states(object)
```

**Arguments**

- `object`  
  An instance of the `MarkovChain`-class

**Methods**

```r
list("signature(object = \"MarkovChain\")")
```

Returns the name of all states of a `MarkovChain` object.

**Author(s)**

Michael Scholz <michael.scholz@uni-passau.de>

---

**summary-methods**

*Prints a summary of a MarkovChain object*

---

**Description**

Prints a summary of a MarkovChain object

**Usage**

```r
## S4 method for signature 'MarkovChain'
summary(object)
```

**Arguments**

- `object`  
  An instance of the `MarkovChain`-class
summary.ClickstreamClusters

Value

Returns a MarkovChainSummary object.

- **list("desc")** A short description of the MarkovChain object.
- **list("observations")** The number of observations from which the MarkovChain object has been fitted.
- **list("k")** The number of estimation parameters.
- **list("logLikelihood")** The LogLikelihood of the MarkovChain object.
- **list("aic")** Akaike's Information Criterion for the MarkovChain object
- **list("bic")** Bayesian Information Criterion for the MarkovChain object

Methods

- **list("signature(object = "MarkovChain")")** Generates a summary for a given MarkovChain object

Author(s)

Michael Scholz <michael.scholz@uni-passau.de>

---

summary.ClickstreamClusters

*Prints a summary of a ClickstreamCluster object*

Description

Prints a summary of a ClickstreamCluster object. A ClickstreamClusters object represents the result of a cluster analysis on a list of clickstreams (see `clusterClickstreams`).

Usage

```r
## S3 method for class 'ClickstreamClusters'
summary(object, ...)  
```

Arguments

- **object** A ClickstreamClusters object returned by `clusterClickstreams`.
- **...** Ignored parameters.

Author(s)

Michael Scholz <michael.scholz@uni-passau.de>

See Also

`clusterClickstreams, print.ClickstreamClusters`
Summary

Example

```r
clickstreams <- c("User1,h,c,c,p,c,h,c,p,p,c,p,p,o",
                   "User2,i,c,i,c,c,c,d",
                   "User3,h,i,c,i,c,p,c,c,p,c,c,i,d",
                   "User4,c,c,p,c,d",
                   "User5,h,c,c,p,p,c,p,p,p,i,p,o",
                   "User6,i,h,c,c,p,p,c,c,d")

csf <- tempfile()
writeLines(clickstreams, csf)
cls <- readClickstreams(csf, header = TRUE)
summary(clusterClickstreams(cls, order = 0, centers = 2))
```

Description

Returns a summary of a list of clickstreams.

Usage

```r
## S3 method for class 'Clickstreams'
summary(object, ...)  
```

Arguments

- `object` A list of clickstreams.
- `...` Ignored parameters.

Author(s)

Michael Scholz <michael.scholz@uni-passau.de>

See Also

`readClickstreams`, `randomClickstreams`

Example

```r
clickstreams <- c("User1,h,c,c,p,c,h,c,p,p,c,p,p,o",
                   "User2,i,c,i,c,c,c,d",
                   "User3,h,i,c,i,c,p,c,c,p,c,c,i,d",
                   "User4,c,c,p,c,d",
                   "User5,h,c,c,p,p,c,p,p,p,i,p,o",
                   "User6,i,h,c,c,p,p,c,c,d")

csf <- tempfile()
writeLines(clickstreams, csf)
cls <- readClickstreams(csf, header = TRUE)
summary(cls)
```
transientStates-methods

Returns all transient states

Description

Returns all transient states

Usage

transientStates(object)

Arguments

object An instance of the MarkovChain-class

Methods

list("signature(object = "MarkovChain")") Returns the names of all states that have a non-zero probability that a user will never return to them (i.e. that are transient).

Author(s)

Michael Scholz <michael.scholz@uni-passau.de>

writeClickstreams Writes a list of clickstreams to a file

Description

Writes a list of clickstream to a csv-file.

Usage

writeClickstreams(clickstreamList, file, header = TRUE, sep = ",", quote = TRUE)

Arguments

clickstreamList The list of clickstreams to be written.
file The name of the file which the clickstreams are written to.
header A logical flag indicating whether the name of each clickstream element should be used as first element.
sep The character used to separate clicks (default is ",").
quote A logical flag indicating whether each element of a clickstream will be surrounded by double quotes (default is TRUE.)
Author(s)
Michael Scholz <michael.scholz@uni-passau.de>

See Also
readClickstreams, clusterClickstreams

Examples

```r
clickstreams <- c("User1,h,c,c,p,c,h,c,p,p,c,p,p,o",
                 "User2,i,c,i,c,c,c,d",
                 "User3,h,i,c,i,c,p,c,c,p,c,c,i,d",
                 "User4,c,c,p,c,d",
                 "User5,h,c,c,p,p,p,p,p,i,p,o",
                 "User6,i,h,c,c,p,c,p,c,d")
csf <- tempfile()
writelines(clickstreams, csf)
cls <- readClickstreams(csf, header=TRUE)
clusters <- clusterClickstreams(cls, order=0, centers=2)
writeClickstreams(cls, file="clickstreams.csv", header=TRUE, sep=",")
```
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