Package 'MmgraphR'

September 14, 2018

Type Package

Title Graphing for Markov, Hidden Markov, and Mixture Transition
Distribution Models

Version 0.3-1

Date 2018-08-23

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Description Produces parallel coordinate plots of probability transition matrices from Markov, hidden Markov, and mixture transition distribution models.

URL https://r-forge.r-project.org/scm/viewvc.php/pkg/MmgraphR/?root=traminer

Depends R(>= 3.1.1), TraMineR, colorspace

Imports march, msm

License GPL (>= 2)

LazyData true

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Repository CRAN

Repository/R-Forge/Project traminer

Repository/R-Forge/Revision 980

Repository/R-Forge/DateTimeStamp 2018-08-23 09:07:58

Date/Publication 2018-09-14 14:30:06 UTC

NeedsCompilation no

R topics documented:

MmgraphR-package   *Graphing for Markov, Hidden Markov, and Mixture Transition Distri-*
                            bution Models

Description

MmgraphR produces parallel coordinate plots which map each element in a probability transition matrix (of any order) as a line. Each line is weighted by probability, and so the thicker the line, the more probable a sequence of states is and vice-versa. Probability transition matrices reflecting higher order dependencies, often useful in life-course studies, can also be mapped.

Additional functionalities of MmgraphR include probability filters that can easily be applied to emphasize the most (or least) probable state sequences overall, or by initial state. Any specific element(s) of the probability transition matrix can also be highlighted. To render the plot more attractive, various color palettes using the Hue-Chroma-Luminance color scheme have been built-in and can be easily selected by the user.

The package is available through CRAN as well as R-forge, where it is developed. Although MmgraphR can be used on its own, it is also compatible with the output of R packages msm, HiddenMarkov, HMM, depmixS4, seqHMM, as well as march.

Details

Package:	MmgraphR
Version:	0.3-1
Date:	2018-08-23
Depends:	R (>= 3.1.1), TraMineR, colorspace
Imports:	march, msm
License:	GPL (>= 2)
LazyData:	true
URL:	https://cran.r-project.org/package=MmgraphR
URL:	https://r-forge.r-project.org/scm/viewvc.php/pkg/MmgraphR/?root=traminer
Encoding:	latin1

Author(s)

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References

Buergin, R. and G. Ritschard (2014), "A decorated parallel coordinate plot for categorical longitudinal data", *The American Statistician*. Vol. 68(2), pp. 98-103.

Zeileis, A.; Hornik, K. and P. Murrell (2009), "Escaping RGBland: Selecting Colors for Statistical Graphics", *Computational Statistics & Data Analysis*. Vol. 53, pp. 3259-3270.

See Also

trmatplot, trmatplot.default, trmatplot.array, trmatplot.depmix.fitted, trmatplot.dthmm, trmatplot.hmm, trmatplot.msm, march.Dcmm.trmatplot

Examples

```
## Plotting a probability transition matrix
############################################

trMat<-matrix(c(0.1, 0.05, 0.05, 0.80,
  0.06, 0.02, 0.03, 0.89,
  0.03, 0.01, 0.01, 0.95,
  0, 0, 0, 1), nrow = 4, ncol = 4, byrow = TRUE)

trmatplot(trMat)

#--- Setting a seed so that the graphic can be replicated

trmatplot(trMat, seed = 2)

#--- Defining a second order probability transition matrix as an array

trMatArray <- array(c(
  0.30, 0.70,
  0.65, 0.35,
  0.05, 0.95,
  0.99, 0.01), dim = c( 1, 2, 4))

#--- Plotting with user-defined colors

trmatplot(trMatArray, seed = 3, morder = 2, cpal = c("grey40", "grey70"))

# cspal: ready-to-use color palettes using colorspace
#####################################################

#--- Color palette "dynamic"

trmatplot(trMat, seed = 2, cspal = "dynamic")

#--- Color palette "harmonic"

trmatplot(trMat, seed = 2, cspal = "harmonic")

## pfilter: Filtering out most (or least) probable sequences
###########################################################

#--- The most probable sequence given a state
```

```
trmatplot(trMat, seed = 2, pfilter = "smax")

#--- The ten least probable sequences

trmatplot(trMat, seed = 2, pfilter = "tmin", num = 10 )
```

---

march.Dcmm.trmatplot   *Transition Matrix Plot for march.Dcmm objects*

Description

A coordinate plot which maps each element in the probability transition matrix (of any order) as
a line, where each line is weighted by probability. Users can apply filters to emphasize the most
(or least) probable state sequences overall, or by initial state. Various color palettes using the Hue-
Chroma-Luminance color scheme can be easily selected by the user. Input is an object of class
march.Dcmm which is the output of march.dcmm.construct.

Usage

```
## For class 'march.Dcmm'

march.Dcmm.trmatplot ( d, seed = NULL, type = "hidden", hstate = 1,
cspal = NULL, cpal = NULL, main = NULL, xlab = NULL,
ylab = NULL, ylim = NULL, xtlab = NULL, ytlab = NULL,
pfilter = NULL, shade.col = "grey80", num = NULL, hide.col = NULL,
lorder = NULL, plot = TRUE, verbose = FALSE, ...)
```

Arguments

d	Object to be plotted. A march.Dcmm object.
seed	A single value, interpreted as an integer, or NULL (default). See Details.
type	Character string. Can be specified as either "hidden", if the hidden matrix is to be plotted (default) or as "visible" if the visible matrix is to be plotted.
hstate	Numeric. Valid when type = "visible". Specifies from which hidden state the (visible) probability transition matrix should be plotted. Default hstate = 1.
cspal	A color palette that can be specified as one of: "dynamic", "harmonic", "cold", "warm", "heat", "terrain". The rainbow_hcl, heat_hcl, and terrain_hcl commands are used to generate color palettes. See Examples in trmatplot.
cpal	Color palette vector when coloring probability sequences. The rainbow_hcl command is used to generate a color palette if none is specified.
main	Title for the graphic. Default is *Probability Transition Matrix*.
xlab	Label for the x axis. Default is *Time*.
ylab	Label for the y axis. Default is *States*.
ylim	Numeric vector of length 2 giving the y coordinates range.

xtlab	Label for the x axis ticks. Default is time (t, t+1,...).
ytlab	Labels for the y axis ticks.
pfilter	Probability filter. Can be specified as one of `"tmax"`, `"tmin"`, `"smax"`, `"smin"`. See Details.
shade.col	The color for sequences shaded out using the `pfilter` argument. Default is `"grey80"`. See Details.
num	Numeric. The number of sequences to be highlighted, a whole number from 1 to `length(d) - 1`. Must be specified only when using `pfilter="tmax"` or `pfilter="tmin"`. Default is NULL.
hide.col	The color for sequences shaded out using the `filter` argument. Default is `"grey80"`. See Details.
lorder	Line order. Either `"background"` or `"foreground"`. When `pfilter` is used `lorder` is set by default.
plot	Logical. Should the object be plotted. Default is TRUE.
verbose	Logical. Reports extra information on progress. Default is FALSE.
...	Additional arguments, such as graphical parameters, to be passed on. See [par](#) and [seqpcplot](#).

Details

Setting a `seed` allows the graphic to be replicated.

The `pfilter` argument serves to highlight probability sequences that are either most probable while shading out those that are less probable in `shade.col` and vice-versa. The four options for `pfilter` are described below, and are illustrated in Examples in [trmatplot](#).

`"smax"` For each initial state the most probable next state is highlighed.

`"smin"` For each initial state the least probable next state is highlighed.

`"tmax"` The sequence of states with the highest probability overall is highlighed. To highlight the *n* most probable sequences of states, set `num = n`.

`"tmin"` The sequence of states with the lowest probability overall is highlighed. To highlight the *n* least probable sequences of states, set `num = n`.

The `filter` and `hide.col` arguments are inherent in and may be passed on to [seqpcplot](#). The `filter` argument serves to specify filters to gray less interesting patterns. The filtered-out patterns are displayed in the `hide.col` color. The filter argument expects a list with at least elements `type` and `value`. Most relevant within the context of probabilities is `type = "sequence"`, which highlights the specific pattern.

See Examples in [trmatplot](#).

Value

`trmatplot` returns an object of class [trmatplot](#). Some of the arguments are inherent in [par](#) and [seqpcplot](#).

Author(s)

Pauline Adamopoulou

References

Buergin, R. and G. Ritschard (2014), "A decorated parallel coordinate plot for categorical longitu-dinal data", *The American Statistician*. Vol. 68(2), pp. 98-103.

Zeileis, A.; Hornik, K. and P. Murrell (2009), "Escaping RGBland: Selecting Colors for Statistical Graphics", *Computational Statistics & Data Analysis*. Vol. 53, pp. 3259-3270.

See Also

trmatplot, trmatplot.default, trmatplot.depmix.fitted, trmatplot.array, seqpcplot, par.

---

trmat   *Extract a Probability Transition Matrix*

Description

Extracts a probability transition matrix.

Usage

```
## S3 method for class 'depmix.fitted'

trmat ( d )
```

Arguments

d   Object of class depmix.fitted.

Details

The function trmat extracts the probability transition matrix from a depmix.fitted object and returns it as a matrix. trmat is used internally by the function trmatplot.depmix.fitted in order to extract the probability transition matrix to be plotted.

Value

trmat returns an the probability transition matrix as an object of class matrix.

Author(s)

Pauline Adamopoulou

See Also

[trmatplot](), [trmatplot.depmix.fitted](), [depmix.fitted](),

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trmatplot	*Transition Matrix Plot*

Description

A parallel coordinate plot which maps each element in the probability transition matrix (of any order) as a line, where each line is weighted by probability. Users can apply filters to emphasize the most (or least) probable state sequences overall, or by initial state. Various color palettes using the Hue-Chroma-Luminance color scheme can be easily selected by the user. Input is either an object of class [matrix](), [array](), [depmix.fitted](), or a [list]() of class [msm](), hmm or of class dthmm.

Usage

```
## S3 method for classes 'matrix', 'array',
## 'depmix.fitted', 'dthmm', 'hmm', and 'msm'

trmatplot ( d, seed = NULL, rowconstraint = TRUE, morder = 1,
cspal = NULL, cpal = NULL, main = NULL,
xlab = NULL, ylab = NULL, ylim = NULL, xtlab = NULL, ytlab = NULL,
pfilter = NULL, shade.col = "grey80", num = NULL,
hide.col = NULL, lorder = NULL, plot = TRUE,
verbose = FALSE, ...)
```

Arguments

d	Object to be plotted. A transition matrix of probabilities. Can be of any order. An object of class [matrix](), [array](), [depmix.fitted](), dthmm, hmm, or [msm](). See Details.
seed	A single value, interpreted as an integer, or NULL (default). See Details.
rowconstraint	Logical. Checks if the row constraint is satisfied, i.e. the sum of each row of the transition probability matrix equals one. Default is TRUE.
morder	Numeric. The order of the probability transition matrix, d, to be plotted. Default is 1. See Details.
cspal	A color palette that can be specified as one of: "dynamic", "harmonic", "cold", "warm", "heat", or "terrain". The [rainbow_hcl](), [heat_hcl](), and [terrain_hcl]() commands are used to generate color palettes. The [rainbow_hcl]() command is used to generate a color palette if none is specified.
cpal	Color palette vector when coloring probability sequences. Cannot specify both cspal and cpal.
main	Title for the graphic. Default is *Probability Transition Matrix*.
xlab	Label for the x axis. Default is *Time*.

ylab	Label for the y axis. Default is *States*.
ylim	Numeric vector of length 2 giving the y coordinates range.
xtlab	Labels for the x axis ticks. Default is time (t, t+1,...).
ytlab	Labels for the y axis ticks.
pfilter	Probability filter. Can be specified as one of "tmax", "tmin", "smax", "smin". See Details.
shade.col	The color for sequences shaded out using the pfilter argument. Default is "grey80". See Details.
num	Numeric. The number of sequences to be highlighted, a whole number from 1 to length(d) - 1. Must be specified only when using pfilter="tmax" or pfilter="tmin". Default is NULL.
hide.col	The color for sequences shaded out using the filter argument. Default is "grey80". See Details.
lorder	Line order. Either "background" or "foreground". When pfilter is used lorder is set by default.
plot	Logical. Should the object be plotted. Default is TRUE.
verbose	Logical. Reports extra information on progress. Default is FALSE.
...	Additional arguments, such as graphical parameters, to be passed on. See par and seqpcplot.

Details

The object d to be plotted, is a probability transition matrix that can be of class matrix, array, depmix.fitted, dthmm, hmm, msm. If the probability transition matrix is the output of packages implemented using S3 methods and classes, such as **msm**, **HiddenMarkov**, **HMM**, or **seqHMM** it is a matrix which is element of a list. More specifically, using the package **HMM**, the function initHMM returns a list containing the element transProbs with the probability transition matrix. Within the **HiddenMarkov**, dthmm returns a list of class dthmm with the element Pi which is a probability transition matrix, either user-defined or estimated. Similarly, the **seqHMM** functions build_mm and build_hmm return a list of class hmm containing the element transition_probs with the estimated probability transition matrix. The package **msm** proposes the pmatrix.msm and pmatrix.piecewise.msm to extract the probability transition matrix from a fitted multi-state model (a list of class msm), as returned by msm. If the object d to be plotted is an object of msm, the function pmatrix.msm is used with the default settings to extract the probability transition matrix. In the case of **depmixS4**, which uses S4 classes, a probability transition matrix may be obtained depending on the type of model computed using depmix followed by fit and is embedded in an object of class depmix.fitted.

Setting a seed allows the graphic to be replicated.

If morder > 1, in other words, the order of the probability transition matrix d is of order greater than one, then d must be specified in reduced form. Structural zeroes are not accepted.

The pfilter argument serves to highlight probability sequences that are either most probable while shading out those that are less probable in shade.col and vice-versa. The four options for pfilter are described below, and are illustrated in Examples.

"smax" For each initial state the most probable next state is highlighed.

"smin" For each initial state the least probable next state is highlighed.

"tmax" The sequence of states with the highest probability overall is highlighed. To highlight the *n* most probable sequences of states, set num = n.

"tmin" The sequence of states with the lowest probability overall is highlighed. To highlight the *n* least probable sequences of states, set num = n.

The filter and hide.col arguments are inherent in and may be passed on to seqpcplot. The filter argument serves to specify filters to gray less interesting patterns. The filtered-out patterns are displayed in the hide.col color. The filter argument expects a list with at least elements type and value. Most relevant within the context of probabilities is type = "sequence", which highlights the specific pattern.

See Examples.

Value

trmatplot returns an object of class trmatplot. Some of the arguments are inherent in par and seqpcplot.

Author(s)

Pauline Adamopoulou

References

Buergin, R. and G. Ritschard (2014), "A decorated parallel coordinate plot for categorical longitudinal data", *The American Statistician*. Vol. 68(2), pp. 98-103.

Zeileis, A.; Hornik, K. and P. Murrell (2009), "Escaping RGBland: Selecting Colors for Statistical Graphics", *Computational Statistics & Data Analysis*. Vol. 53, pp. 3259-3270.

See Also

seqpcplot, par.

Examples

```
###########################################
# Plotting a probability transition matrix
###########################################

trMat<-matrix(c(0.1, 0.05, 0.05, 0.80,
  0.06, 0.02, 0.03, 0.89,
  0.03, 0.01, 0.01, 0.95,
  0, 0, 0, 1), nrow = 4, ncol = 4, byrow = TRUE)

trmatplot(trMat)

#--- Setting a seed so that the graphic can be replicated

trmatplot(trMat, seed = 2)
```

```
#--- Adjusting line width

trmatplot(trMat, seed = 2, lwd = 0.8)

#--- Defining a second order probability transition matrix as an array

trMatArray <- array(c(
  0.30, 0.70,
  0.65, 0.35,
  0.05, 0.95,
  0.99, 0.01), dim = c(1, 2, 4))

#--- Plotting with user-defined colors

trmatplot(trMatArray, seed = 3, morder = 2, cpal = c("grey40", "grey70"))

############################################################
# cspal: ready-to-use color palettes using colorspace
############################################################

#--- Color palette "dynamic"

trmatplot(trMat, seed = 2, cspal = "dynamic")

#--- Color palette "harmonic"

trmatplot(trMat, seed = 2, cspal = "harmonic")

#--- Color palette "cold"

trmatplot(trMat, seed = 2, cspal = "cold")

#--- Color palette "warm"

trmatplot(trMat, seed = 2, cspal = "warm")

#--- Color palette "heat"

trmatplot(trMat, seed = 2, cspal = "heat")

#--- Color palette "terrain"

trmatplot(trMat, seed = 2, cspal = "terrain")

############################################################
# pfilter: Filtering out most (or least) probable sequences
############################################################

#--- The most probable sequence given a state

trmatplot(trMat, seed = 2, pfilter = "smax")

#--- The least probable sequence given a state
```

```
trmatplot(trMat, seed = 2, pfilter = "smin")

#--- The two most probable sequnces

trmatplot(trMat, seed = 2, pfilter = "tmax", num = 2 )

#--- The ten least probable sequences

trmatplot(trMat, seed = 2, pfilter = "tmin", num = 10 )

#######################################################
# filter: Highlighting a specific sequence of interest
#######################################################

#--- Highlight the probability that a sequence is initially in state 1 and then in state 4

trmatplot(trMat, seed = 2, filter = list(type = "sequence", value = "(1)-(4)"))
```

Index