Package 'cfda'

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Title Categorical Functional Data Analysis

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Description Package for the analysis of categorical functional data.
The main purpose is to compute an encoding (real functional variable) for each state <https://hal.inria.fr/hal-02973094>.
It also provides functions to perform basic statistical analysis on categorical functional data.

BugReports https://github.com/modal-inria/cfda/issues

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Imports msm, diagram, ggplot2, mgcv, parallel, pbapply

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R topics documented:

cfda-package 2
biofam2 4

boxplot.timeSpent . . . 5
care . . . 6
compute_duration . . . 7
compute_number_jumps . . . 8
compute_optimal_encoding . . . 9
compute_time_spent . . . 11
cut_data . . . 12
estimate_Markov . . . 13
estimate_pt . . . 14
generate_2State . . . 15
generate_Markov . . . 16
get_encoding . . . 17
get_state . . . 18
hist.duration . . . 19
hist.njump . . . 20
plot.fmca . . . 21
plot.Markov . . . 23
plot.pt . . . 24
plotComponent . . . 25
plotData . . . 26
plotEigenvalues . . . 28
predict.fmca . . . 29
print.fmca . . . 30
remove_duplicated_states . . . 31
statetable . . . 32
summary.fmca . . . 33
summary_cfd . . . 33

Index **35**

`cfda-package` *Categorical Functional Data Analysis*

Description

cfda provides functions for the analysis of categorical functional data.

The main contribution is the computation of an optimal encoding (real functional variable) of each state of the categorical functional data. This can be done using the `compute_optimal_encoding` function that takes in arguments the data in a specific format and a basis of functions created using the `fda` package (cf. `create.basis`). The output can be analysed with `summary.fmca`, `plot.fmca`, `get_encoding`, `plotEigenvalues` and `plotComponent`.

Moreover, `cfda` contains functions to visualize and compute some statistics about categorical functional data. A summary of the dataset is available with `summary_cfd`. `plotData` shows a graphical representation of the dataset. Basic statistics can be computed: the number of jumps (`compute_number_jumps`), the duration (`compute_duration`), the time spent in each state (`compute_time_spent`), the probability to be in each state at any given time (`estimate_pt`), the transition table (`statetable`).

The parameters of a Markov process can be estimated using `estimate_Markov` function.

In order to test the different functions, a real dataset is provided (biofam2) as well as two functions for generating data: (generate_Markov and generate_2State).

Details

See the vignette for a detailed example and mathematical background: `RShowDoc("cfda",package = "cfda")`

References

- Deville J.C. (1982) Analyse de données chronologiques qualitatives : comment analyser des calendriers ?, Annales de l'INSEE, No 45, p. 45-104.
- Deville J.C. et Saporta G. (1980) Analyse harmonique qualitative, DIDAY et al. (editors), Data Analysis and Informatics, North Holland, p. 375-389.
- Saporta G. (1981) Méthodes exploratoires d'analyse de données temporelles, Cahiers du B.U.R.O, Université Pierre et Marie Curie, 37-38, Paris.

See Also

compute_optimal_encoding

Examples

```
# Simulate the Jukes-Cantor model of nucleotide replacement
K <- 4
Tmax <- 5
PJK <- matrix(1/3, nrow = K, ncol = K) - diag(rep(1/3, K))
lambda_PJK <- c(1, 1, 1, 1)
d_JK <- generate_Markov(n = 10, K = K, P = PJK, lambda = lambda_PJK, Tmax = Tmax)
d_JK2 <- cut_data(d_JK, Tmax)

# create basis object
m <- 5
b <- create.bspline.basis(c(0, Tmax), nbasis = m, norder = 4)

# compute encoding
encoding <- compute_optimal_encoding(d_JK2, b, computeCI = FALSE, nCores = 1)
summary(encoding)

# plot eigenvalues
plotEigenvalues(encoding, cumulative = TRUE, normalize = TRUE)

# plot the two first components
plotComponent(encoding, comp = c(1, 2))

# plot the encoding using the first harmonic
plot(encoding)

# extract the encoding using the first harmonic
encod <- get_encoding(encoding)
```

biofam2 *Family life states from the Swiss Household Panel biographical survey*

Description

2000 16 year-long family life sequences built from the retrospective biographical survey carried out by the Swiss Household Panel (SHP) in 2002. Data from `TraMineR` package.

Usage

```
data(biofam2)
```

Format

A data.frame containing three columns:

- *id* id of individuals (2000 different ids)
- *time* age in years where a change occurs
- *state* new state.

Details

The biofam2 dataset derives from the biofam dataset from `TraMineR` package. The biofam2 format is adapted to `cfda` functions. The biofam data set was constructed by Müller et al. (2007) from the data of the retrospective biographical survey carried out by the Swiss Household Panel (SHP) in 2002. The data set contains sequences of family life states from age 15 to 30 (sequence length is 16). The sequences are a sample of 2000 sequences of those created from the SHP biographical survey. It includes only individuals who were at least 30 years old at the time of the survey. The biofam data set describes family life courses of 2000 individuals born between 1909 and 1972.

The eight states are defined from the combination of five basic states, namely Living with parents (Parent), Left home (Left), Married (Marr), Having Children (Child), Divorced: "Parent", "Left", "Married", "Left+Marr", "Child", "Left+Child", "Left+Marr+Child", "Divorced"

Source

Swiss Household Panel https://forscenter.ch/projects/swiss-household-panel/

References

Müller, N. S., M. Studer, G. Ritschard (2007). Classification de parcours de vie à l'aide de l'optimal matching. In XIVe Rencontre de la Société francophone de classification (SFC 2007), Paris, 5 - 7 septembre 2007, pp. 157–160.

Examples

```
data(biofam2)
head(biofam2)


# It is recommended to increase the number of cores to reduce computation time
set.seed(42)
basis <- create.bspline.basis(c(15, 30), nbasis = 4, norder = 4)
fmca <- compute_optimal_encoding(biofam2, basis, nCores = 2)

plot(fmca, harm = 1)
plot(fmca, harm = 2)
plotEigenvalues(fmca, cumulative = TRUE, normalize = TRUE)
plotComponent(fmca, comp = c(1, 2), addNames = FALSE)
```

---

boxplot.timeSpent *Boxplot of time spent in each state*

Description

Boxplot of time spent in each state

Usage

```
## S3 method for class 'timeSpent'
boxplot(x, col = NULL, ...)
```

Arguments

x	output of compute_time_spent function
col	a vector containing color for each state
...	extra parameters for geom_boxplot

Value

a ggplot object that can be modified using ggplot2 package.

Author(s)

Quentin Grimonprez

Examples

```
# Simulate the Jukes-Cantor model of nucleotide replacement
K <- 4
PJK <- matrix(1/3, nrow = K, ncol = K) - diag(rep(1/3, K))
lambda_PJK <- c(1, 1, 1, 1)
d_JK <- generate_Markov(n = 10, K = K, P = PJK, lambda = lambda_PJK, Tmax = 10)

# cut at Tmax = 8
d_JK2 <- cut_data(d_JK, Tmax = 8)

# compute time spent by each id in each state
timeSpent <- compute_time_spent(d_JK2)

# plot the result
boxplot(timeSpent, col = c("#8DA0CB", "#E78AC3", "#A6D854", "#FFD92F"))

# modify the plot using ggplot2
library(ggplot2)
boxplot(timeSpent, notch = TRUE, outlier.colour = "black") +
   coord_flip() +
   labs(title = "Time spent in each state")
```

---

care *Care trajectories*

Description

Care trajectories of patients diagnosed with a serious and chronic condition

Usage

```
data(care)
```

Format

A data.frame containing three columns:

- *id* id of individuals (2929 different ids)
- *time* number of months since the diagnosis
- *state* new state.

Details

In this study, patients were followed from the time they were diagnosed with a serious and chronic condition and their care trajectories were tracked monthly from the time of diagnosis. The status variable contains the care status of each individual for each month of follow-up. Trajectories have different lengths.

The four states are:

- D: diagnosed, but not in care
- C: in care, but not on treatment
- T: on treatment, but infection not suppressed
- S: on treatment and suppressed infection

Source

https://larmarange.github.io/analyse-R/data/care_trajectories.RData https://larmarange.github.io/analyse-R/trajectoires-de-soins.html

Examples

```
data(care)
head(care)

# Individuals has not the same length. In order to compute the encoding,
# we keep individuals with at least 18 months of history and work
# with the 18 first months.
duration <- compute_duration(care)
idToKeep <- as.numeric(names(duration[duration >= 18]))
care2 <- cut_data(care[care$id %in% idToKeep, ], 18)
head(care2)


# It is recommended to increase the number of cores to reduce computation time
set.seed(42)
basis <- create.bspline.basis(c(0, 18), nbasis = 10, norder = 4)
fmca <- compute_optimal_encoding(care2, basis, nCores = 2)

plotEigenvalues(fmca, cumulative = TRUE, normalize = TRUE)
plot(fmca)
plot(fmca, addCI = TRUE)
plotComponent(fmca, addNames = FALSE)
```

---

compute_duration *Compute duration of individuals*

Description

For each individual, compute the duration

Usage

```
compute_duration(data)
```

Arguments

data	data.frame containing id, id of the trajectory, time, time at which a change occurs and state, associated state.

Value

a vector containing the duration of each trajectories

Author(s)

Cristian Preda, Quentin Grimonprez

See Also

hist.duration

Examples

```
# Simulate the Jukes-Cantor model of nucleotide replacement
K <- 4
PJK <- matrix(1/3, nrow = K, ncol = K) - diag(rep(1/3, K))
lambda_PJK <- c(1, 1, 1, 1)
d_JK <- generate_Markov(n = 10, K = K, P = PJK, lambda = lambda_PJK, Tmax = 10)


# compute duration of each individual
duration <- compute_duration(d_JK)

hist(duration)
```

---

compute_number_jumps *Compute the number of jumps*

Description

For each individual, compute the number of jumps performed

Usage

```
compute_number_jumps(data, countDuplicated = FALSE)
```

Arguments

data	data.frame containing id, id of the trajectory, time, time at which a change occurs and state, associated state.
countDuplicated	if TRUE, jumps in the same state are counted as jump

Value

A vector containing the number of jumps for each individual

Author(s)

Cristian Preda, Quentin Grimonprez

See Also

hist.njump

Examples

```
# Simulate the Jukes-Cantor model of nucleotide replacement
K <- 4
PJK <- matrix(1/3, nrow = K, ncol = K) - diag(rep(1/3, K))
lambda_PJK <- c(1, 1, 1, 1)
d_JK <- generate_Markov(n = 10, K = K, P = PJK, lambda = lambda_PJK, Tmax = 10)

# compute the number of jumps
nJump <- compute_number_jumps(d_JK)
```

---

compute_optimal_encoding

Compute the optimal encoding for each state

Description

Compute the optimal encoding for categorical functional data using an extension of the multiple correspondence analysis to a stochastic process.

Usage

```
compute_optimal_encoding(
  data,
  basisobj,
  computeCI = TRUE,
  nBootstrap = 50,
  propBootstrap = 1,
  nCores = max(1, ceiling(detectCores()/2)),
  verbose = TRUE,
  ...
)
```

Arguments

`data`	data.frame containing `id`, id of the trajectory, `time`, time at which a change occurs and `state`, associated state. All individuals must begin at the same time T0 and end at the same time Tmax (use `cut_data`).
`basisobj`	basis created using the `fda` package (cf. `create.basis`).
`computeCI`	if TRUE, perform a bootstrap to estimate the variance of encoding's coefficients
`nBootstrap`	number of bootstrap samples
`propBootstrap`	size of bootstrap samples relative to the number of individuals: propBootstrap * number of individuals
`nCores`	number of cores used for parallelization. Default is the half of cores.
`verbose`	if TRUE print some information
`...`	parameters for `integrate` function (see details).

Details

See the vignette for the mathematical background: `RShowDoc("cfda",package = "cfda")`

Extra parameters (...) for the `integrate` function can be:

- *subdivisions* the maximum number of subintervals.
- *rel.tol* relative accuracy requested.
- *abs.tol* absolute accuracy requested.

Value

A list containing:

- `eigenvalues` eigenvalues
- `alpha` optimal encoding coefficients associated with each eigenvectors
- `pc` principal components
- `F` matrix containing the $F_{(x,i)(y,j)}$
- `V` matrix containing the $V_{(x,i)}$
- `G` covariance matrix of `V`
- `basisobj` `basisobj` input parameter
- `pt` output of estimate_pt function
- `bootstrap` Only if `computeCI = TRUE`. Output of every bootstrap run
- `varAlpha` Only if `computeCI = TRUE`. Variance of alpha parameters
- `runTime` Total elapsed time

Author(s)

Cristian Preda, Quentin Grimonprez

References

- Deville J.C. (1982) Analyse de données chronologiques qualitatives : comment analyser des calendriers ?, Annales de l'INSEE, No 45, p. 45-104.
- Deville J.C. et Saporta G. (1980) Analyse harmonique qualitative, DIDAY et al. (editors), Data Analysis and Informatics, North Holland, p. 375-389.
- Saporta G. (1981) Méthodes exploratoires d'analyse de données temporelles, Cahiers du B.U.R.O, Université Pierre et Marie Curie, 37-38, Paris.

See Also

plot.fmca print.fmca summary.fmca plotComponent get_encoding

Examples

```
# Simulate the Jukes-Cantor model of nucleotide replacement
K <- 4
Tmax <- 5
PJK <- matrix(1/3, nrow = K, ncol = K) - diag(rep(1/3, K))
lambda_PJK <- c(1, 1, 1, 1)
d_JK <- generate_Markov(n = 10, K = K, P = PJK, lambda = lambda_PJK, Tmax = Tmax,
                        labels = c("A", "C", "G", "T"))
d_JK2 <- cut_data(d_JK, Tmax)

# create basis object
m <- 5
b <- create.bspline.basis(c(0, Tmax), nbasis = m, norder = 4)

# compute encoding
encoding <- compute_optimal_encoding(d_JK2, b, computeCI = FALSE, nCores = 1)
summary(encoding)

# plot the optimal encoding
plot(encoding)

# plot the two first components
plotComponent(encoding, comp = c(1, 2))

# extract the optimal encoding
get_encoding(encoding, harm = 1)
```

---

compute_time_spent *Compute time spent in each state*

Description

For each individual, compute the time spent in each state

Usage

```
compute_time_spent(data)
```

Arguments

data	data.frame containing id, id of the trajectory, time, time at which a change occurs and state, associated state.

Value

a matrix with K columns containing the total time spent in each state for each individual

Author(s)

Cristian Preda, Quentin Grimonprez

See Also

boxplot.timeSpent

Examples

```
# Simulate the Jukes-Cantor model of nucleotide replacement
K <- 4
PJK <- matrix(1/3, nrow = K, ncol = K) - diag(rep(1/3, K))
lambda_PJK <- c(1, 1, 1, 1)
d_JK <- generate_Markov(n = 10, K = K, P = PJK, lambda = lambda_PJK, Tmax = 10)

# cut at Tmax = 8
d_JK2 <- cut_data(d_JK, Tmax = 8)

# compute time spent by each id in each state
timeSpent <- compute_time_spent(d_JK2)
```

---

cut_data *Cut data to a maximal given time*

Description

Cut data to a maximal given time

Usage

```
cut_data(data, Tmax)
```

Arguments

data	data.frame containing id, id of the trajectory, time, time at which a change occurs and state, associated state.
Tmax	max time considered

Value

a data.frame with the same format as data where each individual has Tmax as last time entry.

Author(s)

Cristian Preda

Examples

```
# Simulate the Jukes-Cantor model of nucleotide replacement
K <- 4
PJK <- matrix(1/3, nrow = K, ncol = K) - diag(rep(1/3, K))
lambda_PJK <- c(1, 1, 1, 1)
d_JK = generate_Markov(n = 10, K = K, P = PJK, lambda = lambda_PJK, Tmax = 10)
tail(d_JK)

# cut at Tmax = 8
d_JK2 <- cut_data(d_JK, Tmax = 8)
tail(d_JK2)
```

---

estimate_Markov *Estimate transition matrix and spent time*

Description

Calculates crude initial values for transition intensities by assuming that the data represent the exact transition times of the Markov process.

Usage

```
estimate_Markov(data)
```

Arguments

data	data.frame containing id, id of the trajectory, time, time at which a change occurs and state, associated state.

Value

list of two elements: Q, the estimated transition matrix, and lambda, the estimated time spent in each state

Author(s)

Cristian Preda

See Also

plot.Markov

Examples

```
# Simulate the Jukes-Cantor model of nucleotide replacement
K <- 4
PJK <- matrix(1/3, nrow = K, ncol = K) - diag(rep(1/3, K))
lambda_PJK <- c(1, 1, 1, 1)
d_JK <- generate_Markov(n = 100, K = K, P = PJK, lambda = lambda_PJK, Tmax = 10)

# estimation
mark <- estimate_Markov(d_JK)
mark$P
mark$lambda
```

`estimate_pt` *Estimate probabilities to be in each state*

Description

Estimate probabilities to be in each state

Usage

```
estimate_pt(data, NAafterTmax = FALSE)
```

Arguments

`data`	data.frame containing `id`, id of the trajectory, `time`, time at which a change occurs and `state`, associated state.
`NAafterTmax`	if TRUE, return NA if t > Tmax otherwise return the state associated with Tmax (useful when individuals has different lengths)

Value

A list of two elements:

- t: vector of time
- pt: a matrix with K (= number of states) rows and with `length(t)` columns containing the probabilities to be in each state at each time.

Author(s)

Cristian Preda, Quentin Grimonprez

See Also

plot.pt

Examples

```
# Simulate the Jukes-Cantor model of nucleotide replacement
K <- 4
PJK <- matrix(1/3, nrow = K, ncol = K) - diag(rep(1/3, K))
lambda_PJK <- c(1, 1, 1, 1)
d_JK <- generate_Markov(n = 10, K = K, P = PJK, lambda = lambda_PJK, Tmax = 10)

d_JK2 <- cut_data(d_JK, 10)

# estimate probabilities
estimate_pt(d_JK2)
```

---

generate_2State *Generate data following a 2 states model*

Description

Generate individuals such that each individual starts at time 0 with state 0 and then an unique change to state 1 occurs at a time t generated using an uniform law between 0 and 1.

Usage

```
generate_2State(n)
```

Arguments

n	number of individuals

Value

a data.frame with 3 columns: `id`, id of the trajectory, `time`, time at which a change occurs and `state`, new state.

Author(s)

Cristian Preda, Quentin Grimonprez

`generate_Markov` *Generate Markov Trajectories*

Description

Simulate individuals from a Markov process defined by a transition matrix, time spent in each time and initial probabilities.

Usage

```
generate_Markov(
  n = 5,
  K = 2,
  P = 1 - diag(K),
  lambda = rep(1, K),
  pi0 = c(1, rep(0, K - 1)),
  Tmax = 1,
  labels = NULL
)
```

Arguments

`n`	number of trajectories to generate
`K`	number of states
`P`	matrix containing the transition probabilities from one state to another. Each row contains positive reals summing to 1.
`lambda`	time spent in each state
`pi0`	initial distribution of states
`Tmax`	maximal duration of trajectories
`labels`	state names. If `NULL`, integers are used

Details

For one individual, assuming the current state is s_j at time t_j, the next state and time is simulated as follows:

1. generate one sample, d, of an exponential law of parameter `lambda[s_j]`
2. define the next time values as: $t_{j+1} = t_j + d$
3. generate the new state s_{j+1} using a multinomial law with probabilities `Q[s_j,]`

Value

a data.frame with 3 columns: `id`, id of the trajectory, `time`, time at which a change occurs and `state`, new state.

Author(s)

Cristian Preda

Examples

```
# Simulate the Jukes-Cantor model of nucleotide replacement
K <- 4
PJK <- matrix(1/3, nrow = K, ncol = K) - diag(rep(1/3, K))
lambda_PJK <- c(1, 1, 1, 1)
d_JK <- generate_Markov(n = 100, K = K, P = PJK, lambda = lambda_PJK, Tmax = 10,
                            labels = c("A", "C", "G", "T"))

head(d_JK)
```

---

get_encoding *Extract the computed encoding*

Description

Extract the encoding as an fd object or as a matrix

Usage

```
get_encoding(x, harm = 1, fdObject = FALSE, nx = NULL)
```

Arguments

x	Output of compute_optimal_encoding
harm	harmonic to use for the encoding
fdObject	If TRUE returns a fd object else a matrix
nx	(Only if fdObject = TRUE) Number of points to evaluate the encoding

Details

The encoding is $a_x \approx \sum_{i=1}^{m} \alpha_{x,i}\phi_i$.

Value

a fd object or a list of two elements y, a matrix with nx rows containing the encoding of the state and x, the vector with time values.

Author(s)

Cristian Preda

Examples

```
# Simulate the Jukes-Cantor model of nucleotide replacement
K <- 4
Tmax <- 6
PJK <- matrix(1/3, nrow = K, ncol = K) - diag(rep(1/3, K))
lambda_PJK <- c(1, 1, 1, 1)
d_JK <- generate_Markov(n = 10, K = K, P = PJK, lambda = lambda_PJK, Tmax = Tmax)
d_JK2 <- cut_data(d_JK, Tmax)

# create basis object
m <- 6
b <- create.bspline.basis(c(0, Tmax), nbasis = m, norder = 4)


# compute encoding
encoding <- compute_optimal_encoding(d_JK2, b, computeCI = FALSE, nCores = 1)

# extract the encoding using 1 harmonic
encodFd <- get_encoding(encoding, fdObject = TRUE)
encodMat <- get_encoding(encoding, nx = 200)
```

---

get_state *Extract the state of each individual at a given time*

Description

Extract the state of each individual at a given time

Usage

```
get_state(data, t, NAafterTmax = FALSE)
```

Arguments

data	data.frame containing id, id of the trajectory, time, time at which a change occurs and state, associated state.
t	time at which extract the state
NAafterTmax	if TRUE, return NA if t > Tmax otherwise return the state associated with Tmax (useful when individuals has different lengths)

Value

a vector containing the state of each individual at time t

Author(s)

Cristian Preda, Quentin Grimonprez

Examples

```
# Simulate the Jukes-Cantor model of nucleotide replacement
K <- 4
PJK <- matrix(1/3, nrow = K, ncol = K) - diag(rep(1/3, K))
lambda_PJK <- c(1, 1, 1, 1)
d_JK <- generate_Markov(n = 10, K = K, P = PJK, lambda = lambda_PJK, Tmax = 10)

# get the state of each individual at time t = 6
get_state(d_JK, 6)


# get the state of each individual at time t = 12 (> Tmax)
get_state(d_JK, 12)
# if NAafterTmax = TRUE, it will return NA for t > Tmax
get_state(d_JK, 12, NAafterTmax = TRUE)
```

`hist.duration` *Plot the duration*

Description

Plot the duration

Usage

```
## S3 method for class 'duration'
hist(x, breaks = NULL, ...)
```

Arguments

`x`	output of `compute_duration` function
`breaks`	number of breaks. If not given, use the Sturges rule
`...`	parameters for `geom_histogram`

Value

a `ggplot` object that can be modified using `ggplot2` package.

Author(s)

Quentin Grimonprez

Examples

```
# Simulate the Jukes-Cantor model of nucleotide replacement
K <- 4
PJK <- matrix(1/3, nrow = K, ncol = K) - diag(rep(1/3, K))
lambda_PJK <- c(1, 1, 1, 1)
d_JK <- generate_Markov(n = 10, K = K, P = PJK, lambda = lambda_PJK, Tmax = 10)


# compute duration of each individual
duration <- compute_duration(d_JK)

hist(duration)

# modify the plot using ggplot2
library(ggplot2)
hist(duration) +
   labs(title = "Distribution of the duration")
```

---

hist.njump *Plot the number of jumps*

Description

Plot the number of jumps

Usage

```
## S3 method for class 'njump'
hist(x, breaks = NULL, ...)
```

Arguments

x	output of compute_number_jumps function
breaks	number of breaks. If not given, use the Sturges rule
...	parameters for geom_histogram

Value

a ggplot object that can be modified using ggplot2 package.

Author(s)

Quentin Grimonprez

Examples

```
# Simulate the Jukes-Cantor model of nucleotide replacement
K <- 4
PJK <- matrix(1/3, nrow = K, ncol = K) - diag(rep(1/3, K))
lambda_PJK <- c(1, 1, 1, 1)
d_JK <- generate_Markov(n = 10, K = K, P = PJK, lambda = lambda_PJK, Tmax = 10)

nJump <- compute_number_jumps(d_JK)

hist(nJump)

# modify the plot using ggplot2
library(ggplot2)
hist(nJump, fill = "#984EA3") +
   labs(title = "Distribution of the number of jumps")
```

`plot.fmca` *Plot the optimal encoding*

Description

Plot the optimal encoding

Usage

```
## S3 method for class 'fmca'
plot(
  x,
  harm = 1,
  states = NULL,
  addCI = FALSE,
  coeff = 1.96,
  col = NULL,
  nx = 128,
  ...
)
```

Arguments

`x`	output of `compute_optimal_encoding` function
`harm`	harmonic to use for the encoding
`states`	states to plot (default = NULL, it plots all states)
`addCI`	if TRUE, plot confidence interval (only when `computeCI = TRUE` in compute_optimal_encoding)
`coeff`	the confidence interval is computed with +- coeff * the standard deviation
`col`	a vector containing color for each state
`nx`	number of time points used to plot
`...`	not used

Details

The encoding for the harmonic h is $a_x^{(h)} \approx \sum_{i=1}^{m} \alpha_{x,i}^{(h)} \phi_i$.

Value

a ggplot object that can be modified using ggplot2 package.

Author(s)

Quentin Grimonprez

See Also

plotComponent plotEigenvalues

Examples

```
# Simulate the Jukes-Cantor model of nucleotide replacement
K <- 4
Tmax <- 6
PJK <- matrix(1/3, nrow = K, ncol = K) - diag(rep(1/3, K))
lambda_PJK <- c(1, 1, 1, 1)
d_JK <- generate_Markov(n = 10, K = K, P = PJK, lambda = lambda_PJK, Tmax = Tmax)
d_JK2 <- cut_data(d_JK, Tmax)

# create basis object
m <- 6
b <- create.bspline.basis(c(0, Tmax), nbasis = m, norder = 4)


# compute encoding
encoding <- compute_optimal_encoding(d_JK2, b, computeCI = FALSE, nCores = 1)

# plot the encoding produced by the first harmonic
plot(encoding)


# modify the plot using ggplot2
library(ggplot2)
plot(encoding, harm = 2, col = c("red" , "blue", "darkgreen", "yellow")) +
   labs(title = "Optimal encoding")
```

`plot.Markov` *Plot the transition graph*

Description

Plot the transition graph between the different states. A node corresponds to a state with the mean time spent in this state. Each arrow represents the probability of transition between states.

Usage

```
## S3 method for class 'Markov'
plot(x, ...)
```

Arguments

`x`	output of `estimate_Markov` function
`...`	parameters of `plotmat` function from `diagram` package (see details).

Details

Some useful extra parameters:

- `main` main title.
- `dtext` controls the position of arrow text relative to arrowhead (default = 0.3).
- `relsize` scaling factor for size of the graph (default = 1).
- `box.size` size of label box, one value or a vector with dimension = number of rows of `x$P`.
- `box.cex` relative size of text in boxes, one value or a vector with dimension=number of rows of `x$P`.
- `arr.pos` relative position of arrowhead on arrow segment/curve.

Value

No return value, called for side effects

Author(s)

Cristian Preda

Examples

```
# Simulate the Jukes-Cantor model of nucleotide replacement
K <- 4
PJK <- matrix(1/3, nrow = K, ncol = K) - diag(rep(1/3, K))
lambda_PJK <- c(1, 1, 1, 1)
d_JK <- generate_Markov(n = 100, K = K, P = PJK, lambda = lambda_PJK, Tmax = 10)

# estimation
```

```
mark <- estimate_Markov(d_JK)

# transition graph
plot(mark)
```

---

plot.pt *Plot probabilities*

Description

Plot the probabilities of each state at each given time

Usage

```
## S3 method for class 'pt'
plot(x, col = NULL, ribbon = FALSE, ...)
```

Arguments

x	output of estimate_pt
col	a vector containing color for each state
ribbon	if TRUE, use ribbon to plot probabilities
...	only if ribbon = TRUE, parameter addBorder, if TRUE, add black border to the ribbons.

Value

a ggplot object that can be modified using ggplot2 package.

Author(s)

Quentin Grimonprez

Examples

```
# Simulate the Jukes-Cantor model of nucleotide replacement
K <- 4
PJK <- matrix(1/3, nrow = K, ncol = K) - diag(rep(1/3, K))
lambda_PJK <- c(1, 1, 1, 1)
d_JK <- generate_Markov(n = 10, K = K, P = PJK, lambda = lambda_PJK, Tmax = 10)

d_JK2 <- cut_data(d_JK, 10)

pt <- estimate_pt(d_JK2)

plot(pt, ribbon = TRUE)
```

plotComponent *Plot Components*

Description

Plot Components

Usage

```
plotComponent(
  x,
  comp = c(1, 2),
  addNames = TRUE,
  nudge_x = 0.1,
  nudge_y = 0.1,
  size = 4,
  ...
)
```

Arguments

x	output of compute_optimal_encoding function
comp	a vector of two elements indicating the components to plot
addNames	if TRUE, add the id labels on the plot
nudge_x, nudge_y	horizontal and vertical adjustment to nudge labels by
size	size of labels
...	geom_point parameters

Value

a ggplot object that can be modified using ggplot2 package.

Author(s)

Quentin Grimonprez

See Also

plot.fmca plotEigenvalues

Examples

```
# Simulate the Jukes-Cantor model of nucleotide replacement
K <- 4
Tmax <- 6
PJK <- matrix(1/3, nrow = K, ncol = K) - diag(rep(1/3, K))
lambda_PJK <- c(1, 1, 1, 1)
d_JK <- generate_Markov(n = 10, K = K, P = PJK, lambda = lambda_PJK, Tmax = Tmax)
d_JK2 <- cut_data(d_JK, Tmax)

# create basis object
m <- 6
b <- create.bspline.basis(c(0, Tmax), nbasis = m, norder = 4)


# compute encoding
encoding <- compute_optimal_encoding(d_JK2, b, computeCI = FALSE, nCores = 1)

plotComponent(encoding, comp = c(1, 2))

# modify the plot using ggplot2
library(ggplot2)
plotComponent(encoding, comp = c(1, 2), shape = 23) +
   labs(title = "Two first components")
```

`plotData` *Plot categorical functional data*

Description

Plot categorical functional data

Usage

```
plotData(
  data,
  group = NULL,
  col = NULL,
  addId = TRUE,
  addBorder = TRUE,
  sort = FALSE,
  nCol = NULL
)
```

Arguments

`data`	data.frame containing `id`, id of the trajectory, `time`, time at which a change occurs and `state`, associated state.

group	vector, of the same length as the number individuals of data, containing group index. Groups are displayed on separate plots. If group = NA, the corresponding individuals in data is ignored.
col	a vector containing color for each state (can be named)
addId	If TRUE, add id labels
addBorder	If TRUE, add black border to each individual
sort	If TRUE, id are sorted according to the duration in their first state
nCol	number of columns when group is given

Value

a ggplot object that can be modified using ggplot2 package. On the plot, each row represents an individual over [0:Tmax]. The color at a given time gives the state of the individual.

Author(s)

Cristian Preda, Quentin Grimonprez

Examples

```
# Simulate the Jukes-Cantor model of nucleotide replacement
K <- 4
PJK <- matrix(1/3, nrow = K, ncol = K) - diag(rep(1/3, K))
lambda_PJK <- c(1, 1, 1, 1)
d_JK <- generate_Markov(n = 10, K = K, P = PJK, lambda = lambda_PJK, Tmax = 10)

# add a line with time Tmax at the end of each individual
d_JKT <- cut_data(d_JK, Tmax = 10)

plotData(d_JKT)

# modify the plot using ggplot2
library(ggplot2)
plotData(d_JKT, col = c("red", "blue", "green", "brown")) +
   labs(title = "Trajectories of a Markov process")


# use the group variable: create a group with the 3 first variables and one with the others
group <- rep(1:2, c(3, 7))
plotData(d_JKT, group = group)


# use the group variable: remove the id number 5 and 6
group[c(5, 6)] = NA
plotData(d_JKT, group = group)
```

plotEigenvalues *Plot Eigenvalues*

Description

Plot Eigenvalues

Usage

```
plotEigenvalues(x, cumulative = FALSE, normalize = FALSE, ...)
```

Arguments

x	output of compute_optimal_encoding function
cumulative	if TRUE, plot the cumualtive eigenvalues
normalize	if TRUE eigenvalues are normalized for summing to 1
...	geom_point parameters

Value

a ggplot object that can be modified using ggplot2 package.

Author(s)

Quentin Grimonprez

See Also

plot.fmca plotComponent

Examples

```
# Simulate the Jukes-Cantor model of nucleotide replacement
K <- 4
Tmax <- 6
PJK <- matrix(1/3, nrow = K, ncol = K) - diag(rep(1/3, K))
lambda_PJK <- c(1, 1, 1, 1)
d_JK <- generate_Markov(n = 10, K = K, P = PJK, lambda = lambda_PJK, Tmax = Tmax)
d_JK2 <- cut_data(d_JK, Tmax)

# create basis object
m <- 6
b <- create.bspline.basis(c(0, Tmax), nbasis = m, norder = 4)


# compute encoding
encoding <- compute_optimal_encoding(d_JK2, b, computeCI = FALSE, nCores = 1)
```

```
# plot eigenvalues
plotEigenvalues(encoding, cumulative = TRUE, normalize = TRUE)

# modify the plot using ggplot2
library(ggplot2)
plotEigenvalues(encoding, shape = 23) +
   labs(caption = "Jukes-Cantor model of nucleotide replacement")
```

`predict.fmca` *Predict using RMixtComp*

Description

Predict the cluster of new samples.

Usage

```
## S3 method for class 'fmca'
predict(
  object,
  newdata = NULL,
  nCores = max(1, ceiling(detectCores()/2)),
  verbose = TRUE,
  ...
)
```

Arguments

`object`	output of compute_optimal_encoding function.
`newdata`	data.frame containing `id`, id of the trajectory, `time`, time at which a change occurs and `state`, associated state. All individuals must begin at the same time T0 and end at the same time Tmax (use `cut_data`)..
`nCores`	number of cores used for parallelization. Default is the half of cores.
`verbose`	if TRUE print some information
`...`	parameters for `integrate` function (see details).

Value

principal components for the individuals

Author(s)

Quentin Grimonprez

See Also

compute_optimal_encoding

Examples

```
# Simulate the Jukes-Cantor model of nucleotide replacement
K <- 4
Tmax <- 6
PJK <- matrix(1/3, nrow = K, ncol = K) - diag(rep(1/3, K))
lambda_PJK <- c(1, 1, 1, 1)
d_JK <- generate_Markov(n = 10, K = K, P = PJK, lambda = lambda_PJK, Tmax = Tmax,
                            labels = c("A", "C", "G", "T"))
d_JK2 <- cut_data(d_JK, Tmax)

# create basis object
m <- 6
b <- create.bspline.basis(c(0, Tmax), nbasis = m, norder = 4)


# compute encoding
encoding <- compute_optimal_encoding(d_JK2, b, computeCI = FALSE, nCores = 1)

# predict principal components
d_JK_predict <- generate_Markov(n = 5, K = K, P = PJK, lambda = lambda_PJK, Tmax = Tmax,
                            labels = c("A", "C", "G", "T"))
d_JK_predict2 <- cut_data(d_JK, Tmax)

pc <- predict(encoding, d_JK_predict2, nCores = 1)
```

---

print.fmca *Print* fmca *object Print a* fmca *object*

Description

Print fmca object

Print a fmca object

Usage

```
## S3 method for class 'fmca'
print(x, n = 6, ...)
```

Arguments

x	fmca object (see compute_optimal_encoding function)
n	maximal number of rows and cols to print
...	Not used.

Value

No return value, called for side effects

See Also

compute_optimal_encoding summary.fmca

`remove_duplicated_states` *Remove duplicated states*

Description

Remove duplicated consecutive states from data. If for an individual there is two or more consecutive states that are identical, only the first is kept. Only time when the state changes are kept.

Usage

```
remove_duplicated_states(data, keep.last = TRUE)
```

Arguments

`data`	data.frame containing `id`, id of the trajectory, `time`, time at which a change occurs and `state`, associated state.
`keep.last`	if TRUE, keep the last state for every individual even if it is a duplicated state.

Value

`data` without duplicated consecutive states

Author(s)

Quentin Grimonprez

Examples

```
data <- data.frame(id = rep(1:3, c(10, 3, 8)), time = c(1:10, 1:3, 1:8),
                   state = c(rep(1:5, each = 2), 1:3, rep(1:3, c(1, 6, 1))))
out <- remove_duplicated_states(data)
```

`statetable` *Table of transitions*

Description

Calculates a frequency table counting the number of times each pair of states were observed in successive observation times.

Usage

```
statetable(data, removeDiagonal = FALSE)
```

Arguments

`data`	data.frame containing `id`, id of the trajectory, `time`, time at which a change occurs and `state`, associated state.
`removeDiagonal`	if TRUE, does not count transition from a state i to i

Value

a vector of length `K` containing the total time spent in each state

Author(s)

Quentin Grimonprez

Examples

```
# Simulate the Jukes-Cantor model of nucleotide replacement
K <- 4
PJK <- matrix(1/3, nrow = K, ncol = K) - diag(rep(1/3, K))
lambda_PJK <- c(1, 1, 1, 1)
d_JK <- generate_Markov(n = 10, K = K, P = PJK, lambda = lambda_PJK, Tmax = 10)

# table of transitions
statetable(d_JK)
```

summary.fmca *Object Summaries Summary of a* fmca *object*

Description

Object Summaries

Summary of a fmca object

Usage

```
## S3 method for class 'fmca'
summary(object, n = 6, ...)
```

Arguments

object	fmca object (see compute_optimal_encoding function)
n	maximal number of rows and cols to print
...	Not used.

Value

No return value, called for side effects

See Also

compute_optimal_encoding print.fmca

summary_cfd *Summary*

Description

Get a summary of the data.frame containin categorical functional data

Usage

```
summary_cfd(data, max.print = 10)
```

Arguments

data	data.frame containing id, id of the trajectory, time, time at which a change occurs and state, associated state.
max.print	maximal number of states to display

Value

a list containing:

- `nRow` number of rows
- `nInd` number of individuals
- `timeRange` minimal and maximal time value
- `uniqueStart` TRUE, if all individuals have the same time start value
- `uniqueEnd` TRUE, if all individuals have the same time start value
- `states` vector containing the different states
- `visit` number of individuals visiting each state

Author(s)

Quentin Grimonprez

Examples

```
data(biofam2)
summary_cfd(biofam2)
```

Index

∗ **data**
    biofam2, 4
    care, 6
∗ **package**
    cfda-package, 2

biofam2, *3*, 4
boxplot.timeSpent, 5, *12*

care, 6
cfda-package, 2
compute_duration, *2*, 7, *19*
compute_number_jumps, *2*, 8, *20*
compute_optimal_encoding, *2, 3*, 9, *17*, *21*, *25*, *28–31*, *33*
compute_time_spent, *2*, *5*, 11
create.basis, *2*, *10*
cut_data, *10*, 12, *29*

estimate_Markov, *2*, 13, *23*
estimate_pt, *2*, *10*, 14, *24*

generate_2State, *3*, 15
generate_Markov, *3*, 16
get_encoding, *2*, *11*, 17
get_state, 18

hist.duration, *8*, 19
hist.njump, *9*, 20

integrate, *10*, *29*

plot.fmca, *2*, *11*, 21, *25*, *28*
plot.Markov, *14*, 23
plot.pt, *15*, 24
plotComponent, *2*, *11*, *22*, 25, *28*
plotData, *2*, 26
plotEigenvalues, *2*, *22*, *25*, 28
predict.fmca, 29
print.fmca, *11*, 30, *33*

remove_duplicated_states, 31

statetable, *2*, 32
summary.fmca, *2*, *11*, *31*, 33
summary_cfd, *2*, 33