Package 'gfpop'

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Type Package

Title Graph-Constrained Functional Pruning Optimal Partitioning

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Description Penalized parametric change-point detection by functional pruning dynamic programming algorithm. The successive means are constrained using a graph structure with edges defining the nature of the changes These changes can be unconstrained (type std), up or down constrained (type up and down) or constrained by a minimal size jump (type abs). The type null means that the graph allows us to stay on the same segment. To each edge we can associate some additional properties: a minimal gap size, a penalty, some robust parameters (K,a) for biweight (K) and Huber losses (K and a). The user can also constrain the inferred means to lie between some minimal and maximal values. Data is modeled by a cost with possible use of a robust loss, biweight and Huber (see edge parameters K and a). These costs should have a quadratic, log-linear or a log-log representation. This includes quadratic Gaussian cost (type = 'mean'), log-linear cost (type = 'variance', 'poisson' or 'exp') and log-log cost (type = 'negbin'). More details in the paper published in the Journal of Statistical Software: <doi:10.18637/jss.v106.i06>.

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Contents

dataGenerator . . . 2
ECG . . . 3
Edge . . . 4
gfpop . . . 5
graph . . . 7
itergfpop . . . 8
Mono27ac . . . 9
neuroSpike . . . 10
Node . . . 10
paperGraph . . . 11
plot.gfpop . . . 12
print.gfpop . . . 13
profile614chr2 . . . 13
sdDiff . . . 14
StartEnd . . . 15
summary.gfpop . . . 15

Index **17**

`dataGenerator` *Data Generator*

Description

Generating data with a given model = changepoint relative positions + parameters + type of cost + (standard deviation + gamma decay)

Usage

```
dataGenerator(
  n,
  changepoints,
  parameters,
  type = "mean",
  sigma = 1,
  gamma = 1,
```

```
  size = 10
)
```

Arguments

`n`	number of data points to generate
`changepoints`	vector of positions of the changepoints in (0,1] (last element is always 1).
`parameters`	vector of means for the consecutive segments (same length as changepoints)
`type`	a string defining the cost model to use: `"mean"`, `"variance"`, `"poisson"`, `"exp"`, `"negbin"`
`sigma`	a positive number = the standard deviation of the data
`gamma`	a number between 0 and 1 : the coefficient of the exponential decay (by default = 1 for piecewise constant signals)
`size`	parameter of the `rnbinom` function

Value

a vector of size n generated by the chosen model

Examples

```
dataGenerator(500, c(0.3, 0.6, 1), c(1, 2, 3), type = "mean", sigma = 0.5)

dataGenerator(1000, c(0.2, 0.33,0.5, 1), c(4, 0.2, 3,0.5), type = "variance")

dataGenerator(800, c(0.4, 0.8, 1), c(15, 5, 8), type = "mean", gamma  = 0.95, sigma = 0.4)

dataGenerator(400, c(0.4, 0.9, 1), c(2, 1.5, 3), type = "poisson")

dataGenerator(1000, c(0.44, 0.86, 1), c(0.5, 0.2, 0.4), type = "negbin", size = 3)
```

ECG   *Electrocardiogram data*

Description

The goal in these data is to detect the QRS complex, as does the Pan-Tompkins algorithm.

Usage

```
data("ECG")
```

Format

A named list of two data.tables: data has 1001 rows and 2 columns, PanTompkins has 24 rows and 3 columns.

References

https://www.robots.ox.ac.uk/~gari/teaching/cdt/A3/readings/ECG/Pan+Tompkins.pdf

---

`Edge` *Edge generation*

Description

Edge creation for gfpop-R-Package graph

Usage

```
Edge(
  state1,
  state2,
  type = "null",
  decay = 1,
  gap = 0,
  penalty = 0,
  K = Inf,
  a = 0
)
```

Arguments

`state1`	a string defining the starting state of the edge
`state2`	a string defining the ending state of the edge
`type`	a string equal to `"null"`, `"std"`, `"up"`, `"down"` or `"abs"`. Default type is `"null"`, the transition to stay on the same segment.
`decay`	a nonnegative number to give the strength of the exponential decay into the segment
`gap`	a nonnegative number to constrain the size of the gap in the change of state
`penalty`	a nonnegative number. The penality associated to this state transition
`K`	a positive number. Threshold for the Biweight robust loss
`a`	a positive number. Slope for the Huber robust loss

Value

a one-row dataframe with 9 variables

Examples

```
Edge("Dw", "Up", "up", gap = 1, penalty = 10, K = 3)

Edge(0, 1, "abs", penalty = 2, gap = 1)

Edge(0, 0, "null", penalty = 0, K = 2, a = 1)

Edge("Dw", "Dw", type = "null", decay = 0.997)
```

---

gfpop *Graph-Constrained Functional Pruning Optimal Partitioning (gfpop)*

Description

Functional pruning optimal partitioning with a graph structure to take into account constraints on consecutive segment parameters. The user has to specify the graph he wants to use (see the graph function) and a type of cost function. This is the main function of the gfpop package. Its result can be plotted using the S3 gfpop function `gfpop::plot()`

Usage

```
gfpop(data, mygraph, type = "mean", weights = NULL, testMode = FALSE)
```

Arguments

`data`	vector of data to segment. For simulation studies, Data can be generated using gfpop package function `gfpop::dataGenerator()`
`mygraph`	dataframe of class "graph" to constrain the changepoint inference, see `gfpop::graph()`
`type`	a string defining the cost model to use: `"mean"`, `"variance"`, `"poisson"`, `"exp"`, `"negbin"`
`weights`	vector of weights (positive numbers), same size as data
`testMode`	boolean. `FALSE` by default. Used to debug the code

Details

The constrained optimization problem for n data points takes the following general form:

$$Q_n = min(withconstraints)(\sum_{t=1}^{n}(\gamma(e[t])(y[t], \mu[t]) + \beta(e[t]))$$

with data points $y[t]$, edges $e[t]$, edge-dependent penalties $\beta(e[t])$ and cost functions γ. The cost function can take three different forms for parameter x and constants (A, B, C):

- *quadratic*, with representation $Ax^2 + Bx + C$ with x in R
- *log-linear*, with representation $Ax - Blog(x) + C$ with $x \geq 0$
- *log-log*, with representation $-Alog(x) - Blog(1 - x) + C$ with $0 \leq x \leq 1$

For each optimization problem, we consider a unique cost representation. However, the User can define robustness values (K and a) specific to each edge, making the cost function edge-dependent. We give the atomic form of each of the five available types (for one data point of value y with weight w)

- `"mean"` : $A = w, B = -2wy, C = wy^2$
- `"variance"` : $A = wy^2, B = w, C = 0$
- `"poisson"` : $A = w, B = wy, C = 0$
- `"exp"` : $A = wy, B = w, C = 0$
- `"negbin"` : $A = w, B = wy, C = 0$

Value

a gfpop object = (`changepoints`, `states`, `forced`, `parameters`, `globalCost`)

`changepoints` is the vector of changepoints (we give the last element of each segment)

`states` is the vector giving the state of each segment

`forced` is the vector specifying whether the constraints of the graph are active (= `TRUE`) or not (= `FALSE`)

`parameters` is the vector of successive parameters of each segment

`globalCost` is a number equal to the total loss: the minimal cost for the optimization problem with all penalty values excluded

See Also

- `gfpop::dataGenerator()` to generate data for multiple change-point simulations
- `gfpop::graph()` to create graphs complying with the gfpop function
- `gfpop::plot()` to plot the gfpop object and visualize inferred changepoints and parameters

Examples

```
n <- 1000 #data length
### EXAMPLE 1 ### updown graph + poisson loss
 myData <- dataGenerator(n, c(0.1, 0.3, 0.5, 0.8, 1), c(1, 2, 1, 3, 1), type = "poisson")
 myGraph <- graph(penalty = 2 * sdDiff(myData)^2 * log(n), type = "updown")
 gfpop(data = myData, mygraph = myGraph, type = "poisson")

### EXAMPLE 2 ### relevant graph with min gap = 2 + poisson loss
 myData <- dataGenerator(n, c(0.1, 0.3, 0.5, 0.8, 1), c(1, 2, 3, 5, 3), type = "poisson")
 myGraph <- graph(type = "relevant", penalty = 2 * log(n), gap = 2)
 gfpop(data =  myData, mygraph = myGraph, type = "poisson")

### EXAMPLE 3 ### std graph with robust loss + variance loss
 myData <- dataGenerator(n, c(0.1, 0.3, 0.5, 0.8, 1), c(1, 5, 1, 5, 1), type = "variance")
 outliers <- 5 * rbinom(n, 1, 0.05) - 5 * rbinom(n, 1, 0.05)
### with robust parameter K
 myGraph <- graph(type = "std", penalty = 2 * log(n), K = 10)
 gfpop(data =  myData + outliers, mygraph = myGraph, type = "variance")
```

```
### no K
 myGraph <- graph(type = "std", penalty = 2 * log(n))
 gfpop(data =  myData, mygraph = myGraph, type = "variance")

### EXAMPLE 4 ###  3-segment graph with mean (Gaussian) loss
 myData <- dataGenerator(n, c(0.12, 0.31, 0.53, 0.88, 1), c(1, 2, 0, 1, 2), type = "mean")
 outliers <- 5 * rbinom(n, 1, 0.05) - 5 * rbinom(n, 1, 0.05)
 gfpop(data =  myData + outliers, mygraph = paperGraph(8, penalty = 2 * log(n)), type = "mean")
```

`graph` *Graph generation*

Description

Graph creation using component functions `Edge`, `StartEnd` and `Node`

Usage

```
graph(
  ...,
  type = "empty",
  decay = 1,
  gap = 0,
  penalty = 0,
  K = Inf,
  a = 0,
  all.null.edges = FALSE
)
```

Arguments

`...`	This is a list of edges definied by functions `Edge`, `StartEnd` and `Node`. See gfpop functions `gfpop::Edge()`, `gfpop::StartEnd()` and `gfpop::Node()`
`type`	a string equal to `"std"`, `"isotonic"`, `"updown"` or `"relevant"` to build a predefined classic graph
`decay`	a nonnegative number to give the strength of the exponential decay into the segment
`gap`	a nonnegative number to constrain the size of the gap in the change of state
`penalty`	a nonnegative number equals to the common penalty to use for all edges
`K`	a positive number. Threshold for the Biweight robust loss
`a`	a positive number. Slope for the Huber robust loss
`all.null.edges`	a boolean. Add null edges to all nodes automatically

Value

a dataframe with 9 variables : columns are named `"state1"`, `"state2"`, `"type"`, `"parameter"`, `"penalty"`, `"K"`, `"a"`, `"min"`, `"max"` with additional `"graph"` class.

Examples

```
graph(type = "updown", gap = 1.3, penalty = 5)

graph(Edge("Dw","Dw"),
      Edge("Up","Up"),
      Edge("Dw","Up","up", gap = 0.5, penalty = 10),
      Edge("Up","Dw","down"),
      StartEnd("Dw","Dw"),
      Node("Dw",0,1),
      Node("Up",0,1))

graph(Edge("1", "2", type = "std"),
      Edge("2", "3", type = "std"),
      Edge("3", "4", type = "std"),
      StartEnd(start = "1", end = "4"),
      all.null.edges = TRUE)
```

---

itergfpop — *Graph-constrained functional pruning optimal partitioning iterated*

Description

Functional pruning optimal partitioning with a graph structure to take into account constraints on consecutive segment parameters. This is an iterated version of the main gfpop function using a Birgé Massart like penalty

Usage

```
itergfpop(
  data,
  mygraph,
  type = "mean",
  weights = NULL,
  iter.max = 100,
  D.init = 1
)
```

Arguments

`data`	vector of data to segment. For simulation studies, Data can be generated using gfpop package function `gfpop::dataGenerator()`
`mygraph`	dataframe of class "graph" to constrain the changepoint inference, see `gfpop::graph()`
`type`	a string defining the cost model to use: `"mean"`, `"variance"`, `"poisson"`, `"exp"`, `"negbin"`
`weights`	vector of weights (positive numbers), same size as data
`iter.max`	maximal number of iteration of the gfpop function
`D.init`	initialisation of the number of segments

Value

a gfpop object = (`changepoints`, `states`, `forced`, `parameters`, `globalCost`)

`changepoints` is the vector of changepoints (we give the last element of each segment)

`states` is the vector giving the state of each segment

`forced` is the vector specifying whether the constraints of the graph are active (= `TRUE`) or not (= `FALSE`)

`parameters` is the vector of successive parameters of each segment

`globalCost` is a number equal to the total loss: the minimal cost for the optimization problem with all penalty values excluded

`Dvect` is a vector of integers. The successive tested D in the Birgé Massart penalty until convergence

---

`Mono27ac` *A small ChIP-seq data set in which peaks can be found using PeakSegFPOP*

Description

The data come from an H3K27ac ChIP-seq experiment which was aligned to the human reference genome (hg19), aligned read counts were used to produce the coverage data; looking at these data in a genome browser was used to produce the labels.

Usage

```
data("Mono27ac")
```

Format

A list of 2 data.tables: coverage has 4 columns (chrom, chromStart, chromEnd, count=number of aligned reads at each position on chrom:chromStart-chromEnd); labels has 4 columns (chrom, chromStart, chromEnd, annotation=label at chrom:chromStart-chromEnd).

Source

https://github.com/tdhock/feature-learning-benchmark neuroSpike *Neuro spike train data*

Description

The goal in these data is to detect the spikes = abrupt up changes in calcium concentration, which correspond to neurons firing in laboratory animals.

Usage

```
data("neuroSpike")
```

Format

A data frame with 20000 observations on the following 4 variables.

`seconds` time of measurement

`calcium` noisy data measured

`AR1` autoregressive model mean, for comparison

`TrueSpike` logical

Source

Spikefinder challenge, dataset number 7, cell number 13, subset 1:20000, 100 fps, for AR1: 0.98 exp decay parameter, 3.6 penalty parameter.

Node *Node Values*

Description

Constrain the range of values to consider at a node

Usage

```
Node(state = NULL, min = -Inf, max = Inf)
```

Arguments

`state`	a string defining the state to constrain
`min`	minimal value for the inferred parameter
`max`	maximal value for the inferred parameter

Value

a dataframe with 9 variables with only `state1`, `min` and `max` defined (not `NA`).

Examples

```
Node(state = "s0", min = 0, max = 2)

Node(state = 0, min = -1, max = 1)

Node(state = "positive", min = 0)

Node(state = "mu0", min = 0.5, max = 0.5)
```

---

paperGraph *Graphs of our paper in JSS*

Description

Graphs of our paper in JSS (Journal of Statistical Software)

Usage

```
paperGraph(nb, penalty = 0, decay = 1, gap = 0, oneValue = 0, K = Inf, a = 0)
```

Arguments

nb	the number of the Figure in paper
penalty	the penalty to use for change-point
decay	a nonnegative number to give the strength of the exponential decay into the segment
gap	a nonnegative number to constrain the size of the gap in the change of state
oneValue	the value for parameter when we consider the collective anomalies problem
K	a positive number. Threshold for the Biweight robust loss
a	a positive number. Slope for the Huber robust loss

Value

a dataframe with 9 variables : columns are named `"state1"`, `"state2"`, `"type"`, `"parameter"`, `"penalty"`, `"K"`, `"a"`, `"min"`, `"max"` with additional `"graph"` class.

`plot.gfpop` *plot.gfpop*

Description

Plotting inferred segment parameters (the result of gfpop) and data.

Usage

```
## S3 method for class 'gfpop'
plot(x, ..., data, multiple = TRUE)
```

Arguments

`x`	a gfpop class object
`...`	Other parameters
`data`	the data from which we get the gfpop result
`multiple`	if `TRUE` we plot data and the model on different graphs. Only with `"mean"` and `"poisson"` cost functions (as in that case the parameter values represent the data mean value over each segment) we allow the User to plot signal and data on a single graph.

Value

plot data and the inferred gfpop segments

Examples

```
n <- 1000 #data length
data <- dataGenerator(n, c(0.3, 0.4, 0.7, 0.95, 1), c(1, 3, 1, -1, 4), "mean", sigma = 3)
myGraph <- graph(type = "relevant", gap = 0.5, penalty = 2 * sdDiff(data) ^ 2 * log(n))
g <- gfpop(data, myGraph, type = "mean")
plot(x = g, data = data, multiple = FALSE)

data <- dataGenerator(n, c(0.4, 0.8, 1), c(1, 1.7, 2.3), "exp")
g <- gfpop(data,graph(type = "isotonic", penalty = 2 * sdDiff(data) ^ 2 * log(n)), type = "exp")
plot(x = g, data = data, multiple = TRUE)

data <- dataGenerator(n, c(0.22, 0.75, 1), c(1.4,1,0.8), "poisson")
g <- gfpop(data, paperGraph(8), type = "poisson")
plot(x = g, data = data, multiple = TRUE)
```

`print.gfpop` *print.gfpop*

Description

Printing the resulting change-point model found by gfpop function

Usage

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

Arguments

`x`	a gfpop class object
`...`	Other parameters

Value

print the gfpop object

Examples

```
n <- 1000 #data length
data <- dataGenerator(n, c(0.3, 0.4, 0.7, 0.95, 1), c(1, 3, 1, -1, 4), "mean", sigma = 3)
myGraph <- graph(type = "relevant", gap = 0.5, penalty = 2 * sdDiff(data) ^ 2 * log(n))
g <- gfpop(data, myGraph, type = "mean")
print(g)
```

`profile614chr2` *Labeled DNA copy number profile*

Description

This DNA copy number data set has changepoint labels that are impossible to all predict correctly using the maximum likelihood gaussian changepoint model.

Usage

```
data("profile614chr2")
```

Format

Named list of two elements: probes is a data.table with 153663 noisy logratio observations in which we would like to detect changepoints; labels is a data.table with 8 rows that define regions with 1 or 0 breakpoints.

Source

https://github.com/vrunge/gfpop.data

References

Labels created with SegAnnDB software, Hocking et al., Bioinformatics 2014, doi:10.1093/bioinformatics/btu072.

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sdDiff *sdDiff*

Description

sdDiff is a function based on the difference operator (or difference order for HALL method) estimating the time-series standard deviation. The estimation works for time-series generated by Gaussian random variables with constant standard deviation and multiple changes in mean. Three estimators are available:

- `HALL` : the so-called HALL-estimator of order 3. For more details see: *(1990) Asymptotically optimal difference-based estimation of variance in nonparametric regression. Authors: Hall, Peter and Kay, JW and Titterinton, DM. Biometrika, pages 521–528*
- `MAD` : the median absolute deviation estimator computed on `diff(x)/sqrt(2)` with x the vector of datapoints
- `SD` : the standard deviation estimator (function sd) computed on `diff(x)/sqrt(2)` with x the vector of datapoints

Usage

```
sdDiff(x, method = "HALL")
```

Arguments

`x`	vector of datapoints
`method`	Three available methods: `"HALL"`, `"MAD"` and `"SD"`

Value

a value equal to the estimated standard deviation

Examples

```
data <- dataGenerator(300, seq(0.1,1,0.1), sample(10), sigma = 2)
sdDiff(data, method = "HALL")
sdDiff(data, method = "MAD")
sdDiff(data, method = "SD")
```

StartEnd *Start and End nodes for the graph*

Description

Defining the beginning and ending states of a graph

Usage

```
StartEnd(start = NULL, end = NULL)
```

Arguments

start	a vector of states. The beginning nodes for the changepoint inference
end	a vector of states. The ending nodes for the changepoint inference

Value

dataframe with 9 variables with only `state1` and `type` = `"start"` or `"end"` defined (not `NA`).

Examples

```
StartEnd(start = "A", end = c("A","B"))

StartEnd(start = 0)

StartEnd(start = 1, end = 1)

StartEnd(start = "v0", end = "v3")

StartEnd(end = "s0")
```

summary.gfpop *summary.gfpop*

Description

Returns all information contains in gfpop object

Usage

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

Arguments

object	a gfpop class object
...	Other parameters

Value

summary of gfpop object

Examples

```
n <- 1000 #data length
data <- dataGenerator(n, c(0.3, 0.4, 0.7, 0.95, 1), c(1, 3, 1, -1, 4), "mean", sigma = 3)
myGraph <- graph(type = "relevant", gap = 0.5, penalty = 2 * sdDiff(data) ^ 2 * log(n))
g <- gfpop(data, myGraph, type = "mean")
summary(g)
```

Index

∗ **datasets**
    ECG, 3
    Mono27ac, 9
    neuroSpike, 10
    profile614chr2, 13

dataGenerator, 2

ECG, 3
Edge, 4

gfpop, 5
gfpop::dataGenerator(), *5, 6*, *8*
gfpop::Edge(), *7*
gfpop::graph(), *5, 6*, *8*
gfpop::Node(), *7*
gfpop::plot(), *5, 6*
gfpop::StartEnd(), *7*
graph, 7

itergfpop, 8

Mono27ac, 9

neuroSpike, 10
Node, 10

paperGraph, 11
plot.gfpop, 12
print.gfpop, 13
profile614chr2, 13

sdDiff, 14
StartEnd, 15
summary.gfpop, 15