

Package ‘onlineBcp’

July 22, 2025

Type Package

Title Online Bayesian Methods for Change Point Analysis

Version 0.1.8

Description It implements the online Bayesian methods for change point analysis. It can also perform missing data imputation with methods from 'VIM'. The reference is Yigiter A, Chen J, An L, Danacioglu N (2015) <[doi:10.1080/02664763.2014.1001330](https://doi.org/10.1080/02664763.2014.1001330)>. The link to the package is <<https://CRAN.R-project.org/package=onlineBcp>>.

License GPL

Depends R (>= 3.1.0)

Encoding UTF-8

LazyData true

RoxygenNote 7.1.2

Imports VIM

Suggests knitr, rmarkdown, testthat

VignetteBuilder knitr

NeedsCompilation no

Author Hongyan Xu [cre, aut],
Ayten Yigiter [aut],
Jie Chen [aut]

Maintainer Hongyan Xu <hxu@augusta.edu>

Repository CRAN

Date/Publication 2022-05-31 13:40:02 UTC

Contents

aCGH	2
addDatapoint	2
cnv_H2347	3
combine	3
covid	4

imputation	4
online_cp	5
plot.BayesCP	5
summary.BayesCP	6

Index	7
--------------	----------

aCGH	<i>Transformed aCGH data</i>
------	------------------------------

Description

A dataset containing the tranformed aCGH data from the genome of the fibroblast cell line GM02948

Usage

aCGH

Format

A data frame with 2046 rows and 1 variable:

transNorm normalized aCGH intensity

addDatapoint	<i>Add one data point</i>
--------------	---------------------------

Description

Add one data point

Usage

```
addDatapoint(bcp, d)
```

Arguments

bcp	current BayesCP object
d	additional data point to be added to the existing data

Value

a vector with new data point appended

cnv_H2347	<i>GC-corrected data for copy number variation</i>
-----------	--

Description

A dataset containing the raw data and GC-corrected/normalized data

Usage

```
cnv_H2347
```

Format

A data frame with 14189 rows and 2 variables:

raw.count raw read counts

normalized.count normalized read counts

combine	<i>Combine two BayesCP objects</i>
---------	------------------------------------

Description

Combine two BayesCP objects

Usage

```
combine(bcp1, bcp2)
```

Arguments

bcp1 the first BayesCP object to be combined

bcp2 the second BayesCP object to be combined

Value

The combined BayesCP object. Notice that if bcp1 has n_1 change points ($n_1 + 1$ segments), and bcp2 has n_2 change points ($n_2 + 1$ segments), the combined bcp will have $n_1 + n_2$ change points and $n_1 + n_2 + 2$ segments.

covid	<i>US COVID-19 data</i>
-------	-------------------------

Description

A dataset containing new daily cases in the United States downloaded from the World Health Organization on August 25, 2020

Usage

covid

Format

A data frame with 219 rows and 8 variables

Date_reported The report date

Country_code The code for country

Country Country in full name

WHO_region Geographic region defined by WHO

New_cases New COVID-19 cases

Cumulative_cases Cumulative COVID-19 cases

New_deaths New COVID-19 deaths

Cumulative_deaths Cumulative COVID-19 deaths

imputation	<i>Impute missing data</i>
------------	----------------------------

Description

Impute missing data

Usage

```
imputation(x, method = c("Median", "kNN"))
```

Arguments

x	the normalized data with missing
method	the imputation method

Value

The vector of imputed data with no missing values

online_cp	<i>Online change point detection algorithm for normally distributed data.</i>
-----------	---

Description

Online change point detection algorithm for normally distributed data.

Usage

```
online_cp(x, theta = 0.9, alpha = 1, beta = 1, th_cp = 0.5, debug = FALSE)
```

Arguments

x	the normalized data
theta	the probability of occurrence of a change point, default 0.9
alpha	the hyperparameter of posterior distribution, default 1.0
beta	the hyperparameter of posterior distribution, default 1.0
th_cp	threshold level for the posterior distribution of change point, default 0.5
debug	a logical value, when TRUE, will print more information

Value

An object of the BayesCP class

plot.BayesCP	<i>Plot BayesCP object</i>
--------------	----------------------------

Description

Plot BayesCP object

Usage

```
## S3 method for class 'BayesCP'
plot(x, xlab = "Index", ylab = "x", ...)
```

Arguments

x	the BayesCP class object to be plotted
xlab	the default x-axis label, default "Index"
ylab	the default y-axis label, default "x"
...	the plotting parameters passed to plot()

Value

No return value, called for side effects

summary.BayesCP *Summarize BayesCP object*

Description

Summarize BayesCP object

Usage

```
## S3 method for class 'BayesCP'  
summary(object, norm.test = FALSE, ...)
```

Arguments

object	the BayesCP class object to be summarized
norm.test	logical value for normality test, default is false
...	parameters passed to summary()

Value

An object of BayesCP class with updated summary result

Examples

```
x <- c(rnorm(10, 0, 1), rnorm(10, 5, 1))  
bcp <- online_cp(x)  
summary(bcp)
```

Index

* datasets

aCGH, [2](#)

cnv_H2347, [3](#)

covid, [4](#)

aCGH, [2](#)

addDatapoint, [2](#)

cnv_H2347, [3](#)

combine, [3](#)

covid, [4](#)

imputation, [4](#)

online_cp, [5](#)

plot.BayesCP, [5](#)

summary.BayesCP, [6](#)