

# Package ‘onlineBcp’

April 28, 2021

**Type** Package

**Title** Online Bayesian Methods for Change Point Analysis

**Version** 0.1.1

**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>.

**License** GPL

**Depends** R (>= 3.1.0)

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 7.1.0

**Imports** VIM

**Suggests** testthat

**NeedsCompilation** no

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**Repository** CRAN

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aCGH	<i>Transformed aCGH data</i>
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**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

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

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

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

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online_cp	<i>Online change point detection algorithm for normally distributed data.</i>
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**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)
```

**Arguments**

x	the normalized data
theta	the probability of occurrence of a change point
alpha	the hyperparameter of posterior distribution
beta	the hyperparameter of posterior distribution
th_cp	threshold level for the posterior distribution of change point

**Value**

An object of the BayesCP class

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plot.BayesCP	<i>Plot BayesCP object</i>
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**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
ylab	the default y-axis label
...	the plotting parameters passed to plot()

**Value**

No return value, called for side effects

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summary.BayesCP	<i>Summarize BayesCP object</i>
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**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**

The summary of the BayesCP class in a list

**Examples**

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

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