

# Package ‘onlineBcp’

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**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

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

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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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combine	<i>Combine two BayesCP objects</i>
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**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.

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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, 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

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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, default "Index"
ylab	the default y-axis label, default "x"
...	the plotting parameters passed to plot()

**Value**

No return value, called for side effects

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summary.BayesCP      *Summarize BayesCP object*

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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**

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)
```

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