

# Package ‘bwd’

January 4, 2019

**Type** Package

**Title** Backward Procedure for Change-Point Detection

**Version** 0.1.0

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**Description** Implements a backward procedure for single and multiple change point detection proposed by Shin et al. <arXiv:1812.10107>. The backward approach is particularly useful to detect short and sparse signals which is common in copy number variation (CNV) detection.

**License** GPL-2

**Depends** R (>= 3.4.0)

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 6.1.1

**NeedsCompilation** yes

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**Repository** CRAN

**Date/Publication** 2019-01-04 11:10:03 UTC

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bwd

*Backward procedure for the change point detection***Description**

Implements backward procedure for detecting single or multiple change points.

**Usage**

```
bwd(y, alpha = 0.05, kmin = 3, lastkgroup = floor(0.01 * n),
    mu0 = NULL, normal = T, n.permute = 1000, h = 10)
```

**Arguments**

y	observed data
alpha	target level that detemines stopping criterion. Default is 0.05
kmin	minimum length of segements for checking possible change points
lastkgroup	We can abvoid chekcing possible change points when we have less groups than "lastkgroup" to improve computational efficiency. Default is 0.01 * n
mu0	Baseline mean value whe detecting epidemic chang points. Defalut is NULL
normal	if TRUE normal cutoff values are used, and if FALSE residual permuted cutoff values are used. Default is TRUE
n.permute	number of permutation when computing the permuted cutoff. Defalut is 1000
h	bandwidth size for variance esitimator

**Value**

bwd object that contains information of detected segments and significance levels

**Author(s)**

Seung Jun Shin, Yicaho Wu, Ning Hao

**References**

Shin, Wu, and Hao (2018+) A backward procedure for change-point detection with applications to copy number variation detection, arXiv:1812.10107.

**See Also**

[plot.bwd](#)

**Examples**

```
# simulated data
set.seed(1)
n <- 1000
L <- 10

mu0 <- -0.5

mu <- rep(mu0, n)
mu[(n/2 + 1):(n/2 + L)] <- mu0 + 1.6
mu[(n/4 + 1):(n/4 + L)] <- mu0 - 1.6
y <- mu + rnorm(n)
alpha <- c(0.01, 0.05)

# BWD
obj1 <- bwd(y, alpha = alpha)

# Modified for epidemic changes with a known baseline mean, mu0.
obj2 <- bwd(y, alpha = alpha, mu0 = 0)

par(mfrow = c(2,1))
plot(obj1, y)
plot(obj2, y)
```

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plot.bwd

*plot for the backward procedure for the change point detection*

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**Description**

A plot of segments estimated by the backward procedure.

**Usage**

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

**Arguments**

x	bwd object
y	observed data
...	graphical parameters

**Value**

plot of estimated segments

**Author(s)**

Seung Jun Shin, Yicaho Wu, Ning Hao

**References**

Shin, Wu, and Hao (2018+) A backward procedure for change-point detection with applications to copy number variation detection, arXiv:1812.10107.

**See Also**

[bwd](#)

**Examples**

```
# simulated data
set.seed(1)
n <- 1000
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mu0 <- -0.5

mu <- rep(mu0, n)
mu[(n/2 + 1):(n/2 + L)] <- mu0 + 1.6
mu[(n/4 + 1):(n/4 + L)] <- mu0 - 1.6
y <- mu + rnorm(n)
alpha <- c(0.01, 0.05)

# BWD
obj1 <- bwd(y, alpha = alpha)

# Modified for epidemic changes with a known baseline mean, mu0.
obj2 <- bwd(y, alpha = alpha, mu0 = 0)

par(mfrow = c(2,1))
plot(obj1, y)
plot(obj2, y)
```

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