

# Package ‘bwd’

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**Type** Package

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

**Version** 0.1.0

**Maintainer** Seung Jun Shin <sjshin@korea.ac.kr>

**Description** Implements a backward procedure for single and multiple change point detection proposed by Shin et al. <[doi:10.48550/arXiv.1812.10107](https://doi.org/10.48550/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

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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 determines stopping criterion. Default is 0.05                                                                                 |
| kmin       | minimum length of segments for checking possible change points                                                                                   |
| lastkgroup | We can avoid checking possible change points when we have less groups than "lastkgroup" to improve computational efficiency. Default is 0.01 * n |
| mu0        | Baseline mean value when detecting epidemic change points. Default 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. Default is 1000                                                                        |
| h          | bandwidth size for variance estimator                                                                                                            |

**Value**

bwd object that contains information of detected segments and significance levels

**Author(s)**

Seung Jun Shin, Yicah 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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