

# Package ‘kerSeg’

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**Type** Package

**Title** New Kernel-Based Change-Point Detection

**Version** 1.1

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**Description** New kernel-based test and fast tests for detecting change-points or changed-intervals where the distributions abruptly change. They work well particularly for high-dimensional data.

Song, H. and Chen, H. (2022)  
<[doi:10.48550/arXiv.2206.01853](https://doi.org/10.48550/arXiv.2206.01853)>.

**License** GPL (>= 2)

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**LinkingTo** Rcpp

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gaussiankernel      *Compute the Gaussian kernel matrix*

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### Description

This function provides the Gaussian kernel matrix computed with the median heuristic bandwidth.

### Usage

```
gaussiankernel(X)
```

### Arguments

X                      The samples in the sequence.

### Value

Returns a numeric matrix, the Gaussian kernel matrix computed with the specified bandwidth.

### See Also

[kerSeg-package](#), [kerseg1](#), [kerseg2](#)

### Examples

```
## Sequence : change in the mean in the middle of the sequence.
d = 50
mu = 2
tau = 50
n = 100
set.seed(1)
y = rbind(matrix(rnorm(d*tau),tau), matrix(rnorm(d*(n-tau),mu/sqrt(d)), n-tau))

K = gaussiankernel(y) # Gaussian kernel matrix
```

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kerSeg                      *New kernel-based change-point detection*

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### Description

This package can be used to detect change-points where the distributions abruptly change. The Gaussian kernel with the median heuristic, which is the median of all pairwise distances among observations, is used.

**Details**

To compute the Gaussian kernel matrix with the median heuristic bandwidth, the function [gaussiankernel](#) should be used. The main functions are [kerseg1](#) for the single change-point alternative and [kerseg2](#) for the changed-interval alternative.

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**References**

Song, H. and Chen, H. (2022). New kernel-based change-point detection. arXiv:2206.01853

**See Also**

[kerseg1](#), [kerseg2](#), [gaussiankernel](#)

**Examples**

```
## Sequence 1: change in the mean in the middle of the sequence.
d = 50
mu = 2
tau = 15
n = 50
set.seed(1)
y = rbind(matrix(rnorm(d*tau),tau), matrix(rnorm(d*(n-tau),mu/sqrt(d)), n-tau))
K = gaussiankernel(y) # Gaussian kernel matrix
a = kerseg1(n, K, pval.perm=TRUE, B=1000)
# output results based on the permutation and the asymptotic results.
# the scan statistics can be found in a$scanZ.
# the approximated p-values can be found in a$appr.
# the permutation p-values can be found in a$perm.

## Sequence 2: change in both the mean and variance away from the middle of the sequence.
d = 50
mu = 2
sigma = 0.7
tau = 35
n = 50
set.seed(1)
y = rbind(matrix(rnorm(d*tau),tau), matrix(rnorm(d*(n-tau),mu/sqrt(d),sigma), n-tau))
K = gaussiankernel(y)
a = kerseg1(n, K, pval.perm=TRUE, B=1000)

## Sequence 3: change in both the mean and variance happens on an interval.
d = 50
mu = 2
sigma = 0.5
tau1 = 25
tau2 = 35
```

```

n = 50
set.seed(1)
y1 = matrix(rnorm(d*tau1), tau1)
y2 = matrix(rnorm(d*(tau2-tau1), mu/sqrt(d), sigma), tau2-tau1)
y3 = matrix(rnorm(d*(n-tau2)), n-tau2)
y = rbind(y1, y2, y3)
K = gaussiankernel(y)
a = kerseg2(n, K, pval.perm=TRUE, B=1000)

```

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kerseg1	<i>Kernel-based change-point detection for single change-point alternatives</i>
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### Description

This function finds a break point in the sequence where the underlying distribution changes.

### Usage

```

kerseg1(n, K, r1=1.2, r2=0.8, n0=0.05*n, n1=0.95*n,
        pval.appr=TRUE, skew.corr=TRUE, pval.perm=FALSE, B=100)

```

### Arguments

n	The number of observations in the sequence.
K	The kernel matrix of observations in the sequence.
r1	The constant in the test statistics $Z_{W,r1}(t)$ .
r2	The constant in the test statistics $Z_{W,r2}(t)$ .
n0	The starting index to be considered as a candidate for the change-point.
n1	The ending index to be considered as a candidate for the change-point.
pval.appr	If it is TRUE, the function outputs the p-value approximation based on asymptotic properties.
skew.corr	This argument is useful only when pval.appr=TRUE. If skew.corr is TRUE, the p-value approximation would incorporate skewness correction.
pval.perm	If it is TRUE, the function outputs the p-value from doing B permutations, where B is another argument that you can specify. Doing permutation could be time consuming, so use this argument with caution as it may take a long time to finish the permutation.
B	This argument is useful only when pval.perm=TRUE. The default value for B is 100.

**Value**

Returns a list `stat` containing the each scan statistic, `tauhat` containing the estimated location of change-point, `appr` containing the approximated p-values of the fast tests when argument `'pval.appr'` is TRUE, and `perm` containing the permutation p-values of the fast tests and GKCP when argument `'pval.perm'` is TRUE. See below for more details.

<code>seq</code>	A vector of each scan statistic (standardized counts).
<code>Zmax</code>	The test statistics (maximum of the scan statistics).
<code>tauhat</code>	An estimate of the location of the change-point.
<code>fGKCP1_bon</code>	The p-value of <code>fGKCP<sub>1</sub></code> obtained by the Bonferroni procedure.
<code>fGKCP1_sim</code>	The p-value of <code>fGKCP<sub>1</sub></code> obtained by the Simes procedure.
<code>fGKCP2_bon</code>	The p-value of <code>fGKCP<sub>2</sub></code> obtained by the Bonferroni procedure.
<code>fGKCP2_sim</code>	The p-value of <code>fGKCP<sub>2</sub></code> obtained by the Simes procedure.
<code>GKCP</code>	The p-value of GKCP obtained by the random permutation.

**See Also**

[kerSeg-package](#), [kerseg1](#), [gaussiankernel](#), [kerseg2](#)

**Examples**

```
## Sequence 1: change in the mean in the middle of the sequence.
d = 50
mu = 2
tau = 25
n = 50
set.seed(1)
y = rbind(matrix(rnorm(d*tau),tau), matrix(rnorm(d*(n-tau),mu/sqrt(d)), n-tau))
K = gaussiankernel(y) # Gaussian kernel matrix
a = kerseg1(n, K, pval.perm=TRUE, B=1000)
# output results based on the permutation and the asymptotic results.
# the scan statistics can be found in a$scanZ.
# the approximated p-values can be found in a$appr.
# the permutation p-values can be found in a$perm.

## Sequence 2: change in both the mean and variance away from the middle of the sequence.
d = 50
mu = 2
sigma = 0.7
tau = 35
n = 50
set.seed(1)
y = rbind(matrix(rnorm(d*tau),tau), matrix(rnorm(d*(n-tau),mu/sqrt(d),sigma), n-tau))
K = gaussiankernel(y)
a = kerseg1(n, K, pval.perm=TRUE, B=1000)
```

**Description**

This function finds an interval in the sequence where their underlying distribution differs from the rest of the sequence.

**Usage**

```
kerseg2(n, K, r1=1.2, r2=0.8, l0=0.05*n, l1=0.95*n,
        pval.appr=TRUE, skew.corr=TRUE, pval.perm=FALSE, B=100)
```

**Arguments**

n	The number of observations in the sequence.
K	The kernel matrix of observations in the sequence.
r1	The constant in the test statistics $Z_{W,r1}(t_1, t_2)$ .
r2	The constant in the test statistics $Z_{W,r2}(t_1, t_2)$ .
l0	The minimum length of the interval to be considered as a changed interval.
l1	The maximum length of the interval to be considered as a changed interval.
pval.appr	If it is TRUE, the function outputs the p-value approximation based on asymptotic properties.
skew.corr	This argument is useful only when pval.appr=TRUE. If skew.corr is TRUE, the p-value approximation would incorporate skewness correction.
pval.perm	If it is TRUE, the function outputs the p-value from doing B permutations, where B is another argument that you can specify. Doing permutation could be time consuming, so use this argument with caution as it may take a long time to finish the permutation.
B	This argument is useful only when pval.perm=TRUE. The default value for B is 100.

**Value**

Returns a list stat containing the each scan statistic, tauhat containing the estimated changed-interval, appr containing the approximated p-values of the fast tests when argument 'pval.appr' is TRUE, and perm containing the permutation p-values of the fast tests and GKCP when argument 'pval.perm' is TRUE. See below for more details.

seq	A matrix of each scan statistic (standardized counts).
Zmax	The test statistics (maximum of the scan statistics).
tauhat	An estimate of the two ends of the changed-interval.
fGKCP1_bon	The p-value of fGKCP <sub>1</sub> obtained by the Bonferroni procedure.

fGKCP1_sim	The p-value of fGKCP <sub>1</sub> obtained by the Simes procedure.
fGKCP2_bon	The p-value of fGKCP <sub>2</sub> obtained by the Bonferroni procedure.
fGKCP2_sim	The p-value of fGKCP <sub>2</sub> obtained by the Simes procedure.
GKCP	The p-value of GKCP obtained by the random permutation.

**See Also**

[kerSeg-package](#), [kerseg2](#), [gaussiankernel](#), [kerseg1](#)

**Examples**

```
## Sequence 3: change in both the mean and variance happens on an interval.
d = 50
mu = 2
sigma = 0.5
tau1 = 25
tau2 = 35
n = 50
set.seed(1)
y1 = matrix(rnorm(d*tau1), tau1)
y2 = matrix(rnorm(d*(tau2-tau1), mu/sqrt(d), sigma), tau2-tau1)
y3 = matrix(rnorm(d*(n-tau2)), n-tau2)
y = rbind(y1, y2, y3)
K = gaussiankernel(y)
a = kerseg2(n, K, pval.perm=TRUE, B=1000)
```

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skew

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*Compute some components utilized in the third moment formulas.*


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**Description**

This function provides some components used in the third moment formulas.

**Usage**

```
skew(K, Rtemp, Rtemp2, R0, R2)
```

**Arguments**

K	A kernel matrix of observations in the sequence.
Rtemp	A numeric vector of $k_{i.}$ , the sum of kernel values for each row $i$ .
Rtemp2	A numeric vector, the sum of squared kernel values for each row $i$ .
R0	The term $R_0$ , defined in the paper.
R2	The term $R_2$ , defined in the paper.

**Value**

Returns a list of components used in the third moment formulas.

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statint	<i>Compute the test statistics, <math>D</math> and <math>W</math>, for the changed-interval alternatives.</i>
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---

### Description

This function provides the test statistics,  $D(t_1, t_2)$ ,  $W(t_1, t_2)$ , and the weighted  $W(t_1, t_2)$  for the changed-interval alternatives.

### Usage

```
statint(K, Rtemp, R0, r1, r2)
```

### Arguments

K	A kernel matrix of observations in the sequence.
Rtemp	A numeric vector of $k_{i.}$ , the sum of kernel values for each row $i$ .
R0	The term $R_0$ , defined in the paper.
r1	The constant in the test statistics $Z_{W,r1}(t_1, t_2)$ .
r2	The constant in the test statistics $Z_{W,r2}(t_1, t_2)$ .

### Value

Returns a list of test statistics,  $D(t_1, t_2)$ ,  $W(t_1, t_2)$ ,  $W_{r1}(t_1, t_2)$ , and  $W_{r2}(t_1, t_2)$ .

### Examples

```
## Sequence : change in the mean in the middle of the sequence.
d = 50
mu = 2
tau = 50
n = 100
set.seed(1)
y = rbind(matrix(rnorm(d*tau),tau), matrix(rnorm(d*(n-tau),mu/sqrt(d)), n-tau))
K = gaussiankernel(y) # Gaussian kernel matrix
R_temp = rowSums(K)
R0 = sum(K)
a = statint(K, R_temp, R0, r1=1.2, r2=0.8)
```

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