Package 'mHMM'

May 30, 2014

Type Package

Title m-HMM

Version 1.0

Date 2014-05-30

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Description This is the R software for the m-HMM,the mixture hidden Markov model used to detect copy number variation using next generation sequencing data.

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R topics documented:

`mHMM-package` *mHMM-package*

Description

This is the R software for the m-HMM, the mixture hidden Markov model used to detect copy number variation using next generation sequencing data.

Details

Package:	mHMM
Type:	Package
Version:	1.0
Date:	2014-05-30
License:	GPL-2 | GPL-3

Author(s)

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`control_vec` *control_vec*

Description

An example of the original reference read counts.

Usage

```
data(control_vec)
```

Format

The format is: num [1:4121945] 0 0 2 2 0 2 2 2 2 2 ...

Examples

```
data(control_vec)
```

`m_HMM_main` *m_HMM_main*

Description

The main function to use m-HMM.

Usage

```
m_HMM_main(sample_reads_input, reference_reads_input,
loci_input, kmeans1 = TRUE,
C.const = 40, change_point_refine = TRUE)
```

Arguments

`sample_reads_input`
: A vector of sample read counts, with length the same as reference_reads_input and loci_input.

`reference_reads_input`
: A vector of reference read counts, with length the same as sample_reads_input and loci_input.

`loci_input`
: A vector of physical locations of the reads, with length the same as sample_reads_input and reference_reads_input.

`kmeans1` TRUE or FALSE. If kmeans1=TRUE, then the sites are grouped into windows using k-means method.

`C.const` A tuning constant used for site grouping.

`change_point_refine` TRUE or FALSE. Whether the change points will be refined after the initial m-HMM.

Value

A data frame of the resulting CNV detection.

Author(s)

Heng Wang

References

Heng Wang, Dan Nettleton and Kai Ying (2014). Copy Number Variation Detection Using Next Generation Sequencing Read Counts, BMC Bioinformatics 2014, 15:109.

Examples

```
data(control_vec)
data(sample_vec)
data(posi_vec)

reference_reads_input<-control_vec
sample_reads_input<-sample_vec
loci_input<-posi_vec
kmeans1<-TRUE
C.const<-100
change_point_refine<-TRUE

#CNV_detection_result<-m_HMM_main(sample_reads_input, reference_reads_input,
#loci_input, kmeans1=kmeans1, C.const=C.const, change_point_refine=change_point_refine)
```

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posi_vec *posi_vec*

Description

A vector of the physical location of the reads.

Usage

```
data(posi_vec)
```

Format

The format is: num [1:4121945] 33362253 33362255 33362256 33362257 33362261 ...

Examples

```
data(posi_vec)
```

`sample_vec` *sample_vec*

Description

An example of the reference genome read counts.

Usage

```
data(sample_vec)
```

Format

The format is: num [1:4121945] 4 2 0 0 2 0 2 0 2 0 ...

Examples

```
data(sample_vec)
```

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