Package ‘mHMM’

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Type Package
Title m-HMM
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Author Heng Wang
Maintainer Heng Wang <hengwang@msu.edu>
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 ........................................ 1
  control_vec ........................................ 2
  m_HMM_main ........................................ 2
  posi_vec ........................................... 3
  sample_vec ......................................... 4

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

<table>
<thead>
<tr>
<th>Package:</th>
<th>mHMM</th>
</tr>
</thead>
<tbody>
<tr>
<td>Type:</td>
<td>Package</td>
</tr>
<tr>
<td>Version:</td>
<td>1.0</td>
</tr>
<tr>
<td>Date:</td>
<td>2014-05-30</td>
</tr>
<tr>
<td>License:</td>
<td>GPL-2</td>
</tr>
</tbody>
</table>
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

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.
posi_vec

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.

c_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  

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)

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 ...

posi_vec  posi_vec
Examples

data(posi_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)
Index

control_vec, 2
m_HMM_main, 2
mHMM (mHMM-package), 1
mHMM-package, 1

posi_vec, 3
sample_vec, 4