

Package ‘CaTCH’

July 12, 2016

Type Package

Title Call a hierarchy of domains based on Hi-C data

Version 1.0

Date 2016-07-05

Author Yinxu Zhan

Maintainer Yinxu Zhan <yinxu.zhan@fmi.ch>

Imports parallel

Description This package allows building the hierarchy of domains starting from Hi-C data. Each hierarchical level is identified by a minimum value of physical insulation between neighboring domains.

License GPL-2

NeedsCompilation yes

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CaTCH-package	<i>Call a hierarchy of domains based on Hi-C data</i>
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Description

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Details

The DESCRIPTION file:

```
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Type:         Package
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CaTCH-package      Call a hierarchy of domains based on Hi-C data
domain.call        Call a hierarchy of domains based on Hi-C data
```

Author(s)

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References

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domain.call	<i>Call a hierarchy of domains based on Hi-C data</i>
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Description

This package allows building the hierarchy of domains starting from Hi-C data. Each hierarchical level is identified by a minimum value of physical insulation between neighboring domains.

Usage

```
domain.call(input)
domain.call.parallel(inputs, ncpu=parallel::detectCores()-1L)
```

Arguments

<code>input</code>	<p>File containing Hi-C data for the SINGLE CHROMOSOME with 6 columns:</p> <ul style="list-style-type: none"> • col1 = chromosome • col2 = genomic coordinate of the start region • col3 = genomic coordinate of the end region • col4 = bin of the start region • col5 = bin of the end region • col6 = Hi-C counts <p>*****OR*****</p> <p>File containing Hi-C data for the SINGLE CHROMOSOME with 4 columns:</p> <ul style="list-style-type: none"> • col1 = chromosome • col2 = bin of the start region • col3 = bin of the end region • col4 = Hi-C counts
<code>inputs</code>	A character vector of files as <code>input</code>
<code>ncpu</code>	Number of cpu that you want to use (Default ncpu=4)

Value

Output of

<code>domain.call</code>	<p>A list with two elements</p> <ul style="list-style-type: none"> • ncluster: A data.frame with 3 columns <ul style="list-style-type: none"> -Chromosome (chromosome) -Reciprocal insulation (RI) -Number of domains (ndomains) • clusters: A data.frame with 4 columns <ul style="list-style-type: none"> -Chromosome (chromosome) -Reciprocal insulation (RI) -Start of domain (start) -End of domain (end)
<code>domain.call.parallel</code>	A list of outputs as in <code>domain.call</code> for each file

Author(s)

Yinxu Zhan

References

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Examples

```
#R code to be here
fileinput=system.file("Test.dat.gz",package="CaTCH")
library(CaTCH)
domain.call(fileinput)
```