

# Package ‘CaTCH’

February 12, 2018

**Type** Package

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

**Version** 1.0

**Date** 2016-07-05

**Author** Yinxiu Zhan

**Maintainer** Yinxiu Zhan <yinxiu.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 or later

**NeedsCompilation** yes

## R topics documented:

CaTCH-package	1
domain.call	2

<b>Index</b>	<b>4</b>
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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:

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

Version: 1.0  
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 Maintainer: Yinxu Zhan <yinxu.zhan@fmi.ch>  
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 Packaged: 2017-11-07 13:32:41 UTC; yinxu

Index of help topics:

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)

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

### References

Zhan et al, Reciprocal insulation analysis of Hi-C data shows that TADs represent a functionally but not structurally privileged scale in the hierarchical folding of chromosomes, Genome Research 2017

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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

input	File containing Hi-C data for the SINGLE CHROMOSOME with 6 columns: <ul style="list-style-type: none"> <li>• col1 = chromosome</li> <li>• col2 = genomic coordinate of the start region</li> <li>• col3 = genomic coordinate of the end region</li> <li>• col4 = bin of the start region</li> <li>• col5 = bin of the end region</li> <li>• col6 = Hi-C counts</li> </ul>
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\*\*\*\*\*OR\*\*\*\*\*

File containing Hi-C data for the SINGLE CHROMOSOME with 4 columns:

- col1 = chromosome
- col2 = bin of the start region
- col3 = bin of the end region
- col4 = Hi-C counts

inputs      A character vector of files as input  
ncpu        Number of cpu that you want to use (Default ncpu=4)

### Value

Output of

domain.call      A list with two elements

- ncluster: A data.frame with 3 columns
  - Chromosome (chromosome)
  - Reciprocal insulation (RI)
  - Number of domains (ndomains)
- clusters: A data.frame with 4 columns
  - Chromosome (chromosome)
  - Reciprocal insulation (RI)
  - Start of domain (start)
  - End of domain (end)

domain.call.parallel      A list of outputs as in domain.call for each file

### Author(s)

Yinxu Zhan

### References

Zhan et al....

### Examples

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

# Index

\*Topic **TADs, domain calling, Hi-C**

CaTCH-package, [1](#)

\*Topic **TADs**

domain.call, [2](#)

\*Topic **hierarchy**

domain.call, [2](#)

CaTCH (CaTCH-package), [1](#)

CaTCH-package, [1](#)

domain.call, [2](#)