Package 'coolR'

September 10, 2020

Title Convert Cooler HDF5 Contact Matrix To InteractionSet Objects

Version 0.0.0.9000

Description What the package does (one paragraph).

License `use_mit_license()`

Encoding UTF-8

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Imports InteractionSet,
rhdf5

R topics documented:

`cool2IntSet` *Read .cool/.mcool sparse matrix into a GInteractions*

Description

Read .cool/.mcool sparse matrix into a GInteractions

Usage

```
cool2IntSet(files, res = NULL, cores = detectCores())
```

Arguments

files	A character vector of paths to HDF5 stored cool (uni-dimension) or mcool (multi-dimension sparse matrix). If using a multi-dimesion, the resolution of one of the dimension need to be passed to res.
res	'NULL' if using a uni-dimensional cool file or the resolution of one of layer in the mcool file
cores	An integer for the number of parallel thread to convert the file

Value

An InteractionSet of all common pairs with the number of interaction for each pairs

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getBins *Accessing the genomic bins in a cool/mcool file*

Description

Retrieves the chromosome bins forming from a HDF5 stored uni- or multi-dimentional contact matrix (cool or mcool file) into a seqinfo object

Usage

```
getBins(file, res)
```

Arguments

file	Path to a HDF5 stored cool (uni-dimension) or mcool (multi-dimension sparse matrix). If using a multi-dimesion, the resolution of one of the dimension need to be passed to res
res	'NULL' if using a uni-dimensional cool file or the resolution of one of layer in the mcool file

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read.cool *Read .cool/.mcool sparse matrix into a GInteractions*

Description

This function reads a compressed sparse row (CSR) storage scheme for a matrix created by the cooler application (https://github.com/mirnylab/cooler) stored in a HDF5 data storage. This utility can read the matrix or only specfic region of the genome eihter from one pair or a pair of region. If using a multi-dimension dataset (ie .mcool), the resolution needed need to be specified.

Usage

```
read.cool(
  file,
  res = NULL,
  chr1 = NULL,
  start1 = NULL,
  end1 = NULL,
  chr2 = NULL,
  start2 = NULL,
  end2 = NULL
)
```

Arguments

file	Path to a HDF5 stored cool (uni-dimension) or mcool (multi-dimension sparse matrix). If using a multi-dimesion, the resolution of one of the dimension need to be passed to res
res	'NULL' if using a uni-dimensional cool file or the resolution of one of layer in the mcool file
chr1	'NULL' or the chromosome name of the first pairs to return
start1	'NULL' or the start of a region within chr1 to return the pairs from. If chr1 is set and start1 is NULL this will be set to 1 by default
end1	'NULL' or the end of a region within chr1 to return the pairs from. If chr1 is set and end1 is NULL this will be set to the lenght of chr1 by default
chr2	'NULL' or the chromosome name of the first pairs to return
start2	'NULL' or the start of a region within chr2 to return the pairs from. If chr1 is set and start1 is NULL this will be set to 1 by default
end2	'NULL' or the end of a region within chr1 to return the pairs from. If chr2 is set and end1 is NULL this will be set to the lenght of chr2 by default

Value

A GInteraction object of the contact matrix dataset

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seqinfo.cool *Accessing the sequence information in a cool/mcool file*

Description

Convering the chromosomes information from a HDF5 stored uni- or multi-dimentional contact matrix (cool or mcool file) into a seqinfo object

Usage

```
seqinfo.cool(file, res)
```

Arguments

`file`	Path to a HDF5 stored cool (uni-dimension) or mcool (multi-dimension sparse matrix). If using a multi-dimesion, the resolution of one of the dimension need to be passed to res
`res`	'NULL' if using a uni-dimensional cool file or the resolution of one of layer in the mcool file

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