Package: HiCParser (via r-universe)

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Type Package

Title Parser for HiC data in R

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URL https://github.com/emaigne/HiCParser

BugReports https://github.com/emaigne/HiCParser/issues

Description This package is a parser to import HiC data into R. It accepts several type of data: tabular files, Cooler `.cool` or `.mcool` files, Juicer `.hic` files or HiC-Pro `.matrix` and `.bed` files. The HiC data can be several files, for several replicates and conditions. The data is formated in an InteractionSet object.

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`HiCParser-package` *A multiple format Hi-C data parser*

Description

This package is a parser to import HiC data into R. It accepts several type of data: tabular files, Cooler '.cool' or '.mcool' files, Juicer '.hic' files or HiC-Pro '.matrix' and '.bed' files. The HiC data can be several files, for several replicates and conditions. The data is formated in an InteractionSet object.

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See Also

Useful links:

- https://github.com/emaigne/HiCParser
- Report bugs at https://github.com/emaigne/HiCParser/issues

`mergeInteractionSet` *Merge two InteractionSet objects*

Description

Merge two different `InteractionSet`.

Usage

```
mergeInteractionSet(interactionSet1, interactionSet2, fill = NA)
```

Arguments

`interactionSet1`	The first `InteractionSet`.
`interactionSet2`	The second `InteractionSet`.
`fill`	Fill missing values with this.

Value

The merged `InteractionSet`.

Examples

```
# Using the same file for example purpose
matfile <- system.file("extdata", "hicsample_21.matrix",
                       package = "HiCParser")
bedFile <- system.file("extdata", "hicsample_21.bed",
                           package = "HiCParser")
object1 <- parseHiCPro(
  matrixPaths = matfile,
   bedPaths = bedFile,
   conditions = 1,
   replicates = 1)
object2 <- parseHiCPro(
  matrixPaths = matfile,
   bedPaths = bedFile,
   conditions = 2,
   replicates = 1)
objectMerged <- mergeInteractionSet(object1, object2)
```

parseCool *Parser for data in cool format*

Description

Parses interactions in `.cool` or `.mcool` format and returns an InteractionSet object.

Usage

```
parseCool(paths, binSize = NA, conditions, replicates)
```

Arguments

`paths`	A vector of paths to `.cool` or `.mcool` files.
`binSize`	The resolution (span of each position in number of bases). Optionally provided to select the appropriate resolution in `.mcool` files. Defaults to NULL.
`conditions`	A vector of condition names repeated along the replicates.
`replicates`	A vector of replicate names repeated along the conditions.

Details

To read `.cool` of `.mcool` files, the `rhdf5` package is required. Please install it before running the function.

Value

An InteractionSet.

Examples

```
# EXAMPLE FOR .cool FORMAT
# Path to each file
pathsCool <- c(
    "path/to/condition-1.replicate-1.cool",
    "path/to/condition-1.replicate-2.cool",
    "path/to/condition-1.replicate-3.cool",
    "path/to/condition-2.replicate-1.cool",
    "path/to/condition-2.replicate-2.cool",
    "path/to/condition-2.replicate-3.cool"
)
# Condition and replicate of each file. Can be names instead of numbers.
conditions <- c(1, 1, 1, 2, 2, 2)
replicates <- c(1, 2, 3, 1, 2, 3)
if (FALSE) {
    library(rhdf5)
    object <- parseCool(
        paths,
        conditions = conditions,
```

```
        replicates = replicates
    )
}

# EXAMPLE FOR .mcool FORMAT
# Resolution
binSize <- 500000
# Path to each file
paths <- c(
    "path/to/condition-1.replicate-1.mcool",
    "path/to/condition-1.replicate-2.mcool",
    "path/to/condition-1.replicate-3.mcool",
    "path/to/condition-2.replicate-1.mcool",
    "path/to/condition-2.replicate-2.mcool",
    "path/to/condition-2.replicate-3.mcool"
)
# Condition and replicate of each file. Can be names instead of numbers.
conditions <- c(1, 1, 1, 2, 2, 2)
replicates <- c(1, 2, 3, 1, 2, 3)
if (FALSE) {
    # Instantiation of data set
    library(rhdf5)
    object <- parseCool(
        paths,
        conditions = conditions,
        replicates = replicates,
        binSize = binSize
    )
}
```

`parseHiC` *Parser for data in hic format*

Description

Parses interactions in `.hic` format and returns an InteractionSet object.

Usage

```
parseHiC(paths, binSize, conditions, replicates)
```

Arguments

`paths`	A vector of paths to `.hic` files.
`binSize`	The resolution (span of each position in number of bases) to select within the `.hic` files.
`conditions`	A vector of condition names repeated along the replicates.
`replicates`	A vector of replicate names repeated along the conditions.

Value

An InteractionSet.

Examples

```
# Path to each file
paths <- c(
    "path/to/condition-1.replicate-1.hic",
    "path/to/condition-1.replicate-2.hic",
    "path/to/condition-1.replicate-3.hic",
    "path/to/condition-2.replicate-1.hic",
    "path/to/condition-2.replicate-2.hic",
    "path/to/condition-2.replicate-3.hic"
)
# Replicate and condition of each file. Can be names instead of numbers.
conditions <- c(1, 1, 1, 2, 2, 2)
replicates <- c(1, 2, 3, 1, 2, 3)
# Resolution to select
binSize <- 500000
if (FALSE) {
    # Instantiation of data set
    hic.experiment <- parseHiC(
        paths,
        conditions = conditions,
        replicates = replicates,
        binSize = binSize
    )
}
```

---

parseHiCPro *Parser for HiCPro data*

Description

Parses interactions in pairs of `.matrix` and `.bed` files and returns an InteractionSet object.

Usage

```
parseHiCPro(matrixPaths, bedPaths, conditions, replicates)
```

Arguments

`matrixPaths`	A vector of paths to HiC-Pro matrix files.
`bedPaths`	A vector of paths to HiC-Pro bed files.
`conditions`	A vector of condition names repeated along the replicates.
`replicates`	A vector of replicate names repeated along the conditions.

Value

An InteractionSet.

Examples

```
# Path to each matrix file
matrixPaths <- c(
    "path/to/condition-1.replicate-1.matrix",
    "path/to/condition-1.replicate-2.matrix",
    "path/to/condition-1.replicate-3.matrix",
    "path/to/condition-2.replicate-1.matrix",
    "path/to/condition-2.replicate-2.matrix",
    "path/to/condition-2.replicate-3.matrix"
)

# Path to each bed file
bedPaths <- c(
    "path/to/condition-1.replicate-1.bed",
    "path/to/condition-1.replicate-2.bed",
    "path/to/condition-1.replicate-3.bed",
    "path/to/condition-2.replicate-1.bed",
    "path/to/condition-2.replicate-2.bed",
    "path/to/condition-2.replicate-3.bed"
)

# Condition and replicate of each file. Can be names instead of numbers.
conditions <- c(1, 1, 1, 2, 2, 2)
replicates <- c(1, 2, 3, 1, 2, 3)

if (FALSE) {
    # Instantiation of data set
    hic.experiment <- parseHiCPro(
        matrixPaths = matrixPaths,
        bedPaths = bedPaths,
        conditions = conditions,
        replicates = replicates
    )
}
```

---

parseTabular *Parser for tabular data*

Description

Read the file, produce an `InteractionSet` object.

Usage

```
parseTabular(path, sep = '\t')
```

Arguments

path	A path to a tabular file.
sep	The separator of the tabular file. Default to tabulation.

Details

Accepts a tabular file with chromosome, position 1, position 2, and multiple replicate columns listing interaction counts. Null interactions do not have to be listed. Values must be separated by tabulations. The header must be chromosome position 1 position 2 x.y x.y x.y ... with x replaced by condition names and y replaced by replicate names.

Value

An InteractionSet object.

Examples

```
path <- system.file("extdata", "hicsample_21.tsv", package = "HiCParser")
object <- parseTabular(path, sep = "\t")
```

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