# Package ‘HiCParser’

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**Type** Package

**Title** Parser for HiC data in R

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**Version** 1.5.0

**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.

**License** LGPL

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pbapply, BiocGenerics, Seqinfo

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**Config/testthat/edition** 3

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

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### 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`

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## `mergeInteractionSet` *Merge two InteractionSet objects*

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### 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

```
path <- system.file("extdata", "hicsample_21.cool", package = "HiCParser")
object1 <- parseCool(path, conditions = 1, replicates = 1)
# Creating an object with a different condition
object2 <- parseCool(path, 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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