

Package ‘BiocIO’

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Title Standard Input and Output for Bioconductor Packages

Version 1.14.0

Description The `BiocIO` package contains high-level abstract classes and generics used by developers to build IO functionality within the Bioconductor suite of packages. Implements `import()` and `export()` standard generics for importing and exporting biological data formats. `import()` supports whole-file as well as chunk-wise iterative import. The `import()` interface optionally provides a standard mechanism for 'lazy' access via `filter()` (on row or element-like components of the file resource), `select()` (on column-like components of the file resource) and `collect()`. The `import()` interface optionally provides transparent access to remote (e.g. via https) as well as local access. Developers can register a file extension, e.g., `.loom` for dispatch from character-based URIs to specific `import()` / `export()` methods based on classes representing file types, e.g., `LoomFile()`.

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Author Martin Morgan [aut],
 Michael Lawrence [aut],
 Daniel Van Twisk [aut],
 Marcel Ramos [cre] (<<https://orcid.org/0000-0002-3242-0582>>)

Maintainer Marcel Ramos <marcel.ramos@roswellpark.org>

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BiocFile-class	<i>BiocFile class objects</i>
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Description

BiocFile is the base virtual class for high-level file abstractions where subclasses are associated with a particular file format or type. It wraps a low-level representation of a file, currently either a path, URL, or connection object. We can represent a list of BiocFile objects with a BiocFileList.

Usage

```
BiocFileList(files)
```

```
resource(x)
```

```
resource(x) <- value
```

```
## S4 method for signature 'BiocFile'  
resource(x)
```

```
## S4 replacement method for signature 'BiocFile,character_OR_connection'  
resource(x) <- value
```

```
fileFormat(x)
```

```
## S4 method for signature 'character'  
fileFormat(x)
```

```
## S4 method for signature 'BiocFile'
fileFormat(x)

## S4 method for signature 'BiocFile'
path(object, ...)

## S4 method for signature 'BiocFile'
show(object)

FileForFormat(path, format = file_ext(path))

## S4 method for signature 'BiocFile'
as.character(x)
```

Arguments

files	character()	A vector of file paths for the BiocFileList constructor
x		A BiocFile instance
object		A BiocFile instance
...		additional arguments to lower-level functions, not used.
path, value		Either a character or connection object to replace the original resource
format	character(1)	The file extension conducive to a file class name, e.g., CSVFile

Value

For constructors, an instance of that class. For extractors such as resource and path, typically a character vector of the file path. For FileForFormat, a convenient instance of the class for which the input file corresponds to.

Accessor Methods

In the code snippets below, x represents a BiocFile object.

path(x) Gets the path, as a character vector, to the resource represented by the BiocFile object, if possible.

resource(x) Gets the low-level resource, either a character vector (a path or URL) or a connection.

fileFormat(x) Gets a string identifying the file format. Can also be called directly on a character file path, in which case it uses a heuristic based on the file extension.

Author(s)

Michael Lawrence

See Also

Implementing classes include: [BigWigFile](#), [TwoBitFile](#), [BEDFile](#), [GFFFile](#), [WIGFile](#)

Examples

```

## For our examples, we create a class called CSVFILE that extends BiocFile
.CSVFile <- setClass("CSVFile", contains = "BiocFile")

## Constructor
CSVFile <- function(resource) {
  .CSVFile(resource = resource)
}

setMethod("import", "CSVFile", function(con, format, text, ...) {
  read.csv(resource(con), ...)
})

## Define export
setMethod("export", c("data.frame", "CSVFile"),
  function(object, con, format, ...) {
    write.csv(object, resource(con), ...)
  }
)

## Recommend CSVFile class for .csv files
temp <- tempfile(fileext = ".csv")
FileForFormat(temp)

## Create CSVFile
csv <- CSVFile(temp)

## Display path of file
path(csv)

## Display resource of file
resource(csv)

```

compression

File compression

Description

Methods and generics for file compression strategies.

Usage

```

decompress(manager, con, ...)

## S4 method for signature 'ANY'
decompress(manager, con, ...)

## S4 method for signature 'CompressedFile'

```

```
decompress(manager, con, ...)  
  
## S4 method for signature 'character'  
decompress(manager, con, ...)  
  
## S4 method for signature 'CompressedFile'  
fileFormat(x)
```

Arguments

manager	The connection manager, defaults to the internal manager class
con	The connection from which data is loaded or to which data is saved. If this is a character vector, it is assumed to be a file name and a corresponding file connection is created and then closed after exporting the object. If it is a BiocFile derivative, the data is loaded from or saved to the underlying resource. If missing, the function will return the output as a character vector, rather than writing to a connection.
...	Parameters to pass to the format-specific method.
x	A BiocFile instance

Value

A decompressed representation of a CompressedFile or character object

Related functions

`FileForFormat(path, format = file_ext(path))` Determines the file type of path and returns a high-level file object such as `BamFile`, `BEDFile`, `BigWigFile`, etc.

Examples

```
file <- tempfile(fileext = ".gzip")  
decompress(con = file)
```

Description

The functions `import` and `export` load and save objects from and to particular file formats.

Usage

```
import(con, format, text, ...)

## S4 method for signature 'connection,character,ANY'
import(con, format, text, ...)

## S4 method for signature 'connection,missing,ANY'
import(con, format, text, ...)

## S4 method for signature 'character,missing,ANY'
import(con, format, text, ...)

## S4 method for signature 'character,character,ANY'
import(con, format, text, ...)

## S4 method for signature 'missing,ANY,character'
import(con, format, text, ...)

export(object, con, format, ...)

## S4 method for signature 'ANY,connection,character'
export(object, con, format, ...)

## S4 method for signature 'ANY,connection,missing'
export(object, con, format, ...)

## S4 method for signature 'ANY,missing,character'
export(object, con, format, ...)

## S4 method for signature 'ANY,character,missing'
export(object, con, format, ...)

## S4 method for signature 'ANY,character,character'
export(object, con, format, ...)

## S4 method for signature 'CompressedFile,missing,ANY'
import(con, format, text, ...)

## S4 method for signature 'ANY,CompressedFile,missing'
export(object, con, format, ...)
```

Arguments

con The connection from which data is loaded or to which data is saved. If this is a character vector, it is assumed to be a file name and a corresponding file connection is created and then closed after exporting the object. If it is a [BiocFile](#) derivative, the data is loaded from or saved to the underlying resource. If missing, the function will return the output as a character vector, rather than

	writing to a connection.
format	The format of the output. If missing and con is a file name, the format is derived from the file extension. This argument is unnecessary when con is a derivative of BiocFile .
text	If con is missing, this can be a character vector directly providing the string data to import.
...	Parameters to pass to the format-specific method.
object	The object to export.

Value

If con is missing, a character vector containing the string output. Otherwise, nothing is returned.

Author(s)

Michael Lawrence

See Also

Format-specific options for the popular formats: [GFF](#), [BED](#), [BED15](#), [BEDGRAPH](#), [WIG](#), [BIGWIG](#)

Examples

```
## To illustrate export(), import(), and yeild(), we create a class, CSVFILE
.CSVFile <- setClass("CSVFile", contains = "BiocFile")

## Constructor
CSVFile <- function(resource) {
  .CSVFile(resource = resource)
}

## Define import
setMethod("import", "CSVFile",
  function(con, format, text, ...) {
    read.csv(resource(con), ...)
  }
)

## Define export
setMethod("export", c("data.frame", "CSVFile"),
  function(object, con, format, ...) {
    write.csv(object, resource(con), ...)
  }
)

## Usage
temp <- tempfile(fileext = ".csv")
csv <- CSVFile(temp)

export(mtcars, csv)
```

```
df <- import(csv)
```


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