Package 'BiocIO'

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Title Standard Input and Output for Bioconductor Packages

Version 1.19.0

Description The `BiocIO` package contains high-level abstract classes
and generics used by developers to build IO funcionality 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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Encoding UTF-8

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Imports BiocGenerics, S4Vectors, methods, tools

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Contents

BiocFile-class *BiocFile class objects*

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), prefix = NULL, suffix = "File")

## 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`
`prefix`	character(1) The prefix to prepend to the format class name, e.g., `Spatial` for a class `SpatialCSV`.
`suffix`	character(1) The suffix to append to the format class name, e.g., `File` for a class `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.

FileForFormat

The `prefix` and `suffix` arguments are used to filter the class names to those that match the pattern `paste0(prefix, format, suffix)`. If either `prefix` or `suffix` are NULL, they are ignored. Note that the search is case insensitive and does require the `format` to be in the name of the class.

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)
```

IO   *Import and export*

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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