

# Package ‘BiocIO’

June 1, 2023

**Title** Standard Input and Output for Bioconductor Packages

**Version** 1.10.0

**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()`.

**License** Artistic-2.0

**Encoding** UTF-8

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.2.3

**Depends** R (>= 4.3.0)

**Imports** BiocGenerics, S4Vectors, methods, tools

**Suggests** testthat, knitr, rmarkdown, BiocStyle

**Collate** 'BiocFile.R' 'import\_export.R' 'compression.R' 'utils.R'

**VignetteBuilder** knitr

**biocViews** Annotation,DataImport

**BugReports** <https://github.com/Bioconductor/BiocIO/issues>

**git\_url** <https://git.bioconductor.org/packages/BiocIO>

**git\_branch** RELEASE\_3\_17

**git\_last\_commit** 1368ff1

**git\_last\_commit\_date** 2023-04-25

**Date/Publication** 2023-06-01

**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>

## R topics documented:

BiocFile-class . . . . .	2
compression . . . . .	4
IO . . . . .	5
<b>Index</b>	<b>9</b>

---

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

---

## 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 <a href="#">BiocFile</a> 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 <a href="#">BiocFile</a> .
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)
```

# Index

- \* **IO**
  - IO, 5
- \* **classes**
  - BiocFile-class, 2
- \* **methods**
  - BiocFile-class, 2
- as.character, BiocFile-method (BiocFile-class), 2
- bed, 7
- bed15, 7
- BEDFile, 3
- bedgraph, 7
- bigwig, 7
- BigWigFile, 3
- BiocFile, 5–7
- BiocFile (BiocFile-class), 2
- BiocFile-class, 2
- BiocFileList (BiocFile-class), 2
- BiocFileList-class (BiocFile-class), 2
- compress (compression), 4
- CompressedFile-class (compression), 4
- compression, 4
- decompress (compression), 4
- decompress, ANY-method (compression), 4
- decompress, character-method (compression), 4
- decompress, CompressedFile-method (compression), 4
- decompress, GZFile-method (compression), 4
- export (IO), 5
- export, ANY, character, character-method (IO), 5
- export, ANY, character, missing-method (IO), 5
- export, ANY, CompressedFile, missing-method (IO), 5
- export, ANY, connection, character-method (IO), 5
- export, ANY, connection, missing-method (IO), 5
- export, ANY, missing, character-method (IO), 5
- FileForFormat (BiocFile-class), 2
- fileFormat (BiocFile-class), 2
- fileFormat, BiocFile-method (BiocFile-class), 2
- fileFormat, character-method (BiocFile-class), 2
- fileFormat, CompressedFile-method (compression), 4
- gff, 7
- GFFFFile, 3
- import (IO), 5
- import, character, character, ANY-method (IO), 5
- import, character, missing, ANY-method (IO), 5
- import, CompressedFile, missing, ANY-method (IO), 5
- import, connection, character, ANY-method (IO), 5
- import, connection, missing, ANY-method (IO), 5
- import, missing, ANY, character-method (IO), 5
- IO, 5
- path (BiocFile-class), 2
- path, BiocFile-method (BiocFile-class), 2
- resource (BiocFile-class), 2

resource, BiocFile-method  
    (BiocFile-class), [2](#)  
resource<- (BiocFile-class), [2](#)  
resource<- , BiocFile, character\_OR\_connection-method  
    (BiocFile-class), [2](#)  
  
show, BiocFile-method (BiocFile-class), [2](#)  
  
TwoBitFile, [3](#)  
  
wig, [7](#)  
WIGFile, [3](#)