

# Package ‘BiocIO’

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

**Version** 1.17.0

**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

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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), 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 | <i>File compression</i> |
|-------------|-------------------------|

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**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)
```

---

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 <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. |
| 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)
```



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