

# Package ‘BiocIO’

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

**Version** 1.21.0

**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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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)
```

**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 <code>manager</code> 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 <code>BiocFile</code> 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 <code>BiocFile</code> 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 <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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