Package 'RBioFormats'

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Title R interface to Bio-Formats

Description An R package which interfaces the OME Bio-Formats Java library to allow reading of proprietary microscopy image data and metadata.

Encoding UTF-8

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URL https://github.com/aoles/RBioFormats

BugReports https://github.com/aoles/RBioFormats/issues

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License GPL-3

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`AnnotatedImage-class` *AnnotatedImage Class*

Description

Extends the Image class from the **EBImage** package.

Usage

```
AnnotatedImage(..., metadata = ImageMetadata())

## S3 method for class 'AnnotatedImage'
print(x, short = FALSE, ...)

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

## S3 method for class 'AnnotatedImage'
as.Image(x)
```

Arguments

`...`	arguments passed to the Image constructor.
`metadata`	an ImageMetadata object containing image metadata
`x`	an AnnotatedImage object.
`short`	logical, turns off image data preview.
`object`	an AnnotatedImage object

Value

`AnnotatedImage` returns a new AnnotatedImage object.

`as.Image` returns an Image object.

Slots

`metadata` an ImageMetadata object containing image metadata

Author(s)

Andrzej Oleś <<andrzej.oles@gmail.com>>, 2014-2023

See Also

AnnotatedImageList

Examples

```
f = mockFile(sizeX = 256, sizeY = 256)
img = read.image(f)
img
```

`AnnotatedImageList-class` *AnnotatedImageList Class*

Description

A list of AnnotatedImage objects.

Usage

```
AnnotatedImageList(...)
```

Arguments

`...`	a list of AnnotatedImage objects to include in the new object.

Value

`AnnotatedImageList` returns a new AnnotatedImageList object.

Examples

```
f = mockFile(sizeX = 256, sizeY = 256, series = 2)
img = read.image(f)
img
```

checkJavaMemory *Java Memory Settings*

Description

Information about the Java heap space usage.

Usage

```
checkJavaMemory(units = "m")
```

Arguments

units	Units to return the size in: "k", "m" or "g"

Value

The maximum amount of memory that the JVM will attempt to use, measured in units.

Author(s)

Andrzej Oleś <<andrzej.oles@gmail.com>>, 2014-2023

Examples

```
## Not run:
## assign 4 gigabytes of heap space to the Java environment.
options( java.parameters = "-Xmx4g" )
library( "RBioFormats" )

## End(Not run)

checkJavaMemory()
```

coreMetadata *Metadata Accessors*

Description

Get and set image metadata.

Usage

```
coreMetadata(x, series, ...)

globalMetadata(x, series, ...)

seriesMetadata(x, series, ...)

## S4 method for signature 'ANY'
metadata(x)

## S4 method for signature 'AnnotatedImage'
metadata(x)

## S4 method for signature 'AnnotatedImageList'
metadata(x)

## S4 method for signature 'ImageMetadata'
metadata(x)

## S4 method for signature 'ImageMetadataList'
metadata(x)

## S4 replacement method for signature 'AnnotatedImage'
metadata(x) <- value

coreMetadata(y) <- value

## S4 replacement method for signature 'AnnotatedImage'
coreMetadata(y) <- value

## S4 replacement method for signature 'ImageMetadata'
coreMetadata(y) <- value

globalMetadata(y) <- value

## S4 replacement method for signature 'AnnotatedImage'
globalMetadata(y) <- value

## S4 replacement method for signature 'ImageMetadata'
globalMetadata(y) <- value

seriesMetadata(y) <- value

## S4 replacement method for signature 'AnnotatedImage'
seriesMetadata(y) <- value

## S4 replacement method for signature 'ImageMetadata'
seriesMetadata(y) <- value
```

Arguments

x	an AnnotatedImage, AnnotatedImageList, ImageMetadata, or ImageMetadataList object
series	series ID
...	arguments passed to grep
value	depending on the context, an ImageMetadata object or a list
y	an AnnotatedImage or ImageMetadata object

Details

The ... arguments are passed to grep called on metadata names allowing for convenient subsetting.

Value

Named list consisting of key value pairs.

Author(s)

Andrzej Oleś <<andrzej.oles@gmail.com>>, 2014-2023

Examples

```
img = read.image(system.file("images", "nuclei.tif", package="EBImage"))

coreMetadata(img)

# subset for specific names

globalMetadata(img, pattern="Image")
```

---

dimorder *Image Frames Order*

Description

Get the ordering of image frames.

Usage

```
dimorder(x)
```

Arguments

x	An Image object or an array

Value

A character vector giving the dimension names.

Author(s)

Andrzej Oleś <<andrzej.oles@gmail.com>>, 2014-2023

Examples

```
# sample timelapse image
f = mockFile(sizeC=2, sizeT=10)
img = read.image(f)

dimorder(img)
```

FormatTools *Bio-Formats FormatTools Class*

Description

A utility class for format reader and writer implementations.

Usage

```
FormatTools
```

Format

An object of class `jclassName` of length 1.

Author(s)

Andrzej Oleś <<andrzej.oles@gmail.com>>, 2014-2023

Examples

```
# List available pixel types
sapply(0:7, FormatTools$getPixelTypeString)
```

`ImageMetadata-class` *ImageMetadata and ImageMetadataList Class*

Description

Formal representation of image metadata.

Usage

```
ImageMetadata(
  coreMetadata = NULL,
  globalMetadata = NULL,
  seriesMetadata = NULL
)

ImageMetadataList(...)

## S3 method for class 'ImageMetadata'
print(x, list.len = 5L, ...)

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

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

## S3 method for class 'ImageMetadataList'
print(x, ...)
```

Arguments

`coreMetadata`	a list of core metadata entries
`globalMetadata`	a list of global metadata entries
`seriesMetadata`	a list of series metadata entries
`...`	further arguments to be passed to other methods
`x`	An ImageMetadata object
`list.len`	numeric; maximum number of metadata entries to display
`object`	an `ImageMetadata` object

Value

`ImageMetadata` returns a new ImageMetadata object.

`ImageMetadataList` returns a new ImageMetadataList object.

Author(s)

Andrzej Oleś <<andrzej.oles@gmail.com>>, 2014-2023

Examples

```
f = mockFile(sizeX = 256, sizeY = 256)
img = read.image(f)
metadata(img)
```

`mockFile` *Generate Test Images*

Description

Create a mock image of specific parameters for testing.

Usage

```
mockFile(name = "mockfile", ...)
```

Arguments

`name`	File name.
`...`	File parameters; available parameters are listed below.

Details

Generates mock files of specific size or pixel type containing gradient images. The desired parameters can be provided as key value pairs to the `mockFile` function. For a list of available parameters see below.

Value

A character string.

Parameters

Name	Default	Description
sizeX	512	horizontal size in pixels
sizeY	512	vertical size in pixels
sizeZ	1	number of Z sections
sizeC	1	number of channels
sizeT	1	number of time points
pixelType	uint8	string specifying pixel type: int8, uint8, int16, uint16, int32, uint32, float, double
bitsPerPixel	0	number of valid bits (<= number of bits implied by pixel type)
rgb	1	number of channels that are merged together
dimOrder	XYZCT	string describing dimension order

orderCertain	true	
little	true	whether or not the pixel data should be little-endian
interleaved	true	whether or not merged channels are interleaved
indexed	false	whether or not a color lookup table is present
falseColor	false	whether or not the color lookup table is just for making the image look pretty
series	1	number of series (Images)
lutLength	3	number of entries in the color lookup table

Author(s)

Andrzej Oleś <<andrzej.oles@gmail.com>>, 2014-2023

Examples

```
f = mockFile(sizeX = 256, sizeY = 256)
img = read.image(f)
img
```

`RBioFormats` *R Interface to Bio-Formats*

Description

Interfaces the Bio-Formats Java library.

Usage

```
BioFormats.version()
```

Value

A character string containing the Bio-Formats library version.

Functions

- `BioFormats.version()`: Provides the version of the Bio-Formats library embedded in the package.

Author(s)

Andrzej Oleś <<andrzej.oles@gmail.com>>, 2014-2023

References

Bio-Formats website

Examples

```
BioFormats.version()
```

`read.image` *Read Images*

Description

Read image files using the Bio-Formats library. A list of supported formats can be found on the Bio-Formats website.

Usage

```
read.image(
  file,
  filter.metadata = FALSE,
  proprietary.metadata = TRUE,
  normalize = TRUE,
  series,
  resolution,
  subset,
  read.metadata = TRUE
)
```

Arguments

`file`	character, file name
`filter.metadata`	logical, specifies whether ugly metadata (entries with unprintable characters, and extremely large entries) should be discarded from the metadata table
`proprietary.metadata`	logical, should proprietary metadata be populated to OME-XML
`normalize`	logical, should the original image data be mapped to the [0,1] range
`series`	integer vector specifying series to read; if missing all series included in the file are read
`resolution`	integer vector specifying resolution levels to read; if missing all levels read
`subset`	named list specifing image subsetting
`read.metadata`	logical, should image metadata be read

Value

An AnnotatedImage object or an AnnotatedImageList object in case of multi-series data.

Author(s)

Andrzej Oleś <<andrzej.oles@gmail.com>>, 2014-2023

See Also

read.metadata for reading image metadata, read.omexml for reading image metadata as OME-XML

Examples

```
require(EBImage)
f = system.file("images", "sample-color.png", package="EBImage")

img = read.image(f)
img
```

---

read.metadata *Read Image Metadata*

Description

Read image metadata using the Bio-Formats library. The list of supported file formats can be found on the Bio-Formats website.

Usage

```
read.metadata(file, filter.metadata = FALSE, proprietary.metadata = TRUE)
```

Arguments

file	character, file name
filter.metadata	logical, specifies whether ugly metadata (entries with unprintable characters, and extremely large entries) should be discarded from the metadata table
proprietary.metadata	logical, should proprietary metadata be populated to OME-XML

Value

An ImageMetadata or ImageMetadataList object.

Author(s)

Andrzej Oleś <<andrzej.oles@gmail.com>>, 2014-2023

See Also

read.omexml for reading image metadata as OME-XML, read.image for reading image data

Examples

```
require(EBImage)
f = system.file("images", "nuclei.tif", package="EBImage")

metadata = read.metadata(f)
str(metadata)
```

`read.omexml` *Read OME-XML Metadata*

Description

Read the OME-XML DOM tree.

Usage

```
read.omexml(file, filter.metadata = FALSE, proprietary.metadata = TRUE)
```

Arguments

`file`	character, file name
`filter.metadata`	logical, specifies whether ugly metadata (entries with unprintable characters, and extremely large entries) should be discarded from the metadata table
`proprietary.metadata`	logical, should proprietary metadata be populated to OME-XML

Value

A string containing a dumped OME-XML DOM tree.

Author(s)

Andrzej Oleś <<andrzej.oles@gmail.com>>, 2014-2023

See Also

`read.metadata` for reading image metadata, `read.image` for reading image data

Examples

```
require(EBImage)
f = system.file("images", "nuclei.tif", package="EBImage")

omexml = read.omexml(f)
omexml
```

seriesCount *Number of Image Series*

Description

Get the number of image series contained in an object.

Usage

```
seriesCount(x)

## S4 method for signature 'ANY'
seriesCount(x)

## S4 method for signature 'matrix'
seriesCount(x)

## S4 method for signature 'array'
seriesCount(x)

## S4 method for signature 'ImageMetadata'
seriesCount(x)

## S4 method for signature 'AnnotatedImageList'
seriesCount(x)

## S4 method for signature 'ImageMetadataList'
seriesCount(x)
```

Arguments

x	an images object.

Details

Image series are encoded by AnnotatedImageList or ImageMetadataList objects. Therefore, only these objects can possibly yield image series count higher than 1 while for all the rest of image objects this number is expected to be 1.

Value

The number of image series the object contains, see Details.

Author(s)

Andrzej Oleś <<andrzej.oles@gmail.com>>, 2014-2023

Examples

```
f = mockFile(sizeX = 256, sizeY = 256, series = 2)
img = read.image(f)
seriesCount(img)

meta <- metadata(img)
seriesCount(meta)
```

`write.image` *Write Images*

Description

Save image files using the Bio-Formats library. A list of supported formats can be found on the Bio-Formats website.

Usage

```
write.image(x, file, force = FALSE, pixelType, littleEndian)
```

Arguments

`x`	an `Image` or `AnnotatedImage` object
`file`	character, file name
`force`	logical(1), if `TRUE` overwrite existing file
`pixelType`	character(1), data type to store pixel values
`littleEndian`	boolean(1), pixel data endianness

Value

File path to `file` is returned invisibly.

Author(s)

Andrzej Oleś <<andrzej.oles@gmail.com>>, 2014-2023

See Also

`read.image` for reading images.

Examples

```
f = mockFile(sizeX = 256, sizeY = 256)
img = read.image(f)

tempfile = tempfile("", , ".png")
write.image(img, tempfile)
```

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