Package ‘RBioFormats’

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'write.image.R'
'zzz.R'
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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
AnnotatedImageList-class

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

def 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

def 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

```r
## 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.
coreMetadata

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.
- `

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 2014-2023

Examples

```r
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

```r
dimorder(x)
```

Arguments

- `x`: An `Image` object or an array

Value

A character vector giving the dimension names.
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(...)

```r
## 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

```r
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

```r
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

<table>
<thead>
<tr>
<th>Name</th>
<th>Default</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>sizeX</td>
<td>512</td>
<td>horizontal size in pixels</td>
</tr>
<tr>
<td>sizeY</td>
<td>512</td>
<td>vertical size in pixels</td>
</tr>
<tr>
<td>sizeZ</td>
<td>1</td>
<td>number of Z sections</td>
</tr>
<tr>
<td>sizeC</td>
<td>1</td>
<td>number of channels</td>
</tr>
<tr>
<td>sizeT</td>
<td>1</td>
<td>number of time points</td>
</tr>
<tr>
<td>pixelType</td>
<td>uint8</td>
<td>string specifying pixel type: int8, uint8, int16, uint16, int32, uint32, float, double</td>
</tr>
<tr>
<td>bitsPerPixel</td>
<td>0</td>
<td>number of valid bits (&lt;= number of bits implied by pixel type)</td>
</tr>
<tr>
<td>rgb</td>
<td>1</td>
<td>number of channels that are merged together</td>
</tr>
<tr>
<td>dimOrder</td>
<td>XYZCT</td>
<td>string describing dimension order</td>
</tr>
</tbody>
</table>
orderCertain true whether or not the pixel data should be little-endian
little true whether or not merged channels are interleaved
interleaved true whether or not a color lookup table is present
indexed false whether or not the color lookup table is just for making the image look pretty
falseColor false number of series (Images)
series 1 number of entries in the color lookup table
lutLength 3

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
read.image

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

```r
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 specifying 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

```r
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

```r
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

```r
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

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

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

Description

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

Usage

```r
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

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

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