Package ‘RBioFormats’

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Author Andrzej Oleś [aut, cre] (<https://orcid.org/0000-0003-0285-2787>),
   John Lee [ctb] (<https://orcid.org/0000-0001-5884-4247>)
Maintainer Andrzej Oleś <andrzej.oles@gmail.com>
AnnotatedImage-class

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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
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.
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 \texttt{AnnotatedImage}, \texttt{AnnotatedImageList}, \texttt{ImageMetadata}, or \texttt{ImageMetadataList} object

\texttt{series} series ID

... arguments passed to \texttt{grep}

\texttt{value} depending on the context, an \texttt{ImageMetadata} object or a list

\(y\) an \texttt{AnnotatedImage} or \texttt{ImageMetadata} object

Details

The ... arguments are passed to \texttt{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

\begin{verbatim}
img = read.image(system.file("images", "nuclei.tif", package="EBImage"))

coreMetadata(img)

# subset for specific names
globalMetadata(img, pattern="Image")
\end{verbatim}

---

**dimorder** *Image Frames Order*

Description

Get the ordering of image frames.

Usage

\texttt{dimorder}(x)

Arguments

\(x\) An \texttt{Image} object or an array

Value

A character vector giving the dimension names.
Examples

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

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

```r
# 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.
mockFile

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

<table>
<thead>
<tr>
<th>Name</th>
<th>Default</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>name</td>
<td></td>
<td>File name.</td>
</tr>
<tr>
<td>...</td>
<td></td>
<td>File parameters; available parameters are listed below.</td>
</tr>
</tbody>
</table>

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 (\leq 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
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

R BioFormats

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 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

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

img = read.image(f)
```

---

**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**

```r
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
### Description

Get the number of image series contained in an object.

### Usage

```r
seriesCount(x)
```

#### S4 method for signature 'ANY'

```r
seriesCount(x)
```

#### S4 method for signature 'matrix'

```r
seriesCount(x)
```

#### S4 method for signature 'array'

```r
seriesCount(x)
```

#### S4 method for signature 'ImageMetadata'

```r
seriesCount(x)
```

#### S4 method for signature 'AnnotatedImageList'

```r
seriesCount(x)
```

#### S4 method for signature 'ImageMetadataList'

```r
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)
```

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

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

Arguments

- `x`: an `Image` or `AnnotatedImage` object
- `file`: character, file name
- `force`: logical(1), if link 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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