

# Package: picohdr (via r-universe)

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**Type** Package

**Title** Read, Write and Manipulate High Dynamic Range Images

**Version** 0.1.1

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**Description** High Dynamic Range (HDR) images support a large range in luminosity between the lightest and darkest regions of an image. To capture this range, data in HDR images is often stored as floating point numbers and in formats that capture more data and channels than standard image types. This package supports reading and writing two types of HDR images; PFM (Portable Float Map) and OpenEXR images. HDR images can be converted to lower dynamic ranges (for viewing) using tone-mapping. A number of tone-mapping algorithms are included which are based on Reinhard (2002) ``Photographic tone reproduction for digital images" <doi:10.1145/566654.566575>.

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**Encoding** UTF-8

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**Suggests** knitr, rmarkdown, ggplot2, testthat (>= 3.0.0)

**Config/testthat/edition** 3

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**VignetteBuilder** knitr

**URL** <https://github.com/coolbutuseless/picohdr>

**BugReports** <https://github.com/coolbutuseless/picohdr/issues>

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---

adj\_clamp

*Clamp values outside the specified range*

---

### Description

Clamp values outside the specified range

### Usage

```
adj_clamp(arr, lo = -Inf, hi = Inf)
```

### Arguments

arr	array or matrix
lo	low value. Values lower than this will be replaced with this value. Default: -Inf
hi	Values higher than this will be replaced with this value. Default: Inf

### Value

adjusted array

### See Also

Other array adjustment functions: [adj\\_gamma\(\)](#), [adj\\_infinite\(\)](#), [adj\\_rescale\(\)](#), [adj\\_shift\\_negatives\\_global\(\)](#), [adj\\_shift\\_negatives\\_local\(\)](#)

**Examples**

```
arr <- array(1:12, c(4, 3, 1))
arr
adj_clamp(arr, 10, 20)
```

---

adj\_gamma

*Adjust gamma*

---

**Description**

Adjust gamma

**Usage**

```
adj_gamma(arr, gamma = 1/2.2)
```

**Arguments**

arr	array or matrix
gamma	gamma correction factor. Default: 1/2.2

**Value**

adjusted array

**See Also**

Other array adjustment functions: [adj\\_clamp\(\)](#), [adj\\_infinite\(\)](#), [adj\\_rescale\(\)](#), [adj\\_shift\\_negatives\\_global\(\)](#), [adj\\_shift\\_negatives\\_local\(\)](#)

**Examples**

```
arr <- array(1:12, c(4, 3, 1))
arr
adj_gamma(arr)
```

---

adj_infinite	<i>Replace infinite values with the minimum/maximum of the finite values</i>
--------------	--

---

**Description**

Replace infinite values with the minimum/maximum of the finite values

**Usage**

```
adj_infinite(arr)
```

**Arguments**

arr                    array or matrix

**Value**

adjusted array

**See Also**

Other array adjustment functions: [adj\\_clamp\(\)](#), [adj\\_gamma\(\)](#), [adj\\_rescale\(\)](#), [adj\\_shift\\_negatives\\_global\(\)](#), [adj\\_shift\\_negatives\\_local\(\)](#)

**Examples**

```
arr <- array(c(-Inf, Inf, 1:10), c(4, 3, 1))
arr
adj_infinite(arr)
```

---

adj_rescale	<i>Linearly rescale values to lie between the given limits</i>
-------------	--

---

**Description**

Infinite values will be clamped to the limits

**Usage**

```
adj_rescale(arr, lo, hi)
```

**Arguments**

arr                    array or matrix  
lo, hi                 limits

**Value**

adjusted array

**See Also**

Other array adjustment functions: [adj\\_clamp\(\)](#), [adj\\_gamma\(\)](#), [adj\\_infinite\(\)](#), [adj\\_shift\\_negatives\\_global\(\)](#), [adj\\_shift\\_negatives\\_local\(\)](#)

**Examples**

```
arr <- array(1:24, c(4, 3, 2))
arr
adj_rescale(arr, 0, 1)
```

---

`adj_shift_negatives_global`

*Shift all values such that the minimum of the array is 0*

---

**Description**

Shift all values such that the minimum of the array is 0

**Usage**

```
adj_shift_negatives_global(arr)
```

**Arguments**

`arr`                    array or matrix

**Value**

adjusted array

**See Also**

Other array adjustment functions: [adj\\_clamp\(\)](#), [adj\\_gamma\(\)](#), [adj\\_infinite\(\)](#), [adj\\_rescale\(\)](#), [adj\\_shift\\_negatives\\_local\(\)](#)

**Examples**

```
arr <- array(c(-5, 1:23), c(4, 3, 2))
arr
adj_shift_negatives_global(arr)
```

adj\_shift\_negatives\_local

*Shift all values in a plane such that the minimum in every plane is 0*

---

### Description

Shift all values in a plane such that the minimum in every plane is 0

### Usage

```
adj_shift_negatives_local(arr)
```

### Arguments

arr                    array or matrix

### Value

adjusted array

### See Also

Other array adjustment functions: [adj\\_clamp\(\)](#), [adj\\_gamma\(\)](#), [adj\\_infinite\(\)](#), [adj\\_rescale\(\)](#), [adj\\_shift\\_negatives\\_global\(\)](#)

### Examples

```
arr <- array(c(-5, 1:23), c(4, 3, 2))
arr
adj_shift_negatives_local(arr)
```

---

array\_to\_df

*Convert array to a linear data.frame. Preserves array names if present.*

---

### Description

This conversion is useful when preparing the data to summarise with ggplot.

### Usage

```
array_to_df(arr)
```

### Arguments

arr                    array

**Value**

data.frame with 'x', 'y', 'z', 'channel' and 'value.' 'channel' will be the channel name if found, otherwise it is equivalent to 'z'.

**Examples**

```
arr <- array(1:24, dim = c(4, 3, 2))
array_to_df(arr)
```

---

exr\_attrs

*Helper function to create attributes for `write_exr()`*


---

**Description**

The EXR file specification requires particular types to define the metadata for the image. This function helps define these metadata attributes.

**Usage**

```
exr_attrs(
  channels = NULL,
  compression = NULL,
  dataWindow = NULL,
  displayWindow = NULL,
  lineOrder = NULL,
  pixelAspectRatio = NULL,
  screenWindowCenter = NULL,
  screenWindowWidth = NULL,
  ...
)
```

**Arguments**

channels	[ <code>exr_type\$chlist()</code> ] data.frame of channel information with columns name [string], type ['half', 'float', 'uint'], pLinear [0, 1], xSampling [0, 1], ySampling [0, 1]
compression	[ <code>exr_type\$compression()</code> ] 'NONE' or 'ZIP'
dataWindow	[ <code>exr_type\$box2i()</code> ] xmin, ymin, xmax, ymax of data. Default: image size <code>c(0, 0, w-1, h-1)</code>
displayWindow	[ <code>exr_type\$box2i()</code> ] xmin, ymin, xmax, ymax of display. Default: image size <code>c(0, 0, w-1, h-1)</code>
lineOrder	[ <code>exr_type\$lineOrder()</code> ] Line ordering. One of 'increasing', 'decreasing' or 'random'. Default: 'increasing'
pixelAspectRatio	[ <code>exr_type\$float()</code> ]. Default: 1.0

```

screenWindowCenter
    [exr_type$v2f()]. Default: c(0.0, 0.0)
screenWindowWidth
    [exr_type$float()]. Default: 1.0
...
    Other named parameters. value must be of class exr_type e.g. myLabel =
    exr_type$string("potpourri").

```

### Details

In the majority of cases for basic image output, there is no need to specify anything with this function. `write_exr()` will create mandatory attributes required for image output.

Note that all values must be an object with class `exr_type`. To create these types, use `exr_type$<TYPE>(...)`.

### Value

named list of attributes for writing EXR

### Examples

```

exr_attrs(compression = exr_type$compression("ZIP"),
          name         = exr_type$string("Render 032"))

```

---

exr\_info

*Extract the metadata from an EXR file*

---

### Description

This will extract attributes from any of EXR file.

### Usage

```
exr_info(filename, verbosity = 0)
```

### Arguments

```

filename      EXR filename or connection
verbosity     verbosity. Default: 0

```

### Value

Named list of image attributes

### Examples

```

filename <- system.file("image/rstats.exr", package = "picohdr")
exr_info(filename)

```



---

exr_type	<i>Functions for creating valid EXR type objects</i>
----------	--

---

**Description**

This is a list of functions for creating EXR objects of a particular EXR type. Each function does checks for argument validity and calculates size information required for EXR output.

**Usage**

```
exr_type
```

**Format**

An object of class `list` of length 23.

**Details**

Refer to official OpenEXR documentation

**Examples**

```
# Create a v2f type
exr_type$v2f(c(12.1, 2.3))

# Create an attribute
exr_attrs(copyright = exr_type$string("mike"))
```

---

plot.array	<i>Plot method for matrices and arrays</i>
------------	--

---

**Description**

Plot method for matrices and arrays

**Usage**

```
## S3 method for class 'array'
plot(x, interpolate = TRUE, ...)
```

**Arguments**

<code>x</code>	matrix or array
<code>interpolate</code>	Default: TRUE
<code>...</code>	other arguments passed to <code>plot()</code>

**Value**

None.

**Examples**

```
filename <- system.file("image/rstats.pfm.bz2", package = "picohdr")
image <- read_pfm(filename)
image <- adj_gamma(image)
plot(image)
```

---

print.exr\_type      *Print 'exr\_type' objects*

---

**Description**

Print 'exr\_type' objects

**Usage**

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

**Arguments**

x	exr_type object
...	other arguments passed on to NextMethod

**Value**

None

**Examples**

```
bbox <- exr_type$bbox2i(0, 0, 1, 1)
print(bbox)
```

---

read_exr	<i>Read an EXR image</i>
----------	--------------------------

---

**Description**

Currently only single-part scanline images are supported (where the compression is one of NONE, ZIP or ZIPS).

**Usage**

```
read_exr(filename, verbosity = 0)
```

**Arguments**

filename	EXR filename or connection
verbosity	Level of debugging output. Default: 0 (no debugging output)

**Value**

Numeric array with names along the third dimension. Each plane in the array corresponds to a channel in the EXR.

**Examples**

```
filename <- system.file("image/rstats.exr", package = "picohdr")
images <- read_exr(filename)
dimnames(images)[[3]]

# Naively adjust one of the images for display
im <- adj_rescale(images[, , 'dzdy'], lo = 0, hi = 1)
plot(im)
```

---

read_pfm	<i>Read PFM image</i>
----------	-----------------------

---

**Description**

Read PFM image

**Usage**

```
read_pfm(filename)
```

**Arguments**

filename	PFM filename or connection object. If filename ends with 'xz', 'bz2' or 'gz' suffix then it will be uncompressed automatically.
----------	---

**Value**

If input PFM file is grayscale, a 2D numeric array is returned. If PFM file represents RGB color values, a 3D numeric array is returned.

**See Also**

Other PFM functions: [write\\_pfm\(\)](#)

**Examples**

```
file <- system.file("image/rstats.pfm.bz2", package = "picohdr")
arr <- read_pfm(file)
arr[1:5, 1:5, ]

# Tone-map the image, gamma correct and plot
arr <- tm_reinhard_basic(arr)
arr <- adj_gamma(arr)
plot(arr)
```

---

tm\_reinhard

*Reinhard's global tone mapping*

---

**Description**

Tone mapping is a method for adapting an HDR image for display on a low dynamic range device. There are three included variants of Reinhard's global tone mapping operator.

**Usage**

```
tm_reinhard(arr)
```

```
tm_reinhard_basic(arr)
```

```
tm_reinhard_variant(arr)
```

**Arguments**

arr                    array or matrix

**Details**

tm\_reinhard() [RGB] Reinhard's operator with a correction for the maximum luminance

tm\_reinhard\_basic() [RGB images] Reinhard's operator applied equally to all colour channels

tm\_reinhard\_variant() [RGB or Gray images] A combination of the above two methods

These functions are based on Reinhard (2002) "Photographic tone reproduction for digital images"

**Value**

New array with adjusted color values

**Examples**

```
filename <- system.file("image", "rstats.pfm.bz2", package = "picohdr")
image <- read_pfm(filename)
image <- tm_reinhard_basic(image)
image <- adj_gamma(image)
plot(image)
```

---

write\_exr

*Write a numeric array as an EXR image*

---

**Description**

Write a numeric array as an EXR image

**Usage**

```
write_exr(
  arr,
  filename,
  pixel_type = c("half", "float", "uint"),
  channel_names = NULL,
  attrs = exr_attrs(),
  verbosity = 0
)
```

**Arguments**

arr	array representing image
filename	filename
pixel_type	one of 'half', 'float' or 'double'. Default: 'half'
channel_names	character vector. names of each plane in the array. If NULL then channel names are extracted from the array with <code>dimnames(arr)[[3]]</code> . If no names are set on the array, then channel names defaults to "Y", "RGB" and "RGBA" for 1, 3, and 4 plane arrays respectively. For all other array sizes, channel names allocated alphabetically from 'A' to 'Z'
attrs	EXR attributes for image. Use <code>exr_attrs()</code>
verbosity	verbosity. default: 0

**Value**

None

## Examples

```
orig_file <- system.file("image", "rstats.pfm.bz2", package = "picohdr")
arr <- read_pfm(orig_file)
exr_file <- tempfile(fileext = ".exr")
write_exr(arr, exr_file)
```

---

write\_pfm

*Write a numeric array as PFM*

---

## Description

Write a numeric array as PFM

## Usage

```
write_pfm(arr, filename, endian = "little")
```

## Arguments

arr	numeric matrix or array (with 3 planes)
filename	filename or connection object. If filename ends with ".xz", '.bz2' or '.gz', then it will be automatically compressed.
endian	One of 'little' or 'big'. Default: 'little'

## Value

None.

## See Also

Other PFM functions: [read\\_pfm\(\)](#)

## Examples

```
arr <- array(runif(10 * 30 * 3), dim = c(10, 30, 3))
write_pfm(arr, tempfile())
```

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