

# Package ‘convert’

July 27, 2025

**Version** 1.84.0

**Title** Convert Microarray Data Objects

**Author** Gordon Smyth <smyth@wehi.edu.au>,  
James Wettenhall <wettenhall@wehi.edu.au>,  
Yee Hwa (Jean) Yang <jean@biostat.ucsf.edu>,  
Martin Morgan <Martin.Morgan@RoswellPark.org>

**Maintainer** Yee Hwa (Jean) Yang <jean@biostat.ucsf.edu>

**Depends** R (>= 2.6.0), Biobase (>= 1.15.33), limma (>= 1.7.0), marray,  
utils, methods

**Description** Define coerce methods for microarray data objects.

**License** LGPL

**URL** <http://bioinf.wehi.edu.au/limma/convert.html>

**biocViews** Infrastructure, Microarray, TwoChannel

**git\_url** <https://git.bioconductor.org/packages/convert>

**git\_branch** RELEASE\_3\_21

**git\_last\_commit** 801274c

**git\_last\_commit\_date** 2025-04-15

**Repository** Bioconductor 3.21

**Date/Publication** 2025-07-27

## Contents

|                  |          |
|------------------|----------|
| coerce . . . . . | 2        |
| <b>Index</b>     | <b>4</b> |

coerce

*Convert Data Objects***Description**

Convert between limma, marray and Biobase data objects.

**Details**

Objects can be converted (coerced) from one class to another using `as(object, Class)` where `object` is an object to convert and `Class` is the name of the class to convert to. The following conversions are provided:

| From:      | To:           |
|------------|---------------|
| RGList     | marrayRaw     |
| marrayRaw  | RGList        |
| MAList     | marrayNorm    |
| marrayNorm | MAList        |
| RGList     | NChannelSet   |
| marrayRaw  | NChannelSet   |
| MAList     | ExpressionSet |
| marrayNorm | ExpressionSet |

RGList and marrayRaw are coerced to NChannelSet. Channel values are not transformed.

MAList and marrayNorm are coerced so that the ExpressionSet slot contains log-ratios (M-values) and the ExpressionSet object has the same number of columns as the original object. In this case, information on the A-values is lost.

There is intentionally no conversion from RGList or marrayRaw to ExpressionSet, as ExpressionSet is intended for expression values, not intensities.

**Author(s)**

Gordon Smyth and others

**See Also**

[as](#) in the methods package.

**Examples**

```
##first set up some fake intensity matrices
testRed <- matrix(rnorm(5*2),5,2,
  dimnames=list(paste("gene",1:5, sep=""), c("S1", "S2")))
testGreen <- matrix(rnorm(5*2),5,2,
  dimnames=list(paste("gene",1:5, sep=""), c("S1", "S2")))
```

```
##some sample/target info
testTarget <- data.frame(slide=c("S1", "S2"), Cy3=c("T", "C"),
  Cy5=c("C", "T"), row.names=c("S1", "S2"))

maT <- new("marrayInfo", maLabels=c("S1", "S2"),
  maInfo= testTarget)

##now create instances and convert
x <- new("RGList")
x$R <- testRed
x$G <- testGreen
y <- as(x, "marrayRaw")
z <- as(x, "NChannelSet")

x <- new("marrayRaw")
x@maGf <- testGreen
x@maRf <- testRed
x@maTargets = maT
y <- as(x, "RGList")
z <- as(x, "NChannelSet")

x <- new("MAlisT")
y <- as(x, "marrayNorm")

##we construct a reasonably complete fake, small
##instance of the marrayNorm class
x <- new("marrayNorm")
x@maM <- testRed
x@maA <- testGreen
maTargets(x) = maT
y <- as(x, "MAlisT")
y <- as(x, "ExpressionSet")

x <- new("MAlisT")
x$M <- testRed
x$A <- testGreen
x$targets <- testTarget
y <- as(x, "ExpressionSet")
```

# Index

- \* **classes**

- coerce, [2](#)

- \* **data**

- coerce, [2](#)

as, [2](#)

coerce, [2](#)

coerce, MAList, ExpressionSet-method  
(coerce), [2](#)

coerce, MAList, marrayNorm-method  
(coerce), [2](#)

coerce, marrayNorm, ExpressionSet-method  
(coerce), [2](#)

coerce, marrayNorm, MAList-method  
(coerce), [2](#)

coerce, marrayRaw, NChannelSet-method  
(coerce), [2](#)

coerce, marrayRaw, RGList-method  
(coerce), [2](#)

coerce, RGList, marrayRaw-method  
(coerce), [2](#)

coerce, RGList, NChannelSet-method  
(coerce), [2](#)

convert (coerce), [2](#)