

# Package ‘convert’

July 26, 2022

**Version** 1.73.0

**Title** Convert Microarray Data Objects

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**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** master

**git\_last\_commit** 471bdce

**git\_last\_commit\_date** 2022-04-26

**Date/Publication** 2022-07-26

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 coerce

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*Convert Data Objects*


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## 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("MArrayList")
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,"MArrayList")
y <- as(x, "ExpressionSet")

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

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