Package ‘convert’

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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


biocViews Infrastructure, Microarray, TwoChannel

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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:

<table>
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<th>From:</th>
<th>To:</th>
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<tbody>
<tr>
<td>RGList</td>
<td>marrayRaw</td>
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<tr>
<td>marrayRaw</td>
<td>RGList</td>
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<tr>
<td>MAList</td>
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<tr>
<td>marrayNorm</td>
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<tr>
<td>RGList</td>
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</tr>
<tr>
<td>marrayRaw</td>
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<tr>
<td>MAList</td>
<td>ExpressionSet</td>
</tr>
<tr>
<td>marrayNorm</td>
<td>ExpressionSet</td>
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</tbody>
</table>

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**

```r
## 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")
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