

**convert**

November 11, 2009

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**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:

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