Package ‘convert’

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Title Convert Microarray Data Objects
Author Gordon Smyth <smyth@wehi.edu.au>,
James Wittenhall <wittenhall@wehi.edu.au>,
Yee Hwa (Jean) Yang <jean@biostat.ucsf.edu>,
Martin Morgan <mtmorgan@fhcrc.org> Martin Morgan
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
biocViews Infrastructure, Microarray, TwoChannel
NeedsCompilation no

R topics documented:

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ckoerce  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>
</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

```r
x <- new("marrayNorm")
x@maM <- testRed
x@maA <- testGreen
maTargets(x) = maT
y <- as(x,"MAList")
y <- as(x,"ExpressionSet")
```

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