convert

October 25, 2011

---

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.

1

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