Converting Between Microarray Data Classes: the `convert` Package Version 1.1.7

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The convert package provides the ability to convert between microarray data formats (object classes) defined in the packages Biobase, limma and marray. Conversion is done using the function `as` from the methods package. For example, if `x` is a `marrayNorm` object produced by the marrayNorm package, then

```
> y <- as(x, "MAList")
```

will produce a `MAList` object `y`, useful in the limma package.

The following data classes are supported:

- `RGList` (limma). A simple list-based class for storing red and green channel foreground and background intensities and associated information for a batch of spotted microarrays.

- `MAList` (limma). A simple list-based class for storing M-values and A-values and associated information for a batch of spotted microarrays.

- `marrayRaw` (marray). Stores red and green channel foreground and background intensities and associate information for a batch of spotted microarrays. Analogous to `RGList`.

- `marrayNorm` (marray). Stores red and green channel foreground and background intensities and associate information for a batch of spotted microarrays. Analogous to `MAList`.

- `ExpressionSet` (Biobase). Stores microarray expression data, one value for each probe for each array and associated phenotypic data. Links out to an external annotation library for probe information. Commonly used for single channel data such as Affymetrix or for pre-processed two-color data in the form of log-ratios ready for cluster analysis or classification.

The `convert` package provides conversion to and from `RGList` and `marrayRaw`, to and from `MAList` and `marrayNorm`, and from `MAList` and `marrayNorm` to `ExpressionSet`.