

# Bioconductor's marrayClasses package

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October 27, 2003

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## Contents

<b>1</b>	<b>Overview</b>	<b>1</b>
<b>2</b>	<b>Getting started</b>	<b>2</b>
<b>3</b>	<b>Object-oriented programming</b>	<b>3</b>
<b>4</b>	<b>Microarray classes</b>	<b>3</b>
4.1	marrayLayout class . . . . .	3
4.2	marrayInfo class . . . . .	5
4.3	marrayRaw class . . . . .	5
4.4	marrayNorm class . . . . .	6
4.5	marraySpots class . . . . .	7
4.6	marrayTwo class . . . . .	7
4.7	Creating and accessing slots of microarray objects . . . . .	7
4.8	Testing the validity of an object . . . . .	8
<b>5</b>	<b>Basic microarray methods</b>	<b>9</b>
5.1	Printing methods for microarray objects . . . . .	9
5.2	Subsetting methods for microarray objects . . . . .	10
5.3	Methods for accessing slots of microarray objects . . . . .	12
5.4	Methods for assigning slots of microarray objects . . . . .	12
5.5	Methods for coercing microarray objects . . . . .	13
5.6	Functions for computing layout parameters . . . . .	14

## 1 Overview

This document provides a detailed discussion of the `marrayClasses` package, which is part of a suite of four packages for diagnostic plots and normalization of cDNA microarray data. A shorter guide to the package is given in `marrayClassesShort`. Information on the other packages can be found in [Dudoit and Yang \(2002\)](#) and the vignettes for each package. Like most Bioconductor packages, these four packages rely on the object-oriented class/method mechanism, provided by the

R **methods** package, to allow efficient and systematic representation and manipulation of microarray data. **marrayClasses** contains basic class definitions and associated methods for pre- and post-normalization intensity data for batches of arrays. The other three packages are

**marrayInput**. This package provides functionality for reading microarray data into R, such as intensity data from image processing output files (e.g. **.spot** and **.gpr** files for the **Spot** and **GenePix** packages, respectively) and textual information on probes and targets (e.g. from gal files and god lists). **tcltk** widgets are supplied to facilitate and automate data input and the creation of microarray specific R objects for storing these data.

**marrayPlot**. This package provides functions for diagnostic plots of microarray spot statistics, such as boxplots, scatter-plots, and spatial color images. Examination of diagnostic plots of intensity data is important in order to identify printing, hybridization, and scanning artifacts which can lead to biased inference concerning gene expression.

**marrayNorm**. This package implements robust adaptive location and scale normalization procedures, which correct for different types of dye biases (e.g. intensity, spatial, plate biases) and allow the use of control sequences spotted onto the array and possibly spiked into the mRNA samples. Normalization is needed to ensure that observed differences in intensities are indeed due to differential expression and not experimental artifacts; fluorescence intensities should therefore be normalized before any analysis which involves comparisons among genes within or between arrays.

## 2 Getting started

**Installing the package.** To install the **marrayClasses** package for Windows operating systems, first download the file **marrayClasses-snapshot.zip** from the Bioconductor website <http://www.bioconductor.org/packages/html/marrayClasses.html>. Next, after starting R, from the menu select **Packages**, then **Install package from local zip file....** Find and highlight the location of the zip file and click on **open**.

**Loading the package.** To load the **marrayClasses** package in your R session, type **library(marrayClasses)**.

**Help files.** As with any R package, detailed information on functions, classes and methods can be obtained in the help files. For instance, to view the help file for the class **marrayRaw** in a browser, use **help.start()** followed by **? marrayRaw** or alternately the dyadic class **? marrayRaw**.

**Case study.** We demonstrate the functionality of this collection of R packages using gene expression data from the Swirl zebrafish experiment. To load the Swirl dataset, use **data(swirl)**, and to view a description of the experiments and data, type **? swirl**.

Welcome to Bioconductor

Vignettes contain introductory material. To view,  
simply type: **openVignette()**  
For details on reading vignettes, see  
the **openVignette** help page.

**Sweave.** This document was generated using the **Sweave** function from the **R tools** package. The source file is in the `/inst/doc` directory of the package **marrayClasses**.

### 3 Object-oriented programming

Microarray experiments generate large and complex multivariate datasets, which contain textual information on probe sequences (e.g. gene names, annotation, layout parameters) and mRNA target samples (e.g. description of samples, protocols, hybridization and scanning conditions), in addition to the primary fluorescence intensity data. Efficient and coordinated access to these various types of data is an important aspect of computing with microarray data. To facilitate the management of microarray data at different stages of the analysis process, a collection of microarray specific data structures or *classes* were defined (see also the Bioconductor package **Biobase** for microarray classes and methods for normalized data). The packages rely on the class/method mechanism provided by John Chambers' R **methods** package, which allows object-oriented programming in R. Broadly speaking, *classes* reflect how we think of certain objects and what information these objects should contain. Classes are defined in terms of *slots* which contain the relevant data for the application at hand. *Methods* define how a particular function should behave depending on the class of its arguments and allow computations to be adapted to particular classes, that is, data types. For example, a microarray object should contain intensity data as well as information on the probe sequences spotted on the array and the target samples hybridized to it. Useful methods for microarray classes include specializations of printing, subsetting, and plotting functions for the types of data represented by these classes. The use of classes and methods greatly reduces the complexity of handling microarray data, by automatically coordinating various sources of information associated with microarray experiments.

### 4 Microarray classes

The *raw data* from a microarray experiment are the image files produced by the scanner; these are typically pairs of 16-bit tagged image file format (TIFF) files, one for each fluorescent dye (images usually range in size from a few megabytes (MB) to 10 or 20 MB for high resolution scans). Image analysis is required to extract foreground and background fluorescence intensity measurements for each spotted DNA sequence.

Here, we begin our analysis of microarray data with the output files of image processing packages such as **GenePix** or **Spot**. In what follows, red and green background intensities are denoted by  $R_b$  and  $G_b$ , respectively, and red and green foreground intensities by  $R_f$  and  $G_f$ , respectively. Background-corrected red and green fluorescence intensities are denoted by  $R$  and  $G$ , and  $M$  denotes the corresponding base-2 log-ratio,  $M = \log_2 R/G$ .

#### 4.1 marrayLayout class

The term *array layout* refers to the layout of DNA probe sequences on the array, as determined by the printing process. In general, probe sequences are spotted on a glass microscope slide using an arrayer which has an  $n_{gr} \times n_{gc}$  print-head, that is, a regular array of  $n_{gr}$  rows and  $n_{gc}$  columns of print-tips or pins. The resulting microarrays are thus partitioned into an  $n_{gr} \times n_{gc}$  *grid matrix*. The terms *grid*, *sector*, and *print-tip-group* are used interchangeably in the microarray literature. Each grid consists of an  $n_{sr} \times n_{sc}$  *spot matrix* that was printed with a single print-tip. DNA probes

are usually printed sequentially from a collection of 384-well plates (or 96-well plates), thus, in some sense, plates are proxies for time of printing. In addition, a number of control probe sequences may be spotted on the array for normalization or other calibration purposes. The term *array batch* is used to refer to a collection of arrays with the same layout. Keeping track of spot layout information is essential for quality assessment of fluorescent intensity data and for normalization purposes.

Important layout parameters are the dimensions of the spot and grid matrices, and, for each probe on the array, its grid matrix and spot matrix coordinates. In addition, it is useful to keep track of gene names, plate origin of the probes, and information on the spotted control sequences (e.g. probe sequences which should have equal abundance in the two target samples, such as housekeeping genes). The class `marrayLayout` was designed to keep track of these various layout parameters and contains the following slots (the classes of the slots are listed below the slot names)

```
> getClassDef("marrayLayout")
```

Slots:

Name:	<code>maNgr</code>	<code>maNgc</code>	<code>maNsr</code>	<code>maNsc</code>	<code>maNspots</code>	<code>maSub</code>
Class:	numeric	numeric	numeric	numeric	numeric	logical

Name:	<code>maPlate</code>	<code>maControls</code>	<code>maNotes</code>
Class:	factor	factor	character

`maNgr`: Object of class "numeric", number of rows for the grid matrix.

`maNgc`: Object of class "numeric", number of columns for the grid matrix.

`maNsr`: Object of class "numeric", number of rows for the spot matrices.

`maNsc`: Object of class "numeric", number of columns for the spot matrices.

`maNspots`: Object of class "numeric", total number of spots on the array, equal to  $maNgr \times maNgc \times maNsr \times maNsc$ .

`maSub`: Object of class "logical", indicating which spots are currently being considered.

`maPlate`: Object of class "factor", recording the plate origin of the spotted probe sequences.

`maControls`: Object of class "factor", recording the control status of the spotted probe sequences.

`maNotes`: Object of class "character", any notes concerning the microarray layout, e.g., printing conditions.

In addition, a number of *methods* were defined to compute other important layout parameters, such as print-tip, grid matrix, and spot matrix coordinates: `maPrintTip`, `maGridRow`, `maGridCol`, `maSpotRow`, and `maSpotCol` (see Section 5). No slots were defined for these quantities for memory management reasons.

## 4.2 marrayInfo class

Information on the target mRNA samples co-hybridized to the arrays is stored in objects of class `marrayInfo`. Such objects may include the names of the arrays, the names of the Cy3 and Cy5 labeled samples, notes on the hybridization and scanning conditions, and other textual information. Descriptions of the spotted probe sequences (e.g. matrix of gene names, annotation, notes on printing conditions) are also stored in object of class `marrayInfo`. The `marrayInfo` class is not specific to the microarray context and has the following definition

```
> getClassDef("marrayInfo")
```

Slots:

```
Name:      maLabels      maInfo      maNotes
Class:     character data.frame character
```

## 4.3 marrayRaw class

Pre-normalization intensity data for a batch of arrays are stored in objects of class `marrayRaw`, which contain slots for the matrices of Cy3 and Cy5 background and foreground intensities (`maGb`, `maRb`, `maGf`, `maRf`), spot quality weights (`maW`), layout parameters of the arrays (`marrayLayout`), description of the probes spotted onto the arrays (`maGnames`) and mRNA target samples hybridized to the arrays (`maTargets`).

```
> getClassDef("marrayRaw")
```

Slots:

```
Name:      maRf      maGf      maRb      maGb      maW
Class:     matrix   matrix   matrix   matrix   matrix
```

```
Name:      maLayout   maGnames   maTargets   maNotes
Class: marrayLayout marrayInfo marrayInfo   character
```

`maRf`: Object of class "matrix", red foreground intensities, rows correspond to spotted probe sequences, columns to arrays in the batch.

`maGf`: Object of class "matrix", green foreground intensities, rows correspond to spotted probe sequences, columns to arrays in the batch.

`maRb`: Object of class "matrix", red background intensities, rows correspond to spotted probe sequences, columns to arrays in the batch.

`maGb`: Object of class "matrix", green background intensities, rows correspond to spotted probe sequences, columns to arrays in the batch.

`maW`: Object of class "matrix", spot quality weights, rows correspond to spotted probe sequences, columns to arrays in the batch.

`maLayout`: Object of class "marrayLayout", layout parameters for cDNA microarrays.

**maNames:** Object of class "marrayInfo", description of spotted probe sequences.

**maTargets:** Object of class "marrayInfo", description of target samples hybridized to the arrays.

**maNotes:** Object of class "character", any notes concerning the microarray experiments, e.g. hybridization or scanning conditions.

#### 4.4 marrayNorm class

Post-normalization intensity data are stored in similar objects of class **marrayNorm**. These objects store the normalized intensity log-ratios **maM**, the location and scale normalization values (**maMloc** and **maMscale**), and the average log-intensities (**maA**). In addition, the **marrayNorm** class has a slot for the function call used to normalize the data, **maNormCall**. For more details on the creation of normalized microarray objects, the reader is referred to the vignette for the **marrayNorm** package.

```
> getClassDef("marrayNorm")
```

Slots:

Name:	maA	maM	maMloc	maMscale	maW
Class:	matrix	matrix	matrix	matrix	matrix

Name:	maLayout	maNames	maTargets	maNotes	maNormCall
Class:	marrayLayout	marrayInfo	marrayInfo	character	call

**maA:** Object of class "matrix", average log-intensities (base 2)  $A$ , rows correspond to spotted probe sequences, columns to arrays in the batch.

**maM:** Object of class "matrix", intensity log-ratios (base 2)  $M$ , rows correspond to spotted probe sequences, columns to arrays in the batch.

**maMloc:** Object of class "matrix", location normalization values, rows correspond to spotted probe sequences, columns to arrays in the batch.

**maMscale:** Object of class "matrix", scale normalization values, rows correspond to spotted probe sequences, columns to arrays in the batch.

**maW:** Object of class "matrix", spot quality weights, rows correspond to spotted probe sequences, columns to arrays in the batch.

**maLayout:** Object of class "marrayLayout", layout parameters for cDNA microarrays.

**maNames:** Object of class "marrayInfo", description of spotted probe sequences.

**maTargets:** Object of class "marrayInfo", description of target samples hybridized to the arrays.

**maNotes:** Object of class "character", any notes concerning the microarray experiments, e.g. hybridization or scanning conditions.

**maNormCall:** Object of class "call", function call for normalizing the batch of arrays.

## 4.5 marraySpots class

This class is used to store information on the spotted probe sequences for a batch of arrays. The class contains slots for the layout of the arrays, `maLayout`, and a description of the probe sequences spotted onto the arrays, `maGnames`.

```
> getClassDef("marraySpots")
```

Slots:

```
Name:      maGnames      maLayout
Class:     marrayInfo marrayLayout
```

## 4.6 marrayTwo class

The `marrayTwo` class can be viewed as a leaner version of the `marrayRaw` and `marrayNorm` classes. It can be used to represent pre- or post-normalization intensity data for a batch of cDNA microarrays. The class contains slots for only two types of spot statistics (`maX` and `maY`), the layout of the arrays (`maLayout`), and a description of the target samples hybridized to the arrays (`maTargets`). The two spot statistics can be, for example, the unnormalized green (Cy3) and red (Cy5) foreground intensities, or the normalized log-ratios  $M$  and average intensities  $A = \log_2 \sqrt{RG}$ .

```
> getClassDef("marrayTwo")
```

Slots:

```
Name:      maX      maY      maLayout      maTargets
Class:     matrix   matrix marrayLayout  marrayInfo
```

Most microarray objects contain an `maNotes` slots which may be used to store any string of characters describing the experiments, for examples, notes on the printing, hybridization, or scanning conditions.

## 4.7 Creating and accessing slots of microarray objects

**Creating new objects.** The function `new` from the `methods` package may be used to create new objects from a given class. For example, to create an object of class `marrayInfo` describing the target samples in the Swirl experiment, one could use the following code

```
> zebra.RG <- as.data.frame(cbind(c("swirl", "WT", "swirl", "WT"),
+   c("WT", "swirl", "WT", "swirl")))
> dimnames(zebra.RG)[[2]] <- c("Cy3", "Cy5")
> zebra.samples <- new("marrayInfo", maLabels = paste("Swirl array ",
+   1:4, sep = ""), maInfo = zebra.RG, maNotes = "Description of targets for Swirl experiment")
> zebra.samples
```

Object of class `marrayInfo`.

```
maLabels  Cy3  Cy5
```

```

1 Swirl array 1 swirl    WT
2 Swirl array 2    WT swirl
3 Swirl array 3 swirl    WT
4 Swirl array 4    WT swirl

```

Number of labels: 4

Dimensions of maInfo matrix: 4 rows by 2 columns

Notes:

Description of targets for Swirl experiment

Slots which are not specified in `new` are initialized to the prototype for the corresponding class. These are usually "empty", e.g., `matrix(0,0,0)`. In most cases, microarray objects can be created automatically using the input functions and their corresponding widgets in the `marrayInput` package. These were used to create the object `swirl` of class `marrayRaw`.

**Accessing slots.** Different components or slots of the microarray objects may be accessed using the operator `@`, or alternately, the function `slot`, which evaluates the slot name. For example, to access the `maLayout` slot in the object `swirl` and the `maNgr` slot in the layout object `L`

```

> L <- slot(swirl, "maLayout")
> L@maNgr

```

```
[1] 4
```

The function `slotNames` can be used to get information on the slots of a formally defined class or an instance of the class. For example, to get information on the slots for the `marrayLayout` class or on the slots for the object `swirl` use

```
> slotNames("marrayLayout")
```

```

[1] "maNgr"      "maNgc"      "maNsr"      "maNsc"      "maNspots"
[6] "maSub"      "maPlate"    "maControls" "maNotes"

```

```
> slotNames(swirl)
```

```

[1] "maRf"      "maGf"      "maRb"      "maGb"      "maW"      "maLayout"
[7] "maGnames"  "maTargets" "maNotes"

```

## 4.8 Testing the validity of an object

The function `validObject` from the R package `methods` may be used to test the validity of an object with respect to its class definition. This function has two arguments: `object`, the object to be tested; and `test`. If `test` is `TRUE`, the function returns a vector of strings describing the problems, if any.

```
> validObject(maLayout(swirl), test = TRUE)
```

```
[1] TRUE
```



## 5 Basic microarray methods

The following basic methods were defined to facilitate manipulation of microarray data objects. To see all methods available for a particular class, e.g., `marrayLayout`, or just the print methods

```
> showMethods(classes = "marrayLayout")
> showMethods("print", classes = "marrayLayout")
```

### 5.1 Printing methods for microarray objects

Since there is usually no need to print out fluorescence intensities for thousands of genes, the `print` method was overloaded for microarray classes by simple report generators. For an overview of the available microarray printing methods, type `methods ? print`, or to see all print methods for the session

```
> showMethods("print")
```

```
Function "print":
x = "ANY"
x = "marrayLayout"
x = "marrayInfo"
x = "marrayRaw"
x = "marrayNorm"
x = "marrayTwo"
x = "marraySpots"
x = "data.frame"
      (inherited from x = "ANY")
```

For example, summary statistics for an object of class `marrayRaw`, such as `swirl`, can be obtained by `print(swirl)` or simply `swirl`.

```
> swirl
```

```
Pre-normalization intensity data:          Object of class marrayRaw.
```

```
Number of arrays:          4 arrays.
```

```
A) Layout of spots on the array:
```

```
Array layout:          Object of class marrayLayout.
```

```
Total number of spots:          8448
Dimensions of grid matrix:          4 rows by 4 cols
Dimensions of spot matrices:          22 rows by 24 cols
```

```
Currently working with a subset of 8448 spots.
```

```
Control spots:
```

```
There are    2 types of controls :
```

```
Control      N
      768    7680
```

Notes on layout:  
No Input File

B) Samples hybridized to the array:  
Object of class `marrayInfo`.

	maLabels	# of slide	Names	experiment Cy3	experiment Cy5	date
1	81	81	swirl.1.spot	swirl	wild type	2001/9/20
2	82	82	swirl.2.spot	wild type	swirl	2001/9/20
3	93	93	swirl.3.spot	swirl	wild type	2001/11/8
4	94	94	swirl.4.spot	wild type	swirl	2001/11/8
	comments					
1	NA					
2	NA					
3	NA					
4	NA					

Number of labels: 4  
Dimensions of `maInfo` matrix: 4 rows by 6 columns

Notes:  
C:/GNU/R/rw1041/library/marrayInput/data/SwirlSample.txt

C) Summary statistics for log-ratio distribution:

	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
swirl.1.spot	-2.73	-0.79	-0.58	-0.48	-0.29	4.42
swirl.2.spot	-2.72	-0.15	0.03	0.03	0.21	2.35
swirl.3.spot	-2.29	-0.75	-0.46	-0.42	-0.12	2.65
swirl.4.spot	-3.21	-0.46	-0.26	-0.27	-0.06	2.90

D) Notes on intensity data:

## 5.2 Subsetting methods for microarray objects

In many instances, one is interested in accessing only a subset of arrays in a batch and/or spots in an array. Subsetting methods `"["` were defined for this purpose. For an overview of the available microarray subsetting methods, type `methods ? "["` or to see all subsetting methods for the session `showMethods("[")`. When using the `"["` operator, the first index refers to spots and the second to arrays in a batch. Thus, to access the first 100 probe sequences in the second and third arrays in the batch `swirl` use

```
> swirl[1:100, 2:3]
```

Pre-normalization intensity data:                    Object of class marrayRaw.

Number of arrays:                    2 arrays.

A) Layout of spots on the array:

Array layout:                    Object of class marrayLayout.

Total number of spots:                    8448

Dimensions of grid matrix:                    4 rows by 4 cols

Dimensions of spot matrices:                    22 rows by 24 cols

Currently working with a subset of 100 spots.

Control spots:

There are    2 types of controls :

Control	N
48	52

Notes on layout:

No Input File

B) Samples hybridized to the array:

Object of class marrayInfo.

maLabels	# of slide	Names	experiment	Cy3	experiment	Cy5	date
2	82	82 swirl.2.spot	wild type		swirl		2001/9/20
3	93	93 swirl.3.spot	swirl		wild type		2001/11/8
comments							
2	NA						
3	NA						

Number of labels: 2

Dimensions of maInfo matrix: 2 rows by 6 columns

Notes:

C:/GNU/R/rw1041/library/marrayInput/data/SwirlSample.txt

C) Summary statistics for log-ratio distribution:

	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
swirl.2.spot	-1.08	-0.26	-0.12	-0.12	0.0	1.72
swirl.3.spot	-1.78	-0.84	-0.44	-0.40	0.1	1.28

D) Notes on intensity data:

### 5.3 Methods for accessing slots of microarray objects

A number of simple methods were defined to access slots of the microarray classes. Using such methods is more general than using the `slot` function or `@` operator. In particular, if the class definitions are changed, any function which uses the `@` operator will need to be modified. When using a method to access the data in the slot, only that particular method needs to be modified. Thus, to access the layout information for the array batch `swirl` one may also use `maLayout(swirl)`.

In addition, various methods were defined to compute basic statistics from microarray object slots. For instance, for memory management reasons, objects of class `marrayLayout` do not store the spot coordinates of each probe. Rather, these can be obtained from the dimensions of the grid and spot matrices by applying methods: `maGridRow`, `maGridCol`, `maSpotRow`, and `maSpotCol` to objects of class `marrayLayout`. Print-tip-group coordinates are given by `maPrintTip`. Similar methods were also defined to operate directly on objects of class `marrayRaw`, `marrayNorm`, `marraySpots`, and `marrayTwo`. The commands below may be used to display the number of spots on the array, the dimensions of the grid matrix, and the print-tip-group coordinates.

```
> swirl.layout <- maLayout(swirl)
> maNspots(swirl)
```

```
[1] 8448
```

```
> maNspots(swirl.layout)
```

```
[1] 8448
```

```
> maNgr(swirl)
```

```
[1] 4
```

```
> maNgc(swirl.layout)
```

```
[1] 4
```

```
> maPrintTip(swirl[1:10, 3])
```

```
[1] 1 1 1 1 1 1 1 1 1 1
```

### 5.4 Methods for assigning slots of microarray objects

A number of methods were defined to replace slots of microarray objects, without explicitly using the `@` operator or `slot` function. These make use of the `setReplaceMethod` function from the `R.methods` package. As with the accessor methods just described, the assignment methods are named after the slots. For example, to replace the `maNotes` slot of `swirl.layout`

```
> maNotes(swirl.layout)
```

```
[1] "No Input File"
```

```
> maNotes(swirl.layout) <- "New value"
```

```
> maNotes(swirl.layout)
```

```
[1] "New value"
```

To initialize slots of an empty `marrayLayout` object

```
> L <- new("marrayLayout")
> L
```

Array layout:                    Object of class `marrayLayout`.

Total number of spots:

Dimensions of grid matrix:                    rows by cols

Dimensions of spot matrices:                    rows by cols

Currently working with a subset of spots.

Control spots:

Notes on layout:

```
> maNgr(L) <- 4
```

Similar methods were defined to operate on objects of class `marrayInfo`, `marrayRaw`, `marrayNorm`, `marraySpots`, and `marrayTwo`.

## 5.5 Methods for coercing microarray objects

To facilitate navigation between different classes of microarray objects, we have defined methods for coercing microarray objects from one class into another. A list of such methods can be obtained by `methods ? coerce`. For example, to coerce an object of class `marrayRaw` into an object of class `marrayNorm`

```
> swirl.norm <- as(swirl, "marrayNorm")
```

It is also possible to convert objects of class `marrayRaw` or `marrayNorm` into objects of class `exprSet` (see definition in the `Biobase` package)

```
> as(swirl, "exprSet")
```

Expression Set (`exprSet`) with

8448 genes

4 samples

          phenoData object with 6 variables and 4 cases

varLabels

  : # of slide

  : Names

  : experiment Cy3

  : experiment Cy5

  : date

  : comments

## 5.6 Functions for computing layout parameters

In some cases, plate information is not stored in `marrayLayout` objects when the data are first read into R. We have defined a function `maCompPlate` which computes plate indices from the dimensions of the grid matrix and number of wells in a plate. For example, the Swirl arrays were printed from 384-well plates, but the plate IDs were not stored in the `fish.gal` file. To generate plate IDs (arbitrarily labeled by integers starting with 1) and store these in the `maPlate` slot of the `marrayLayout` object use

```
> maPlate(swirl) <- maCompPlate(swirl, n = 384)
```

Similar functions were defined to generate and manipulate spot coordinates: `maCompCoord`, `maCompInd`, `maCoord2Ind`, `maInd2Coord`. The function `maGeneTable` produces a table of spot coordinates and gene names for objects of class `marrayRaw`, `marrayNorm`, and `marraySpots`.

## References

S. Dudoit and Y. H. Yang. Bioconductor R packages for exploratory analysis and normalization of cDNA microarray data. In G. Parmigiani, E. S. Garrett, R. A. Irizarry, and S. L. Zeger, editors, *The Analysis of Gene Expression Data: Methods and Software*. Springer, New York, 2002. [1](#)