Introduction to the Bioconductor marray package : Classes structure component

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Contents

1 Overview

This document provides a tutorial on the class structures used in the `marray` package. The `marray` packages contains basic class definitions and associated methods for pre– and post–normalization intensity data for batches of arrays. To load the `marray` package in your R session, type `library(marray)`. 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

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browser, use `help.start()` followed by `? marrayRaw` or alternately the dyadic `class ? marrayRaw`. Furthermore, se 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`.
Getting started:

```
Loading required package: limma
```

2   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.

3   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, $M = \log_2 R/G$.

3.1 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 $ngr \times ngc$ print–head, that is, a regular array of ngr rows and ngc columns of print–tips or pins. The resulting microarrays are thus partitioned into an $ngr \times ngc$ *grid matrix*. The terms *grid*, *sector*, and *print–tip–group* are used interchangeably in the microarray literature. Each grid consists of an $nsr \times nsc$ *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:	maNgr	maNgc	maNsr	maNsc	maNspots	maSub
Class:	numeric	numeric	numeric	numeric	numeric	logical

Name:	maPlate	maControls	maNotes
Class:	factor	factor	character

Extends: "ShowLargeObject"

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 4). No slots were defined for these quantities for memory management reasons.

3.2 `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

Extends: "ShowLargeObject"
```

3.3 `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

Extends: "ShowLargeObject"
```

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.

maGnames: 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.

3.4 `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	maGnames	maTargets	maNotes	maNormCall
Class:	marrayLayout	marrayInfo	marrayInfo	character	call

Extends: "ShowLargeObject"

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.

maGnames: 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.

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.

3.5 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

An object of class "marrayInfo"
@maLabels
[1] "Swirl array 1" "Swirl array 2" "Swirl array 3" "Swirl array 4"

@maInfo
    Cy3   Cy5
1 swirl    WT
2    WT swirl
3 swirl    WT
4    WT swirl

@maNotes
[1] "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"
```

3.6 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
```

4 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("show", classes = "marrayLayout")
```

4.1 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 ?   summary`, or to see all summary methods for the session

```
> showMethods("summary")

Function "summary":
 object = "ANY"
 object = "marrayLayout"
 object = "marrayInfo"
 object = "marrayRaw"
 object = "marrayNorm"
```

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

```
> summary(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 8448spots.

Control spots:
There are   2 types of controls :

Control   probes
    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:
```

4.2   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]

An object of class "marrayRaw"
Slot "maRf":
      swirl.2.spot swirl.3.spot
  [1,]   16138.7200    2895.1600
  [2,]   17247.6700    2976.6230
  [3,]   17317.1500    2735.6190
  [4,]    6794.3810     318.9524
  [5,]    6043.5420     780.6667
  [6,]   21093.5100   12210.6900
```

[7,]	11325.5700	10695.5000
[8,]	16539.6100	12782.4200
[9,]	13287.2000	8841.6600
[10,]	5374.7080	894.3333
[11,]	5003.7620	515.1739
[12,]	5496.0950	588.3810
[13,]	16850.3600	10578.2400
[14,]	14441.1900	6767.5580
[15,]	9396.6130	2346.6790
[16,]	5535.5710	1051.0000
[17,]	984.6667	133.9821
[18,]	363.8400	142.3659
[19,]	6184.0000	1456.1900
[20,]	5816.1360	1322.5450
[21,]	6683.3810	1237.2270
[22,]	6025.9520	336.3810
[23,]	249.6667	119.7500
[24,]	221.5758	117.5143
[25,]	839.5600	135.5769
[26,]	10444.2000	8452.8440
[27,]	7068.7650	3032.6880
[28,]	2220.9320	851.9157
[29,]	13875.6800	5830.3540
[30,]	781.5238	167.8293
[31,]	802.5301	277.3370
[32,]	1436.1370	646.7500
[33,]	3910.6900	4933.1110
[34,]	12905.6500	6197.6960
[35,]	5864.1720	5396.9480
[36,]	22630.7500	14455.2200
[37,]	817.7652	545.3434
[38,]	5452.3540	5421.1600
[39,]	1054.4760	182.4474
[40,]	10903.3300	11882.6900
[41,]	15596.1200	15082.5400
[42,]	16356.6100	11997.7900
[43,]	684.7783	418.8528
[44,]	1563.1400	1232.0100
[45,]	9222.3540	11276.8200
[46,]	9708.6670	8655.7960
[47,]	588.0952	343.4286
[48,]	19457.6400	11943.1000
[49,]	9658.0500	1708.6920
[50,]	1496.3810	1392.0000
[51,]	8572.7140	1611.8800

```
[52,]    10312.3200     1658.0970
[53,]     4651.2170     1007.5000
[54,]      327.1786      160.6250
[55,]    12139.0000     4031.8650
[56,]     3103.6960      668.0455
[57,]     5968.1250     1404.7360
[58,]    17958.7700    12866.6600
[59,]     1894.0950      249.6667
[60,]     5621.5910     1369.5000
[61,]     7509.2610     2317.0250
[62,]     1597.3810     7394.2790
[63,]    17557.2000     2067.3810
[64,]     1927.5910      711.6957
[65,]     6663.5000     1242.7780
[66,]    13084.2000     7794.6740
[67,]     3531.2170      172.8542
[68,]     7771.0600     4459.9540
[69,]      871.5714      330.1905
[70,]     1184.6190      634.6190
[71,]    13852.2400    10288.2200
[72,]     7127.7430     2717.3980
[73,]     4782.0830      979.8864
[74,]     1082.8890      170.0000
[75,]     1957.4090      388.5714
[76,]     4175.7730      899.8077
[77,]     2469.0950      209.3611
[78,]    21232.7100    11359.7000
[79,]     6218.3410     1377.4940
[80,]     6164.2580     1580.5610
[81,]    13873.3000     6497.3830
[82,]    10492.1400     4554.0890
[83,]    10158.3100     1694.9410
[84,]     1733.3330      305.4348
[85,]     3961.8110     1174.8370
[86,]      794.0000      341.1250
[87,]     3291.6820      381.6667
[88,]    16694.0000     7443.3810
[89,]     9587.0870     3755.0370
[90,]     6762.8400     2455.1670
[91,]    11006.6700     3734.7620
[92,]     3560.1600     1094.2330
[93,]     8434.6670     3489.4000
[94,]    13451.9500     4989.5860
[95,]     6410.3210     2228.8630
[96,]    20840.1600     8639.1330
```

```
 [97,]     4644.7600        674.5238
 [98,]     1462.4760        160.5185
 [99,]      498.5000        244.3333
[100,]      615.4400        255.0476
Slot "maGf":
        swirl.2.spot swirl.3.spot
  [1,]    19278.7700     2727.5600
  [2,]    21438.9600     2787.0330
  [3,]    20386.4700     2419.8810
  [4,]     6677.6190      383.2381
  [5,]     6576.2920      901.0000
  [6,]    23769.1000    23377.9700
  [7,]    14280.5700     8839.4550
  [8,]    21246.3100    10529.9300
  [9,]    16792.9700     7426.0710
 [10,]     5023.9580     1095.9050
 [11,]     5136.9520      609.8696
 [12,]     5857.5240      540.0952
 [13,]    19186.3000    18701.8900
 [14,]    16336.1600    12034.6600
 [15,]    10861.8900     4735.3330
 [16,]     6255.6190     1050.7730
 [17,]      398.6923      125.8750
 [18,]      401.2800      113.2195
 [19,]     6190.4760     1634.5710
 [20,]     5821.8180     1401.3180
 [21,]     6519.1900     1353.0000
 [22,]     5814.8100      391.0476
 [23,]      323.1429      115.5278
 [24,]      231.5455       99.4000
 [25,]      801.9200      227.8077
 [26,]    20153.0700     9256.0560
 [27,]     7237.8040     3347.7920
 [28,]     2582.3070     1323.5540
 [29,]    18180.0600     8318.6670
 [30,]      905.3333      236.0976
 [31,]      916.1687      307.7283
 [32,]     1983.5880     1097.8570
 [33,]     7469.1380     2808.1780
 [34,]    13037.0000    11780.8600
 [35,]     7443.3230     6927.5000
 [36,]    30251.7000    14544.6900
 [37,]      996.9217      446.0808
 [38,]     5651.6880     5400.2230
 [39,]     1090.9520      191.6579
```

```
[40,]    13169.3000     9836.5160
[41,]    18169.2300    12243.4900
[42,]    17881.7600     9598.6040
[43,]      920.8227      469.2147
[44,]     1670.0000     1405.8420
[45,]    10613.0500     6251.4520
[46,]    11913.5000     7279.2240
[47,]      675.8571      292.6667
[48,]    21280.3300     9411.6890
[49,]     9289.7000     3339.1350
[50,]     1405.5710      621.3636
[51,]     9315.7710     4400.7600
[52,]    10768.9100     5569.3870
[53,]     5701.3910     1371.5830
[54,]      581.2500      154.8333
[55,]    15414.4300     9679.0140
[56,]     3838.5220      744.4545
[57,]     6317.6500     2151.6230
[58,]    17548.6200    18144.9300
[59,]     1045.9050      539.9048
[60,]     5512.4550     2184.3550
[61,]     8839.6670     6692.5700
[62,]     1817.3330    10838.2400
[63,]    15584.5500     3028.1900
[64,]     2056.3180      895.7391
[65,]     6543.0420     1743.4810
[66,]    15058.7300     9255.9070
[67,]     3363.5220      125.8958
[68,]     8058.6540     6607.1380
[69,]      845.3810      709.9524
[70,]     1120.7620      940.6190
[71,]    16116.2200    18166.0600
[72,]     7704.8380     5161.7230
[73,]     6126.3500     2295.3640
[74,]      986.4444      210.1905
[75,]     1976.3640      584.8571
[76,]     4541.2270     1726.4230
[77,]     2101.2860      187.4444
[78,]    30593.6700    18597.4400
[79,]     7640.1360     2818.8440
[80,]     6726.2260     2631.8780
[81,]    17953.3000    12975.0800
[82,]    14121.2500    12474.1300
[83,]    13422.4400     5581.2350
[84,]     1665.5240      467.7391
```

```
[85,]     4089.9250     2505.0820
[86,]      923.2857      296.9167
[87,]     3563.1360      559.6296
[88,]    13719.5500    10272.9800
[89,]    10427.7400    10020.6500
[90,]     6793.5400     4856.3520
[91,]    10935.3800     7954.9180
[92,]     2774.6400     1014.3000
[93,]     7140.6540     6329.7470
[94,]    13120.6900     8697.0570
[95,]     7107.1070     2975.8430
[96,]    23280.5600    18000.2800
[97,]     4827.4800     1323.9520
[98,]     1606.7140      143.1111
[99,]      610.8636      345.8571
[100,]     680.3600      336.5714
Slot "maRb":
      swirl.2.spot swirl.3.spot
  [1,]          136           82
  [2,]          133           82
  [3,]          133           76
  [4,]          105           61
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  [6,]          105           61
  [7,]          106           61
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 [19,]          117           52
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 [25,]          136           76
 [26,]          133           76
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[94,]             99          50
[95,]             97          50
[96,]            101          50
[97,]            167          53
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[99,]            140          51
[100,]           137          51
Slot "maGb":
       [,1] [,2]
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  [2,]  183   86
  [3,]  183   86
  [4,]  142   71
  [5,]  142   71
  [6,]  142   71
  [7,]  132   65
  [8,]  132   69
  [9,]  132   69
 [10,]  132   69
 [11,]  142   68
 [12,]  142   60
 [13,]  172   60
 [14,]  172   59
 [15,]  172   53
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[23,]    97    45
[24,]    97    45
[25,]   167    86
[26,]   187    86
[27,]   187    86
[28,]   163    71
[29,]   154    71
[30,]   151    71
[31,]   148    65
[32,]   166    69
[33,]   183    69
[34,]   183    69
[35,]   174    68
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[37,]   172    60
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[44,]   163    57
[45,]    90    57
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[48,]    97    47
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[52,]   164    66
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[55,]   187    65
[56,]   192    59
[57,]   192    64
[58,]   186    64
[59,]   186    64
[60,]   174    56
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 [66,]   189    51
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 [71,]    96    46
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 [93,]   111    53
 [94,]   102    48
 [95,]   101    46
 [96,]   108    47
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 [98,]   206    60
 [99,]   205    58
[100,]   175    58
Slot "maW":
<0 x 0 matrix>
Slot "maLayout":
An object of class "marrayLayout"
Slot "maSub":
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 [38] 2 2 2 2 2 2 2 2 2 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 4 4
 [75] 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 5 5 5 5
Levels: 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22
Slot "maControls":
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 [10] Control Control Control Control Control Control Control Control Control
 [19] Control Control Control Control Control Control Control Control Control
 [28] Control Control Control Control Control Control Control Control Control
 [37] Control Control Control Control Control Control Control Control Control
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  [91] probes   probes   probes   probes   probes   probes   probes   probes   probes
 [100] probes
Levels: Control probes
Slot "maNgr":
[1] 4
Slot "maNgc":
[1] 4
Slot "maNsr":
[1] 22
Slot "maNsc":
[1] 24
Slot "maNspots":
[1] 8448
Slot "maNotes":
[1] "No Input File"
Slot "maGnames":
An object of class "marrayInfo"
Slot "maLabels":
  [1] "geno1"      "geno2"      "geno3"      "3XSSC"      "3XSSC"
  [6] "EST1"       "geno1"      "geno2"      "geno3"      "3XSSC"
 [11] "3XSSC"      "3XSSC"      "EST2"       "EST3"       "EST4"
 [16] "3XSSC"      "Actin"      "Actin"      "3XSSC"      "3XSSC"
 [21] "3XSSC"      "3XSSC"      "Actin"      "Actin"      "ath1"
 [26] "Cad-1"      "DeltaB"     "Dlx4"       "ephrinA4"   "FGF8"
 [31] "flk-1"      "GB3 Raldh2" "GB7 tbxa"   "groucho1"   "Her1"
 [36] "Her7 geno"  "HrT"        "MyoD"       "Ndr3"       "geno1"
 [41] "geno2"      "geno3"      "notch6"     "OR2"        "ORF2"
 [46] "geno1"      "geno2"      "geno3"      "1-A1"       "1-A5"
 [51] "1-A9"       "1-A13"      "1-A17"      "1-A21"      "1-E1"
 [56] "1-E5"       "1-E9"       "1-E13"      "1-E17"      "1-E21"
 [61] "1-I1"       "1-I5"       "1-I9"       "1-I13"      "1-I17"
 [66] "1-I21"      "1-M1"       "1-M5"       "1-M9"       "1-M13"
 [71] "1-M17"      "1-M21"      "2-A1"       "2-A5"       "2-A9"
 [76] "2-A13"      "2-A17"      "2-A21"      "2-E1"       "2-E5"
 [81] "2-E9"       "2-E13"      "2-E17"      "2-E21"      "2-I1"
 [86] "2-I5"       "2-I9"       "2-I13"      "2-I17"      "2-I21"
 [91] "2-M1"       "2-M5"       "2-M9"       "2-M13"      "2-M17"
 [96] "2-M21"      "3-A1"       "3-A5"       "3-A9"       "3-A13"
Slot "maInfo":
       "ID"       "Name"
1    control      geno1
2    control      geno2
3    control      geno3
4    control      3XSSC
5    control      3XSSC
```

```
6    control       EST1
7    control      geno1
8    control      geno2
9    control      geno3
10   control      3XSSC
11   control      3XSSC
12   control      3XSSC
13   control       EST2
14   control       EST3
15   control       EST4
16   control      3XSSC
17   control      Actin
18   control      Actin
19   control      3XSSC
20   control      3XSSC
21   control      3XSSC
22   control      3XSSC
23   control      Actin
24   control      Actin
25   control       ath1
26   control      Cad-1
27   control     DeltaB
28   control       Dlx4
29   control    ephrinA4
30   control       FGF8
31   control      flk-1
32   control GB3 Raldh2
33   control   GB7 tbxa
34   control   groucho1
35   control       Her1
36   control  Her7 geno
37   control        HrT
38   control       MyoD
39   control       Ndr3
40   control      geno1
41   control      geno2
42   control      geno3
43   control     notch6
44   control        OR2
45   control       ORF2
46   control      geno1
47   control      geno2
48   control      geno3
49   fb16a01       1-A1
50   fb16a03       1-A5
```

```
51   fb16a05      1-A9
52   fb16a07      1-A13
53   fb16a09      1-A17
54   fb16a11      1-A21
55   fb17a01      1-E1
56   fb17a03      1-E5
57   fb17a05      1-E9
58   fb17a07      1-E13
59   fb17a09      1-E17
60   fb17a11      1-E21
61   fb18a01      1-I1
62   fb18a03      1-I5
63   fb18a05      1-I9
64   fb18a07      1-I13
65   fb18a09      1-I17
66   fb18a11      1-I21
67   fb19a01      1-M1
68   fb19a03      1-M5
69   fb19a05      1-M9
70   fb19a07      1-M13
71   fb19a09      1-M17
72   fb19a11      1-M21
73   fb20a01      2-A1
74   fb20a03      2-A5
75   fb20a05      2-A9
76   fb20a07      2-A13
77   fb20a09      2-A17
78   fb20a11      2-A21
79   fb21a01      2-E1
80   fb21a03      2-E5
81   fb21a05      2-E9
82   fb21a07      2-E13
83   fb21a09      2-E17
84   fb21a11      2-E21
85   fb22a01      2-I1
86   fb22a03      2-I5
87   fb22a05      2-I9
88   fb22a07      2-I13
89   fb22a09      2-I17
90   fb22a11      2-I21
91   fb23a01      2-M1
92   fb23a03      2-M5
93   fb23a05      2-M9
94   fb23a07      2-M13
95   fb23a09      2-M17
```

```
96   fb23a11      2-M21
97   fb24a01       3-A1
98   fb24a03       3-A5
99   fb24a05       3-A9
100 fb24a07       3-A13
Slot "maNotes":
[1] "C:/GNU/R/rw1041/library/marrayInput/data/fish.gal"
Slot "maTargets":
An object of class "marrayInfo"
Slot "maLabels":
[1] "82" "93"
Slot "maInfo":
  # of slide       Names experiment Cy3 experiment Cy5     date comments
2         82 swirl.2.spot      wild type           swirl 2001/9/20      NA
3         93 swirl.3.spot          swirl       wild type 2001/11/8      NA
Slot "maNotes":
[1] "C:/GNU/R/rw1041/library/marrayInput/data/SwirlSample.txt"
Slot "maNotes":
[1] ""
```

4.3 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` and `marrayNorm`. 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
```

4.4   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

An object of class "marrayLayout"
@maNgr
numeric(0)

@maNgc
numeric(0)

@maNsr
numeric(0)

@maNsc
numeric(0)

@maNspots
numeric(0)

@maSub
```

```
[1] TRUE

@maPlate
factor(0)
Levels:

@maControls
factor(0)
Levels:

@maNotes
character(0)

> maNgr(L) <- 4
```

Similar methods were defined to operate on objects of class `marrayInfo`, `marrayRaw` and `mar-rayNorm`.

4.5 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), see package `convert` package for more details.

```
> library(convert)
> as(normdata, "exprSet")
```

4.6 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` and `marrayNorm`.