

Classes and Methods in R

Computing for Data Analysis

- A system for doing object oriented programming
- R was originally quite interesting because it is both interactive *and* has a system for object orientation.
 - Other languages which support OOP (C++, Java, Lisp, Python, Perl) generally speaking are not interactive languages
- In R much of the code for supporting classes/methods is written by John Chambers himself (the creator of the original S language) and documented in the book *Programming with Data: A Guide to the S Language*
- A natural extension of Chambers' idea of allowing someone to cross the user → programmer spectrum
- Object oriented programming is a bit different in R than it is in most languages — even if you are familiar with the idea, you may want to pay attention to the details

Two styles of classes and methods

S3 classes/methods

- Included with version 3 of the S language.
- Informal, a little kludgy
- Sometimes called *old-style* classes/methods

S4 classes/methods

- more formal and rigorous
- Included with S-PLUS 6 and R 1.4.0 (December 2001)
- Also called *new-style* classes/methods

Two worlds living side by side

- For now (and the foreseeable future), S3 classes/methods and S4 classes/methods are separate systems (but they can be mixed to some degree).
- Each system can be used fairly independently of the other.
- Developers of new projects (you!) are encouraged to use the S4 style classes/methods.
 - Used extensively in the Bioconductor project
- But many developers still use S3 classes/methods because they are “quick and dirty” (and easier).
- In this lecture we will focus primarily on S4 classes/methods
- The code for implementing S4 classes/methods in R is in the **methods** package, which is usually loaded by default (but you can load it with `library(methods)` if for some reason it is not loaded)

Object Oriented Programming in R

- A *class* is a description of an thing. A class can be defined using `setClass()` in the **methods** package.
- An *object* is an instance of a class. Objects can be created using `new()`.
- A *method* is a function that only operates on a certain class of objects.
- A generic function is an R function which dispatches methods. A generic function typically encapsulates a “generic” concept (e.g. `plot`, `mean`, `predict`, ...)
 - The generic function does not actually do any computation.
- A *method* is the implementation of a generic function for an object of a particular class.

Things to look up

- The help files for the 'methods' package are extensive — do read them as they are the primary documentation
- You may want to start with ?Classes and ?Methods
- Check out ?setClass, ?setMethod, and ?setGeneric
- Some of it gets technical, but try your best for now—it will make sense in the future as you keep using it.
- Most of the documentation in the **methods** package is oriented towards developers/programmers as these are the primary people using classes/methods

All objects in R have a class which can be determined by the class function

```
> class(1)
```

```
[1] "numeric"
```

```
> class(TRUE)
```

```
[1] "logical"
```

```
> class(rnorm(100))
```

```
[1] "numeric"
```

```
> class(NA)
```

```
[1] "logical"
```

```
> class("foo")
```

```
[1] "character"
```

Data classes go beyond the atomic classes

```
> x <- rnorm(100)
> y <- x + rnorm(100)
> fit <- lm(y ~ x)  ## linear regression model
> class(fit)

[1] "lm"
```


- S4 and S3 style generic functions look different but conceptually, they are the same (they play the same role).
- When you program you can write new methods for an existing generic OR create your own generics and associated methods.
- Of course, if a data type does not exist in R that matches your needs, you can always define a new class along with generics/methods that go with it

An S3 generic function (in the 'base' package)

The mean function is generic

```
> mean
```

```
function (x, ...)
UseMethod("mean")
<bytecode: 0x7fc25c27afc0>
<environment: namespace:base>
```

So is the print function

```
> print
```

```
function (x, ...)
UseMethod("print")
<bytecode: 0x7fc25bd8ee00>
<environment: namespace:base>
```

```
> methods("mean")  
  
[1] mean.data.frame mean.Date  
[3] mean.default    mean.diffftime  
[5] mean.POSIXct    mean.POSIXlt
```

An S4 generic function (from the 'methods' package)

The S4 equivalent of `print` is `show`

```
> show
```

```
standardGeneric for "show" defined from package "methods"
```

```
function (object)
```

```
  standardGeneric("show")
```

```
<bytecode: 0x7fc25b5ced08>
```

```
<environment: 0x7fc25c51aea0>
```

Methods may be defined for arguments: `object`

Use `showMethods("show")` for currently available ones.

(This generic function excludes non-simple inheritance; see `?setIs`)

The `show` function is usually not called directly (much like `print`) because objects are auto-printed

S4 methods

There are many different methods for the show generic function

```
> showMethods("show")
```

```
Function: show (package methods)
```

```
object="ANY"
```

```
object="classGeneratorFunction"
```

```
object="classRepresentation"
```

```
object="envRefClass"
```

```
object="function"
```

```
    (inherited from: object="ANY")
```

```
object="genericFunction"
```

```
object="genericFunctionWithTrace"
```

```
object="MethodDefinition"
```

```
object="MethodDefinitionWithTrace"
```

```
object="MethodSelectionReport"
```

```
object="MethodWithNext"
```

```
object="MethodWithNextWithTrace"
```

```
object="namedList"
```

The first argument of a generic function is an object of a particular class (there may be other arguments)

- 1 The generic function checks the class of the object.
- 2 A search is done to see if there is an appropriate method for that class.
- 3 If there exists a method for that class, then that method is called on the object and we're done.
- 4 If a method for that class does not exist, a search is done to see if there is a default method for the generic. If a default exists, then the default method is called.
- 5 If a default method doesn't exist, then an error is thrown.

Examining Code for Methods

Examining the code for an S3 or S4 method requires a call to a special function

- You cannot just print the code for a method like other functions because the code for the method is usually hidden.
- If you want to see the code for an S3 method, you can use the function `getS3method`.
- The call is `getS3method(<generic>, <class>)`
- For S4 methods you can use the function `getMethod`
- The call is `getMethod(<generic>, <signature>)` (more details later)

S3 Class/Method: Example 1

What's happening here?

```
> set.seed(2)
> x <- rnorm(100)
> mean(x)
```

```
[1] -0.03069816
```

- 1 The class of `x` is “numeric”
- 2 But there is no `mean` method for “numeric” objects!
- 3 So we call the default function for `mean`.

S3 Class/Method: Example 1

```
> head(getS3method("mean", "default"))

1 function (x, trim = 0, na.rm = FALSE, ...)
2 {
3     if (!is.numeric(x) && !is.complex(x) && !is.logical(x)) {
4         warning("argument is not numeric or logical: returning NA")
5         return(NA_real_)
6     }
7
8     if (na.rm) {
9         x = x[is.finite(x)]
10    }
11
12    if (trim > 0) {
13        lo <- floor(n * trim) + 1
14        hi <- n + 1 - lo
15        x <- sort.int(x, partial = unique(c(lo, hi)))[lo:hi]
16    }
17
18    .Internal(mean(x))
19 }
20
21
22
23
24
```

S3 Class/Method: Example 2

What happens here?

```
> set.seed(3)
> df <- data.frame(x = rnorm(100), y = 1:100)
> sapply(df, mean)
```

```
           x           y
0.01103557 50.50000000
```

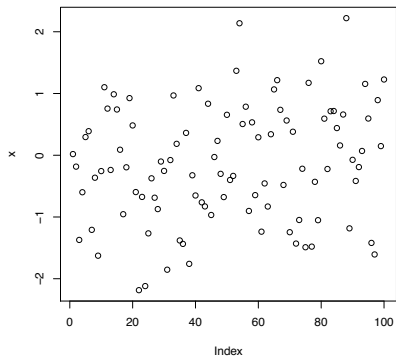
- 1 The class of `df` is “`data.frame`”; in a data frame each column can be an object of a different class
- 2 We `sapply` over the columns and call the `mean` function
- 3 In each column, `mean` checks the class of the object and dispatches the appropriate method.
- 4 Here we have a `numeric` column and an `integer` column; in both cases `mean` calls the default method

NOTE: Some methods are visible to the user (i.e. `mean.default`), but you should **never** call methods directly. Rather, use the generic function and let the method be dispatched automatically.

S3 Class/Method: Example 3

The plot function is generic and its behavior depends on the object being plotted.

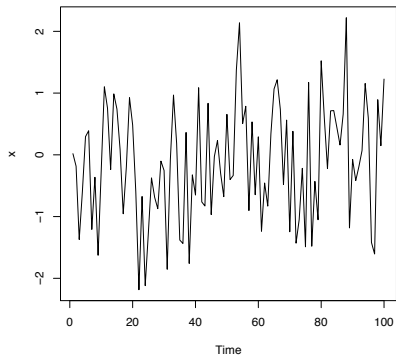
```
> set.seed(10)
> x <- rnorm(100)
> plot(x)
```



S3 Class/Method: Example 3

For time series objects, plot connects the dots

```
> set.seed(10)
> x <- rnorm(100)
> x <- as.ts(x)  ## Convert to a time series object
> plot(x)
```



Write your own methods!

If you write new methods for new classes, you'll probably end up writing methods for the following generics:

- `print/show`
- `summary`
- `plot`

There are two ways that you can extend the R system via classes/methods

- Write a method for a new class but for an existing generic function (i.e. like `print`)
- Write new generic functions and new methods for those generics

Why would you want to create a new class?

- To represent new types of data (e.g. gene expression, space-time, hierarchical, sparse matrices)
- New concepts/ideas that haven't been thought of yet (e.g. a fitted point process model, mixed-effects model, a sparse matrix)
- To abstract/hide implementation details from the user

I say things are “new” meaning that R does not know about them (not that they are new to the statistical community).

S4 Class/Method: Creating a New Class

A new class can be defined using the `setClass` function

- At a minimum you need to specify the name of the class
- You can also specify data elements that are called *slots*
- You can then define methods for the class with the `setMethod` function
- Information about a class definition can be obtained with the `showClass` function

S4 Class/Method: Polygon Class

Creating new classes/methods is usually not something done at the console; you likely want to save the code in a separate file

```
setClass("polygon",  
        representation(x = "numeric",  
                       y = "numeric"))
```

The slots for this class are x and y. The slots for an S4 object can be accessed with the @ operator.

S4 Class/Method: Polygon Class

A plot method can be created with the `setMethod` function.

- For `setMethod` you need to specify a generic function (`plot`), and a *signature*.
- A signature is a character vector indicating the classes of objects that are accepted by the method. In this case, the `plot` method will take one type of object—a polygon object.

```
setMethod("plot", "polygon",  
  function(x, y, ...) {  
    plot(x@x, x@y, type = "n", ...)  
    xp <- c(x@x, x@x[1])  
    yp <- c(x@y, x@y[1])  
    lines(xp, yp)  
  })
```

Notice that the slots of the polygon (the x- and y-coordinates) are accessed with the `@` operator.

S4 Class/Method: Polygon Class

Create a new class

```
> setClass("polygon",  
+         representation(x = "numeric",  
+                        y = "numeric"))
```

Create a plot method for this class

```
> setMethod("plot", "polygon",  
+          function(x, y, ...) {  
+              plot(x@x, x@y, type = "n", ...)  
+              xp <- c(x@x, x@x[1])  
+              yp <- c(x@y, x@y[1])  
+              lines(xp, yp)  
+          })
```

```
[1] "plot"
```

If things go well, you will not get any messages or errors and nothing useful will be returned by either `setClass` or `setMethod`.

S4 Class/Method: Polygon Class

After calling `setMethod` the new `plot` method will be added to the list of methods for `plot`.

```
> showMethods("plot")
```

```
Function: plot (package graphics)
```

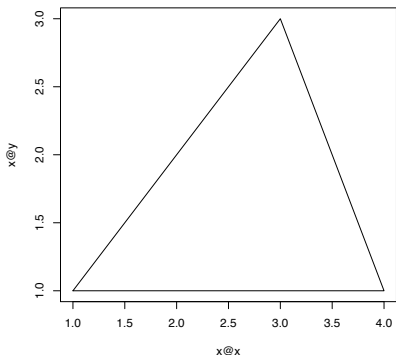
```
x="ANY"
```

```
x="polygon"
```

Notice that the signature for class `polygon` is listed. The method for `ANY` is the default method and it is what is called when now other signature matches

S4 Class/Method: Polygon class

```
> p <- new("polygon", x = c(1, 2, 3, 4), y = c(1, 2, 3, 1))  
> plot(p)
```



Where to Look, Places to Start

- The best way to learn this stuff is to look at examples (and try the exercises for the course)
- There are now quite a few examples on CRAN which use S4 classes/methods.
- Bioconductor (<http://www.bioconductor.org>) — a rich resource, even if you know nothing about bioinformatics
- Some packages on CRAN (as far as I know) — SparseM, gpclib, flexmix, its, lme4, orientlib, pixmap
- The stats4 package (comes with R) has a bunch of classes/methods for doing maximum likelihood analysis.