Classes and Methods in R

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Classes and Methods

- 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 $\longrightarrow$ 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 kludgey
- 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 forseeable 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

Classes

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"
```

Classes (cont'd)

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"
```

Generics/Methods in R

- 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>
```

S3 methods

```
> methods("mean")
[1] mean.data.frame mean.Date
[3] mean.default    mean.difftime
[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

```
> 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"
...
```

Generic/method mechanism

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

- 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"))
function (x, trim = 0, na.rm = FALSE, ...)
{
    if (!is.numeric(x) && !is.complex(x) && !is.logical(x)) {
        warning("argument is not numeric or logical: returning NA")
        return(NA_real_)
    }

> tail(getS3method("mean", "default"))
         lo <- floor(n * trim) + 1
         hi <- n + 1 - lo
         x <- sort.int(x, partial = unique(c(lo, hi)))[lo:hi]
    }
    .Internal(mean(x))
}
```

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

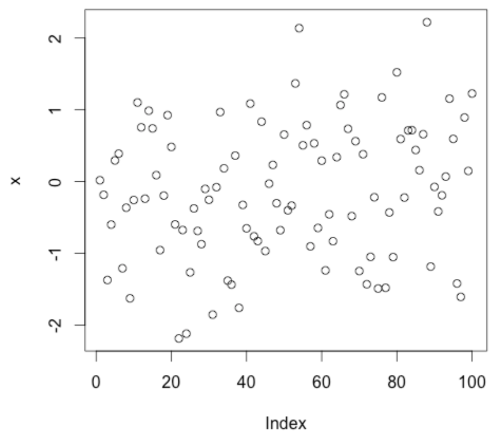
Calling Methods

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.

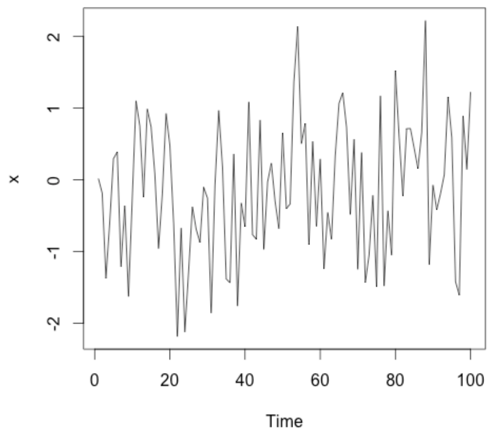
```
> set.seed(10)
> x <- rnorm(100)
> plot(x)
```



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

S4 Classes

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-effcts 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"))
```

S4 Class/Method: Polygon Class

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

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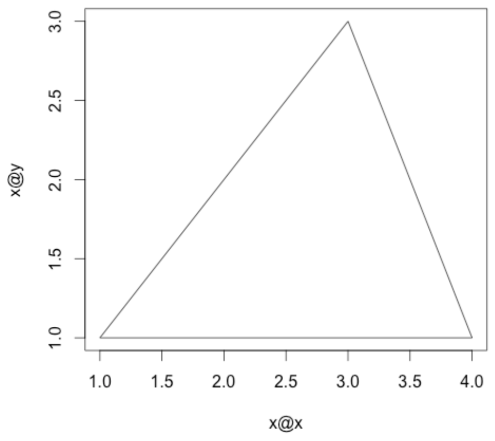
S4 Class/Method: Polygon class

```
> 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.