

# ETC4500/ETC5450

## Advanced R programming

Week 8: Object-oriented Programming  
(S3)



# Outline

1 Object oriented programming

2 S3

3 S3 vctrs

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5 R6

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# Object oriented programming

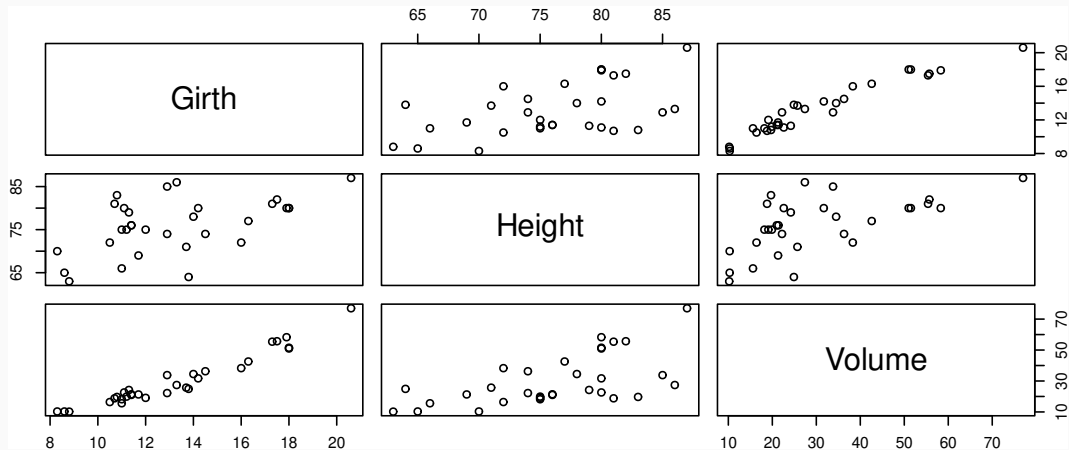
- **Encapsulation:** objects have secret internals that you don't need to understand
- **Polymorphism:** the same function can do different things to different data as appropriate
- **Inheritance:** you can take an existing kind of object and make a new, more specialised one

Inheritance turns out to be useful mostly for data infrastructure, but encapsulation and polymorphism are generally valuable

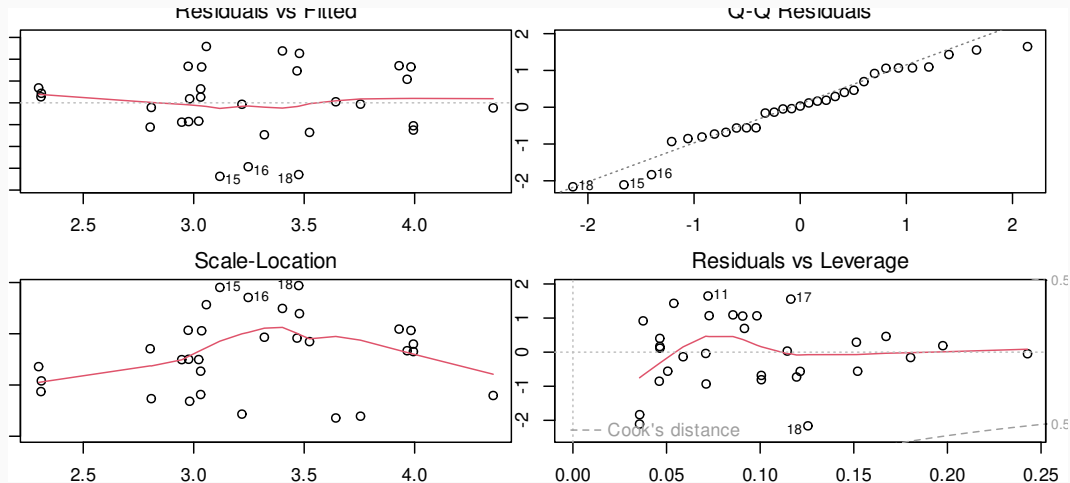
# Generic functions and methods

A simple example: `plot`

```
plot(trees)
```

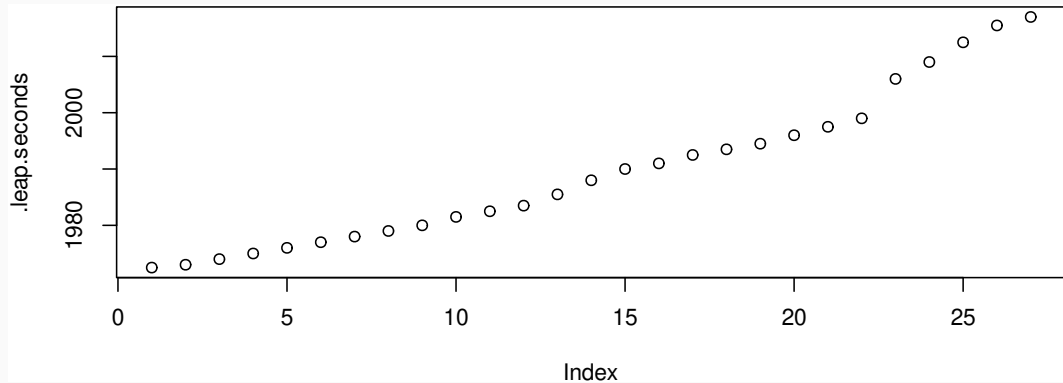


```
m<-lm(log(Volume)~log(Girth)+log(Height),  
      data=trees)  
par(mfrow=c(2,2),mar=c(3,1,1,1))  
plot(m)
```





```
plot(.leap.seconds)
```



```
plot(nhtemp)
```



## How?

- Giant `switch` statement...
- ...that gets updated every time you load a package...
- ???

Generic functions and methods!

# Object systems

R has **a lot** of object systems

- S3
- S3 vctrs
- S4
- R6
- R.oo, proto, R7

## Main topic for today

- easy to start writing
- no safeguards
- especially good for single-person, small to medium projects
- can be used for large projects with a lot of attention to documentation and communication
- limited use of inheritance
- basis of tidyverse and most of CRAN

## S3 vctrs

A tidyverse package for making different sorts of vectors

- handles a lot of formatting and subsetting details
- allows for binary operators
- useful if you want your vectors in a tibble
- enforces some safeguards

- more work to start writing
- objects know their structure
- enforces object structure
- better for large-scale collaborative programming
- better at inheritance
- basis of Bioconductor

- Supports modifiable (mutable) objects
  - ▶ database connections, files, etc
  - ▶ large data objects we don't want to copy
  - ▶ interfacing to eg tensorflow
  - ▶ shared state between copies of an object
- not widely used otherwise
- more similar to other languages



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## Back to `plot`

- `plot()` doesn't *do* anything
- All the work is done by *methods* for different types of object
- Methods are just ordinary functions
- When you call `plot`, R calls the appropriate `plot` method

## Generic functions

- Generic functions don't *do* anything
- All the work is done by *methods* for different types of object
- Methods are just ordinary functions
  - ▶ with declarations in a package NAMESPACE
  - ▶ or R can guess based on function name

When you call the generic function R calls the appropriate method

## Try these

```
print  
methods("print")  
stats:::print.acf  
tools:::print.CRAN_package_reverse_dependencies_and_views  
plot  
methods("plot")  
plot.ts  
stats::plot.lm
```

Also, try `methods("plot")` after loading another package

## What do we notice?

- `print` functions are all different
- names start with `print.`, then the sort of thing they print
- mostly aren't visible just by name
- 
-

## Generic functions

- *methods* that actually do the work 'belong to' *generic functions*
- This is unusual: most popular OOP systems (Java, C++, Python) have methods belonging to data objects
- Important in R because functions are first-class objects (Week 5)
- Useful for functional programming with objects

# Classes

- S3 classes are the things that specify which method to use
- Use `class` to attach a class to an object like a Post-It note
- That's all

```
x<-1
```

```
class(x)<-"numbat"
```

## Try it

```
print.numbat <- function(x,...){  
  cat(x,"numbats\n")  
  invisible(x)  
}
```



## Defining classes

- R doesn't care what `class` you attach to an object
- **You** have to care
- `class(x) <- "lm"` makes R call `lm` methods on `x`
- **You** are responsible for these methods being appropriate
- Documentation is important
- No real enforcement of encapsulation

## Ways to set up classes

- vectors plus attributes (`ts`, `POSIXct`, `matrix`)
- lists plus attributes (`lm`, `data.frame`)
- environments plus attributes

## Try it

```
unclass(.leap.seconds)
unclass(nhtemp)
unclass(trees)
m<-lm(log(Volume)~log(Girth)+log(Height),data=trees)
str(m)
```

## Defining classes safely

- Document what all is in a valid object of your class
- Have a limited set of places where one is created
- Consider having a pure constructor function (ARP 13.3.1)
- Consider having a validator function (ARP 13.3.1)
- Have a user-friendly function to make valid objects

This is more important if *someone else* might want to make an object from your class

## Constructors

- user-friendly: `tibble`, `lm`, `acf`, `svydesign`
- pure: `new_factor`, `new_difftime` (ARP 13.3.1)

Makes a new object and ensures that it is valid. Stops users creating the object themselves.

## Defining methods

- A method should have **the same** arguments as the generic (plus maybe more)
- The name of the method is  
`paste(generic, class, sep=".")`
- Less ambiguous: use a package and declare the functions
  - ▶ `S3method(generic, class) in NAMESPACE`
  - ▶ `@method generic class with devtools`
- `sloop::ftype` tells you about the type of a function
- `sloop::s3_get_method` or `getAnywhere` finds methods even if they're hidden

## default methods

Called when there is no specific method for the object (no class, or no matching class)

- `mean.default`
- `summary.default`
- `head.default`

## Adding methods to your class

No *rules* on which methods, but informal standards

- Start with `print`, `[`
- `summary` for more information
- `plot` or `image` if possible (`ggplot` methods take more work)
- `coef`, `vcov`, maybe `logLik` and `AIC` for models
- `resid` for models with residuals

## Base S3 classes

- The class for method choice isn't just `class(x)` for base types
- Use `sloop::s3_class` to be sure

```
> s3_class(1)
[1] "double" "numeric"
> s3_class(matrix(1,1,1))
[1] "matrix" "double" "numeric"
> class(1)
[1] "numeric"
> class(matrix(1,1,1))
[1] "matrix" "array"
```



## Ambiguous cases

- `t` is a generic
- `t.test` is a generic
- `t.test.formula` is a method for `t.test`
- `t.data.frame` is a method for `t`
- `list` is not generic
- `list.files` isn't a method

Avoid using `.` as a word separator in function names that aren't methods. Use `camelCase` or `snake_case` or some other consistent approach

## Defining generics

A typical generic function includes **only** a call to `UseMethod`  
`print`

```
function (x, ...)  
  UseMethod("print")  
<bytecode: 0x56bc655a7960>  
<environment: namespace:base>
```

## Dispatch on another argument

Specify which argument to use for choosing the method  
(default is the first)

```
> survey::svymean  
function (x, design, na.rm = FALSE, ...)  
{  
  .svycheck(design)  
  UseMethod("svymean", design)  
}
```

## Inheritance

The `class` attribute of an object can have multiple elements

- `UseMethod()` uses the first method that matches, or `default`
- `NextMethod()` uses the next method that matches

## Polite conduct

- if you define a new generic, you can define methods for new and existing classes
- if you define a new class, you can define methods for new and existing generics
- don't define methods for someone else's class and generic (ask them)
- try not to define a generic with the same name as an existing one

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A package for defining new S3 vectors

- makes it easy to have them as `tibble` columns
- requires a *pure constructor* to make new objects, so they will all be valid
- supports *double dispatch* for binary operators (eg: +,-)
- has a complicated but reliable system for type conversion
- requires a lot of method definitions to get started

[vctrs.r-lib.org](https://vctrs.r-lib.org)

## An example: S3 and vctrs

The `rimu` package represents multiple-response questions

```
remotes::install_github("tslumley/rimu")
```



```
data(usethnicity)
race<-as.mr(strsplit(as.character(usethnicity$Q5),""))
race<-mr_drop(race," ")
mtable(race)
hispanic<-as.mr(usethnicity$Q4==1,"Hispanic")
ethnicity<-mr_union(race,hispanic)
plot(ethnicity)
e_S3<-ethnicity[101:120]
e_vctr<-as.vmr(e_S3,na.rm=TRUE)
```

# Inheritance

```
mr_union<-function(x,y,...) UseMethod("mr_union")

mr_union.default<-function(x,y,...){
  x<-as.mr(x)
  y<-as.mr(y)
  if (length(x)!=length(y))
    stop("different numbers of observations in x and y")

  ....
}
```

```
mr_union.vmr<-function(x,y,...) {  
  r<-NextMethod()  
  as.vmr(r)  
}
```

## Encapsulation

- base S3 version is matrix of logical, plus levels attribute
  - ▶ works in `data.frame`
- vctrs S3 version is list of vectors of strings
  - ▶ works in `tibble`

## Pure constructor

```
new_vmr <- function(x, levels=unique(do.call(c,x))) {  
  vctr::new_list_of(x, ptype = character(),  
    class = "vmr", levs=levels)  
}
```

## 'helper' functions

```
> methods("as.mr")  
[1] as.mr.character*  as.mr.data.frame*  as.mr.default*  
[4] as.mr.factor*     as.mr.list*         as.mr.logical*  
[7] as.mr.mr*         as.mr.ms*          as.mr.vmr*  
  
> methods("as.vmr")  
[1] as.vmr.default*  as.vmr.mr*
```

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S4 requires classes and methods to be registered in R code (not just in packages)

- `setClass` defines the structure of a class
- `new` creates a new object from a class
- `setMethod` defines a method

It's possible to ask an object what methods it supports and get a reliable response.

S4 also allows multiple inheritance and multiple dispatch



## Bioconductor

- Package system for high-throughput molecular biology
- Large data
- Structured data
- Annotated data
- New data types/structures all the time

It needs consistent infrastructure and large-scale  
collaboration: S4  
[bioconductor.org](http://bioconductor.org)

## Multiple dispatch

Choosing a method based on the class of more than one argument

- not very often useful
- important for matrices
- can be useful for plots

## Multiple inheritance

AnnDbObjBimap is a class for storing look-up tables between different genomic identifiers (eg from different manufacturers)

It is

- (by purpose) a two-way lookup object (BiMap)
- (by construction) an object containing a SQLite database (DbObj)

so it inherits generic functions from both these parents

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Remember function factories from last week?

- Create a function closure with useful variables in its environment
- These variables are visible inside the function

Now do this with

- multiple variables in the shared environment
- multiple functions inheriting this environment
- allow the shared variables to be modified

## R6 is good for...

- large data objects, to reduce copying
- external objects that R can't just copy (database connections, files,... )
- shared state such as games

R6 is more similar to C++/Java/Python OOP. It doesn't really support functional programming

[R6.r-lib.org](http://R6.r-lib.org)