

# ETC4500/ETC5450

## Advanced R programming

Week 8: Object-oriented Programming



# Programming paradigms

## Functional programming (W5)

- Functions are created and used like any other object.
- Output should only depend on the function's inputs.

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## Functional programming (W5)

- Functions are created and used like any other object.
- Output should only depend on the function's inputs.

## Literate programming (W6)

- Natural language is interspersed with code.
- Aimed at prioritising documentation/comments.
- Now used to create reproducible reports/documents.

# Programming paradigms

## Reactive programming (W7)

- Objects are expressed using code based on inputs.
- When inputs change, the object's value updates.

# Programming paradigms

## Reactive programming (W7)

- Objects are expressed using code based on inputs.
- When inputs change, the object's value updates.

## Object-oriented programming (W8-W9)

- Functions are associated with object types.
- Methods of the same 'function' produce object-specific output.

# Object oriented programming

- **Encapsulation:** Bundles data and methods in a class, restricting access to internal details.
- **Abstraction:** Simplifies complexity by exposing only essential features of an object.
- **Polymorphism:** Allows the same function to operate differently on different object types.
- **Inheritance:** Enables a new class to inherit properties and behaviors from an existing class.

# Object oriented programming

**Inheritance** is primarily useful for structuring data infrastructure by allowing reuse and extension of existing classes.

**Encapsulation** helps protect object integrity by restricting access to internal states.

**Polymorphism** enables flexibility by allowing a single interface to operate on various data types.

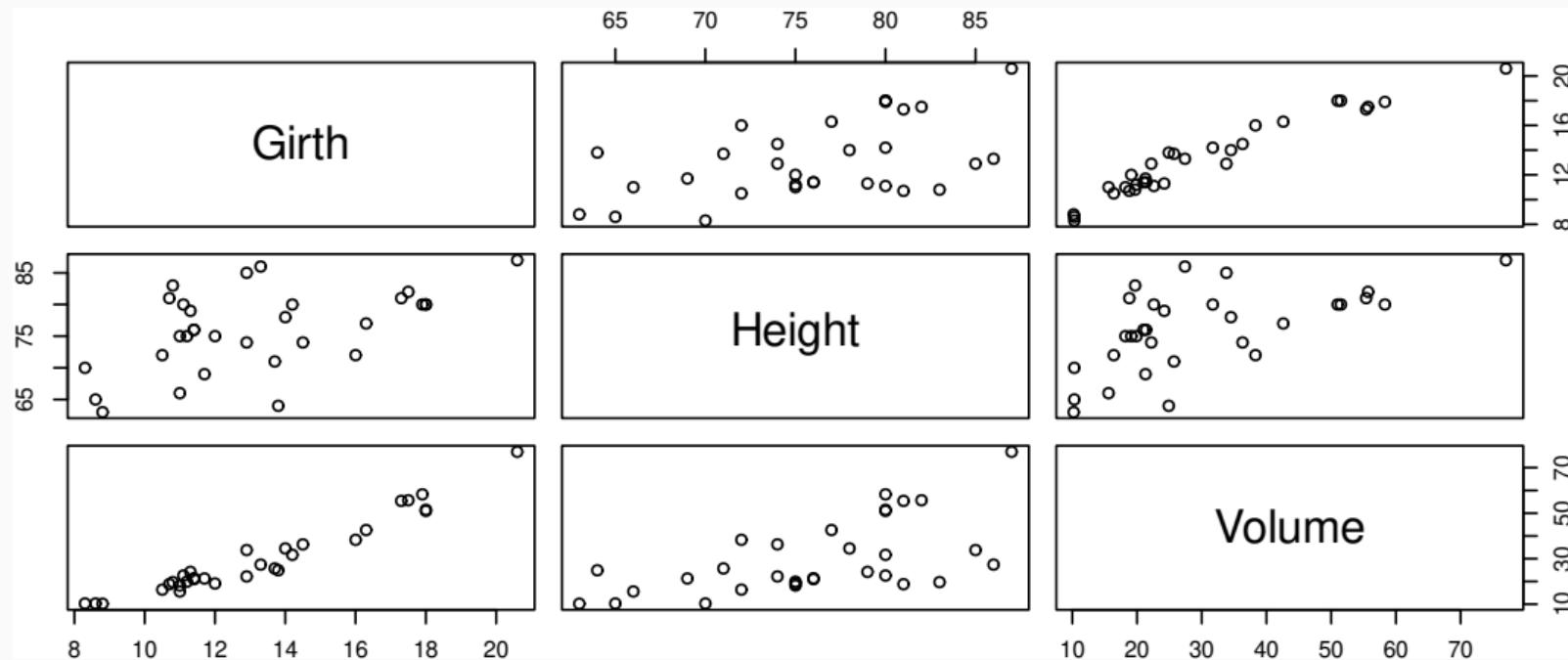
**Abstraction** simplifies complexity by highlighting essential features, making systems easier to understand and use.

# Generic functions and methods

A simple example: plot

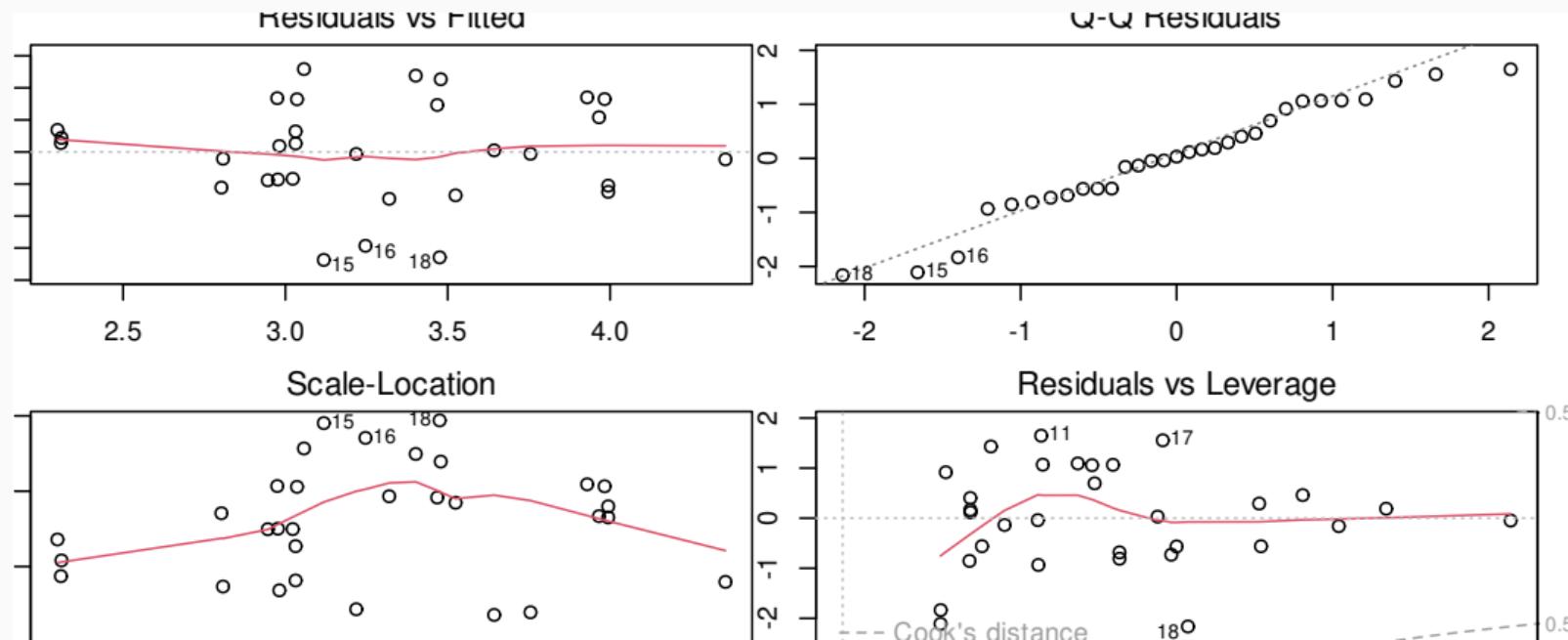
# Generic functions and methods

```
plot(trees)
```



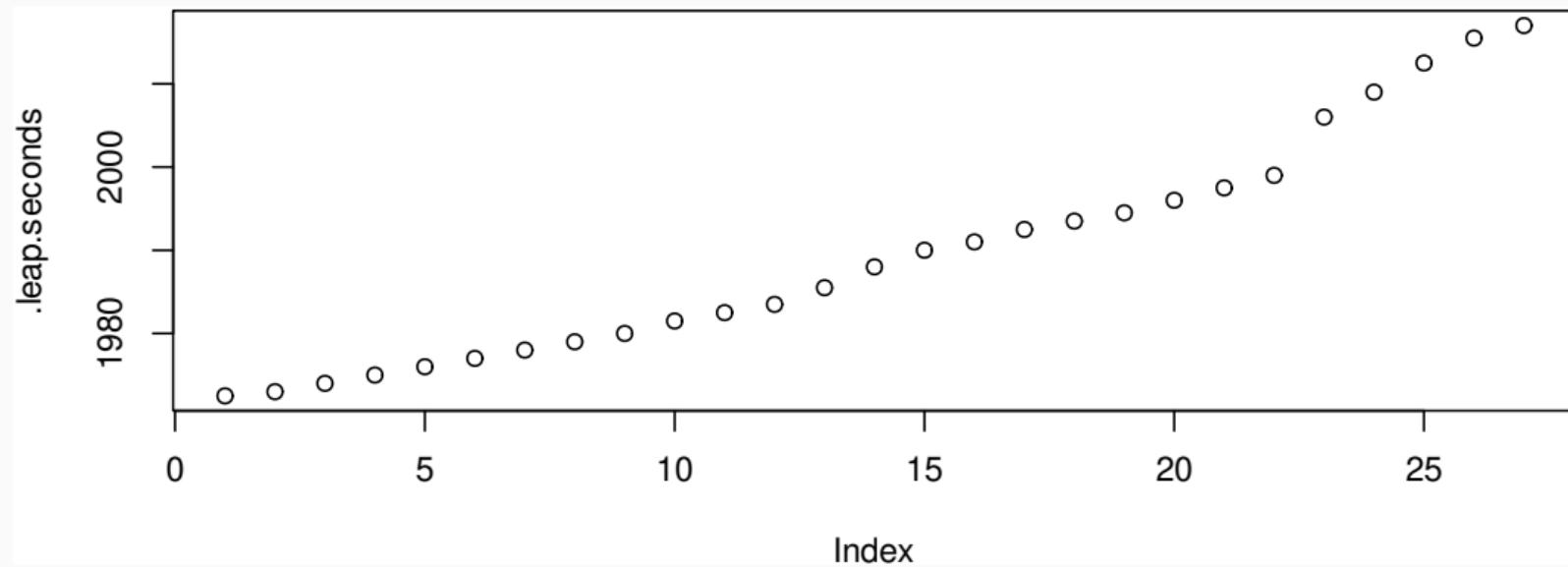
# Generic functions and methods

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



# Generic functions and methods

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



# Generic functions and methods

```
plot(nhtemp)
```



# Generic functions and methods

## How does plot() work?

- Giant switch statement...
- Lots of if statements...
- How does the behaviour update when you load packages?
- ???

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S3 generic functions and methods!

# Object systems

R has **a lot** of object systems

- S3
- [S3 vctrs]
- S4
- R6
- R.oo, proto, ggproto,
- R7
- S7

# Object oriented programming

## S3

- The OO system used by most of CRAN.
- Very simple (and ‘limited’) compared to other systems.

# Object oriented programming

## S3

- The OO system used by most of CRAN.
- Very simple (and ‘limited’) compared to other systems.

## vctrs

- Builds upon S3 to make creating vectors easier.
- Good practices inherited by default.

# Object oriented programming

## S4

- Formal class definitions with validation.
- Supports multiple inheritance and method dispatch.

# Object oriented programming

## S4

- Formal class definitions with validation.
- Supports multiple inheritance and method dispatch.

## S7

- Planned to be the successor of S3 and S4.
- More general than S3, but still easy to use.

# Object oriented programming

R6

- Provides reference semantics for mutable objects.
- Simple and efficient compared to reference classes.

# Object oriented programming

## R6

- Provides reference semantics for mutable objects.
- Simple and efficient compared to reference classes.

## ggproto

- Used in ggplot2 for extensibility.
- Supports inheritance and method overloading.

## Main topic for today

- easy to start writing
- no safeguards
- especially good for simple, small-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 with vctrs

A helpful package for making different sorts of S3 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

We'll learn more about vctrs next week!

Back to the plot function...

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

## S3: 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

# S3: Generics and methods

🔥 Your turn!

Investigate these functions.

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

How do generic functions relate to methods?

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

## S3: Classes

- S3 classes are attributes that specify which method to use
- The `class()` function can access (and modify) an object's class
- Classed S3 objects are typically produced with `structure()`

For example,

```
x <- structure(83, class = "grade")  
class(x)
```

```
[1] "grade"
```

```
x
```

```
[1] 83
```

## S3: Methods

- *methods that actually do the work ‘belong to’ generic functions*
- This is unusual: most other 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

## S3: Creating a method

```
print.grade <- function(x, ...){  
  letter <- if (x < 50) "N"  
  else if (x < 60) "P"  
  else if (x < 70) "C"  
  else if (x < 80) "D"  
  else "HD"  
  cat(x, " [", letter, "]", sep = "")  
  invisible(x)  
}  
x
```

83 [HD]

# Creating an S3 generic

S3 generics work like any ordinary function, but they include `UseMethod()` which calls the appropriate method.

## 🔥 Your turn!

Create an S3 generic called “reverse”.

This function will reverse objects. For example,

- `reverse("stressed")` becomes "desserts",
- `reverse(7919)` becomes 9197,
- `reverse(1.9599)` becomes 9959.1.

# Writing S3 methods

An S3 method is an ordinary function with some constraints:

- The function's name is of the form <generic>.<class>,
- The function's arguments match the generic's arguments,
- The function is registered as an S3 method (for packages).

This looks like:

```
#' Documentation for the method
#' @method <generic> <class>
<generic>.<class> <- function(<generic args>, <method args>, ...) {
  # The code for the method
}
```

# Writing S3 methods

## 🔥 Your turn!

Write methods for reversing character, integer, and double objects.

- `reverse("stressed")` becomes "desserts",
- `reverse(7919L)` becomes 9197L,
- `reverse(1.9599)` becomes 9959.1.

*Hint: `stringi::stri_reverse()` will reverse a string.*

*The integer and double methods should return an integer and double respectively.*

## S3: .default methods

Default methods are called when there is no specific method for the object (no class, or no matching class).

Some examples include:

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

# Writing S3 defaults

What if we tried to reverse the current date;  
`reverse(Sys.Date())?`

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 Your turn!

Question: what should the default behaviour be?

# Writing S3 defaults

What if we tried to reverse the current date;  
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Your turn!

Question: what should the default behaviour be?

- Raise an error?
- Return a reversed string?
- Something else entirely?

## S3: Defining classes

The S3 class system is simple!

- 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

## S3: Classed objects

You can class any object, including:

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



Your turn!

Use unclass() and str() to explore classed objects, e.g.:

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

## S3: Constructors functions

These functions return classed S3 objects. They should handle input validation and be user-friendly.

Constructor functions typically come in two forms:

- complex: `tibble`, `lm`, `acf`, `svydesign`
- pure: `new_factor`, `new_difftime`

Pure constructor functions simply validate inputs and produce the classed object, while complex constructor functions involve calculations.

# Creating your own S3 objects

The `structure()` function is usually used within packages.

- `lm()` returns a list with class "lm", and
- `tibble()` returns a list classed "tbl\_df", "tbl", and "data.frame".

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Your turn!

Create `fraction()`, which returns fraction objects.

The underlying data type is a list containing two vectors for the two arguments: numerator and denominator.

This function should check that the inputs are suitable.

# Creating your own S3 objects

```
fraction <- function(numerator, denominator) {  
  if (!is.numeric(numerator) || !is.numeric(denominator)) {  
    stop("Both numerator and denominator must be numeric.")  
  }  
  if (denominator == 0) {  
    stop("Denominator cannot be zero.")  
  }  
  
  structure(  
    list(numerator = numerator, denominator = denominator),  
    class = "fraction"  
  )  
}
```

# Creating your own S3 objects

The fraction class doesn't yet have any methods, so it inherits methods from its list type.

```
e <- fraction(numerator = 2721, denominator = 1001)
print(e)
```

```
$numerator
[1] 2721
```

```
$denominator
[1] 1001
```

```
attr(,"class")
[1] "fraction"
```

# Creating your own S3 objects

Usually we would create a method for printing S3 objects.

```
print.fraction <- function(x, ...) {  
  paste(x$numerator, x$denominator, sep = "/")  
}  
print(e)
```

```
[1] "2721/1001"
```

# Creating your own S3 objects

 Your turn!

Create a `reverse()` method for the `fraction` object class, which inverts the numerator and denominator.

*Finished early?*

Write a method for converting a fraction into a number.

## S3: Method dispatch

Method dispatch describes the process of calling the appropriate method for the object's class.

This mostly matches `class()`, but not always for some primitive R object types. `sloop::s3_class()` shows the extra s3 dispatch classes.

```
> 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"
```

## S3: Naming ambiguity

- 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

## S3: 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

## S3: 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

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

## S4: 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)

## S4: 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

## S4: 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

## S4: Creating a class

The structure of your S4 class is defined with `setClass()`.

```
setClass(  
  "StudentGrades",  
  slots = list(  
    name = "character",  
    grades = "numeric"  
  )  
)
```

# S4: Creating S4 objects

S4 objects are created with the new() function.

```
studentGrades <- function(name, grades) {  
  if (!is.character(name) || length(name) != 1) {  
    stop("Name must be a single string.")  
  }  
  if (!is.numeric(grades)) {  
    stop("Grades must be numeric.")  
  }  
  
  new("StudentGrades", name = name, grades = grades)  
}
```

## S4: Creating methods

Methods are registered to S4 classes with `setGeneric()` and `setMethod()`.

```
setGeneric("averageGrade", function(object) {  
  standardGeneric("averageGrade")  
})
```

```
[1] "averageGrade"
```

```
setMethod("averageGrade", "StudentGrades", function(object) {  
  mean(object@grades)  
})
```

## S4: Using S4 objects

```
student <- studentGrades("Alice", c(85, 90, 78))
print(student)
```

An object of class "StudentGrades"

Slot "name":

```
[1] "Alice"
```

Slot "grades":

```
[1] 85 90 78
```

```
average <- averageGrade(student)
print(paste("Average Grade:", average))
```

```
[1] "Average Grade: 84.33333333333333"
```

## S4: Accessing S4 slots

Contents of an S4 object are extracted with @.

For example, the student's name can be obtained with:

```
student@name
```

```
[1] "Alice"
```

# S7

$S7 = S3 + S4$

It aims to maintain the simplicity of S3, while adding useful features from S4.

(and unify CRAN and Bioconductor packages!)

It's not yet in R-Core, but it can be used via the S7 package.

```
library(S7)
```

## S7: Creating a class

Like S4, S7 starts by defining the data structure.

```
student <- new_class(  
  name = "student",  
  properties = list(  
    name = class_character,  
    grades = class_double  
)  
)
```

## S7: Self-validation

S7 additionally supports property validation

```
student <- new_class(  
  name = "student",  
  properties = list(  
    name = class_character,  
    grades = class_double  
,  
  validator = function(self) {  
    if (any(self@grades < 0 | self@grades > 100)) {  
      "@grades must be between 0 and 100"  
    }  
  }  
)
```

## S7: S7 classes are also constructors

The S7 class student is also a (pure) constructor function.

```
x <- student(name = "Alice", grades = c(85, 90, 78))  
x
```

```
<student>  
@ name : chr "Alice"  
@ grades: num [1:3] 85 90 78
```

The validator prevents invalid grades.

```
student(name = "Mitch", grades = c(-10, 140))
```

Error:

```
! <student> object is invalid:  
- @grades must be between 0 and 100
```

## S7: Creating generics

S7 generics are created with `new_generic()`.

```
best_grade <- new_generic("best_grade", dispatch_args = "x")
```

Here we explicitly specify which argument(s) are used in finding the appropriate method. Double (or multiple) dispatch is supported!

## S7: Creating methods

S7 methods are created with `method<-:`:

```
method(best_grade, student) <- function(x) {  
  max(x@grades)  
}  
best_grade(x)
```

```
[1] 90
```