

# Intro. to OOP and S3 System in R

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<https://github.com/ravichas/OOP-S3-in-R>

# Scope

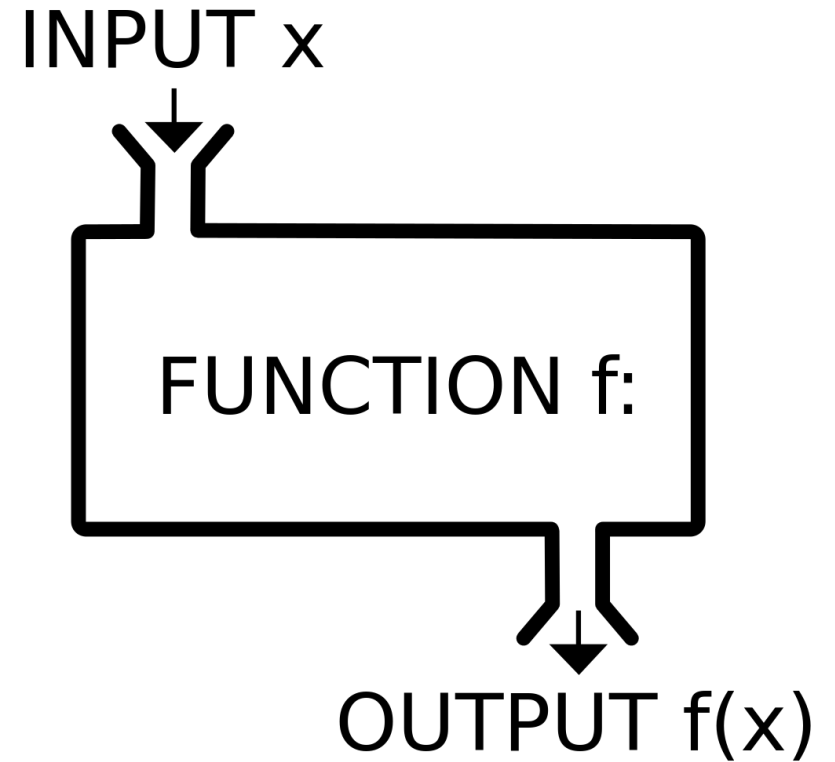
- OOP
  - Concepts might be similar to other languages, but ...
- Specific to R
- Examples

# Specific goals

- Note I am !here to teach OOP
- Reinforce concepts that you already know and associate them with OOP. In that process, I will remind/provide some definitions/examples of OOP
- Specific to R ; One-liners easy for other programmers

# Functional programming

- Commonly used
- Focus is on functions
- Chain functions together to accomplish things
- Good for?
  - Data analysis, modeling etc.

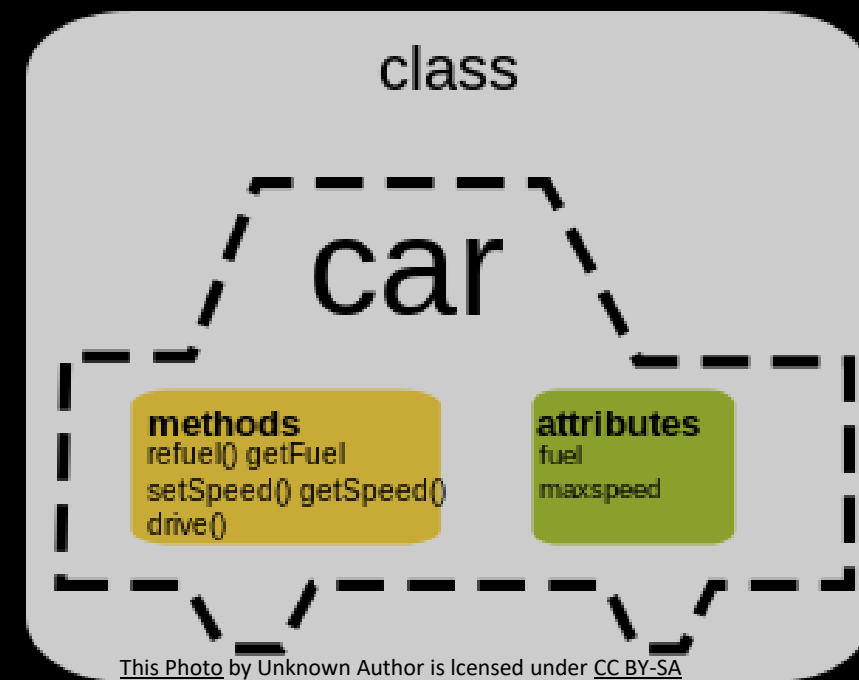


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```
my_add <- function(x,y)
{
  # do some task
  return(x + y)
}
```

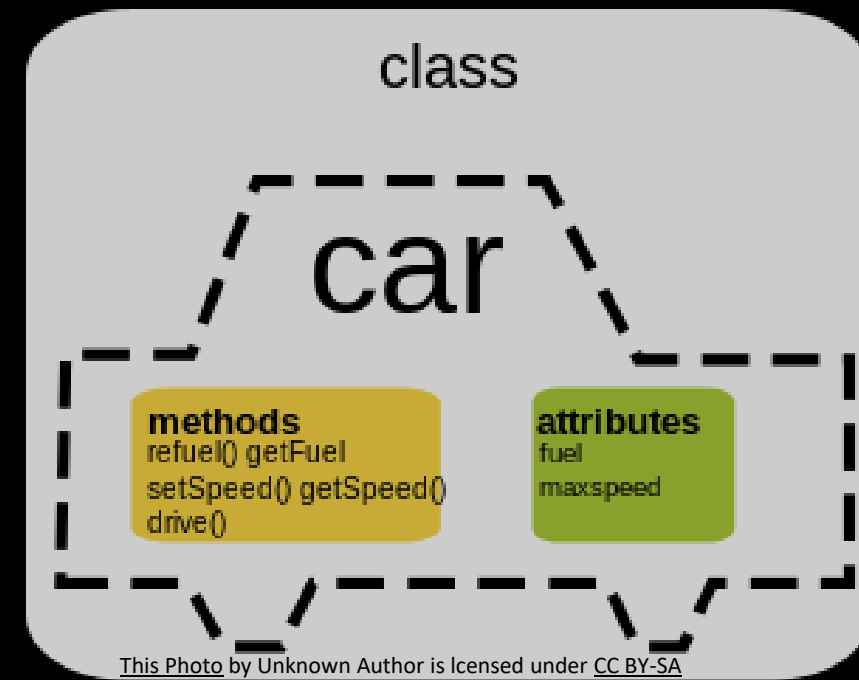
# OOP

- Focus on objects
- Steps
  - Define Object
  - Describe its attributes (size, seats etc.)
  - Define methods to describe what object can do
- Note in OOP, functions are called METHODS



# OOP

- What is OOP good for?
  - Developing tools, GUIs
  - Complex limited # of objects
  - Specifically when you know you can define the objects clearly
  - Developing GUIs (limited # of options)
    - Interface that can handle limited # of inputs
    - Bioconductor objects (complex but can be reused)



# Object types in R

- ~ 20 types
- Integer, logical, numeric, data.frame, List, matrix, array, factor, formula, environment, etc
- Most important types (create complex objects are:
  - List
  - Environment
- These constitute the building blocks that are needed for analysis

# Interrogating the variables

- For OOP to work, R has to identify the class of the variables
- How does R identify the class variables?
- Class (command: *class*)
  - Doesn't tell the whole story
- Typeof (command: *typeof* ; c-code)
  - Supplements *class* command



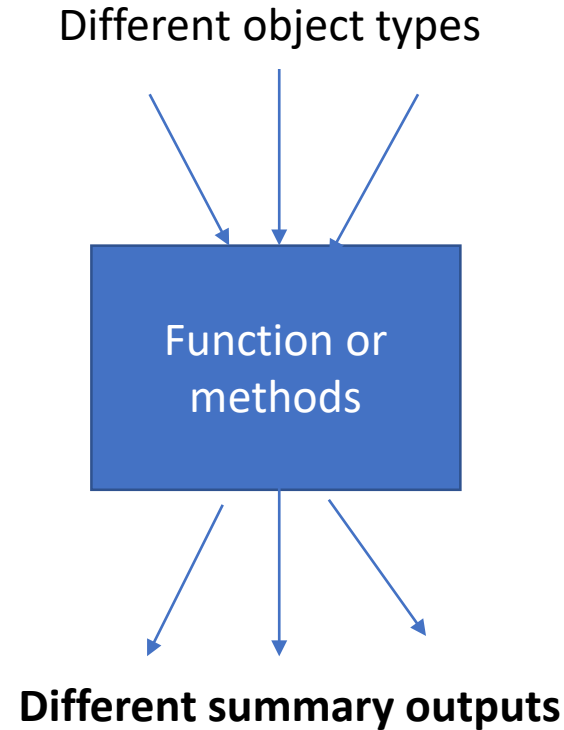


# Hands-on 1

Object Types  
Class of objects

A simple function to show that it behaves differently for different input types

# OOP concept: Functions behave differently for different objects



```
>
>
> x_num <- rnorm(50)
> x_fac <- factor(sample(letters[1:10],50,replace=T))
> model <- lm(mpg ~ wt, mtcars)
>
>
> summary(x_num)
      Min.   1st Qu.   Median     Mean   3rd Qu.    Max.
-2.50817 -0.64324 -0.08345 -0.14963  0.47288  1.71476
> summary(x_fac)
 a  b  c  d  e  f  g  h  i  j
6  1  5  9  3  6  7  1 10  2
> summary(model)

Call:
lm(formula = mpg ~ wt, data = mtcars)

Residuals:
      Min       1Q   Median       3Q      Max
-4.5432  -2.3647  -0.1252   1.4096   6.8727

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)  37.2851     1.8776   19.858  < 2e-16 ***
wt           -5.3445     0.5591   -9.559  1.29e-10 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 3.046 on 30 degrees of freedom
Multiple R-squared:  0.7528,    Adjusted R-squared:  0.7446
F-statistic: 91.38 on 1 and 30 DF,  p-value: 1.294e-10
```

## Polymorphism; Function Overloading

# OOP Systems (frameworks) in R

- Important systems
- S3 (Introduced in 3rd version of S Language)
- S4 (4th version of S)
  - Bioconductor
- R6 (introduced in 6 version of S; more matured)
- ReferenceClasses (RC)

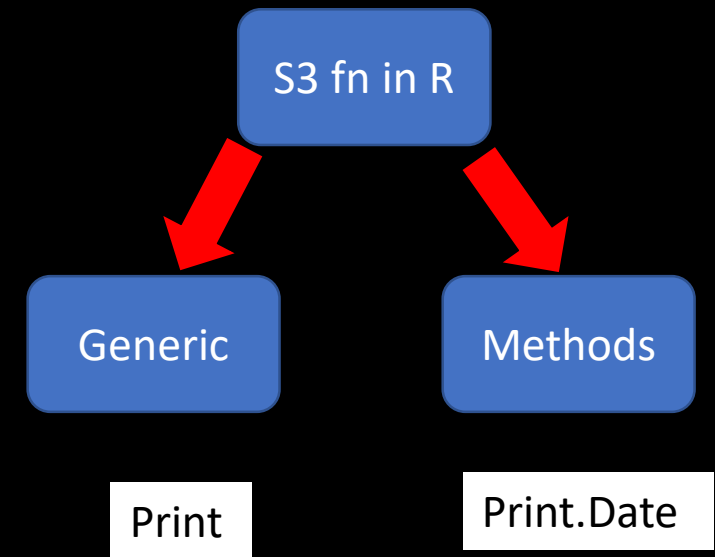
***You can think  
of the systems  
as different  
packages for  
implementing  
OOP***

# S3 System

- Why learn S3?
  - Most commonly used type
  - Simple; lacks formal definition
  - Freedom to be creative (comes with cost!)
  - Create custom class of objects and use S3 to accomplish complex tasks

# S3 Object System in R

- Central players
  - Class & Method
- CLASS
  - defines type of object, its properties, how it works with other objects
- METHOD
  - Function associated with a particular object type
- OOP style in R is different than C++ or Java etc
- A generic function will decide what appropriate method to call



# Generics and Methods

- If we have no overloading then we need a lot more functions
- S3 was created to solve this problem
  - Takes a function for each class and splits into two parts:
    - generic function & method function

# How to name a Method?

- Standard notation for S3
- Print.Date
  - generic.class
- Arguments should be same for both generic and UseMethod
- To avoid from being mistaken, don't name your variable/function with "dot"
  - DON'T: my.print
  - Maybe: my\_print\_function

```
> print
function (x, ...)
UseMethod("print")
<bytecode: 0x000000001e689540>
<environment: namespace:base>
```

	<i>UseMethod</i>
<i>generic</i>	<b>generic.class</b>
print	print.data.frame
	print.data.table*
	print.Date
	print.default
	print.dendrogram

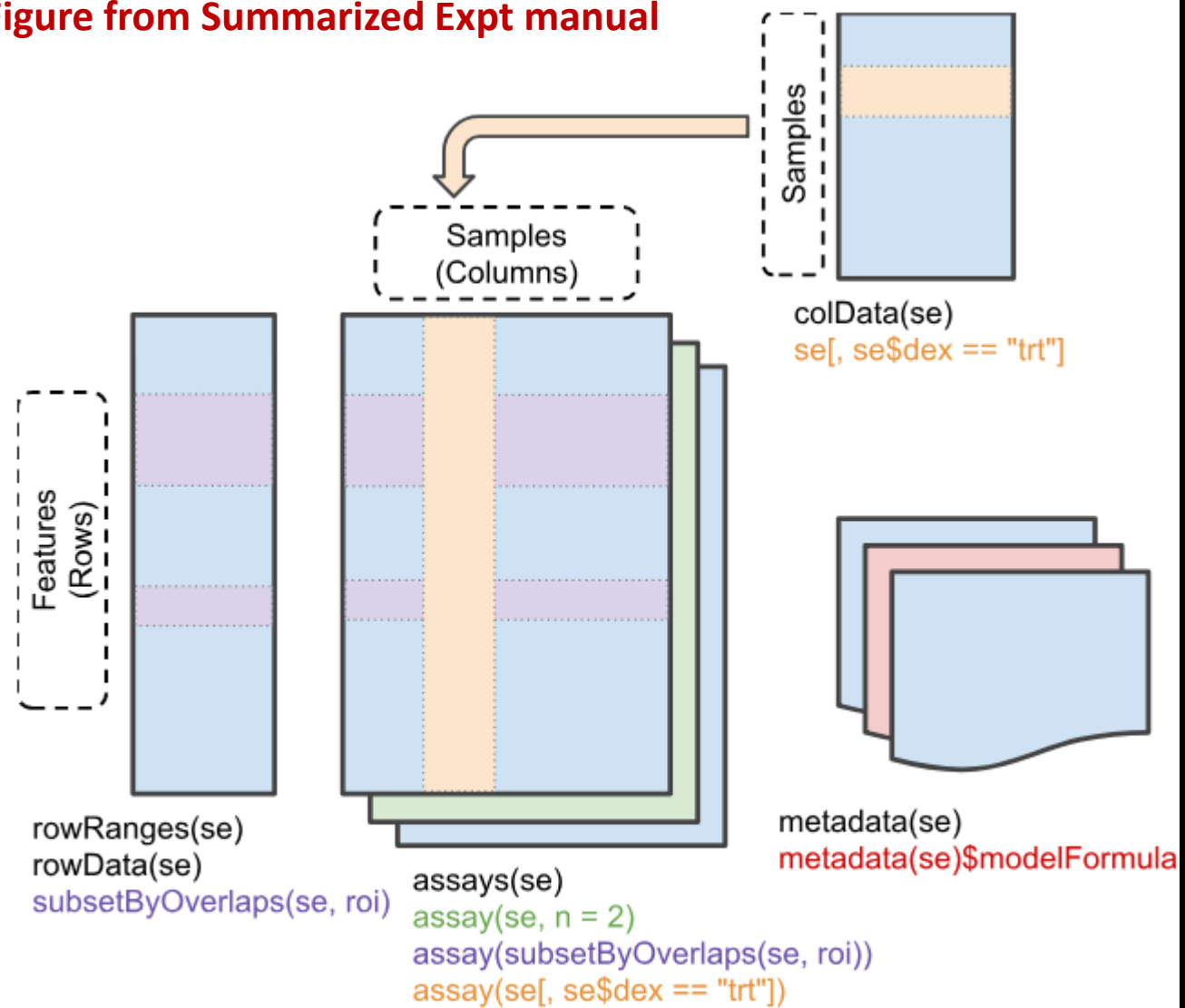
# Hands-on 2



S4

- Very useful to create new class
  - SummarizedExperiment
- Complex objects
  - Genomic objects
  - Elements of class are called slots
  - SetMethod to define methods for a class
- Reused in many contexts

**Figure from Summarized Expt manual**



## Summarized Experiment

```

> se <- airway
> se
class: RangedSummarizedExperiment
dim: 64102 8
metadata(1): ''
assays(1): counts
rownames(64102): ENSG00000000003 ENSG00000000005 ... LRG_98 LRG_99
rowData names(0):
colnames(8): SRR1039508 SRR1039509 ... SRR1039520 SRR1039521
colData names(9): SampleName cell ... Sample BioSample
> |

```

## metadata accessor

```

> metadata(se)
[[1]]
Experiment data
  Experimenter name: Himes BE
  Laboratory: NA
  Contact information:
  Title: RNA-Seq transcriptome profiling identifies CRISPLD2 as a glucocorticoid responsive gene that modulates cytokine function in airway smooth muscle cells.
  URL: http://www.ncbi.nlm.nih.gov/pubmed/24926665
  PMIDs: 24926665

  Abstract: A 226 word abstract is available. Use 'abstract' method.

```

# Acknowledgements

- Statistics for lunch team
- Presentations/Lectures/Tutorials from the following people
- Hadley Wickham
  - [Adv. R tutorial](#)
- Richie Cotton
  - [Youtube](#)
- Kelly Black, Univ Georgia
  - [cyclismo.org](#)

THANK YOU