

Classes in R

R is not actually an object-oriented language in any real sense.

But it has things that it calls “classes”, and things that it calls “methods.”

They look more like “types” and “polymorphic functions” as used in the functional-programming world.

There are two types of classes in R.

- S3 (older)
- S4 (newer)

An S3 class is a list with an extra attribute, called "class"

```
> l <- list(foo = "bar", baz = "qux")  
> class(l) <- "myclass"  
> l
```

```
$foo  
[1] "bar"
```

```
$baz  
[1] "qux"
```

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

Let's revisit our simple regression function from the Functions course:

```
run_regression <- function(y, x) {  
  coef <- cov(x,y) / var(x)  
  se <- calc_se(y, x, coef)  
  list(coef=coef, se=se)  
}
```

Now let's make it return a class:

```
run_regression <- function(y, x) {  
  coef <- cov(x,y) / var(x)  
  se <- calc_se(y, x, coef)  
  model <- list(coef=coef, se=se)  
  class(model) <- "simple_model"  
  model  
}
```

Classes are not useful in-and-of themselves. They are only useful when we use them together with polymorphic functions, called “generic methods” in R.

Polymorphic means that the same function can operate on different types (in R, “classes”), with different behavior.

Consider the `eval_model()` function from the Functions course:

```
eval_model <- function(coef, se, beta, conf = 1.96) {  
  up <- coef + se*conf  
  down <- coef - se*conf  
  beta > down & beta < up  
}
```

This function requires the user to manually input the coefficients and the standard errors. This is good, because it makes the function general. But it requires the user to be a bit sophisticated.

It would be simpler to use, if the user only had to give us the model:

```
eval_model <- function(model, beta, conf = 1.96) {  
  coef <- model$coef  
  se <- model$se  
  up <- coef + se*conf  
  down <- coef - se*conf  
  beta > down & beta < up  
}
```

But now the function is very specialized. What if I have a different model, and it does not have the standard errors under a field called "se"?

This function only works for the exact regression function we created.

We would have to use a different `eval_model()` function for every model we create.

That sounds tedious, and hard to remember all the different function names.

Polymorphic Functions

This is solved with polymorphic functions.

Let's create a polymorphic eval_model() function:

```
eval_model <- function(model, beta, conf) {  
  UseMethod("eval_model")  
}
```

Now, we write a specific function for each “class” that needs to be evaluated:

```
eval_model.simple_model <- function(model, beta, conf) {  
  coef <- model$coef  
  se <- model$se  
  up <- coef + se*conf  
  down <- coef - se*conf  
  beta > down & beta < up  
}
```

This “method”, as it’s called in R, encapsulates intimate knowledge about the class “simple_model”. Like a method in Object-Oriented programming!

Now we can use `eval_model()` without us needing to know what the regression model actually looks like, or what `eval_model()` uses:

```
model <- run_regression(y, x)
eval_model(model, true_beta)
```

Polymorphic Functions

Many functions you will use, and maybe have already used, are polymorphic.

For example, the `mean()` function is polymorphic:

```
> methods(mean)
```

```
[1] mean.Date      mean.default  mean.difftime mean.POSIXct
```

In addition to the default version, the creators of R wanted to be able to take the mean of date and timestamp objects.

Similarly, the `coef()` function is polymorphic:

```
> methods(coef)
```

```
[1] coef.aov*      coef.Arima*    coef.default* coef.listof*  
[6] coef.nls*
```

The `coef()` function gets the coefficients from a model.

Let's implement a `coef()` method for our new class. That way, users can get the coefficients without needing to know where we've put them:

```
coef.simple_model <- function(model) model$coef
```

```
> coef(model)
```

```
[1] 0.4677848
```

