

Class 2: Regression and classification

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Learning outcomes

- ▶ Be able to understand the structure of regression and classification models
- ▶ Know how to read and interpret the output of a statistical model
- ▶ Be familiar with some of the extensions to basic regression and classification models

Why regression and classification?

- ▶ t-tests are only really useful when you have a continuous outcome variable and one discrete variable with two groups (e.g. treatment vs control)
- ▶ For almost any real life situation you have multiple variables of all different types
- ▶ For these situations you need a *statistical model*
- ▶ A statistical model allows to perform *probabilistic prediction* of the outcome variable from the remaining variable, and/or to explain how the other variables are causing the outcome variable to change

Regression vs Classification: what's the difference?

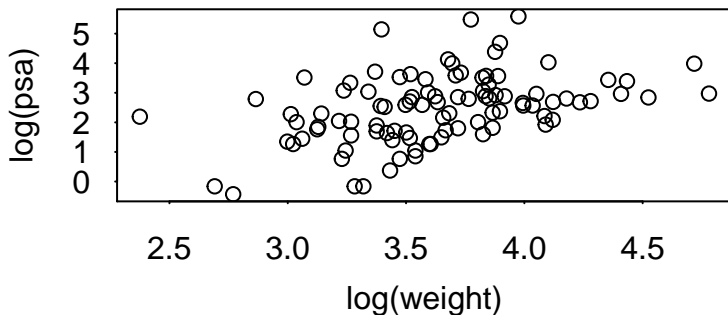
- ▶ In regression we have a single *continuous* outcome variable and lots of other variables which we think might be causing the outcome to change
- ▶ In classification we have a single *discrete* outcome variable and lots of other variables
- ▶ In the machine learning literature this is often known as *supervised learning*
- ▶ Situations where there are multiple outcome variables are beyond the scope of this course

Response and explanatory variables

- ▶ The outcome variable is more commonly known as the *response* variable
- ▶ The other variables which we think might be causing the response variable to change are called the *explanatory variables* (though be careful with causation)
- ▶ We will use these words from now on, but beware there are lots of other terms in the literature

A basic regression model

- ▶ Let's go back to the prostate cancer data
- ▶ Recall the key outcome variable is `lpsa` the log of the prostate specific antigen value. This is our response variable
- ▶ Suppose we had one explanatory variable `lweight`



Creating the model

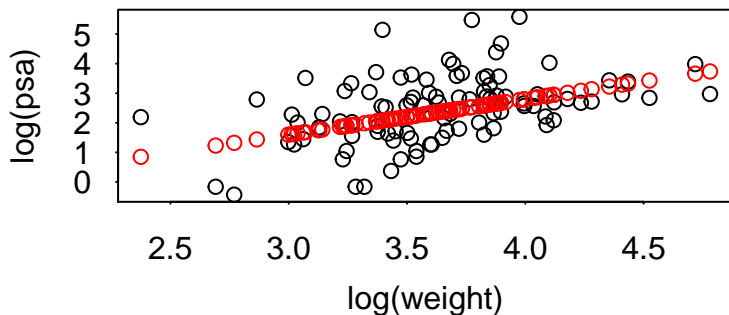
- ▶ Looking at the plot, there may be a positive, linear relationship between $\log(\text{weight})$ and $\log(\text{psa})$
- ▶ Perhaps we can create a prediction model that allows us to predict $\log(\text{psa})$ from $\log(\text{weight})$
- ▶ Suppose, for each patient we multiplied the $\log(\text{weight})$ value by 1.2 and then subtracted the value 2 so:

$$\text{prediction} = 1.2 \times \log(\text{weight}) - 2$$

- ▶ If we do this repeatedly for every value in the data set we get
...

A first model

```
par(mar=c(3,3,2,1), mgp=c(2,.7,0), tck=-.01, las=1)
prediction = 1.2 * prostate$weight - 2
plot(prostate$weight, prostate$lpsa, xlab = 'log(weight)',
points(prostate$weight, prediction, col='red')
```



Refining the model

- ▶ Is this model any good?
- ▶ How might we measure how close our predictions are to the truth?
- ▶ How can we choose the values (here 1.2 and -2) better?

Getting R to do the work

- Luckily the R function `lm` will do the work for us

```
model_1 = lm(formula = lpsa ~ lweight, data = prostate)
summary(model_1)
```

```
##
## Call:
## lm(formula = lpsa ~ lweight, data = prostate)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.27976 -0.67507 -0.03503  0.53984  2.93649
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  -1.7586     0.9103   -1.932   0.0564 .
## lweight       1.1676     0.2491    4.686 9.28e-06 ***
## ---
```

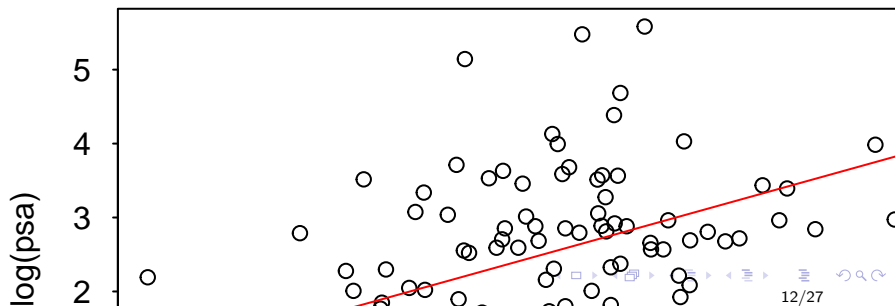
Background details

- ▶ The two values here are the y -intercept and the slope of the line
- ▶ R chooses these values by minimising the vertical distances between the black and the red points (called least squares)
- ▶ A key assumption in the model is that these vertical distances (known as *residuals*) are normally distributed
- ▶ R uses this assumption to run t-tests on the parameters, which you can see the results of in the `summary` output

Plotting the fit

- One way is to type `plot(model_1)` but this perhaps gives too much info. Better:

```
par(mar=c(3,3,2,1), mgp=c(2,.7,0), tck=-.01, las=1)
plot(prostate$lweight, prostate$lpsa, xlab = 'log(weight)',
abline(model_1, col='red'))
```



Reading the output of the model

Expanding the model with two explanatory variables

Expanding the fit even more

Regularisation and shrinkage

Lasso; Ridge and Elastic Net

Dealing with interactions

Even more advanced regression approaches

Intro to classification models

The logit transformation

Example: SA Heart rate

Extending the model

Understanding the output

Plotting the fitted model

Regularisation and shrinkage for classification

More advanced classification approaches