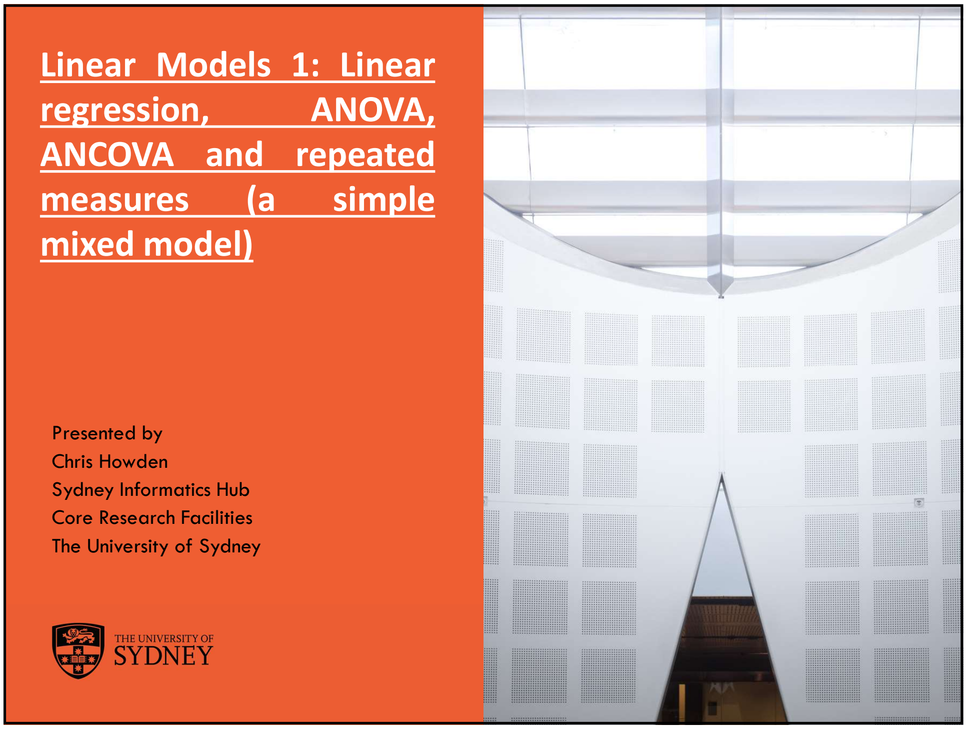

Linear Models 1: Linear regression, ANOVA, ANCOVA and repeated measures (a simple mixed model)

Presented by
Chris Howden
Sydney Informatics Hub
Core Research Facilities
The University of Sydney

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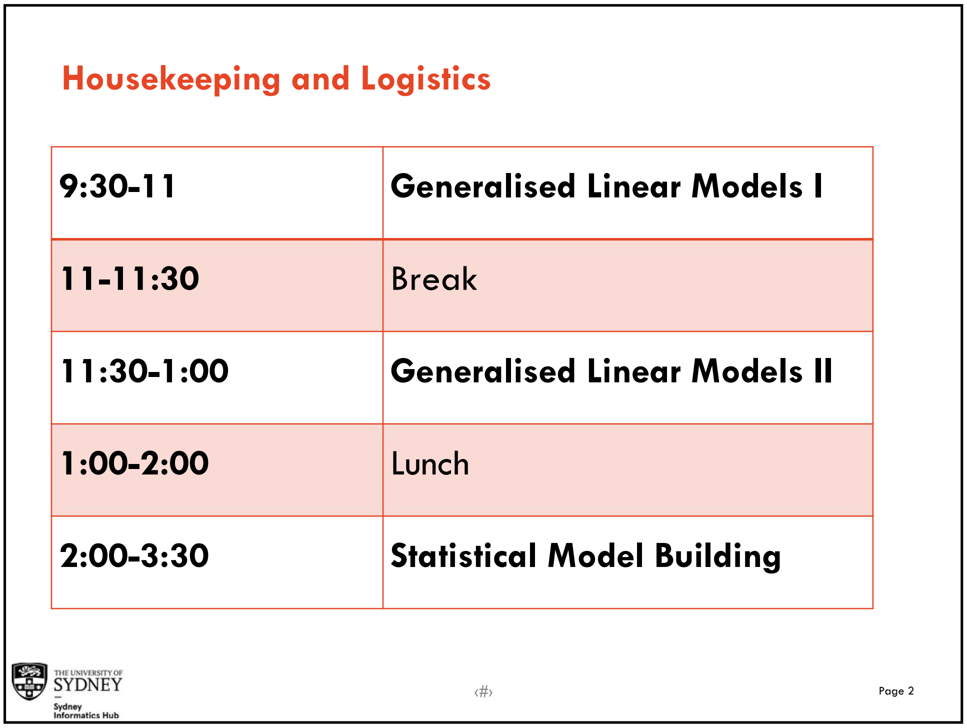

Housekeeping and Logistics

9:30-11	**Generalised Linear Models I**
11-11:30	Break
11:30-1:00	**Generalised Linear Models II**
1:00-2:00	Lunch
2:00-3:30	**Statistical Model Building**

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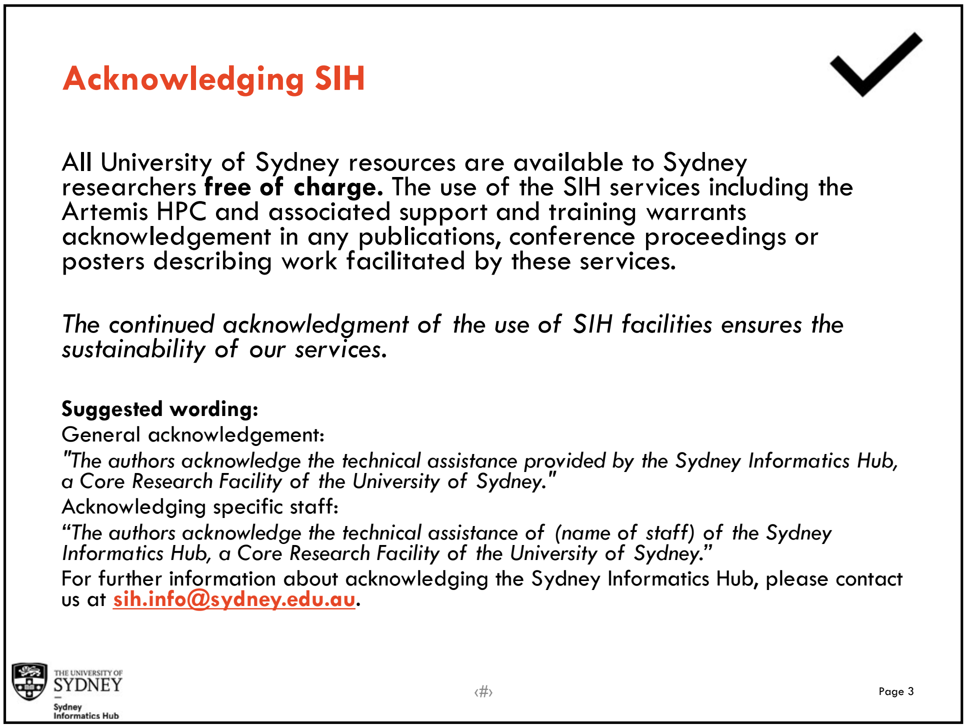
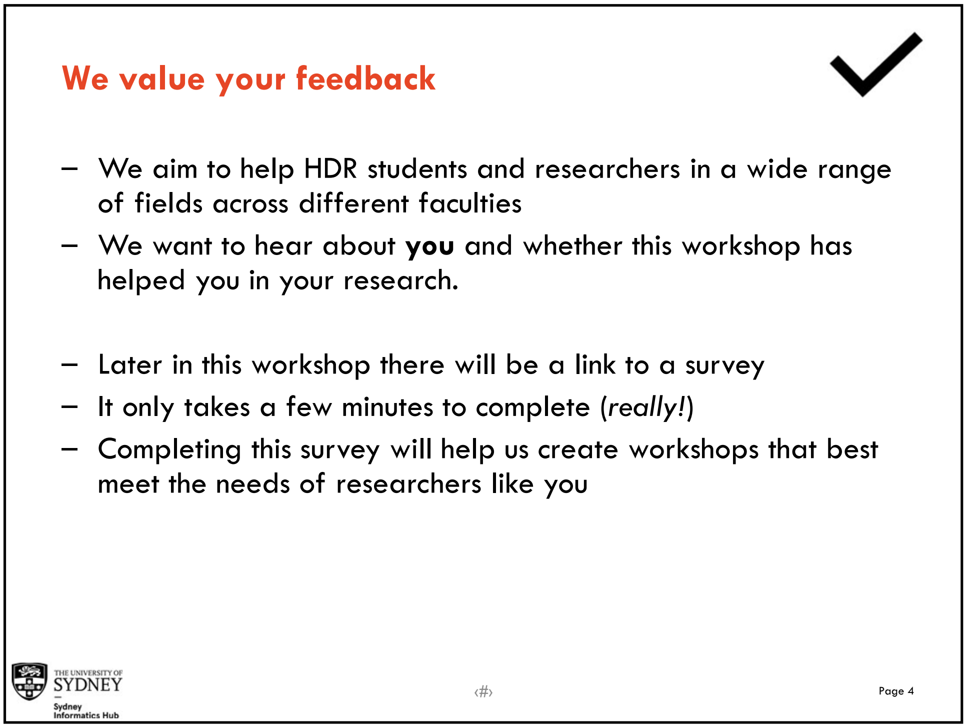


Acknowledging SIH

All University of Sydney resources are available to Sydney researchers **free of charge.** The use of the SIH services including the Artemis HPC and associated support and training warrants acknowledgement in any publications, conference proceedings or posters describing work facilitated by these services.

The continued acknowledgment of the use of SIH facilities ensures the sustainability of our services.

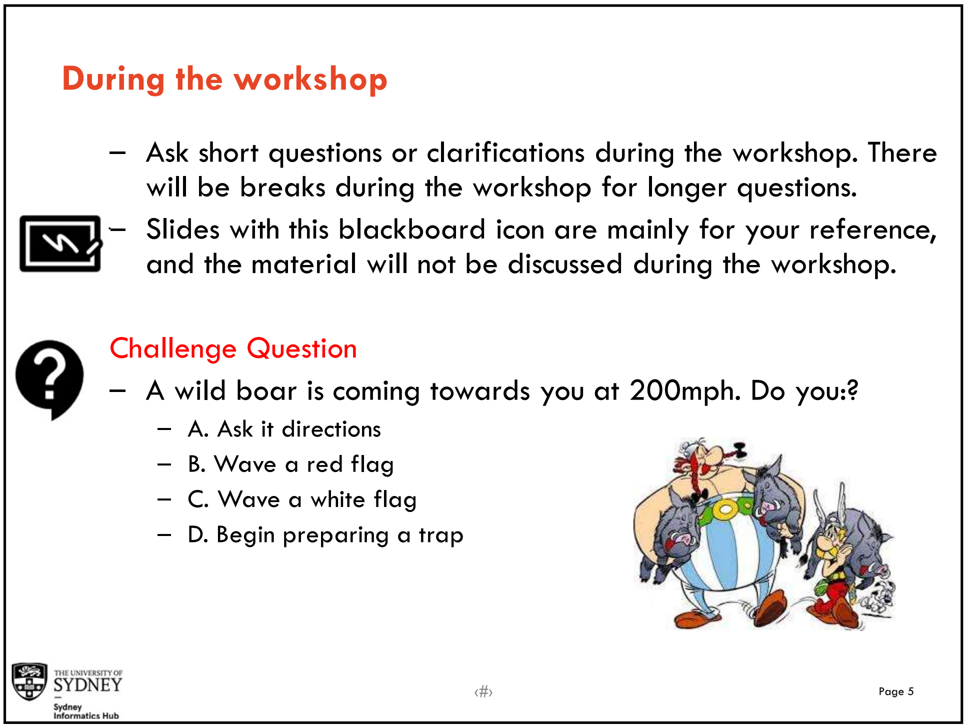
Suggested wording:
General acknowledgement:
"The authors acknowledge the technical assistance provided by the Sydney Informatics Hub, a Core Research Facility of the University of Sydney."
Acknowledging specific staff:
"The authors acknowledge the technical assistance of (name of staff) of the Sydney Informatics Hub, a Core Research Facility of the University of Sydney."
For further information about acknowledging the Sydney Informatics Hub, please contact us at sih.info@sydney.edu.au.



We value your feedback

- We aim to help HDR students and researchers in a wide range of fields across different faculties
- We want to hear about **you** and whether this workshop has helped you in your research.

- Later in this workshop there will be a link to a survey
- It only takes a few minutes to complete (*really!*)
- Completing this survey will help us create workshops that best meet the needs of researchers like you



During the workshop

- Ask short questions or clarifications during the workshop. There will be breaks during the workshop for longer questions.
- Slides with this blackboard icon are mainly for your reference, and the material will not be discussed during the workshop.

Challenge Question

- A wild boar is coming towards you at 200mph. Do you:?
  - A. Ask it directions
  - B. Wave a red flag
  - C. Wave a white flag
  - D. Begin preparing a trap

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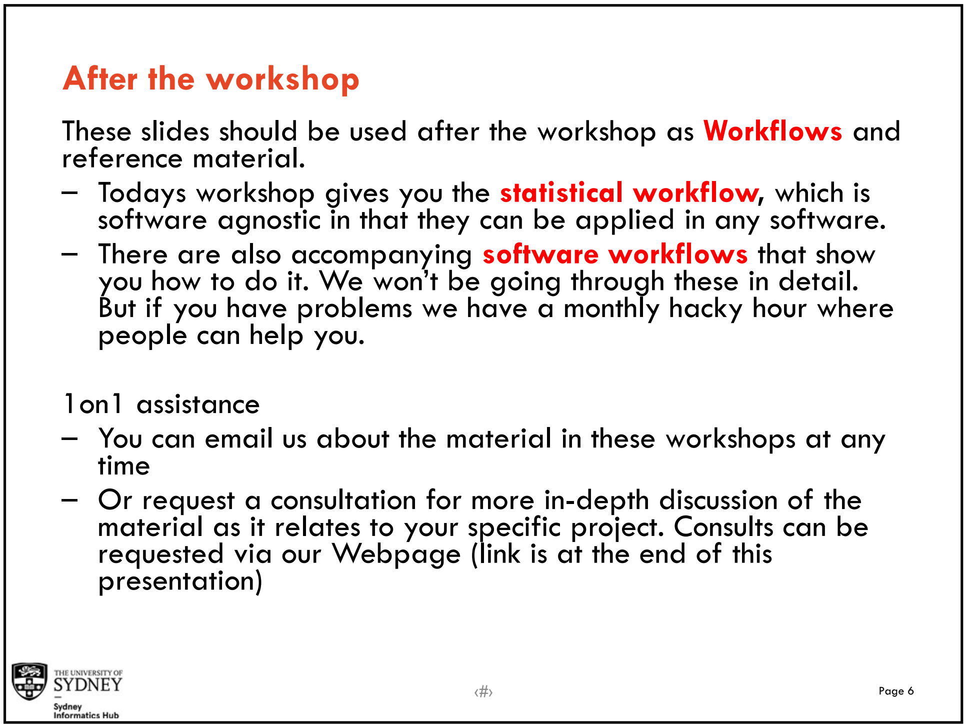

After the workshop

These slides should be used after the workshop as **Workflows** and reference material.

- Todays workshop gives you the **statistical workflow**, which is software agnostic in that they can be applied in any software.
- There are also accompanying **software workflows** that show you how to do it. We won't be going through these in detail. But if you have problems we have a monthly hacky hour where people can help you.

1on1 assistance

- You can email us about the material in these workshops at any time
- Or request a consultation for more in-depth discussion of the material as it relates to your specific project. Consults can be requested via our Webpage (link is at the end of this presentation)

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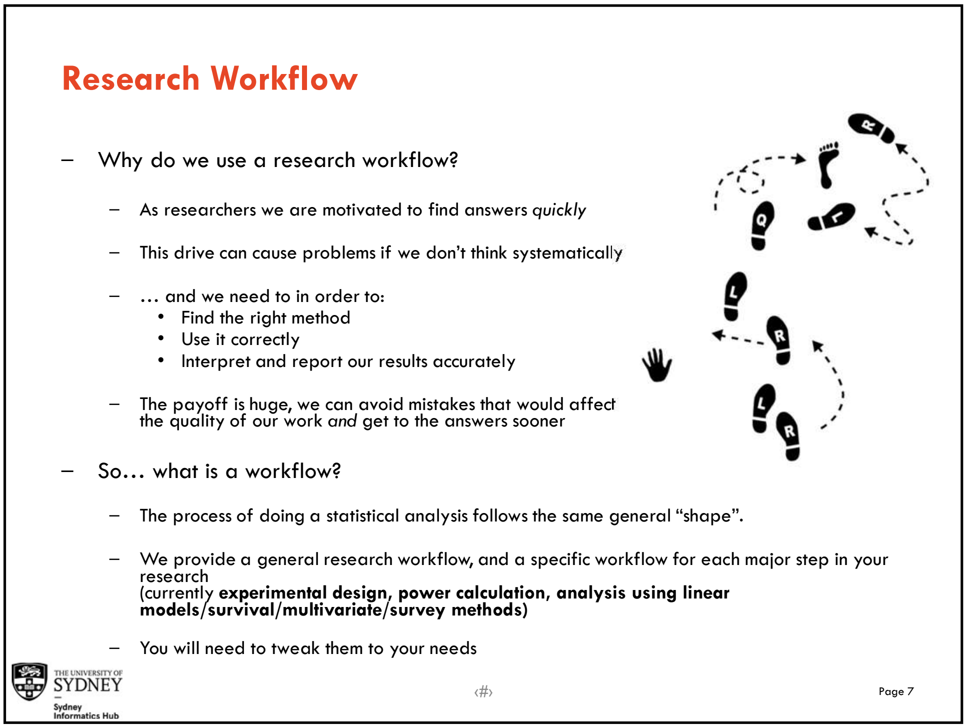

Research Workflow

- Why do we use a research workflow?
  - As researchers we are motivated to find answers *quickly*
  - This drive can cause problems if we don't think systematically
  - … and we need to in order to:
    - Find the right method
    - Use it correctly
    - Interpret and report our results accurately
  - The payoff is huge, we can avoid mistakes that would affect the quality of our work *and* get to the answers sooner
- So… what is a workflow?
  - The process of doing a statistical analysis follows the same general "shape".
  - We provide a general research workflow, and a specific workflow for each major step in your research
    (currently **experimental design, power calculation, analysis using linear models/survival/multivariate/survey methods)**
  - You will need to tweak them to your needs

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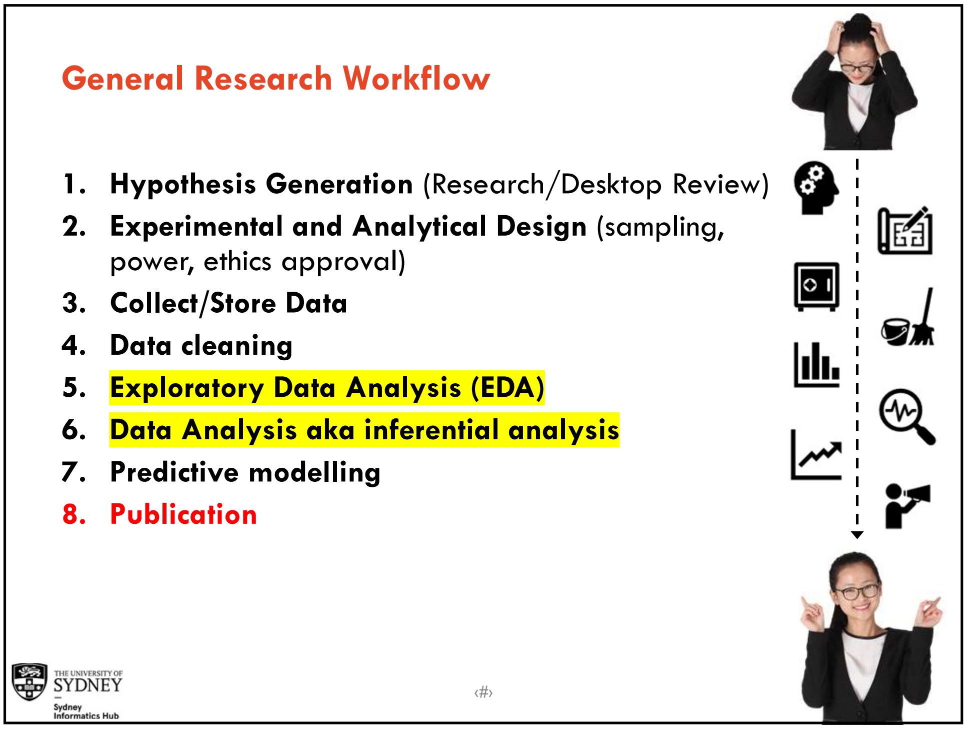

General Research Workflow

1. **Hypothesis Generation** (Research/Desktop Review)
2. **Experimental and Analytical Design** (sampling, power, ethics approval)
3. **Collect/Store Data**
4. **Data cleaning**
5. **Exploratory Data Analysis (EDA)**
6. **Data Analysis aka inferential analysis**
7. **Predictive modelling**
8. **Publication**

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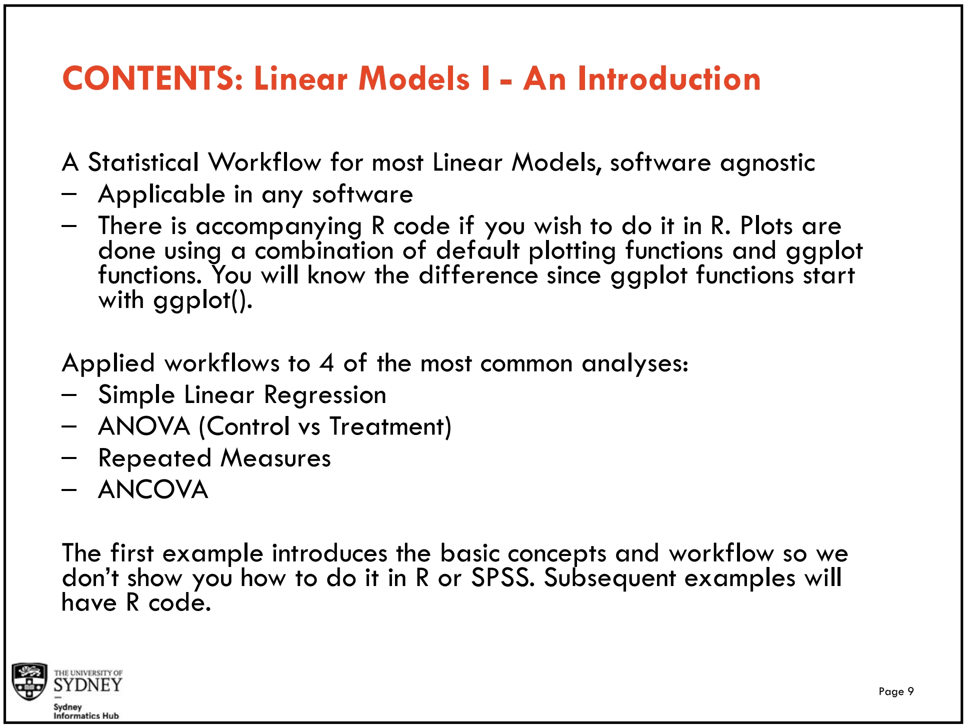

CONTENTS: Linear Models I - An Introduction

A Statistical Workflow for most Linear Models, software agnostic

- Applicable in any software
- There is accompanying R code if you wish to do it in R. Plots are done using a combination of default plotting functions and ggplot functions. You will know the difference since ggplot functions start with ggplot().

Applied workflows to 4 of the most common analyses:

- Simple Linear Regression
- ANOVA (Control vs Treatment)
- Repeated Measures
- ANCOVA

The first example introduces the basic concepts and workflow so we don't show you how to do it in R or SPSS. Subsequent examples will have R code.

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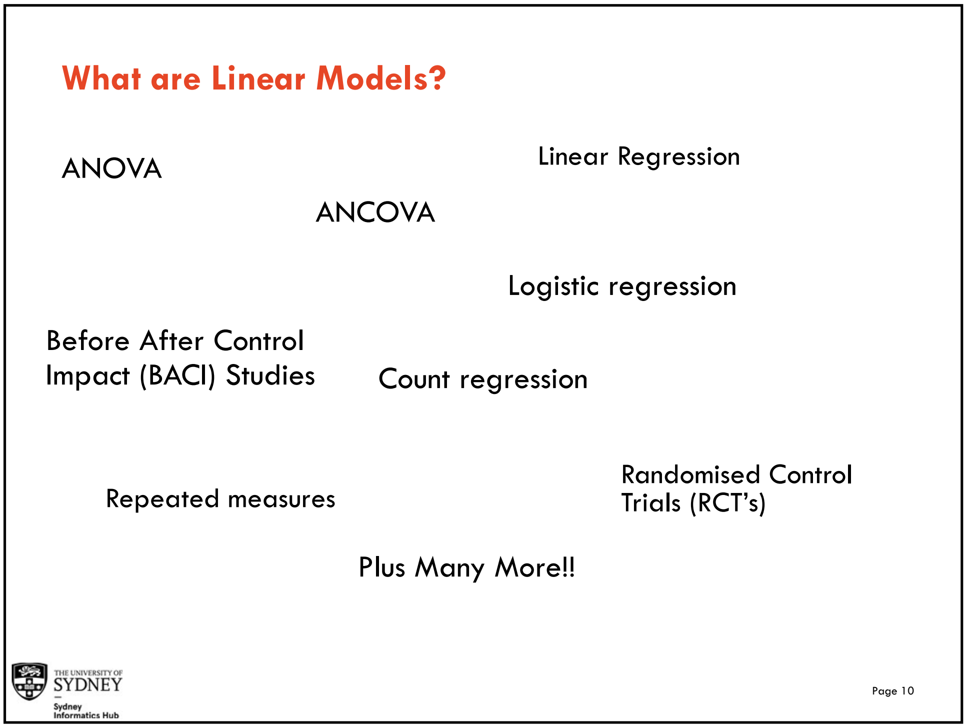

What are Linear Models?

ANOVA

Linear Regression

ANCOVA

Logistic regression

Before After Control Impact (BACI) Studies

Count regression

Repeated measures

Randomised Control Trials (RCT's)

Plus Many More!!

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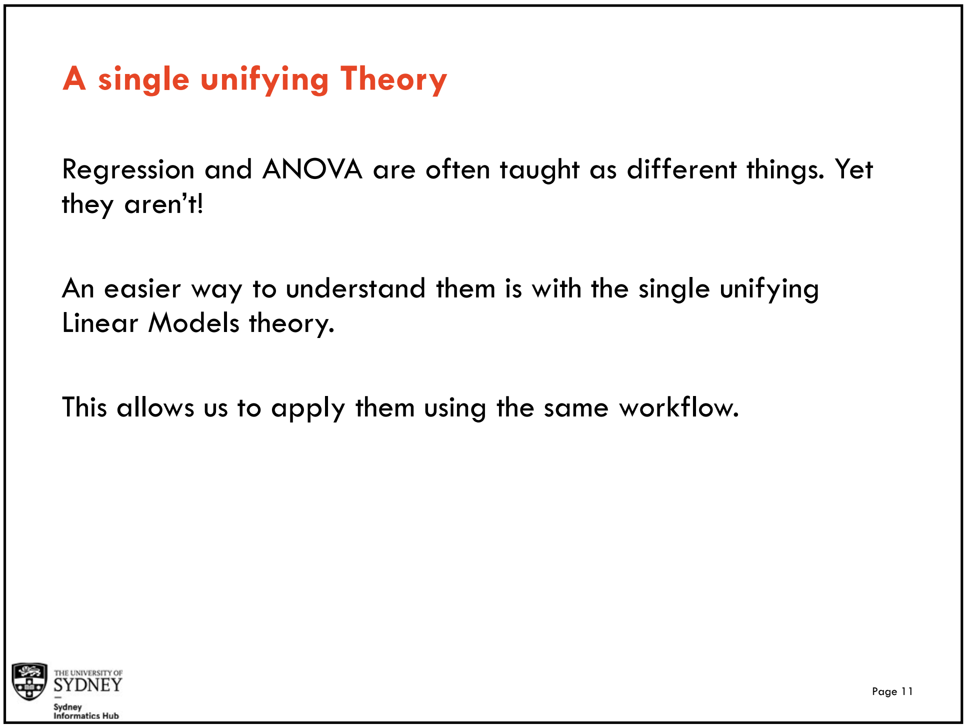

A single unifying Theory

Regression and ANOVA are often taught as different things. Yet they aren't!

An easier way to understand them is with the single unifying Linear Models theory.

This allows us to apply them using the same workflow.

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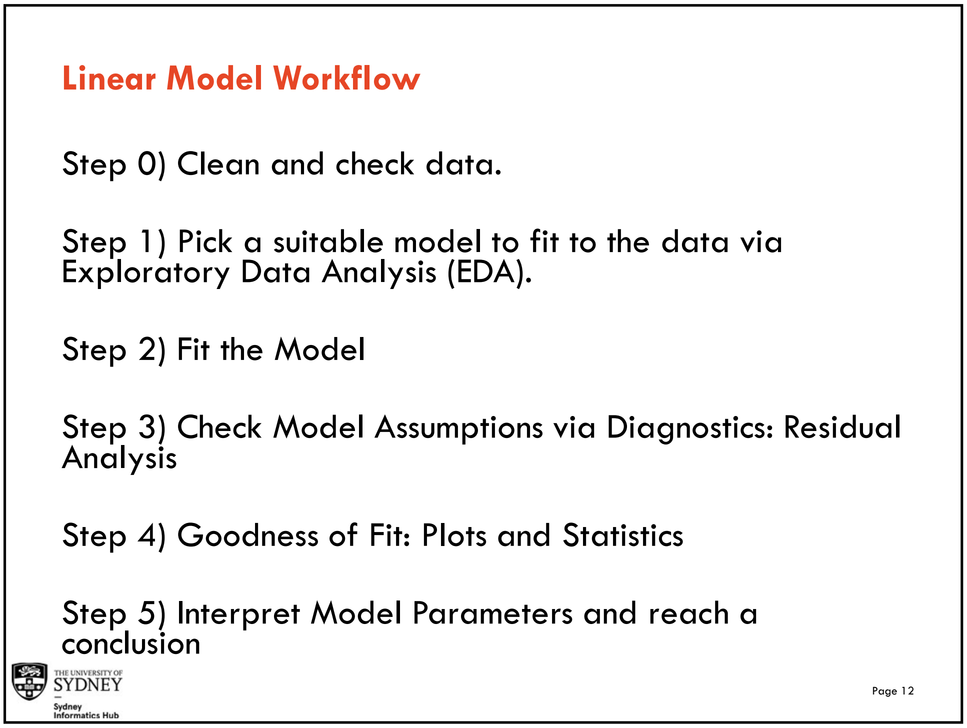

Linear Model Workflow

Step 0) Clean and check data.

Step 1) Pick a suitable model to fit to the data via Exploratory Data Analysis (EDA).

Step 2) Fit the Model

Step 3) Check Model Assumptions via Diagnostics: Residual Analysis

Step 4) Goodness of Fit: Plots and Statistics

Step 5) Interpret Model Parameters and reach a conclusion

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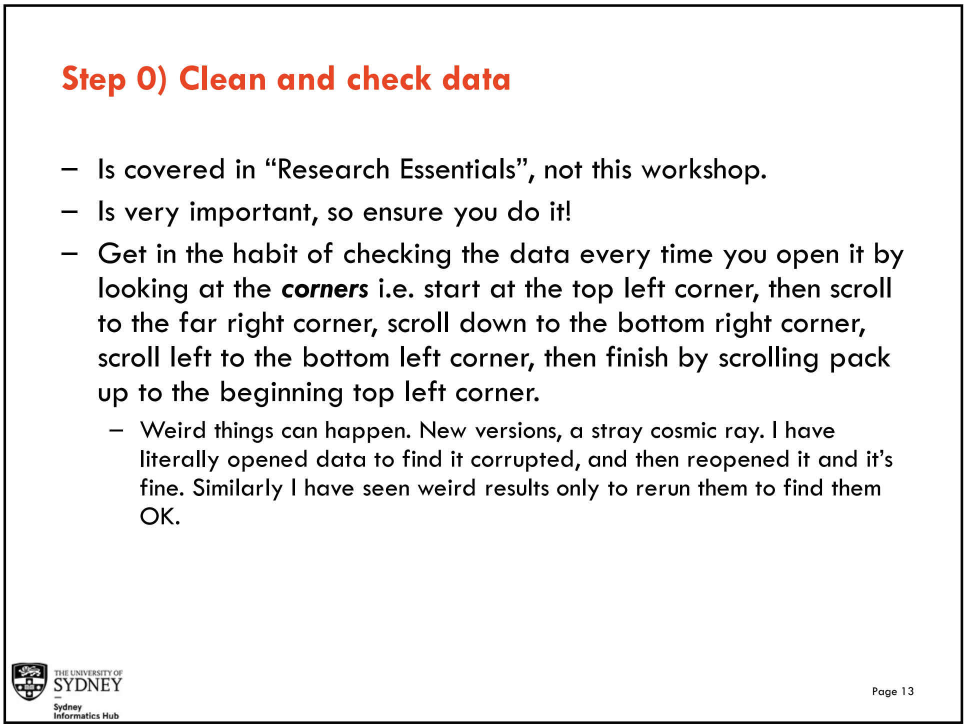

Step 0) Clean and check data

- Is covered in “Research Essentials”, not this workshop.
- Is very important, so ensure you do it!
- Get in the habit of checking the data every time you open it by looking at the ***corners*** i.e. start at the top left corner, then scroll to the far right corner, scroll down to the bottom right corner, scroll left to the bottom left corner, then finish by scrolling pack up to the beginning top left corner.
  - Weird things can happen. New versions, a stray cosmic ray. I have literally opened data to find it corrupted, and then reopened it and it’s fine. Similarly I have seen weird results only to rerun them to find them OK.

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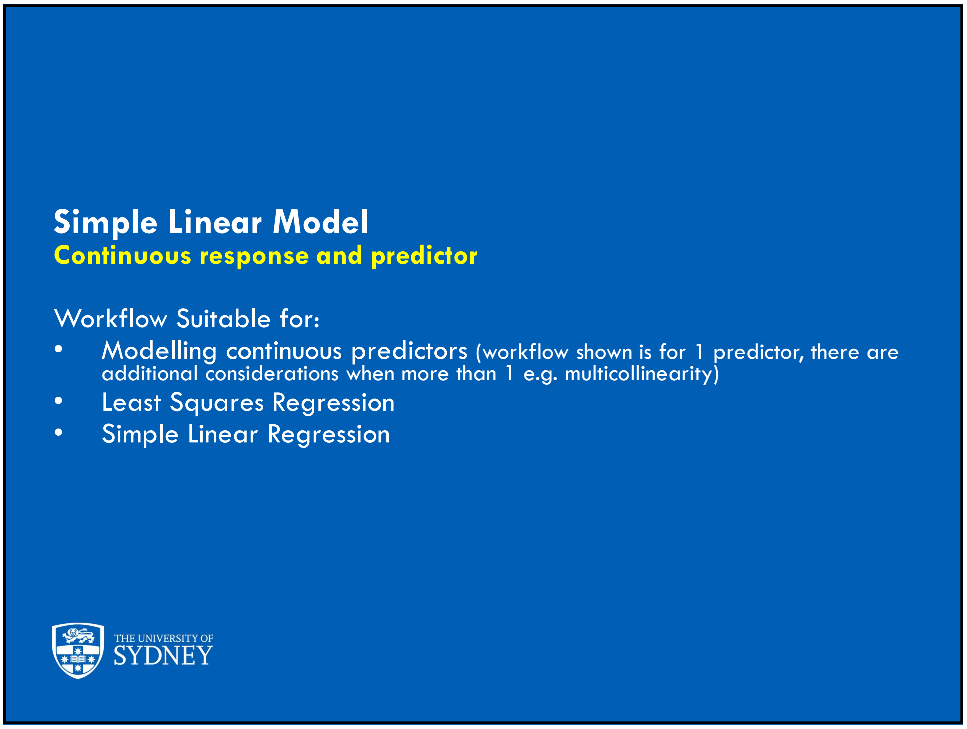

Simple Linear Model

Continuous response and predictor

Workflow Suitable for:

- Modelling continuous predictors (workflow shown is for 1 predictor, there are additional considerations when more than 1 e.g. multicollinearity)
- Least Squares Regression
- Simple Linear Regression

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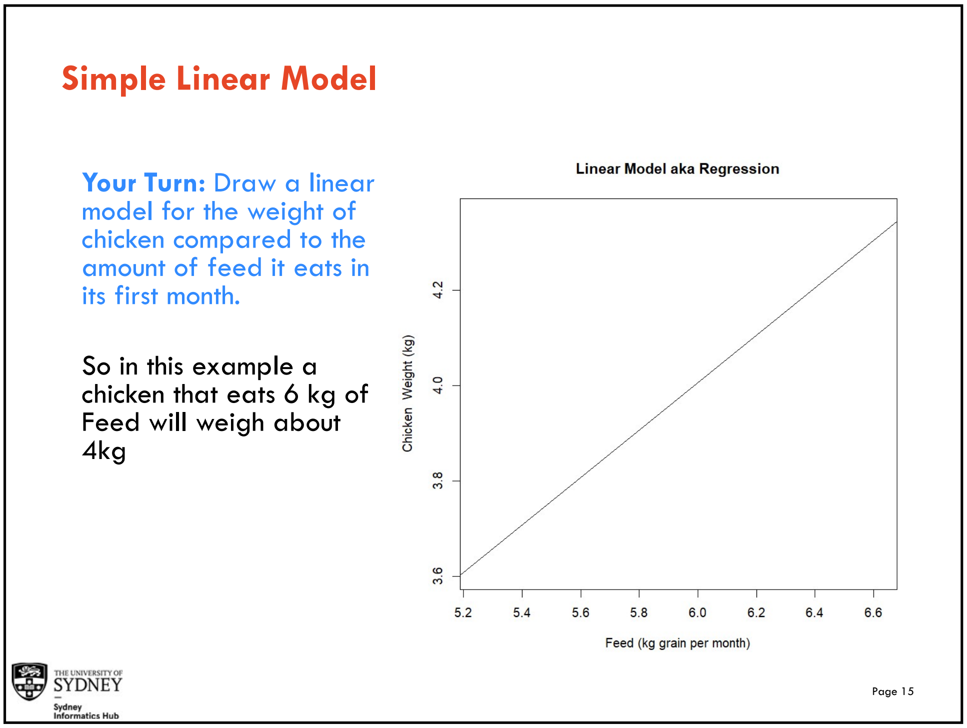

Simple Linear Model

Your Turn: Draw a linear model for the weight of chicken compared to the amount of feed it eats in its first month.

So in this example a chicken that eats 6 kg of Feed will weigh about 4kg

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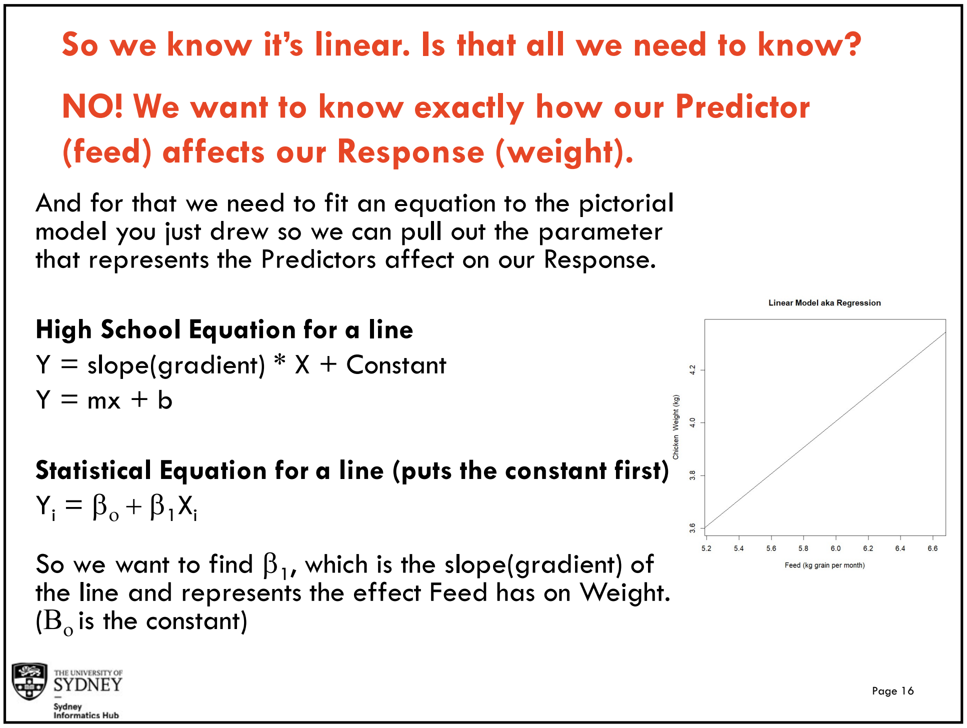

So we know it's linear. Is that all we need to know?

NO! We want to know exactly how our Predictor (feed) affects our Response (weight).

And for that we need to fit an equation to the pictorial model you just drew so we can pull out the parameter that represents the Predictors affect on our Response.

High School Equation for a line

Y = slope(gradient) * X + Constant

Y = mx + b

Statistical Equation for a line (puts the constant first)

$Y_i = \beta_o + \beta_1 X_i$

So we want to find β_1, which is the slope(gradient) of the line and represents the effect Feed has on Weight. (B_o is the constant)

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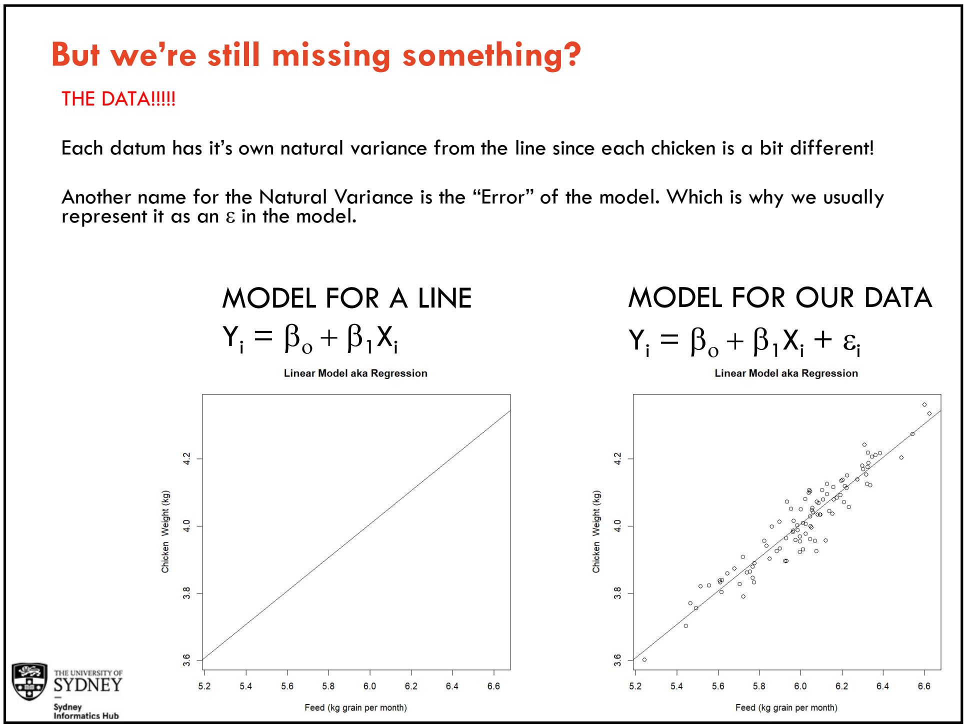

But we're still missing something?

THE DATA!!!!!

Each datum has it's own natural variance from the line since each chicken is a bit different!

Another name for the Natural Variance is the "Error" of the model. Which is why we usually represent it as an ε in the model.

MODEL FOR A LINE

$Y_i = \beta_o + \beta_1 X_i$

MODEL FOR OUR DATA

$Y_i = \beta_o + \beta_1 X_i + \varepsilon_i$

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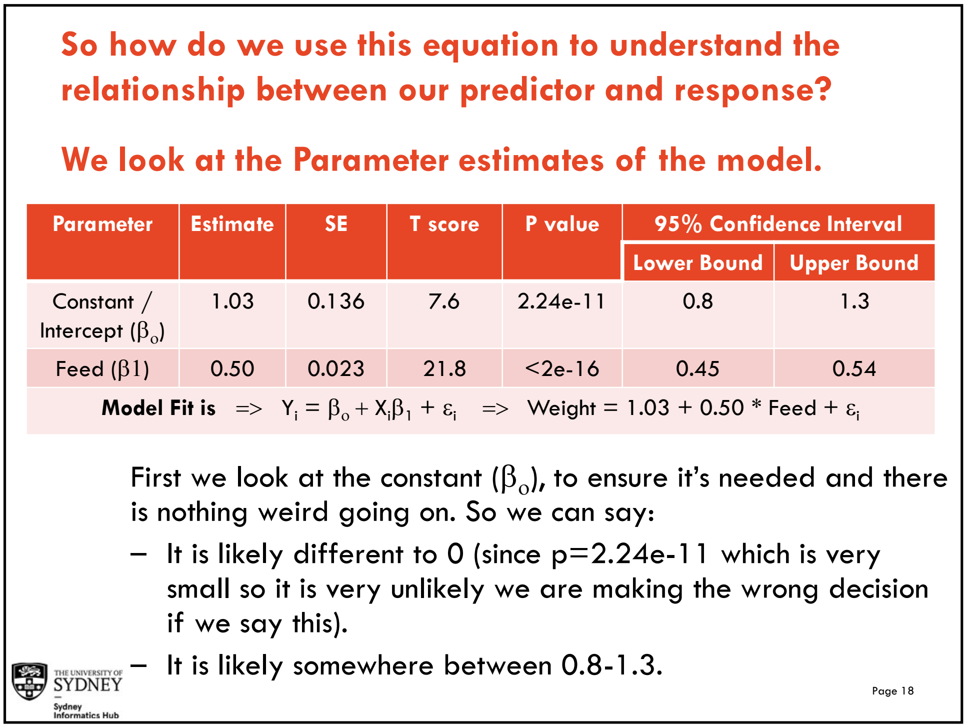

So how do we use this equation to understand the relationship between our predictor and response?

We look at the Parameter estimates of the model.

Parameter	Estimate	SE	T score	P value	95% Confidence Interval	
					Lower Bound	Upper Bound
Constant / Intercept (β_o)	1.03	0.136	7.6	2.24e-11	0.8	1.3
Feed (β1)	0.50	0.023	21.8	<2e-16	0.45	0.54
Model Fit is => $Y_i = \beta_o + X_i\beta_1 + \varepsilon_i$ => Weight = 1.03 + 0.50 * Feed + ε_i						

First we look at the constant (β_o), to ensure it's needed and there is nothing weird going on. So we can say:

- It is likely different to 0 (since p=2.24e-11 which is very small so it is very unlikely we are making the wrong decision if we say this).
- It is likely somewhere between 0.8-1.3.

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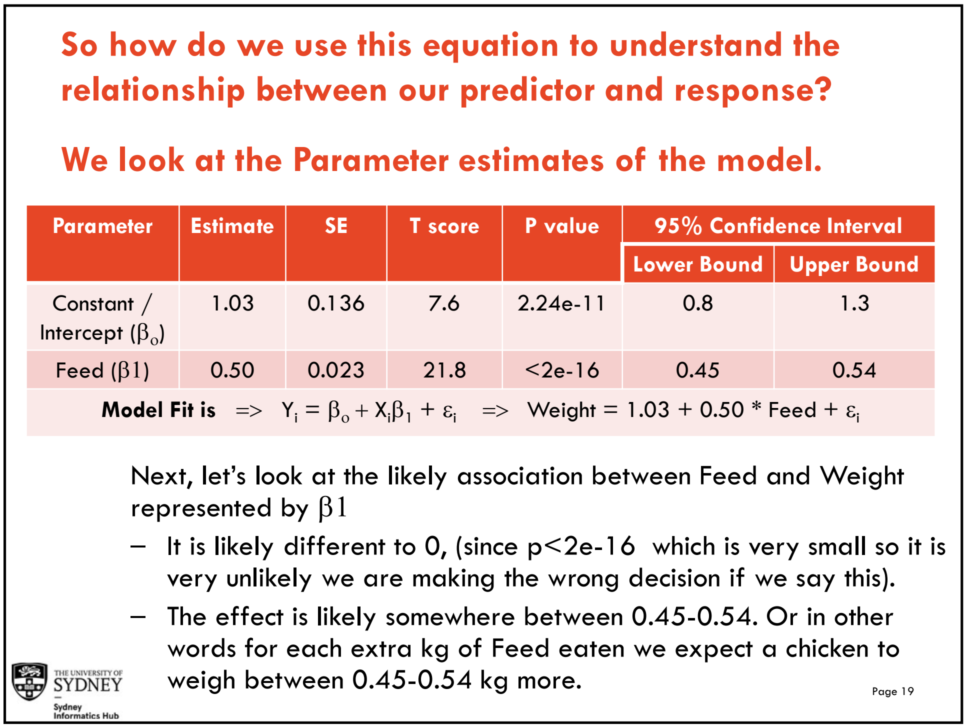

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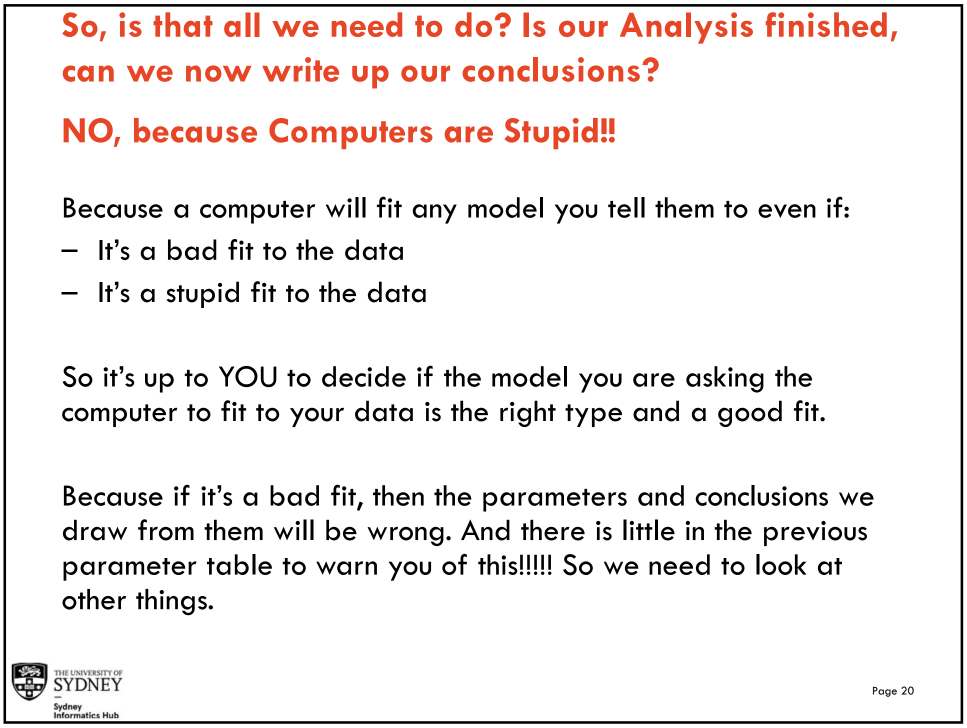
Feed ($\beta 1$)	0.50	0.023	21.8	<2e-16	0.45	0.54
Model Fit is => $Y_i = \beta_o + X_i\beta_1 + \varepsilon_i$ => Weight = 1.03 + 0.50 * Feed + ε_i						

Next, let's look at the likely association between Feed and Weight represented by $\beta 1$

- It is likely different to 0, (since p<2e-16 which is very small so it is very unlikely we are making the wrong decision if we say this).
- The effect is likely somewhere between 0.45-0.54. Or in other words for each extra kg of Feed eaten we expect a chicken to weigh between 0.45-0.54 kg more.



So, is that all we need to do? Is our Analysis finished, can we now write up our conclusions?

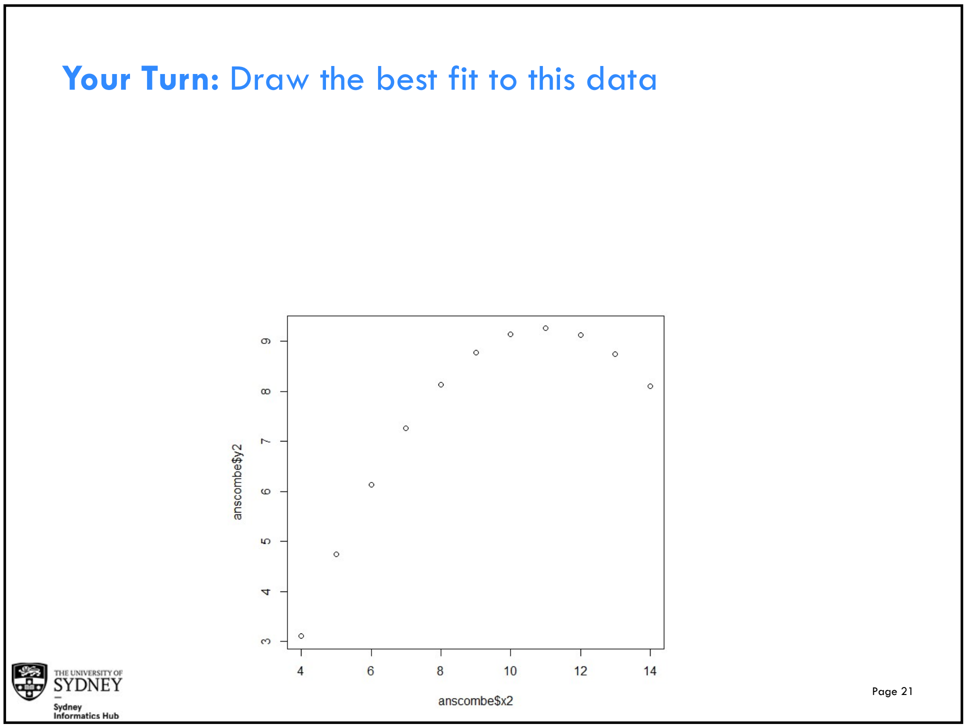
NO, because Computers are Stupid!!

Because a computer will fit any model you tell them to even if:

- It's a bad fit to the data
- It's a stupid fit to the data

So it's up to YOU to decide if the model you are asking the computer to fit to your data is the right type and a good fit.

Because if it's a bad fit, then the parameters and conclusions we draw from them will be wrong. And there is little in the previous parameter table to warn you of this!!!!! So we need to look at other things.



Your Turn: Draw the best fit to this data

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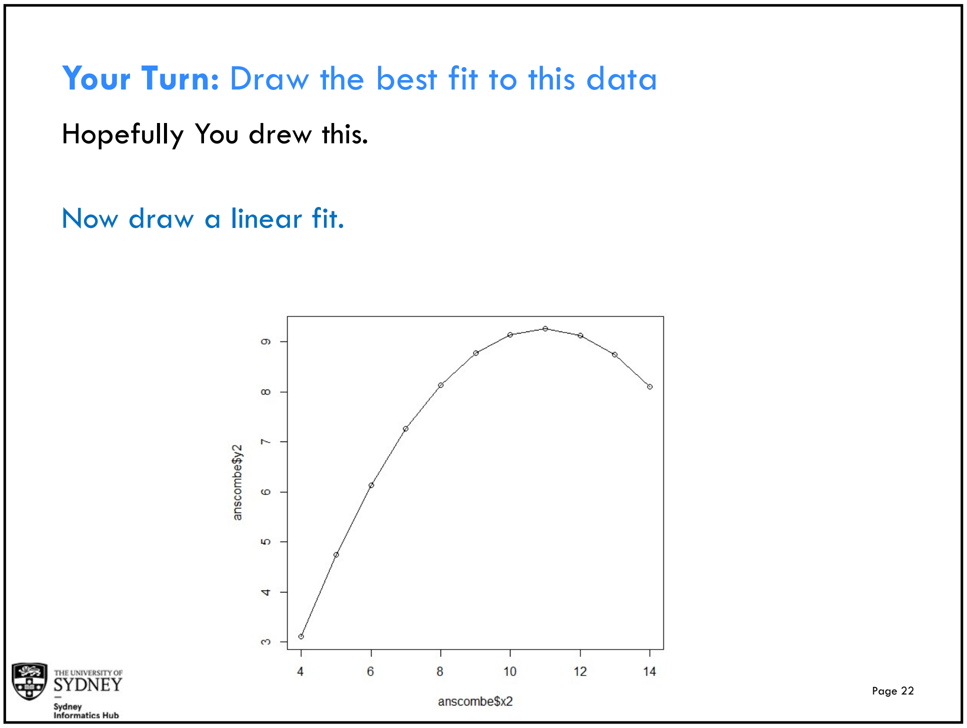

Your Turn: Draw the best fit to this data

Hopefully You drew this.

Now draw a linear fit.

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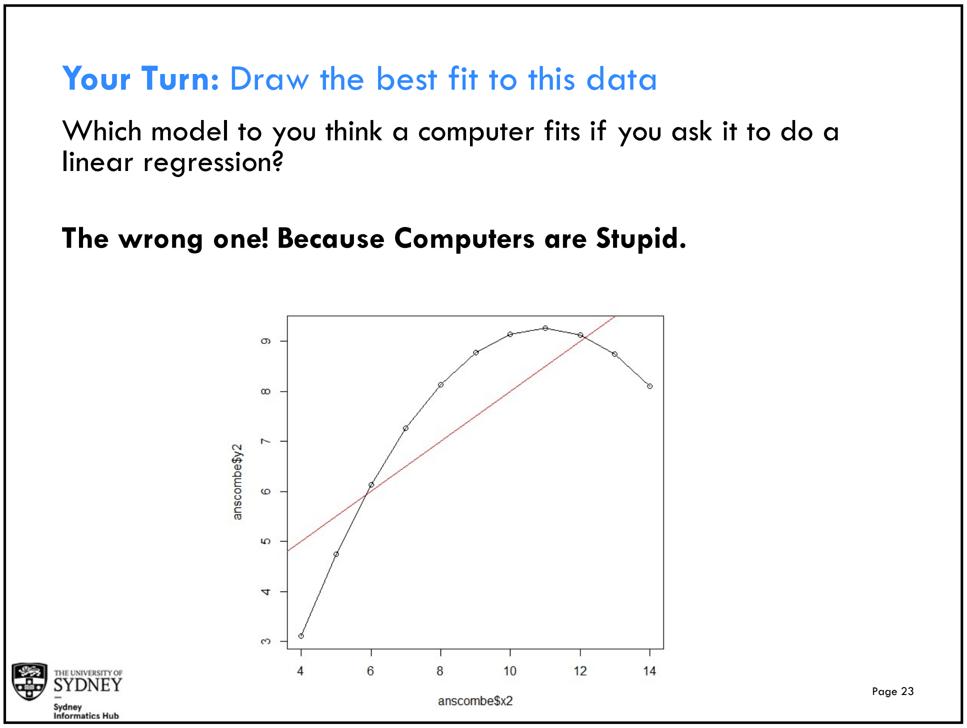

Your Turn: Draw the best fit to this data

Which model to you think a computer fits if you ask it to do a linear regression?

The wrong one! Because Computers are Stupid.

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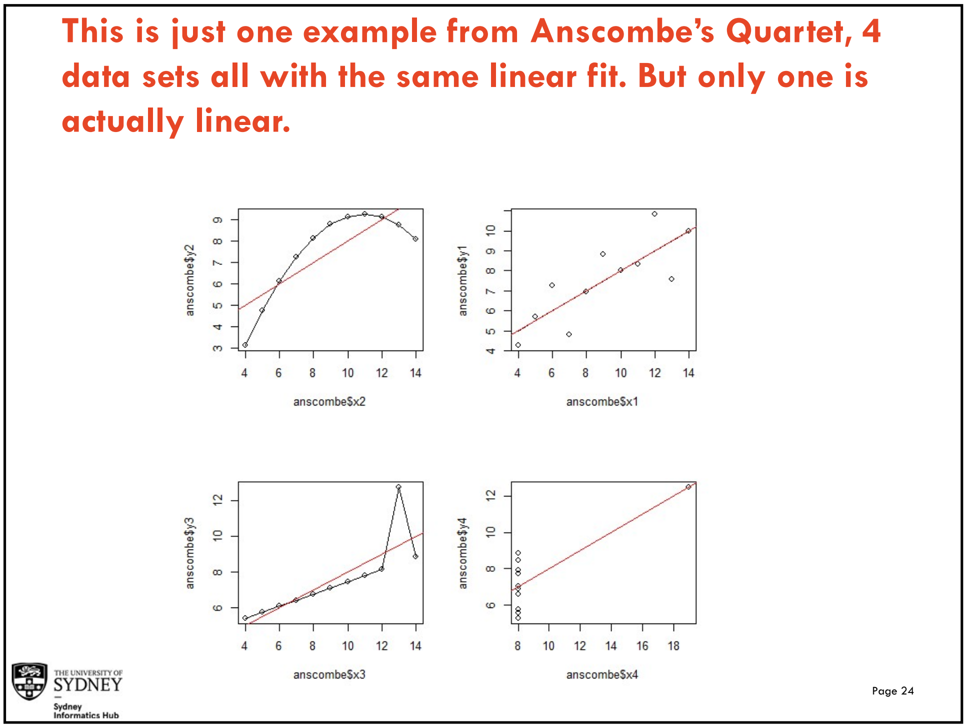

This is just one example from Anscombe's Quartet, 4 data sets all with the same linear fit. But only one is actually linear.

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So how do we decide if the model we are asking the computer to use is a good enough fit to the data that the parameters, and the conclusions we make from them, make sense?

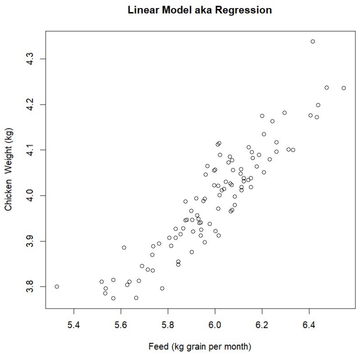
1) Check Model Assumptions via Diagnostics
   1) Linearity
   2) Normal Error
   3) Independence

2) Check Model Goodness of Fit
   1) How much of the response variance does the model explain?
   2) Is the model a good fit of the data overall, or is it biased towards explaining just a couple datum?

Step 1) Pick a suitable model to fit to the data via Exploratory Data Analysis (EDA)

Linearity: Draw A Graphical model of the data

1. Simply plot the data and have a look. Is a linear model a good fit to the data?
2. Try to write down the model you want to fit as well
   1. $Y_i = \beta_o + X_i\beta_1 + \varepsilon_i$



Step 1) Pick a suitable model to fit to the data via Exploratory Data Analysis (EDA)

Independence: Consider your experimental design

Is there anything about it that might lead to datum being correlated with each other. For example, if we had repeated measures on the same patient (chicken) then we would expect these to be correlated i.e. dependant on each other.

Modelling independence correctly is important for 3 main reasons:

1) Ensures the correct sample size is used. For example if I measured the chickens weight 100 times a second for 60 seconds do a really have 6000 samples per chicken? NO, of course not. Because the 6000 samples aren't independent. This is known as **Pseudo Replication** and inflates our sample size, lowering our SE's and making our p-values too low and confidence intervals too narrow.

2) Partitioning extra sources of error/noise which makes our analysis more accurate, which is done using mixed models for designs such as split-plots, blocked, repeated measures.

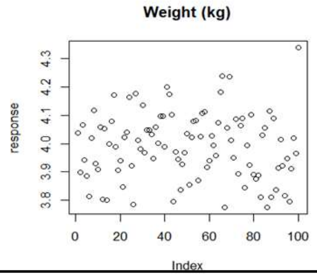
3) Structural Correlation that should be added to the model e.g. serial correlation such as Auto-regressive correlation.

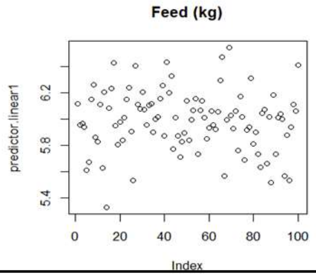
Step 1) Pick a suitable model to fit to the data via Exploratory Data Analysis (EDA)

Independence: Plot the data using a "Serial Plot"

This is simply a plot of the data, one after each other, as recorded in your data. You are looking for unexplained sequences of high or low values i.e. unexplained correlations.

- You can also organise your data into different structures to look for different types of Dependence e.g. if repeated measures then organise so each persons (chickens) data is sequential.
- You can also plot lag correlations.





Step 1) Pick a suitable model to fit to the data via Exploratory Data Analysis (EDA)

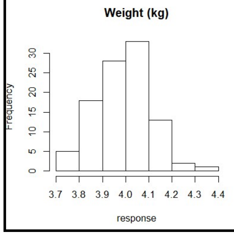
Normality

This is a very poorly understood assumption. The Assumption is that the ***Error, not the Response*** is normal. Meaning we can't test it until we fit a model. So don't make the mistake of thinking just because your data isn't normal this assumption has been violated.

What we can do is consider exactly what it is we are modelling and also look at the response using a histogram to see if a normal error might not fit. Obviously if the response looks normal there is a good chance the errors will be too. However a non-normal response can have a normal error (which I will show you when we look at ANOVA).

The main thing we are looking for here are things that usually prevent the error from being normal and are better fit using different models such as the response being non continuous e.g. binary, counts, extreme outliers, extreme skewness, truncation.

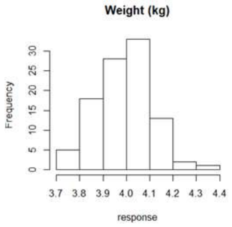
It's worth noting that discrete data can be modelled using a normal error under some circumstances e.g. weight rounded to the nearest gram is technically discrete, but can be fit using a normal error. Counts can also be fit using a normal error if large enough.

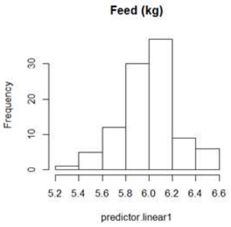


Step 1) Pick a suitable model to fit to the data via Exploratory Data Analysis (EDA)

Outliers

This is a also very poorly understood assumption. We want a model represent the bulk of the data. We don't want it biased towards 1 or 2 outlying influential points. Just like checking the normality assumption we can only test this for sure once we have fit a model. However it is always worth looking at all our data to see if there are any outliers we might need to deal with. The best way to do this is via histograms.





Step 1) Fixing Model Assumption Problems

This is a complex business and is beyond the scope of this workshop. It is covered in more detail in other Linear Model courses we give. The quick answer is that you will usually need to use a different model. In Brief:

Non linear fit

1. Add in quadratic and non linear terms for either the predictors or the response (GLM's can add such terms for the response via the link function).
2. Use a non linear model such as a GAM.

Normal error is inappropriate

1. Use a different type of linear model. A Generalised Linear Model (GLM) with a different Error distribution often works e.g. binomial for binary data (logistic regression), Poisson for count data.

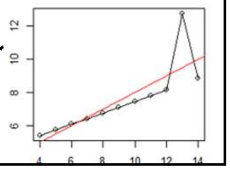
Lack of Independence

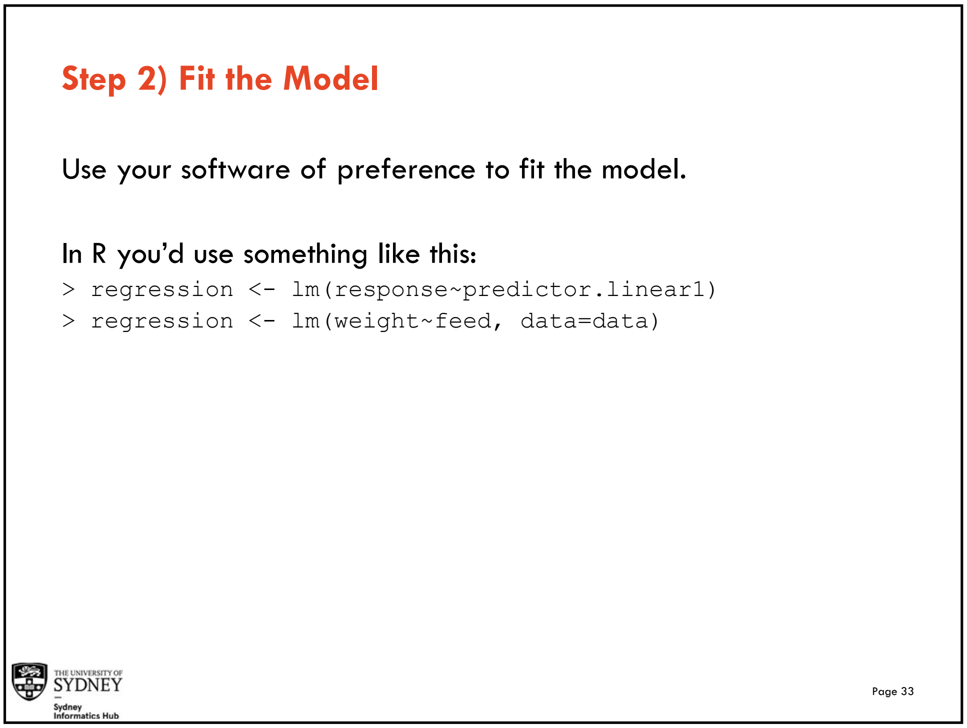
1. Fit a mixed model that accounts for the correlation structure.
2. Remove datum until they are independent (censuring).
3. Average the independent data e.g. average the 6000 chicken weights so we have a single score. Has the advantage that usually makes the data normally distributed (by invoking the CLT)

Step 1) Fixing Model Assumption Problems

Outliers

1. Check to see if they are a data entry or collection mistake and can be removed.
2. Consider transformations that reduce their influence e.g. log transforms will reduce the influence of large outliers.
3. Consider removing them to get a model that is a better fit to the majority of the data. If this is done one ***must*** say so in any reporting. For example: looking at the Anscombe example on the right. What is a better model. A line through the datum in a straight line, while saying there was a single large outlier. Or the red line shown?
4. Consider other models that can handle the outliers.





Step 2) Fit the Model

Use your software of preference to fit the model.

In R you'd use something like this:

```
> regression <- lm(response~predictor.linear1)
> regression <- lm(weight~feed, data=data)
```

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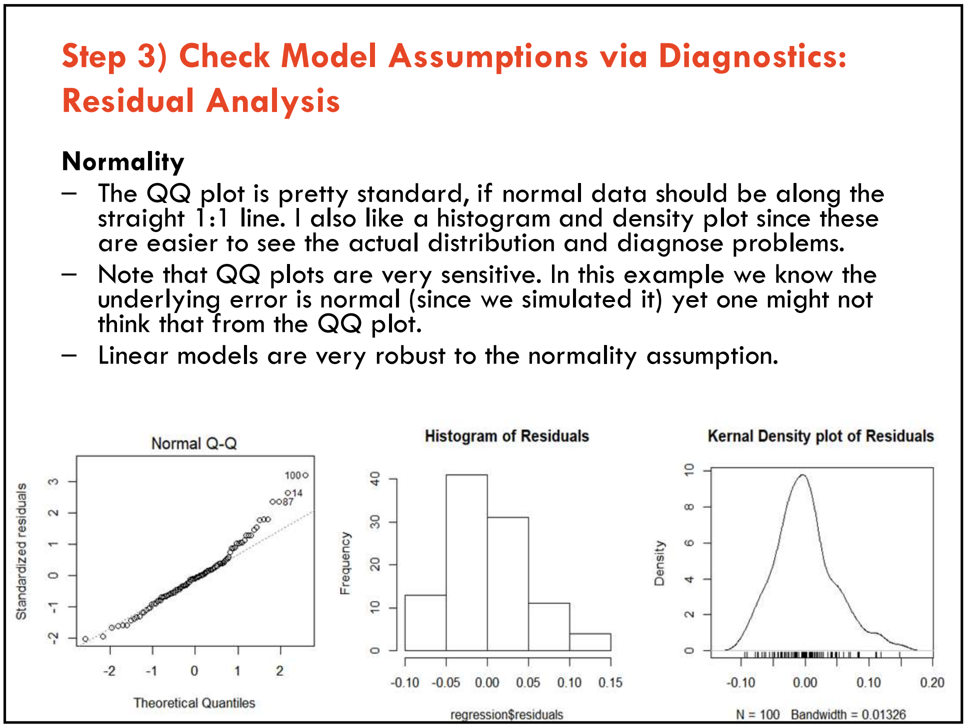

Step 3) Check Model Assumptions via Diagnostics: Residual Analysis

Normality

- The QQ plot is pretty standard, if normal data should be along the straight 1:1 line. I also like a histogram and density plot since these are easier to see the actual distribution and diagnose problems.
- Note that QQ plots are very sensitive. In this example we know the underlying error is normal (since we simulated it) yet one might not think that from the QQ plot.
- Linear models are very robust to the normality assumption.

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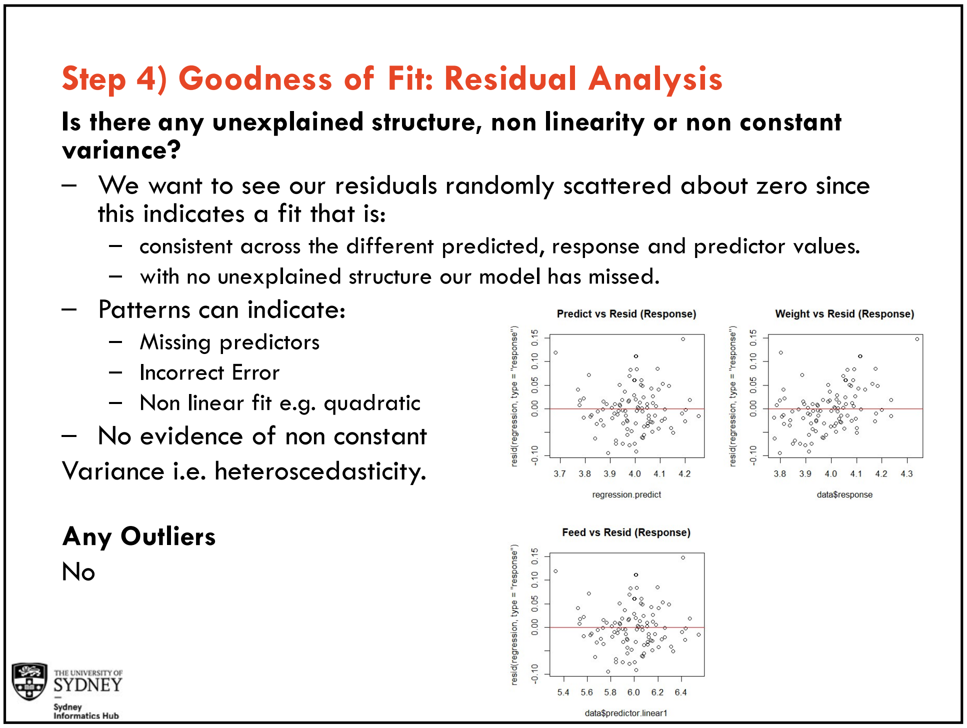

Step 4) Goodness of Fit: Residual Analysis

Is there any unexplained structure, non linearity or non constant variance?

- We want to see our residuals randomly scattered about zero since this indicates a fit that is:
  - consistent across the different predicted, response and predictor values.
  - with no unexplained structure our model has missed.
- Patterns can indicate:
  - Missing predictors
  - Incorrect Error
  - Non linear fit e.g. quadratic
- No evidence of non constant

Variance i.e. heteroscedasticity.

Any Outliers

No

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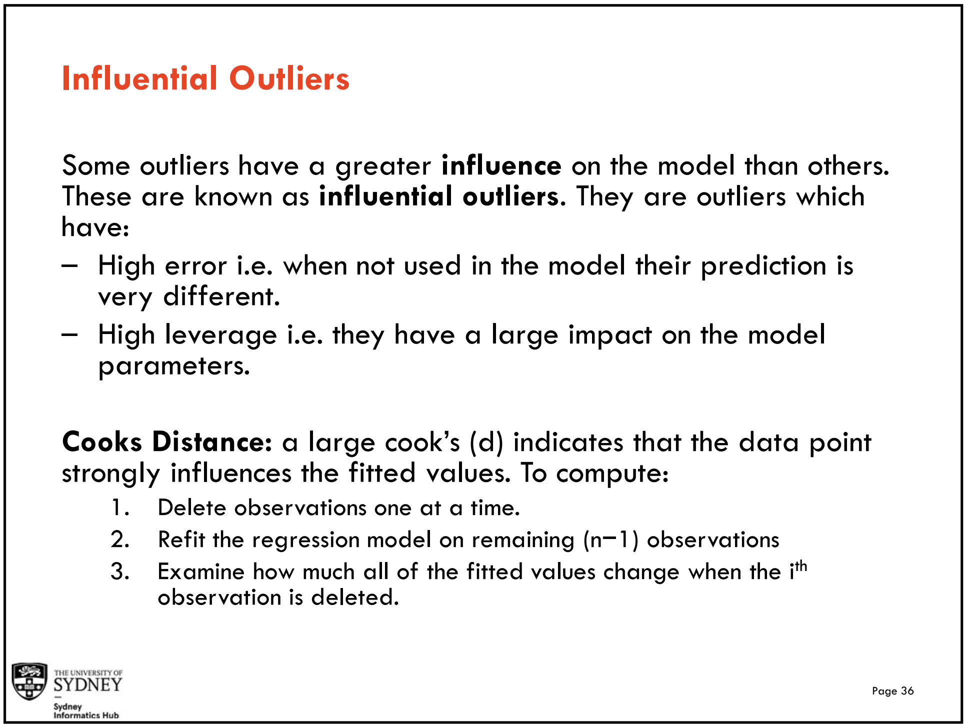

Influential Outliers

Some outliers have a greater **influence** on the model than others. These are known as **influential outliers**. They are outliers which have:

- High error i.e. when not used in the model their prediction is very different.
- High leverage i.e. they have a large impact on the model parameters.

Cooks Distance: a large cook's (d) indicates that the data point strongly influences the fitted values. To compute:

1. Delete observations one at a time.
2. Refit the regression model on remaining (n−1) observations
3. Examine how much all of the fitted values change when the i^{th} observation is deleted.

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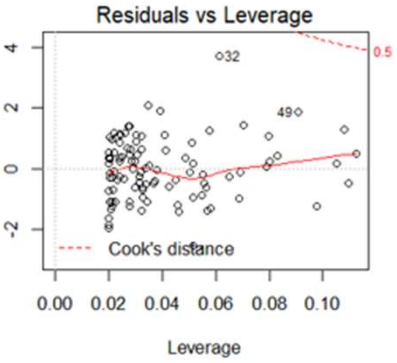
Influential Outliers



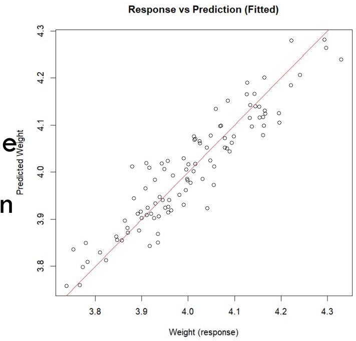
All points within the Cooks distance red dotted lines - so no evidence of influential outliers.

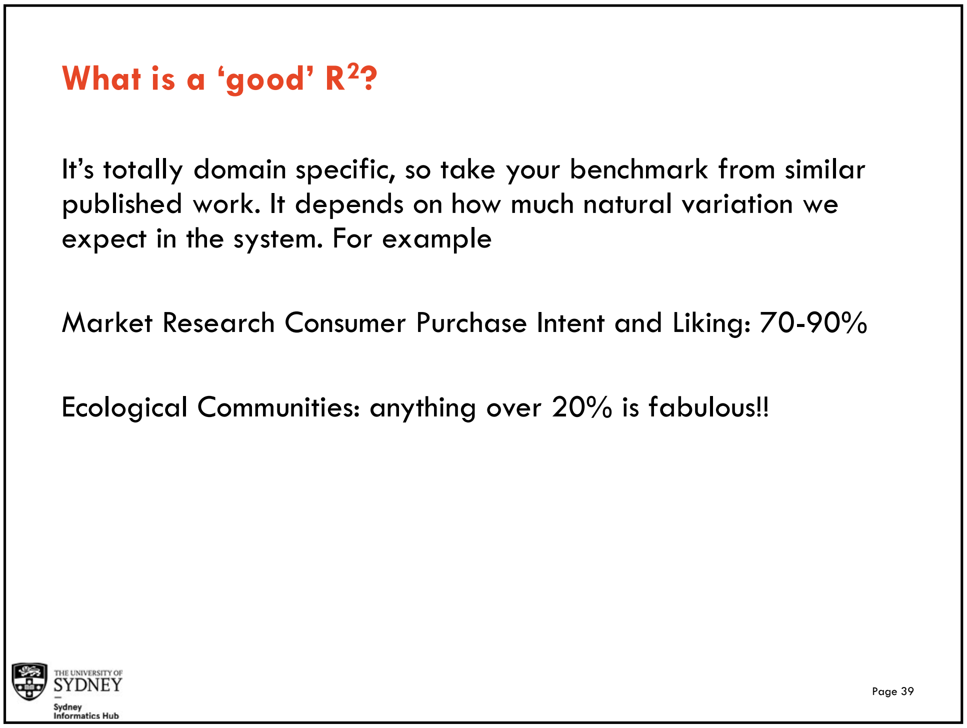
Step 4) Goodness of Fit: Plots and Statistics

So far we have established our model is a ***good fit to our data*** and there is ***nothing obvious we have missed***. Next question. ***How well does it predict i.e. fit, the data?***

This plot is a good visual representation of model fit. If the response is being exactly predicted than we expect it to fall along the 1:1 line.

The correlation along this line is the most commonly used Goodness of Fit Statistic: called R^2. It is literally the correlation of the response and prediction squared. And represents the % of the responses variation the prediction i.e. model, explains. In this example it is 88%.



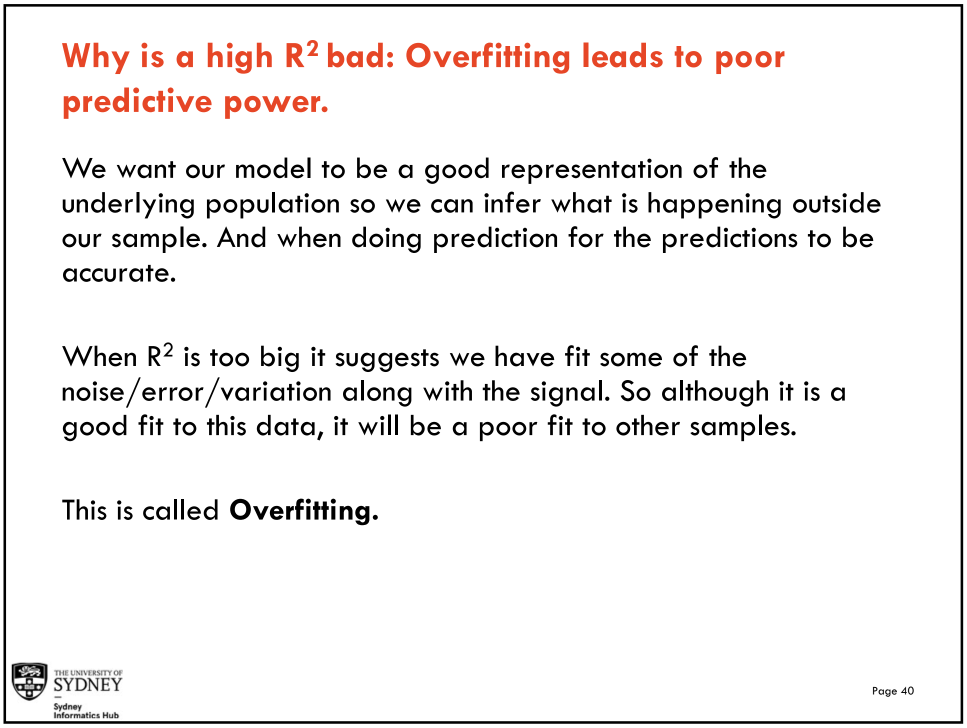


What is a ‘good’ R^2?

It’s totally domain specific, so take your benchmark from similar published work. It depends on how much natural variation we expect in the system. For example

Market Research Consumer Purchase Intent and Liking: 70-90%

Ecological Communities: anything over 20% is fabulous!!

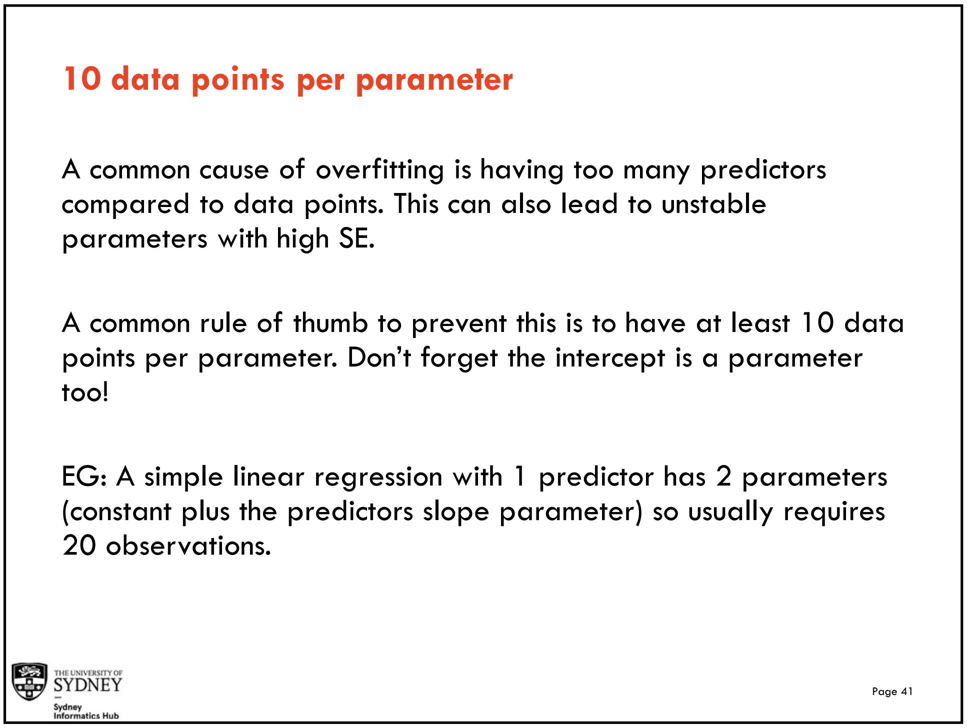


Why is a high R^2 bad: Overfitting leads to poor predictive power.

We want our model to be a good representation of the underlying population so we can infer what is happening outside our sample. And when doing prediction for the predictions to be accurate.

When R^2 is too big it suggests we have fit some of the noise/error/variation along with the signal. So although it is a good fit to this data, it will be a poor fit to other samples.

This is called **Overfitting.**



10 data points per parameter

A common cause of overfitting is having too many predictors compared to data points. This can also lead to unstable parameters with high SE.

A common rule of thumb to prevent this is to have at least 10 data points per parameter. Don't forget the intercept is a parameter too!

EG: A simple linear regression with 1 predictor has 2 parameters (constant plus the predictors slope parameter) so usually requires 20 observations.

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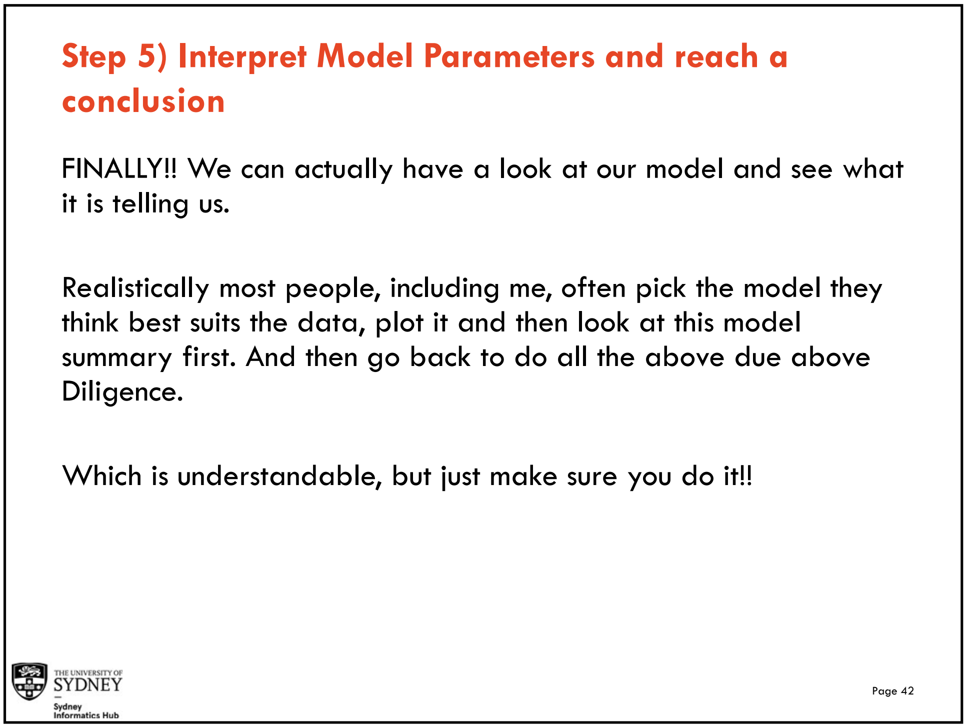

Step 5) Interpret Model Parameters and reach a conclusion

FINALLY!! We can actually have a look at our model and see what it is telling us.

Realistically most people, including me, often pick the model they think best suits the data, plot it and then look at this model summary first. And then go back to do all the above due above Diligence.

Which is understandable, but just make sure you do it!!

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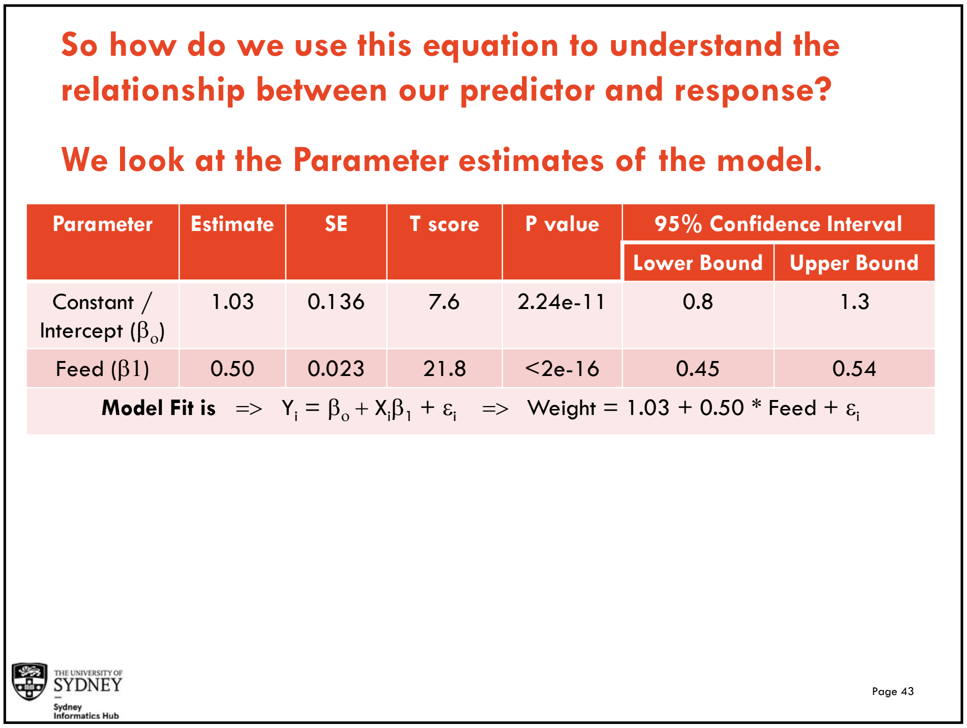

So how do we use this equation to understand the relationship between our predictor and response?

We look at the Parameter estimates of the model.

Parameter	Estimate	SE	T score	P value	95% Confidence Interval	
					Lower Bound	Upper Bound
Constant / Intercept (β_o)	1.03	0.136	7.6	2.24e-11	0.8	1.3
Feed (β1)	0.50	0.023	21.8	<2e-16	0.45	0.54
Model Fit is => $Y_i = \beta_o + X_i\beta_1 + \varepsilon_i$ => Weight = 1.03 + 0.50 * Feed + ε_i						

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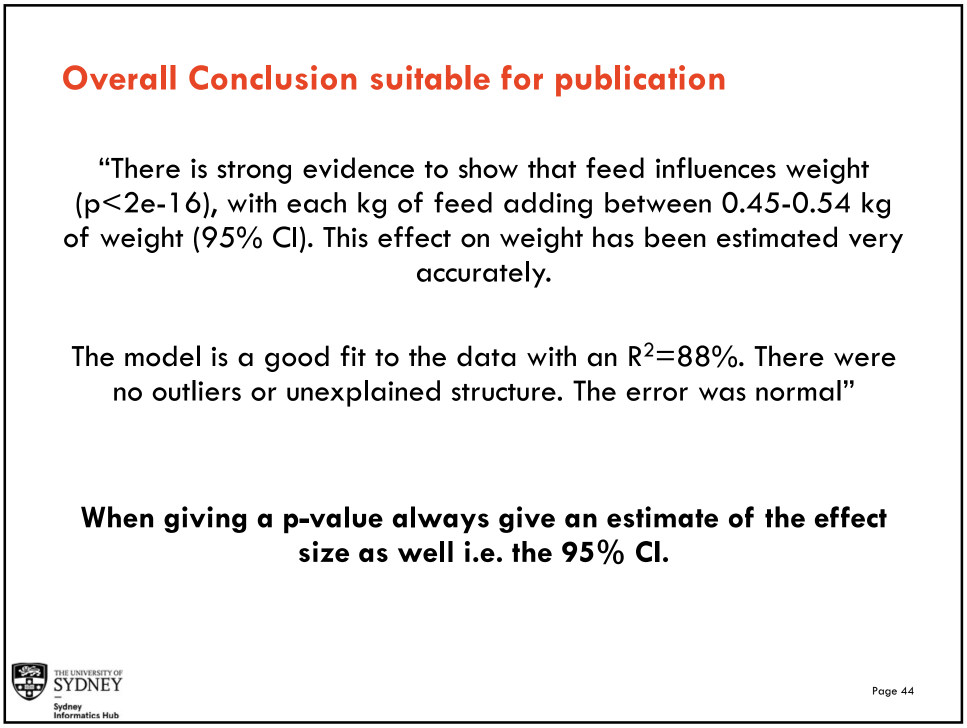

Overall Conclusion suitable for publication

"There is strong evidence to show that feed influences weight (p<2e-16), with each kg of feed adding between 0.45-0.54 kg of weight (95% CI). This effect on weight has been estimated very accurately.

The model is a good fit to the data with an R^2=88%. There were no outliers or unexplained structure. The error was normal"

When giving a p-value always give an estimate of the effect size as well i.e. the 95% CI.

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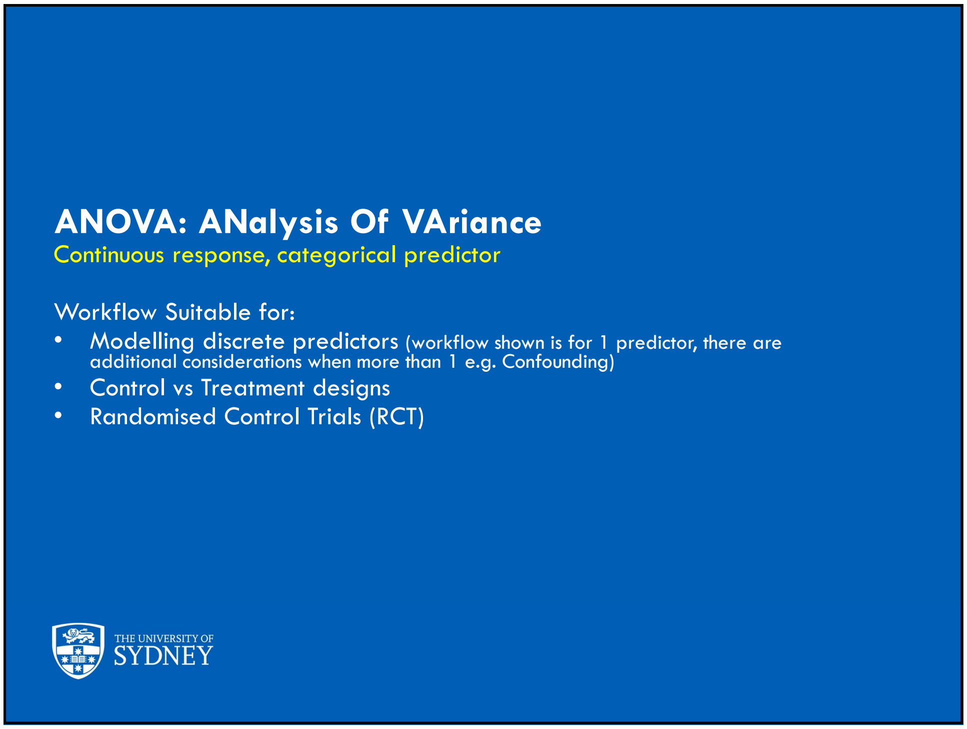

ANOVA: ANalysis Of VAriance

Continuous response, categorical predictor

Workflow Suitable for:

- Modelling discrete predictors (workflow shown is for 1 predictor, there are additional considerations when more than 1 e.g. Confounding)
- Control vs Treatment designs
- Randomised Control Trials (RCT)

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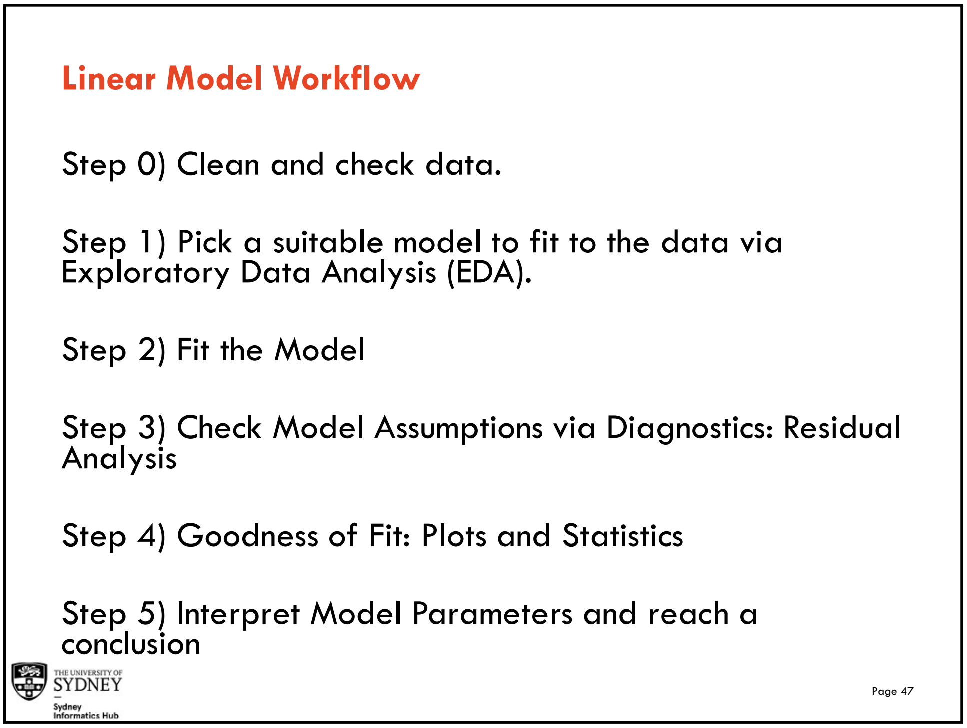

Linear Model Workflow

Step 0) Clean and check data.

Step 1) Pick a suitable model to fit to the data via Exploratory Data Analysis (EDA).

Step 2) Fit the Model

Step 3) Check Model Assumptions via Diagnostics: Residual Analysis

Step 4) Goodness of Fit: Plots and Statistics

Step 5) Interpret Model Parameters and reach a conclusion

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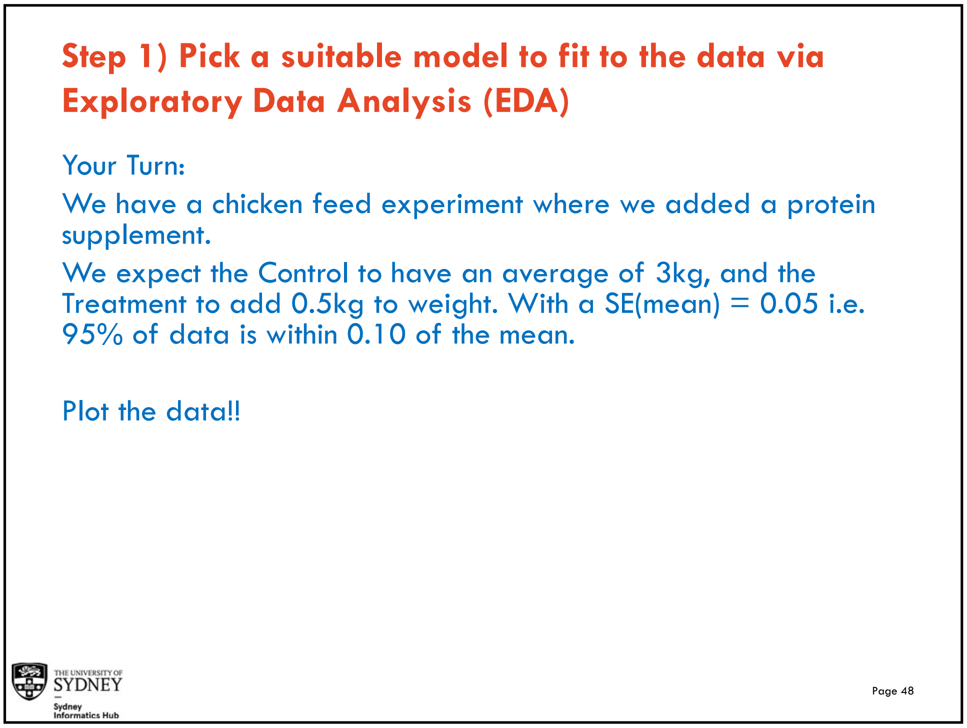

Step 1) Pick a suitable model to fit to the data via Exploratory Data Analysis (EDA)

Your Turn:

We have a chicken feed experiment where we added a protein supplement.

We expect the Control to have an average of 3kg, and the Treatment to add 0.5kg to weight. With a SE(mean) = 0.05 i.e. 95% of data is within 0.10 of the mean.

Plot the data!!

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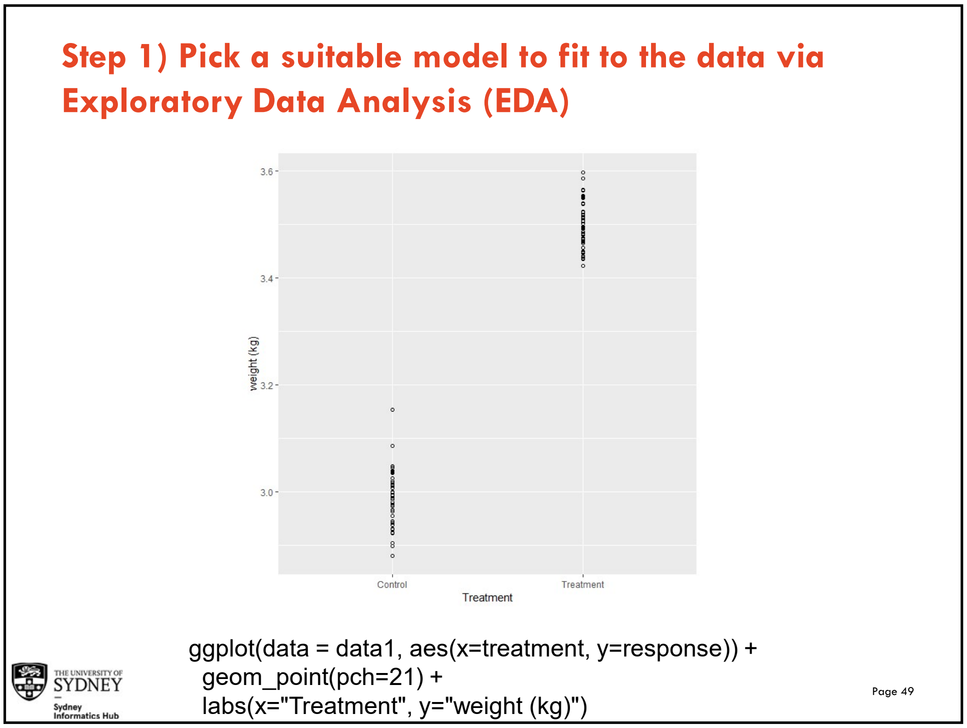
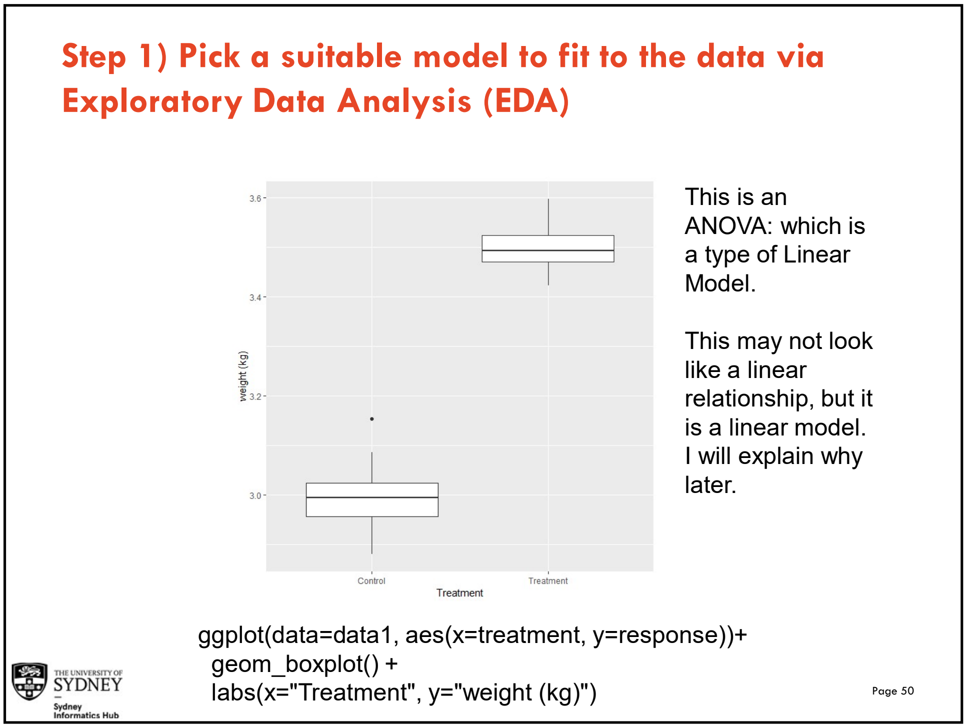


Step 1) Pick a suitable model to fit to the data via Exploratory Data Analysis (EDA)

```
ggplot(data = data1, aes(x=treatment, y=response)) +
  geom_point(pch=21) +
  labs(x="Treatment", y="weight (kg)")
```



Step 1) Pick a suitable model to fit to the data via Exploratory Data Analysis (EDA)

This is an ANOVA: which is a type of Linear Model.

This may not look like a linear relationship, but it is a linear model. I will explain why later.

```
ggplot(data=data1, aes(x=treatment, y=response))+
  geom_boxplot() +
  labs(x="Treatment", y="weight (kg)")
```

Step 1) Pick a suitable model to fit to the data via Exploratory Data Analysis (EDA)

Independence: Consider your experimental design

Your Turn:

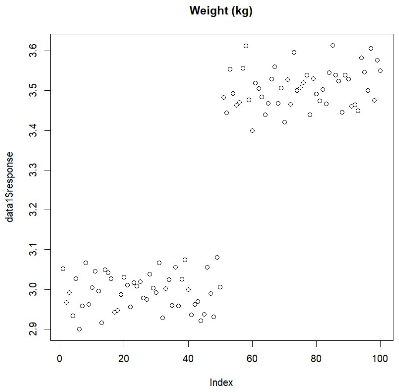
Is there anything about this design that might lead to datum being correlated with each other? For example, if we had repeated measures on the same patient (chicken) then we would expect these to be correlated i.e. dependant on each other.

YES! Chickens in the same treatment might be correlated, but our model will account for that since it's fitting a different mean to the control vs treatment.

ANY OTHERS?

Step 1) Pick a suitable model to fit to the data via Exploratory Data Analysis (EDA)

Independence and Outliers: Plot the data using a Serial Plot



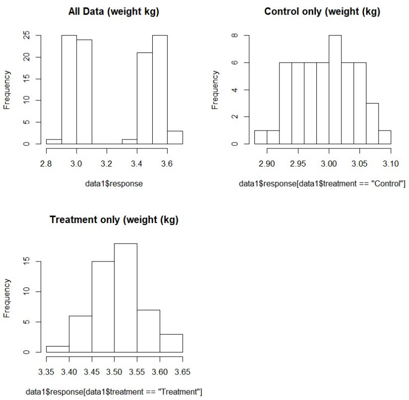
Notice the serial correlation i.e. data at the start are more similar to those at the end. As control data are at the beginning and Treatment at the end this is expected. And our model will account for that.

No Outliers

plot(data1$response, main="Weight (kg)")

Step 1) Pick a suitable model to fit to the data via Exploratory Data Analysis (EDA)

Normality and Outliers



The combined data is clearly bimodal and is certainly not normal!!!

YR Turn: So do we have a problem??

NO: The error needs to be normal, not the response. And as we can see here the error about the mean of each treatment is roughly normal.

(Even though the control might not look like it we know it is since its simulated data. A good example of just how non–normal something can look and we're still OK).

```
par(mfrow=c(2,2))
hist(data1$response, main="All Data (weight kg)")
hist(data1$response[data1$treatment=="Control"], main="Control only (weight (kg)")
hist(data1$response[data1$treatment=="Treatment"], main="Treatment  (weight (kg)")
```

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Step 2) Fit the Model

R Code:

```
lm.anova <- lm(data1$response~data1$treatment)
```

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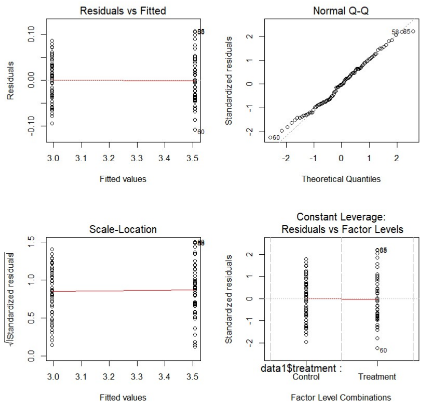
Step 3) Check Model Assumptions via Diagnostics: Residual Analysis

Normality

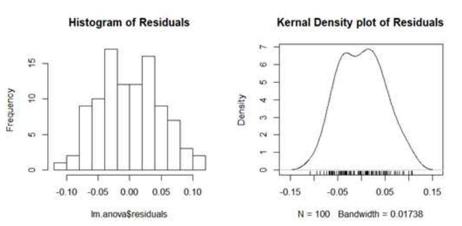


Residuals appear normal.

```
par(mfrow=c(2,2))
plot(lm.anova)
```

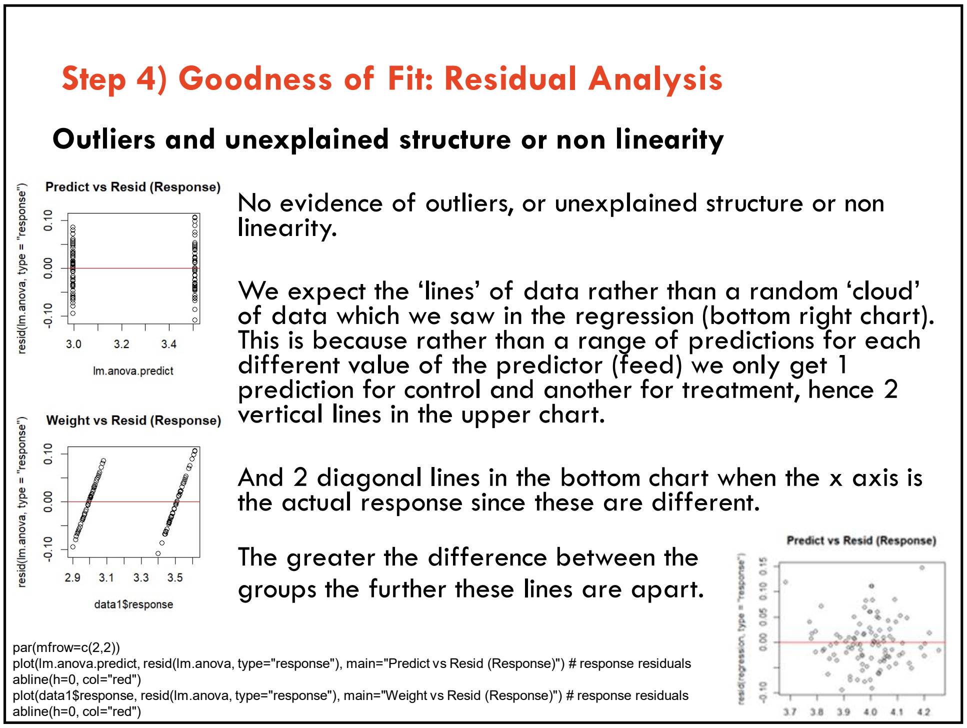
Step 3) Check Model Assumptions via Diagnostics: Residual Analysis

Normality



Residuals appear normal.

```
par(mfrow=c(2,2))
hist(lm.anova$residuals, main="Histogram of Residuals")
plot(density(lm.anova$residuals), main="Kernal Density plot of Residuals")
rug(lm.anova$residuals)
```



Step 4) Goodness of Fit: Residual Analysis

Outliers and unexplained structure or non linearity

No evidence of outliers, or unexplained structure or non linearity.

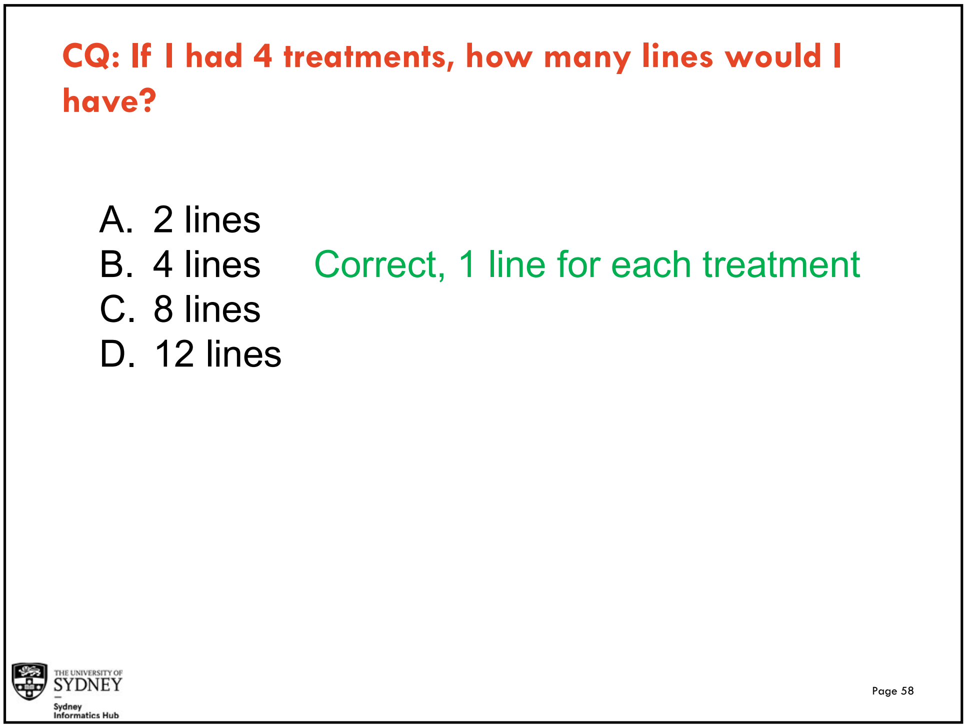
We expect the 'lines' of data rather than a random 'cloud' of data which we saw in the regression (bottom right chart). This is because rather than a range of predictions for each different value of the predictor (feed) we only get 1 prediction for control and another for treatment, hence 2 vertical lines in the upper chart.

And 2 diagonal lines in the bottom chart when the x axis is the actual response since these are different.

The greater the difference between the groups the further these lines are apart.

Predict vs Resid (Response)
resid(regression, type = "response")
-0.10
0.00
0.05
0.10
0.15
3.7
3.8
3.9
4.0
4.1
4.2

```
par(mfrow=c(2,2))
plot(lm.anova.predict, resid(lm.anova, type="response"), main="Predict vs Resid (Response)") # response residuals
abline(h=0, col="red")
plot(data1$response, resid(lm.anova, type="response"), main="Weight vs Resid (Response)") # response residuals
abline(h=0, col="red")
```



CQ: If I had 4 treatments, how many lines would I have?

A. 2 lines
B. 4 lines   Correct, 1 line for each treatment
C. 8 lines
D. 12 lines

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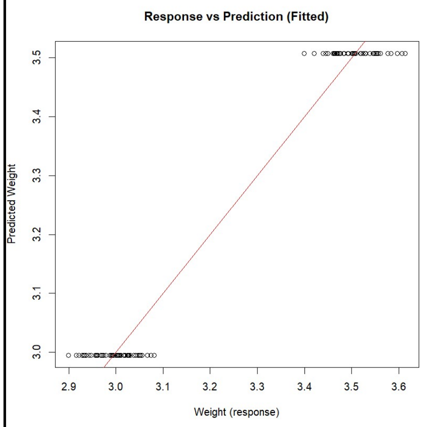
Step 4) Goodness of Fit: Plots and Statistics



For the same reason used previously we expect 2 lines of data here, not a cloud of points i.e. we only have 2 prediction.

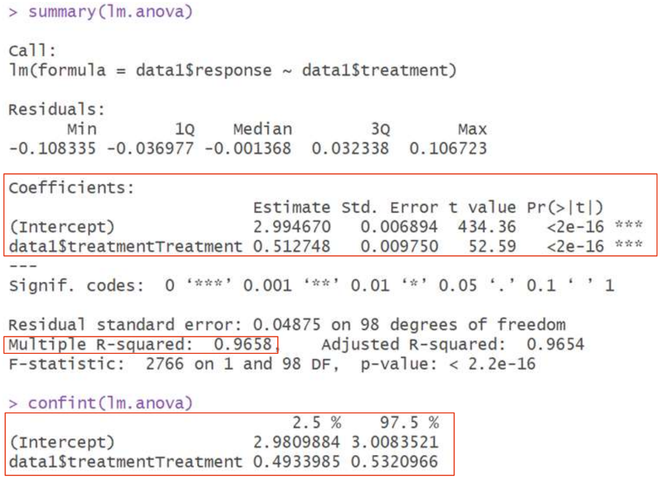
We expect the 2 lines of data to be centred on the red line.

If they aren't this suggests there is some bias to the fit worth investigating further.

```
plot(data1$response, lm.anova.predict, main="Response vs Prediction (Fitted)",
xlab="Weight (response)", ylab="Predicted Weight")
abline(a=0, b=1, col="red")
```

Step 5) Interpret Model Parameters and reach a conclusion

R CODE and output used to create Tables



```
> summary(lm.anova)

Call:
lm(formula = data1$response ~ data1$treatment)

Residuals:
      Min        1Q    Median        3Q       Max 
-0.108335 -0.036977 -0.001368  0.032338  0.106723 

Coefficients:
                         Estimate Std. Error t value Pr(>|t|)    
(Intercept)              2.994670   0.006894  434.36   <2e-16 ***
data1$treatmentTreatment 0.512748   0.009750   52.59   <2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.04875 on 98 degrees of freedom
Multiple R-squared:  0.9658,	Adjusted R-squared:  0.9654 
F-statistic:  2766 on 1 and 98 DF,  p-value: < 2.2e-16

> confint(lm.anova)
                             2.5 %    97.5 %
(Intercept)              2.9809884 3.0083521
data1$treatmentTreatment 0.4933985 0.5320966
```

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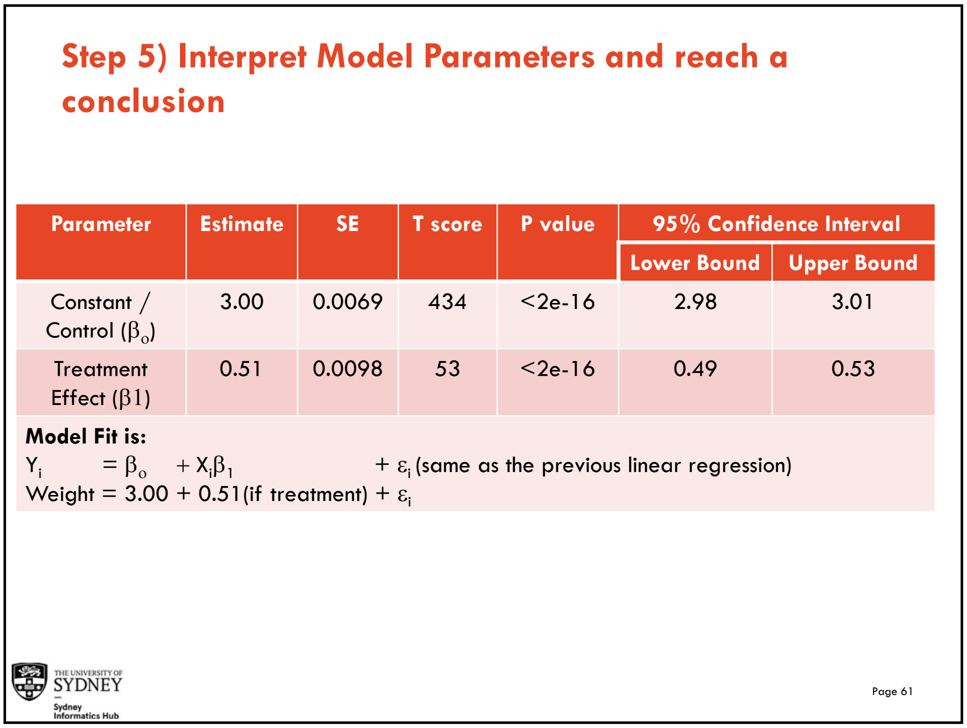

Step 5) Interpret Model Parameters and reach a conclusion

Parameter	Estimate	SE	T score	P value	95% Confidence Interval	
					Lower Bound	Upper Bound
Constant / Control (β_o)	3.00	0.0069	434	<2e-16	2.98	3.01
Treatment Effect ($\beta 1$)	0.51	0.0098	53	<2e-16	0.49	0.53

Model Fit is:

$Y_i = \beta_o + X_i\beta_1 + \varepsilon_i$ (same as the previous linear regression)

Weight = 3.00 + 0.51(if treatment) + ε_i

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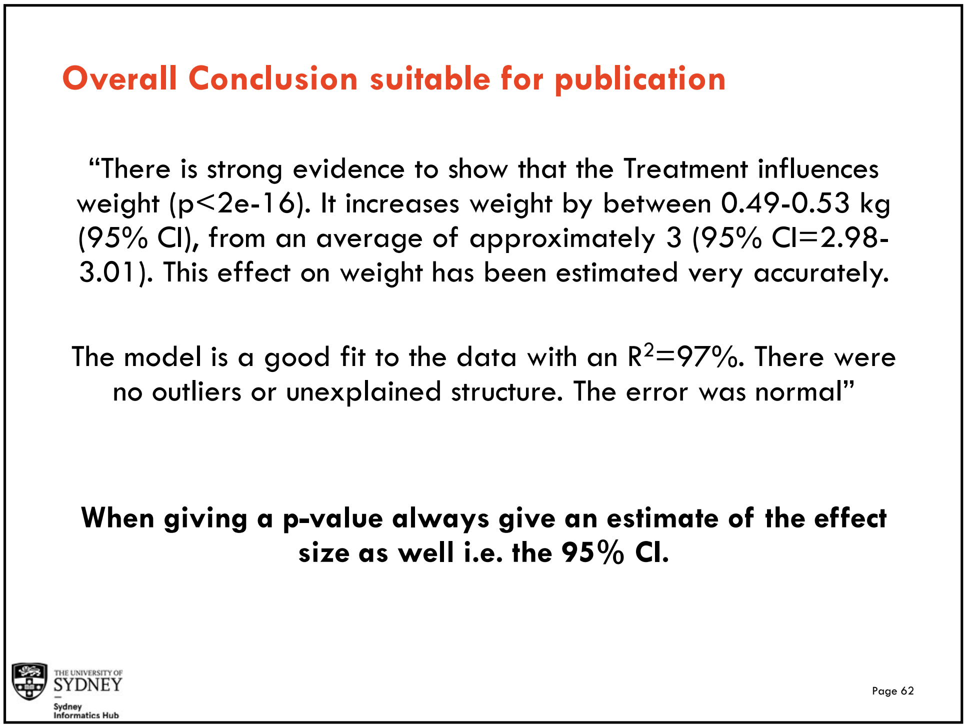

Overall Conclusion suitable for publication

"There is strong evidence to show that the Treatment influences weight (p<2e-16). It increases weight by between 0.49-0.53 kg (95% CI), from an average of approximately 3 (95% CI=2.98-3.01). This effect on weight has been estimated very accurately.

The model is a good fit to the data with an R^2=97%. There were no outliers or unexplained structure. The error was normal"

When giving a p-value always give an estimate of the effect size as well i.e. the 95% CI.

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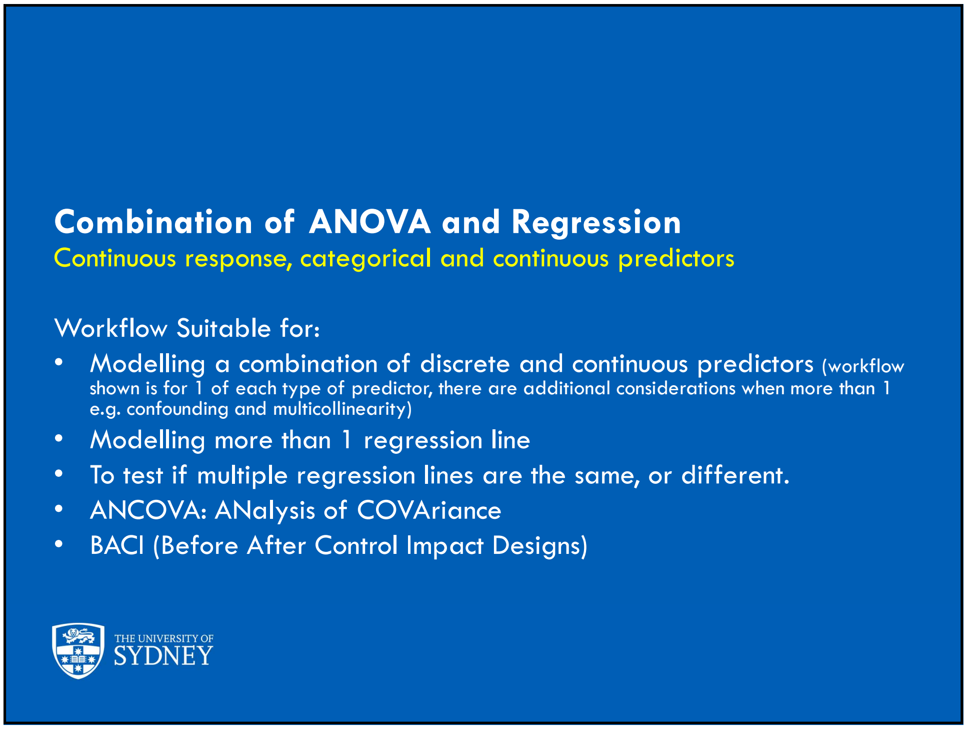

Combination of ANOVA and Regression

Continuous response, categorical and continuous predictors

Workflow Suitable for:

- Modelling a combination of discrete and continuous predictors (workflow shown is for 1 of each type of predictor, there are additional considerations when more than 1 e.g. confounding and multicollinearity)
- Modelling more than 1 regression line
- To test if multiple regression lines are the same, or different.
- ANCOVA: ANalysis of COVAriance
- BACI (Before After Control Impact Designs)

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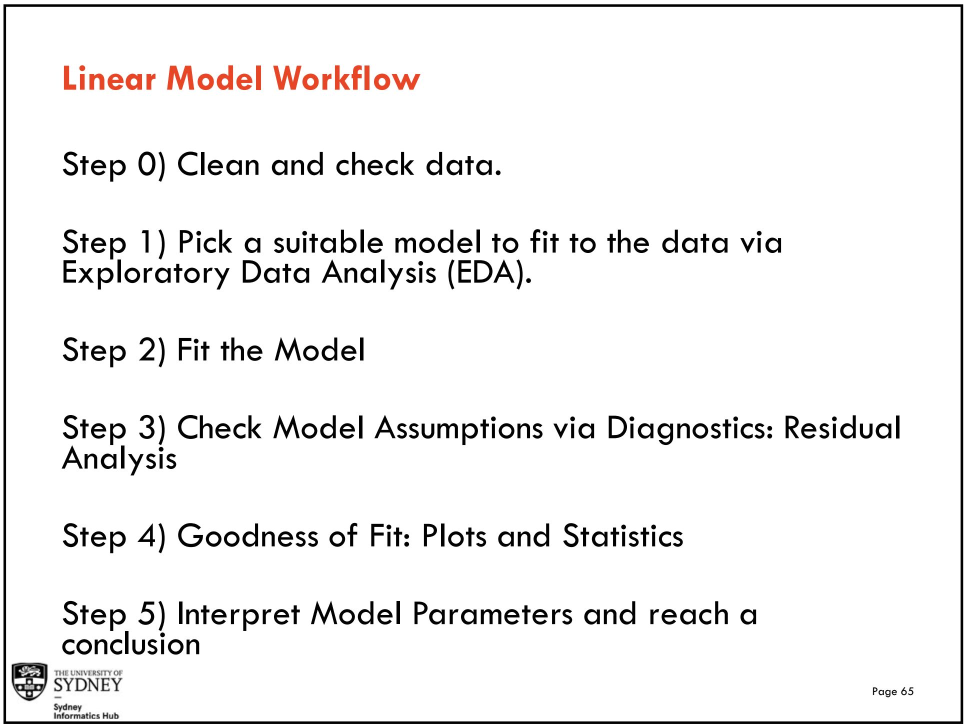

Linear Model Workflow

Step 0) Clean and check data.

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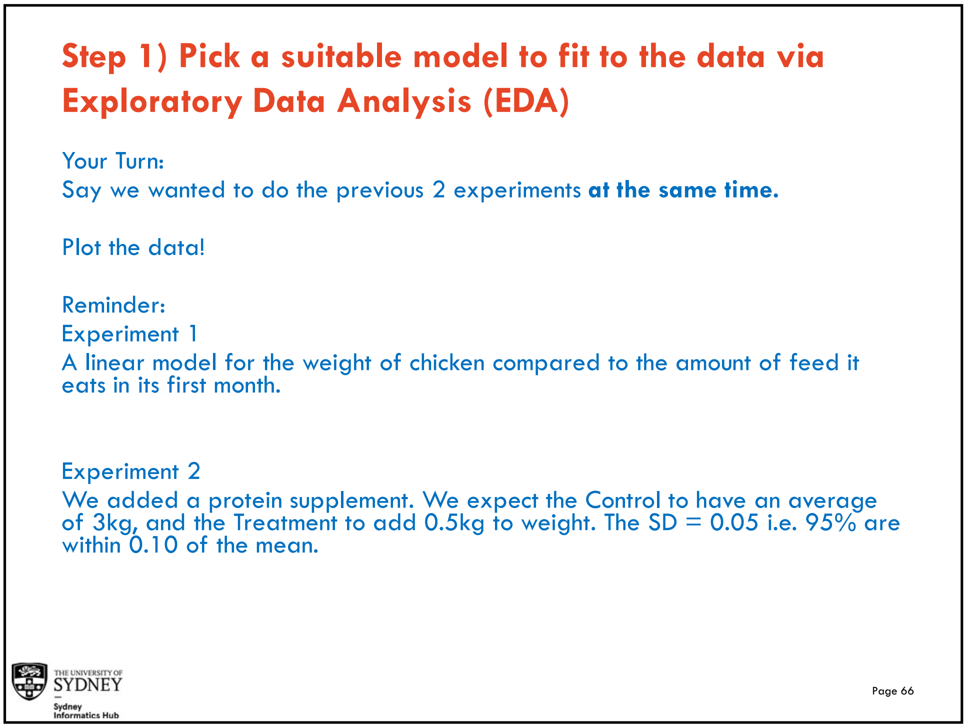
Step 4) Goodness of Fit: Plots and Statistics

Step 5) Interpret Model Parameters and reach a conclusion



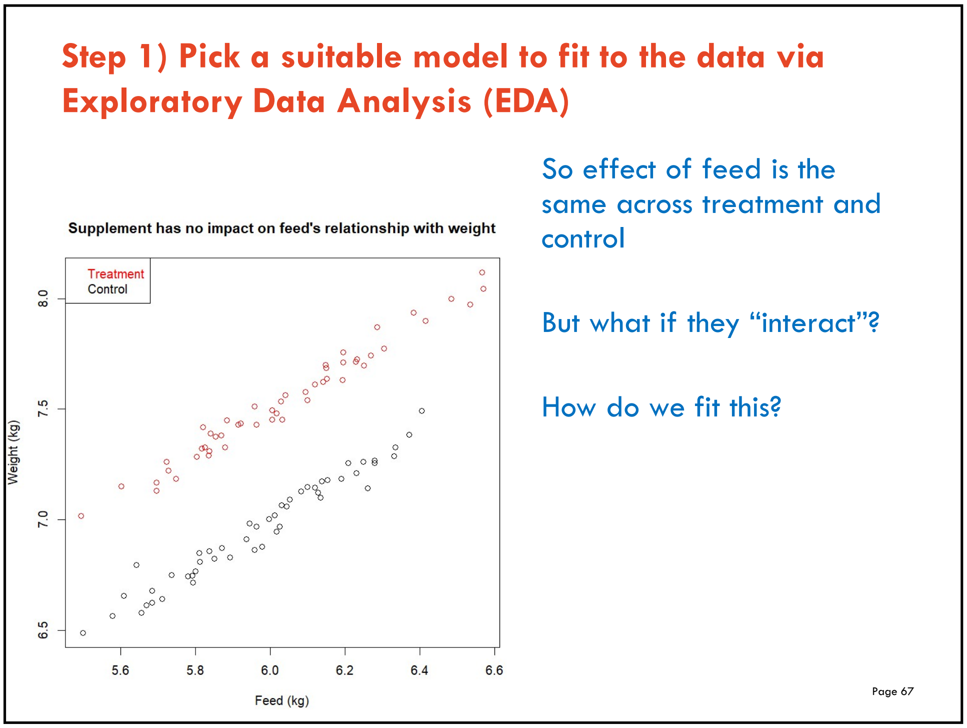
Step 1) Pick a suitable model to fit to the data via Exploratory Data Analysis (EDA)

Your Turn:
Say we wanted to do the previous 2 experiments **at the same time.**

Plot the data!

Reminder:
Experiment 1
A linear model for the weight of chicken compared to the amount of feed it eats in its first month.

Experiment 2
We added a protein supplement. We expect the Control to have an average of 3kg, and the Treatment to add 0.5kg to weight. The SD = 0.05 i.e. 95% are within 0.10 of the mean.



Step 1) Pick a suitable model to fit to the data via Exploratory Data Analysis (EDA)

So effect of feed is the same across treatment and control

But what if they "interact"?

How do we fit this?

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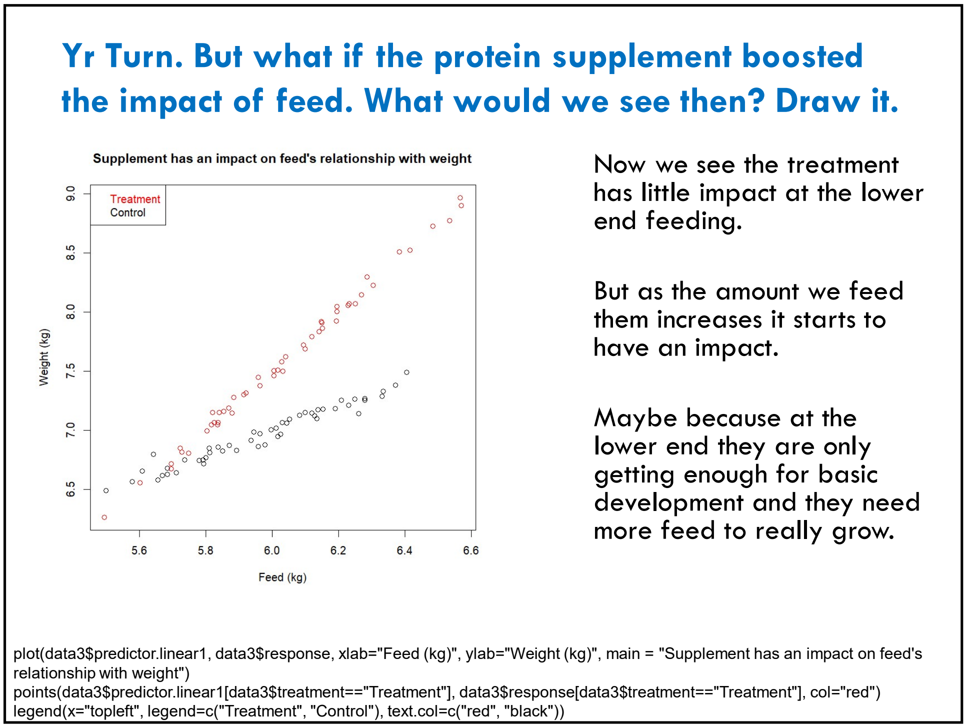

Yr Turn. But what if the protein supplement boosted the impact of feed. What would we see then? Draw it.

Now we see the treatment has little impact at the lower end feeding.

But as the amount we feed them increases it starts to have an impact.

Maybe because at the lower end they are only getting enough for basic development and they need more feed to really grow.

```
plot(data3$predictor.linear1, data3$response, xlab="Feed (kg)", ylab="Weight (kg)", main = "Supplement has an impact on feed's
relationship with weight")
points(data3$predictor.linear1[data3$treatment=="Treatment"], data3$response[data3$treatment=="Treatment"], col="red")
legend(x="topleft", legend=c("Treatment", "Control"), text.col=c("red", "black"))
```

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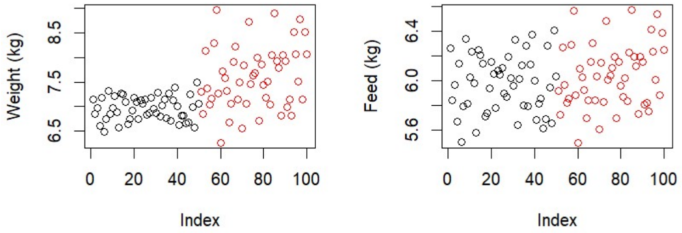
Step 1) Pick a suitable model to fit to the data via Exploratory Data Analysis (EDA)

Independence: Consider your experimental design and serial plot

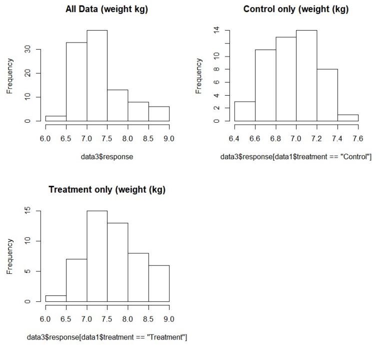
As with the ANOVA we expect there might be dependence within each treatment for the response. However the linear predictors (feed) should be independent, if they're not then we have a big problem!



```
par(mfrow=c(1,2))
plot(data3$response, col=ifelse(data3$treatment=="Treatment","red", "black"), ylab="Weight (kg)")
plot(data3$predictor.linear1, col=ifelse(data3$treatment=="Treatment","red", "black"), ylab="Feed (kg)")
```

Step 1) Pick a suitable model to fit to the data via Exploratory Data Analysis (EDA)

Normality and Outliers

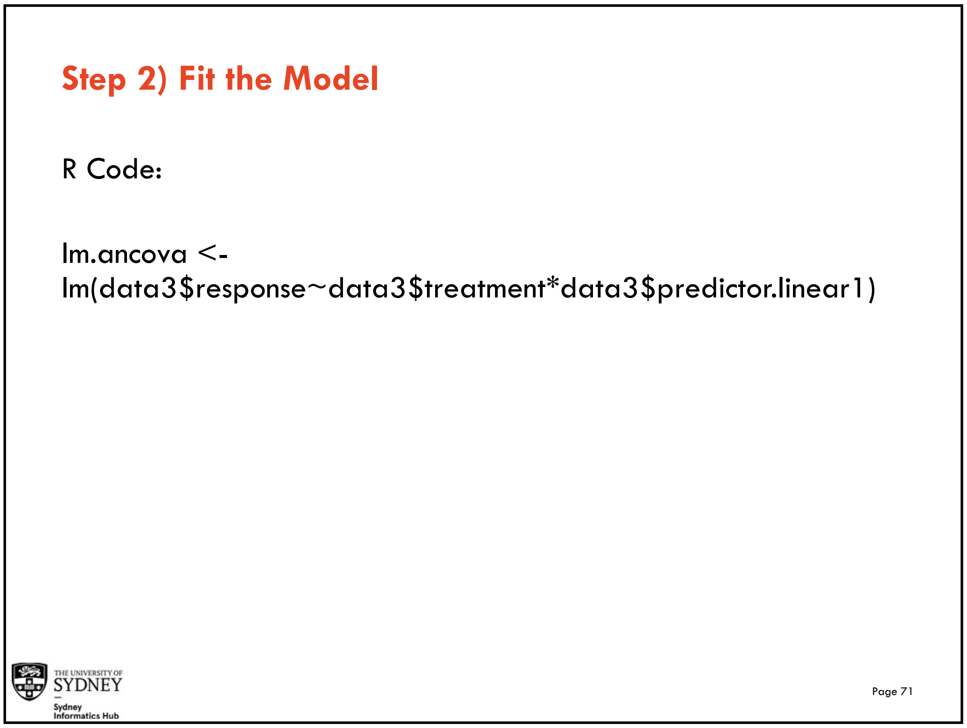


The combined data is clearly skewed and is certainly not normal!!!

Which is what we would expect given that both treatments have the same response at low Feed, but one of them has higher weight at a higher Feed.

If we didn't include treatment this is an example of where our residuals might not be normal and it's **because of missing structure i.e. treatment**.

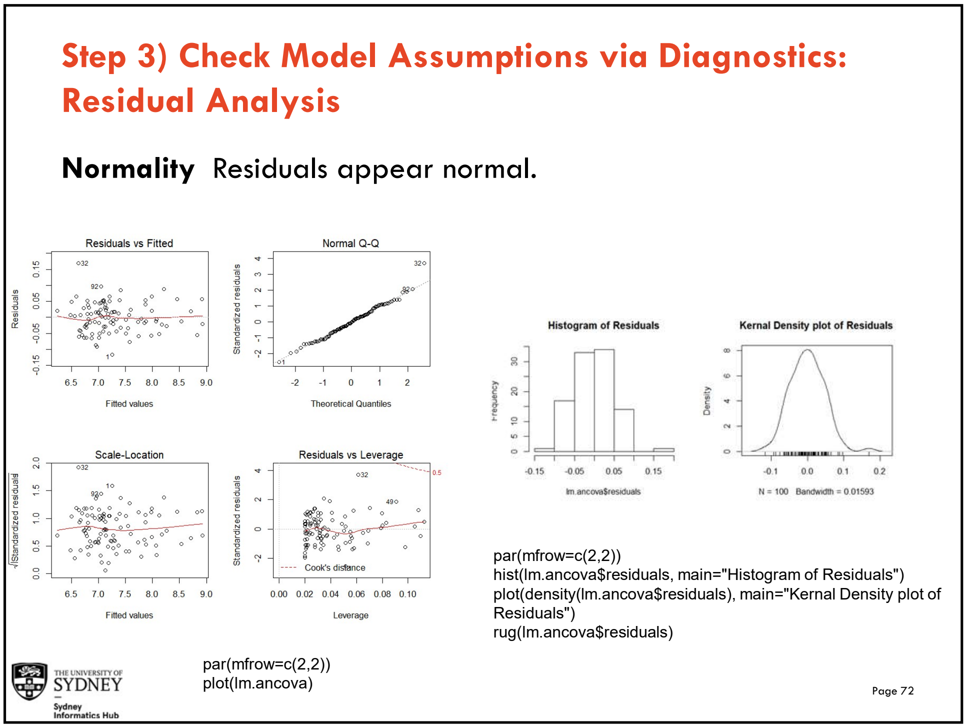
```
par(mfrow=c(2,2))
hist(data3$response, main="All Data (weight kg)")
hist(data3$response[data1$treatment=="Control"], main="Control only (weight (kg)")
hist(data3$response[data1$treatment=="Treatment"], main="Treatment  (weight (kg)")
```



Step 2) Fit the Model

R Code:

```
lm.ancova <-
lm(data3$response~data3$treatment*data3$predictor.linear1)
```

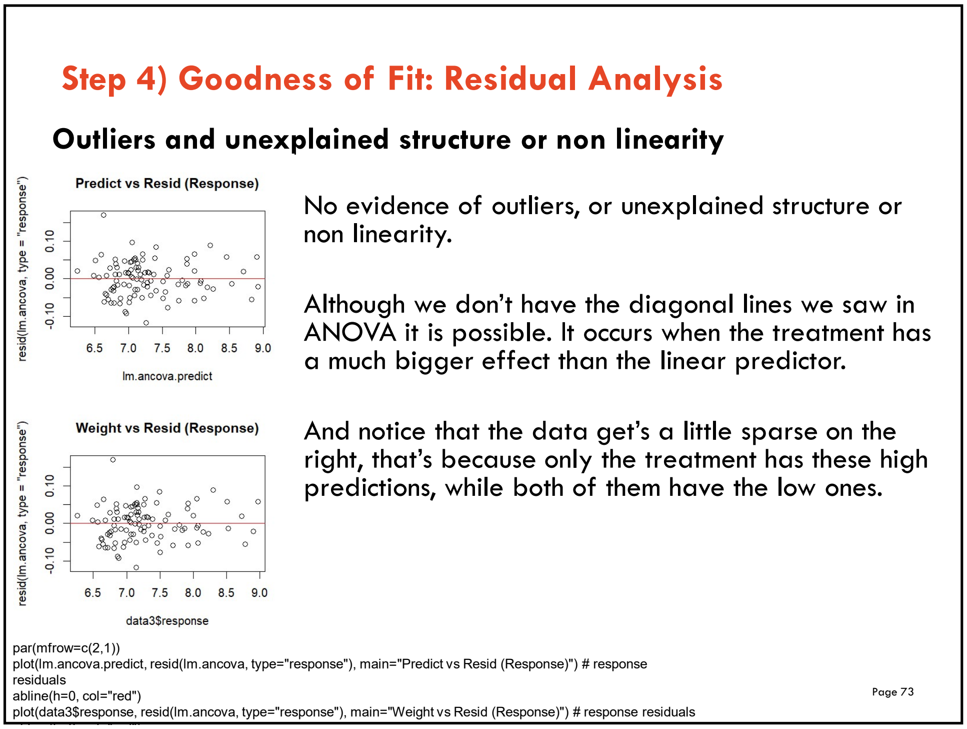


Step 3) Check Model Assumptions via Diagnostics: Residual Analysis

Normality Residuals appear normal.

```
par(mfrow=c(2,2))
hist(lm.ancova$residuals, main="Histogram of Residuals")
plot(density(lm.ancova$residuals), main="Kernal Density plot of
Residuals")
rug(lm.ancova$residuals)
```

```
par(mfrow=c(2,2))
plot(lm.ancova)
```



Step 4) Goodness of Fit: Residual Analysis

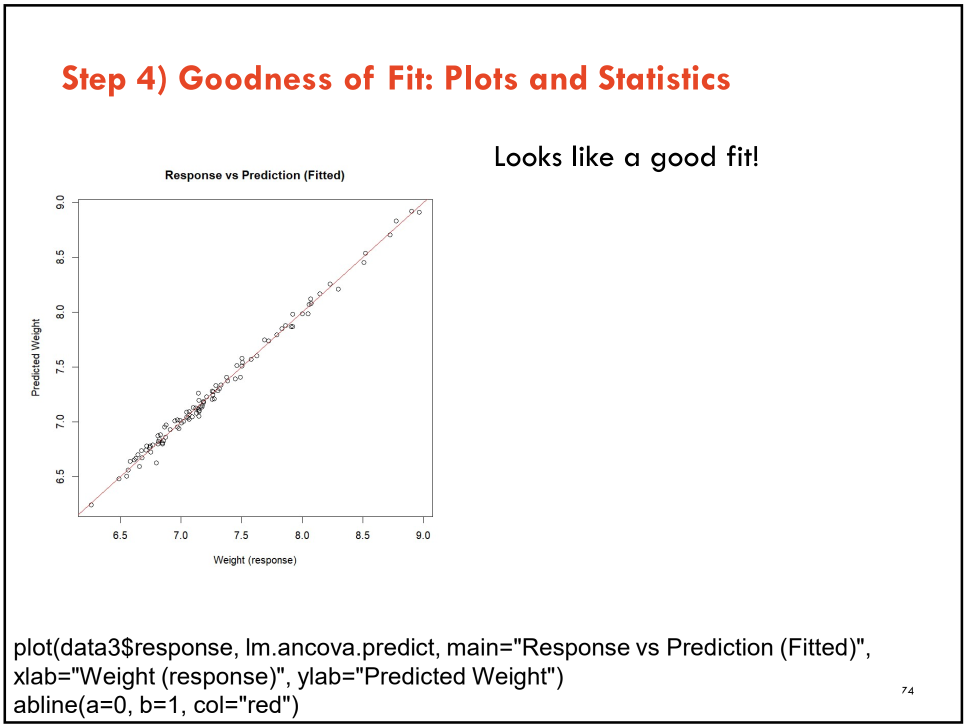
Outliers and unexplained structure or non linearity

No evidence of outliers, or unexplained structure or non linearity.

Although we don't have the diagonal lines we saw in ANOVA it is possible. It occurs when the treatment has a much bigger effect than the linear predictor.

And notice that the data get's a little sparse on the right, that's because only the treatment has these high predictions, while both of them have the low ones.

```
par(mfrow=c(2,1))
plot(lm.ancova.predict, resid(lm.ancova, type="response"), main="Predict vs Resid (Response)") # response
residuals
abline(h=0, col="red")
plot(data3$response, resid(lm.ancova, type="response"), main="Weight vs Resid (Response)") # response residuals
```



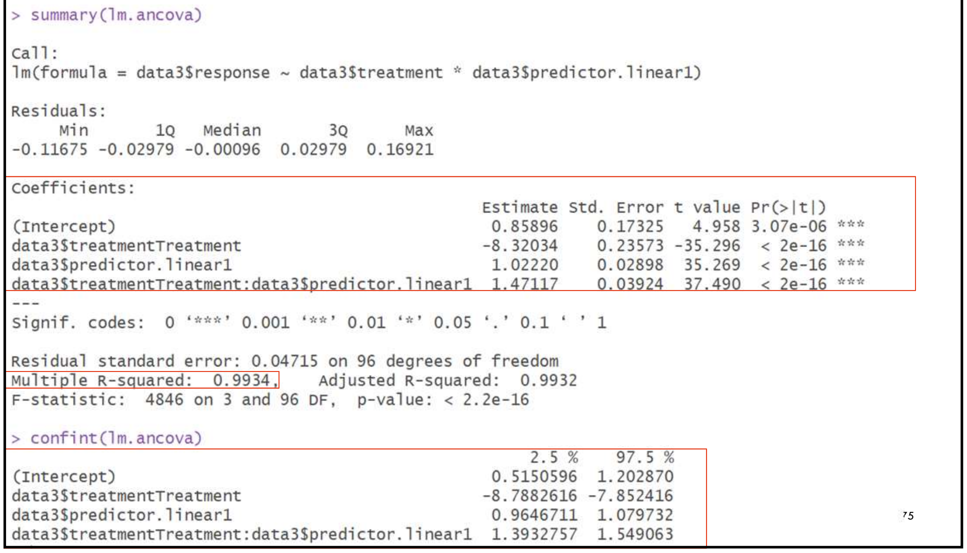
Step 4) Goodness of Fit: Plots and Statistics

Looks like a good fit!

```
plot(data3$response, lm.ancova.predict, main="Response vs Prediction (Fitted)",
xlab="Weight (response)", ylab="Predicted Weight")
abline(a=0, b=1, col="red")
```

Step 5) Interpret Model Parameters and reach a conclusion

R CODE and output used to create Tables



```
> summary(lm.ancova)

Call:
lm(formula = data3$response ~ data3$treatment * data3$predictor.linear1)

Residuals:
     Min       1Q   Median       3Q      Max 
-0.11675 -0.02979 -0.00096  0.02979  0.16921 

Coefficients:
                                                 Estimate Std. Error t value Pr(>|t|)    
(Intercept)                                       0.85896    0.17325   4.958 3.07e-06 ***
data3$treatmentTreatment                         -8.32034    0.23573 -35.296  < 2e-16 ***
data3$predictor.linear1                           1.02220    0.02898  35.269  < 2e-16 ***
data3$treatmentTreatment:data3$predictor.linear1  1.47117    0.03924  37.490  < 2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.04715 on 96 degrees of freedom
Multiple R-squared:  0.9934,	Adjusted R-squared:  0.9932 
F-statistic:  4846 on 3 and 96 DF,  p-value: < 2.2e-16

> confint(lm.ancova)
                                                      2.5 %    97.5 %
(Intercept)                                       0.5150596  1.202870
data3$treatmentTreatment                         -8.7882616 -7.852416
data3$predictor.linear1                           0.9646711  1.079732
data3$treatmentTreatment:data3$predictor.linear1  1.3932757  1.549063
```

Step 5) Interpret Model Parameters and reach a conclusion

Parameter	Estimate	SE	T score	P value	95% Confidence Interval	
					Lower Bound	Upper Bound
Constant Control (β_o)	0.86	0.17	5	<3e-6	0.51	1.2
Constant Adjustment Treatment (β_1)	-8.32	0.24	-35	<2e-16	-8.8	-7.9
Slope Control (β_3)	1.0	0.029	35	<2e-16	0.96	1.08
Slope Adjustment Treatment (β_4)	1.5	0.039	37	<2e-16	1.39	1.55

Model Fit is => $Y_i = \beta_o + X_i\beta_1 + X_i\beta_3 + X_i\beta_4 + \varepsilon_i$ =>

Weight = 0.86 + 1.0*Feed – 8.32(if treatment) + 1.5*Feed(if treatment) + ε_i

Weight (if Control) = 0.86 + 1*Feed + ε_i

Weight (if Treatment) = -7.46 + 2.5*Feed + ε_i

Overall Conclusion suitable for publication

“There is strong evidence to show that feed impacts weight (p<2e-16), with each kg of feed adding between 0.96-1.08 kg of weight (95% CI).

There is strong evidence that Protein supplements have a positive effect on the impact of Feed (p<2e-16), increasing its effect by between 1.39-1.55 (95% CI), for a total average effect of 2.5kg weight increase for each kg of extra Feed.

This effect of feed on weight has been estimated very accurately.

The model is a good fit to the data with an R^2=99%. There were no outliers or unexplained structure. The error was normal”

When giving a p-value always give an estimate of the effect size as well i.e. the 95% CI.

ANCOVA: is a special case of this model

Adjusts for continuous covariates so we get a clean read on the discrete predictors impacts. Often used in observational studies to help remove the effect of covariates.

For example: To understand the effect of the protein supplement after accounting for the different amount of feed each chicken ate we can add feed is a covariate in an ANCOVA. This would account for the scenario where chickens that had the supplement happened to eat more food and as such weighed more for that reason, not due to the supplement.

The key difference is that an ANCOVA makes an additional assumption called **Homogeneity of covariate regression coefficients; i.e. "parallel lines model"**. Which states that the regression lines must be parallel, i.e. the covariate has the same effect for each treatment.

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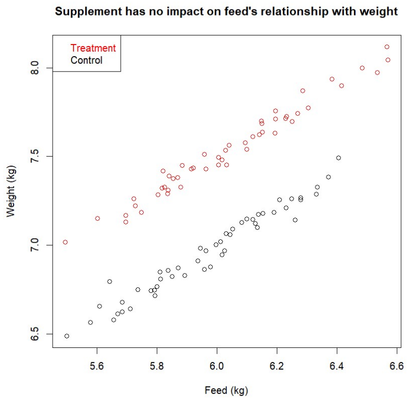
ANCOVA: is a special case of this model

This allows us to measure the effect of each discrete parameter after accounting for the continuous covariate.

For example: The below model shows that the protein supplement increases the chickens weight by 0.5 kg, irrelevant to amount of feed it ate.

Statistically the Homogeneity of covariate regression coefficients; i.e. "parallel lines model" means the interaction is not required in the model.



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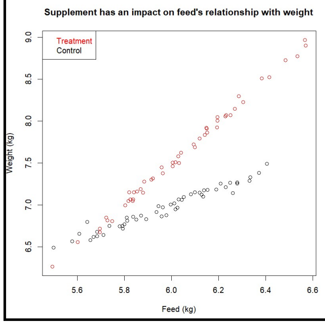
ANCOVA: what happens when the homogeneity of regression covariates is failed?

Don't worry! Its not a big deal. It just means that the covariate doesn't have a consistent effect overall treatments. Meaning we can't directly compare the treatments overall effects with each other and instead need to look at each treatments regression line.

Statistically it's the same model, but we also include an interaction.



So rather than the protein supplement consistently increasing weight by 0.5kg we see it has little impact at the lower end feeding.

But as the amount we feed them increases it starts to have an impact.

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Mixed Models: Random Intercept Model

Response is measured more than once on each respondent (sampling unit)

Workflow Suitable for:

- Modelling the variance associated with the respondents (sampling units). Usually gives a more accurate analysis by partitioning out the noise/variance associated with the respondents (sampling units).
- Repeated Measures
- Longitudinal Analysis
- More advanced workflows suitable for:
  - Cluster Designs
  - More complex designs with repeated measures on clusters of sampling units and experimental units
  - Variance Decomposition
  - Random Slopes

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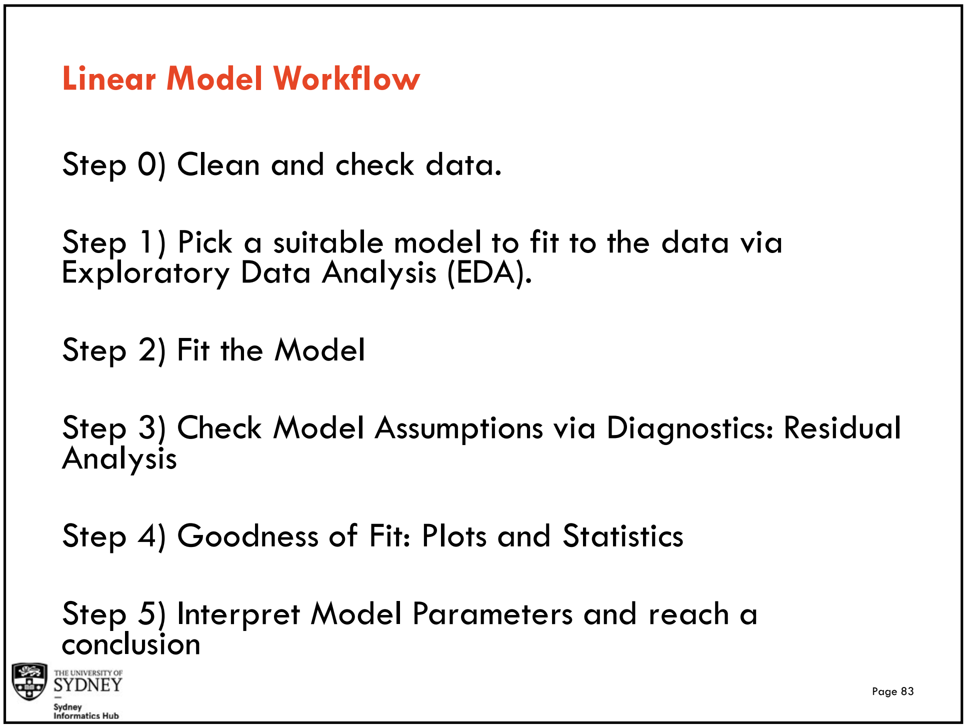

Linear Model Workflow

Step 0) Clean and check data.

Step 1) Pick a suitable model to fit to the data via Exploratory Data Analysis (EDA).

Step 2) Fit the Model

Step 3) Check Model Assumptions via Diagnostics: Residual Analysis

Step 4) Goodness of Fit: Plots and Statistics

Step 5) Interpret Model Parameters and reach a conclusion

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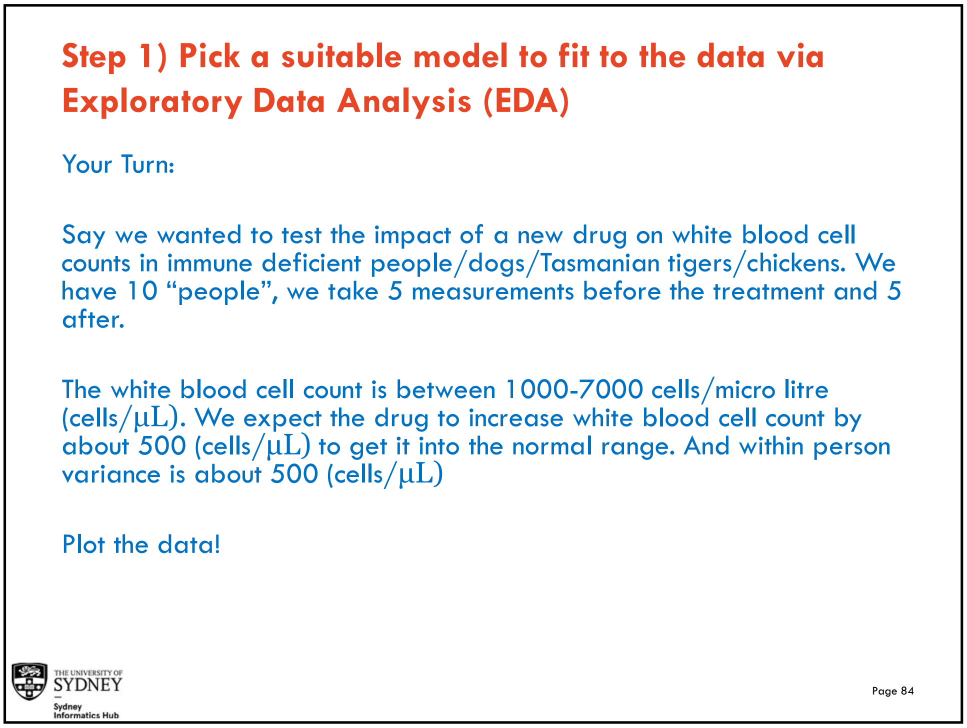

Step 1) Pick a suitable model to fit to the data via Exploratory Data Analysis (EDA)

Your Turn:

Say we wanted to test the impact of a new drug on white blood cell counts in immune deficient people/dogs/Tasmanian tigers/chickens. We have 10 “people”, we take 5 measurements before the treatment and 5 after.

The white blood cell count is between 1000-7000 cells/micro litre (cells/μL). We expect the drug to increase white blood cell count by about 500 (cells/μL) to get it into the normal range. And within person variance is about 500 (cells/μL)

Plot the data!

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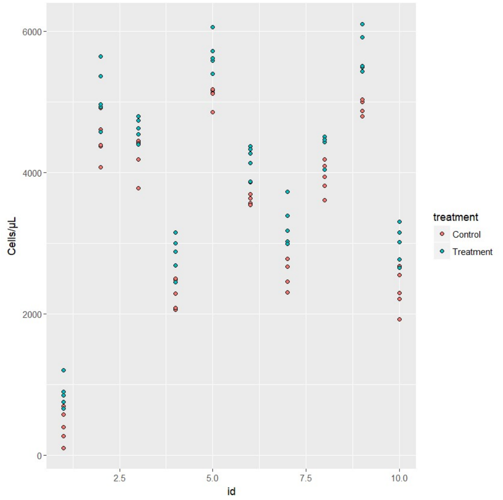
Step 1) Pick a suitable model to fit to the data via Exploratory Data Analysis (EDA)



```
ggplot(data = data6, aes(x=id, y=response, fill=treatment)) +
    geom_point(pch=21) +
    labs(x="id", y="Cells (µL)")
```

Notice how the difference between people is much bigger than the effect of the drug?

The models so far ignore this information.

A ***Mixed Model*** that includes person as a random effect accounts for this. Effectively removing this extra variance and making the model more accurate.

This is a classic example of where mixed models out perform those that ignore this extra info i.e. when the difference between sampling units is bigger than the effect we are looking for.

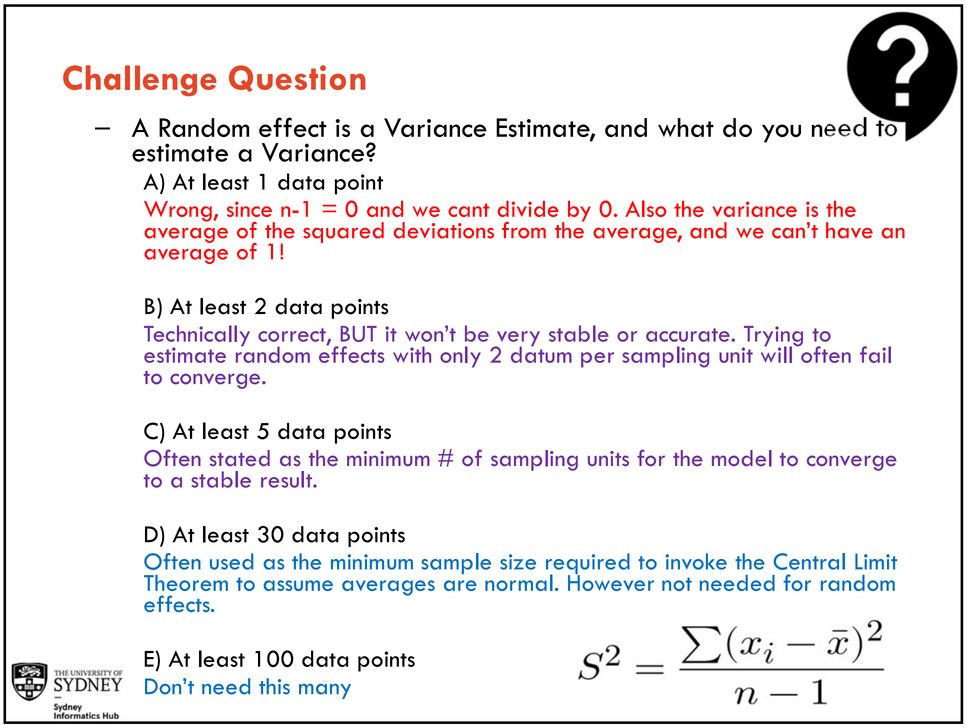
Mixed models: Random & Fixed Effects

Fixed Effects

- Measure a single **fixed effect** for **each** factor level e.g. if we had 50 treatments and we want to understand each of their effects then we need to estimate 50 fixed effects, 1 for each treatment.
- 1 parameter for each Treatment i.e. its's effect. So 50 parameters in total.
- Standard models you are used to.

Random Effects

- Measure the **randomness** of **all** factor levels e.g. if we had 50 treatments and we want to understand the amount of difference between all of them we could estimate the variance of their effects.
- 1 parameter for all Treatments effects i.e. their variance. So 1 parameter in total.
- Usually added to a fixed effects model to make a mixed effects model. Or less often used by themselves to partition the Variance.



Challenge Question

- A Random effect is a Variance Estimate, and what do you need to estimate a Variance?

A) At least 1 data point

Wrong, since n-1 = 0 and we cant divide by 0. Also the variance is the average of the squared deviations from the average, and we can't have an average of 1!

B) At least 2 data points

Technically correct, BUT it won't be very stable or accurate. Trying to estimate random effects with only 2 datum per sampling unit will often fail to converge.

C) At least 5 data points

Often stated as the minimum # of sampling units for the model to converge to a stable result.

D) At least 30 data points

Often used as the minimum sample size required to invoke the Central Limit Theorem to assume averages are normal. However not needed for random effects.

E) At least 100 data points

Don't need this many

$$S^2 = \frac{\sum(x_i - \bar{x})^2}{n-1}$$

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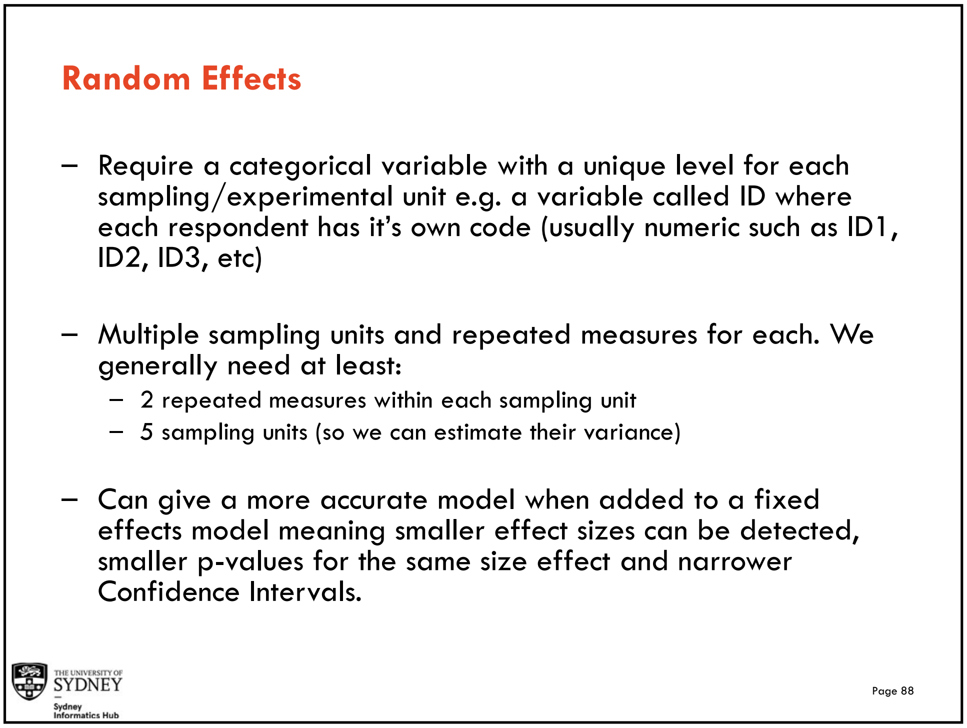

Random Effects

- Require a categorical variable with a unique level for each sampling/experimental unit e.g. a variable called ID where each respondent has it's own code (usually numeric such as ID1, ID2, ID3, etc)
- Multiple sampling units and repeated measures for each. We generally need at least:
  - 2 repeated measures within each sampling unit
  - 5 sampling units (so we can estimate their variance)
- Can give a more accurate model when added to a fixed effects model meaning smaller effect sizes can be detected, smaller p-values for the same size effect and narrower Confidence Intervals.

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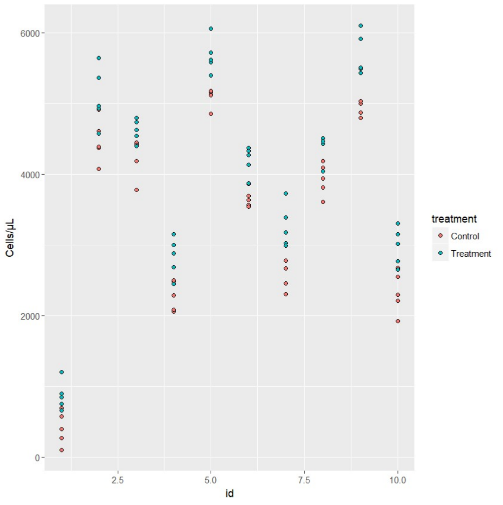
Random Effects: A more efficient use of your Data

- We want to understand the effects of new fishing nets on bycatch, but remove the effect of different boats due to various levels of experience, technology and size. We have randomly sampled 10 boats from the entire NSW East Coast Fleet. We have 2 treatments (existing and new nets).
- We could do this be including a fixed effect for each boat, i.e. old school Blocking. Meaning we need a model with 2 Treatment parameters and 10 boat parameters. Using the rule of thumb of 10 datum / fixed parameter we would need at least 120 datum.
- But as these boats are a sample of all boats and we don't really care what each got we can do a similar thing using a random effect with 1 parameter. This model only requires 2 Treatment parameters and 1 variance parameter for the boats. So a minimum of 20 datum and a much more efficient use of data.
- The Random effects method can be sued on a ***much smaller sample size*** than the Blocking Method using Fixed Effects.

Step 1) Pick a suitable model to fit to the data via Exploratory Data Analysis (EDA)



Notice how the difference between people is much bigger than the effect of the drug?

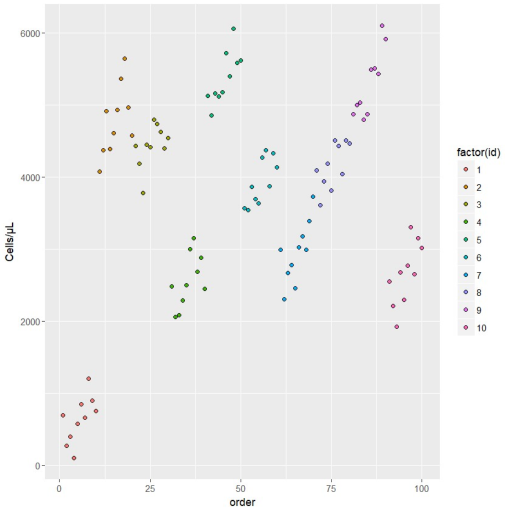
The models so far ignore this information.

A ***Mixed Model*** that includes person as a random effect accounts for this. Effectively removing this extra variance and making the model more accurate.

This is a classic example of where mixed models out perform those that ignore this extra info i.e. when the difference between sampling units is bigger than the effect we are looking for.

```
ggplot(data = data6, aes(x=id, y=response, fill=treatment)) +
   geom_point(pch=21) +
   labs(x="id", y="Cells (µL)")
```

Step 1) Pick a suitable model to fit to the data via Exploratory Data Analysis (EDA)



Independence: Consider your experimental design and serial plot

As with the ANOVA we expect there might be dependence within each treatment.

And since we have repeated measures we also expect dependence (auto-correlation) within patients.

```
ggplot(data = data6, aes(x=id, y=response, fill=treatment)) +
   geom_point(pch=21) +
   labs(x="id", y="Cells (µL)")
```

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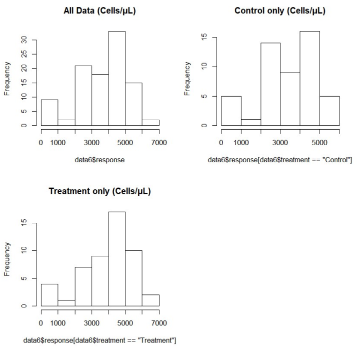
Step 1) Pick a suitable model to fit to the data via Exploratory Data Analysis (EDA)

Normality and Outliers



Could be normal, however there does look like there might be a bit of a negative skew.

But as the assumption is the model Errors are normal, not the response, we aren't too worried about this. But it's worth remembering and paying special attention to whether out model errors are normal.

```
windows()
par(mfrow=c(2,2))
hist(data6$response, main="All Data (Cells/µL)")
hist(data6$response[data6$treatment=="Control"], main="Control only (Cells/µL)")
hist(data6$response[data6$treatment=="Treatment"], main="Treatment only (Cells/µL)")
```

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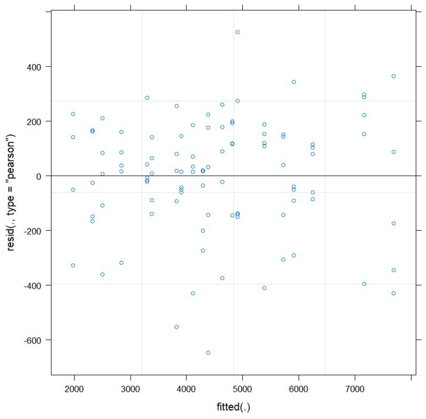
Step 2) Fit the Model

R Code:

```
lm.mm2 <- lmer(response~treatment + (1|id), data=data6)
```

Step 3) Check Model Assumptions via Diagnostics: Residual Analysis

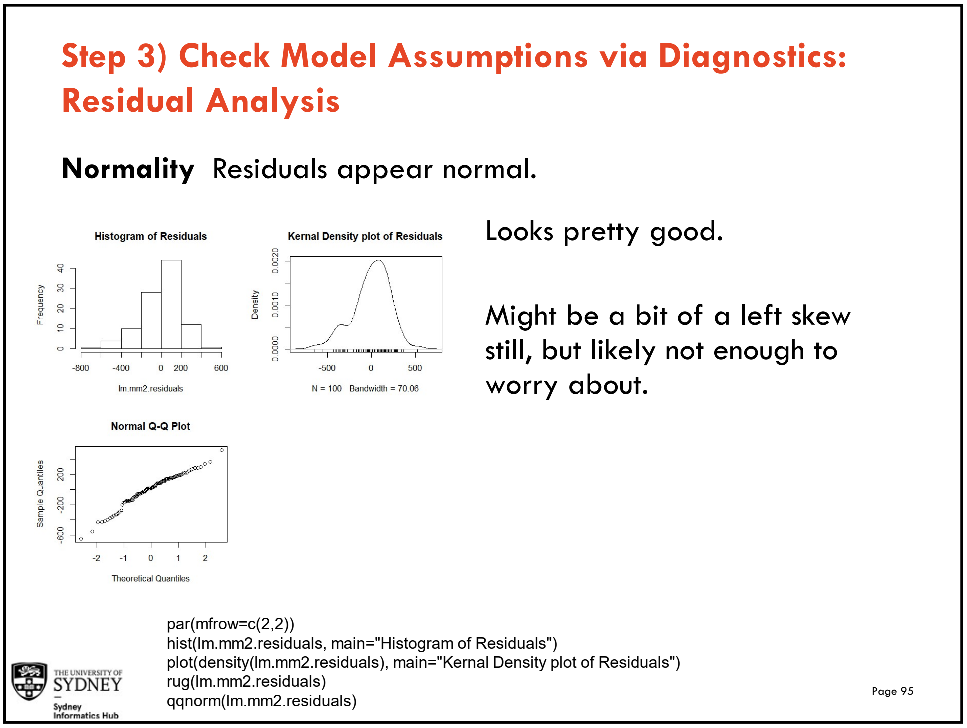
Normality Residuals appear normal.



Standard plots we get from the R function lmer() to fit the model are different to what we get when we use lm(), which is what we have been using previously.

So we are missing the QQ plot, amongst others.

plot(lm.mm2)



Step 3) Check Model Assumptions via Diagnostics: Residual Analysis

Normality Residuals appear normal.

Looks pretty good.

Might be a bit of a left skew still, but likely not enough to worry about.

```
par(mfrow=c(2,2))
hist(lm.mm2.residuals, main="Histogram of Residuals")
plot(density(lm.mm2.residuals), main="Kernal Density plot of Residuals")
rug(lm.mm2.residuals)
qqnorm(lm.mm2.residuals)
```

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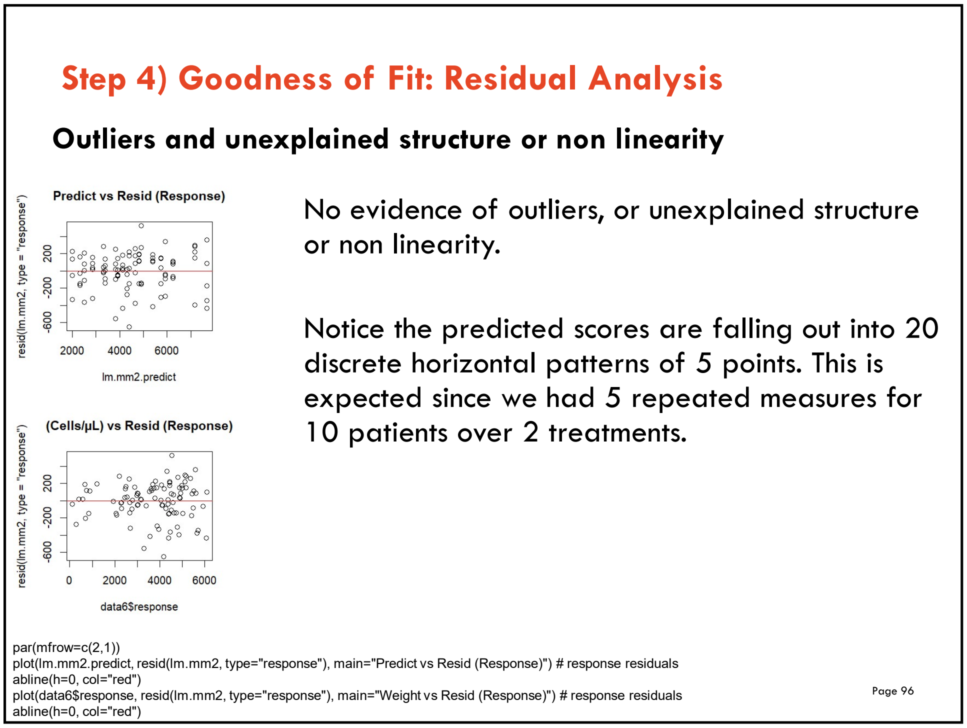


Step 4) Goodness of Fit: Residual Analysis

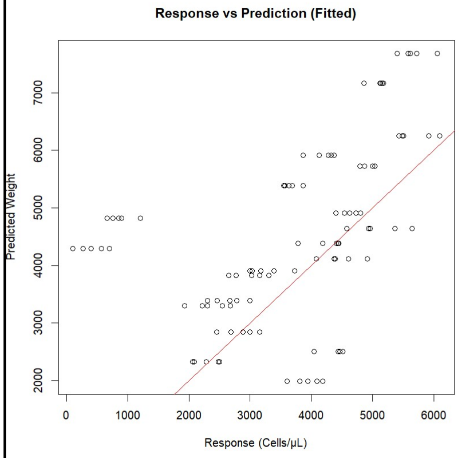
Outliers and unexplained structure or non linearity

No evidence of outliers, or unexplained structure or non linearity.

Notice the predicted scores are falling out into 20 discrete horizontal patterns of 5 points. This is expected since we had 5 repeated measures for 10 patients over 2 treatments.

```
par(mfrow=c(2,1))
plot(lm.mm2.predict, resid(lm.mm2, type="response"), main="Predict vs Resid (Response)") # response residuals
abline(h=0, col="red")
plot(data6$response, resid(lm.mm2, type="response"), main="Weight vs Resid (Response)") # response residuals
abline(h=0, col="red")
```

Step 4) Goodness of Fit: Plots and Statistics



Whoa… That doesn't look right!!

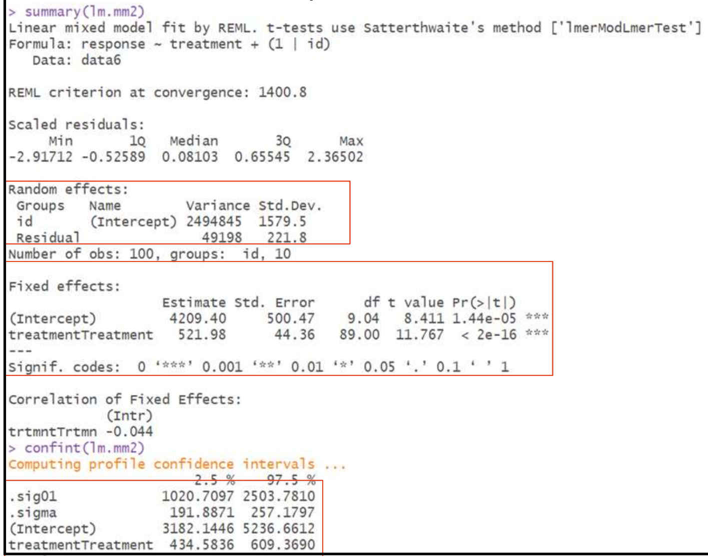
This plot doesn't work for mixed models since it ignores the random effect we added.

Which includes a different baseline intercept for each patient. Hence why it's called the Random Intercept Model.

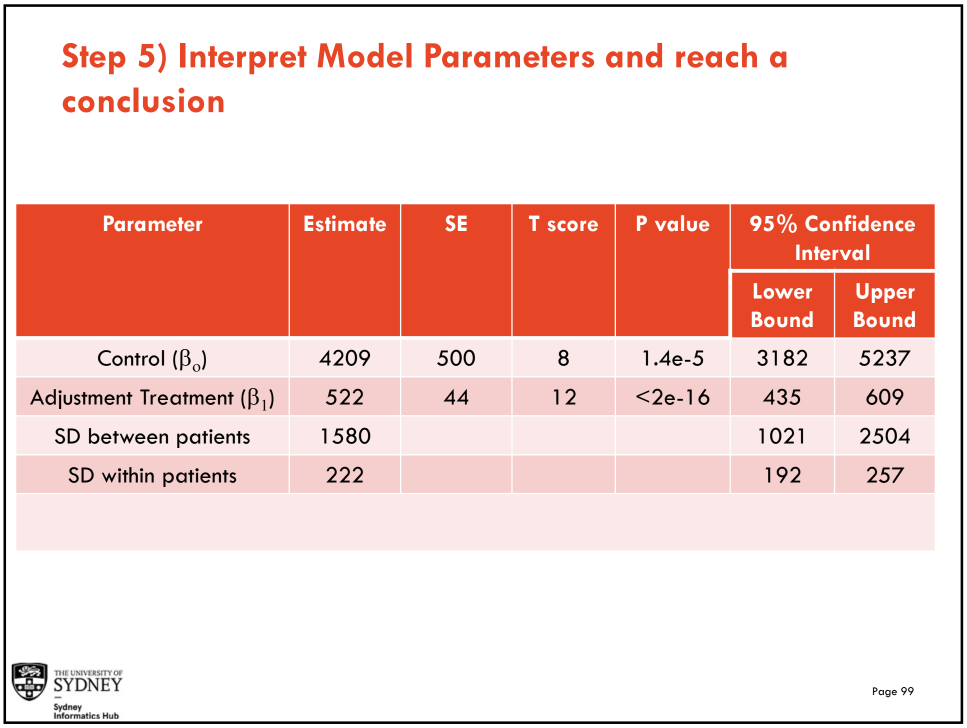
plot(data6$response, lm.mm2.predict, main="Response vs Prediction (Fitted)", xlab="Weight (response)", ylab="Predicted Weight")
abline(a=0, b=1, col="red")

Step 5) Interpret Model Parameters and reach a conclusion

R CODE and output used to create Tables

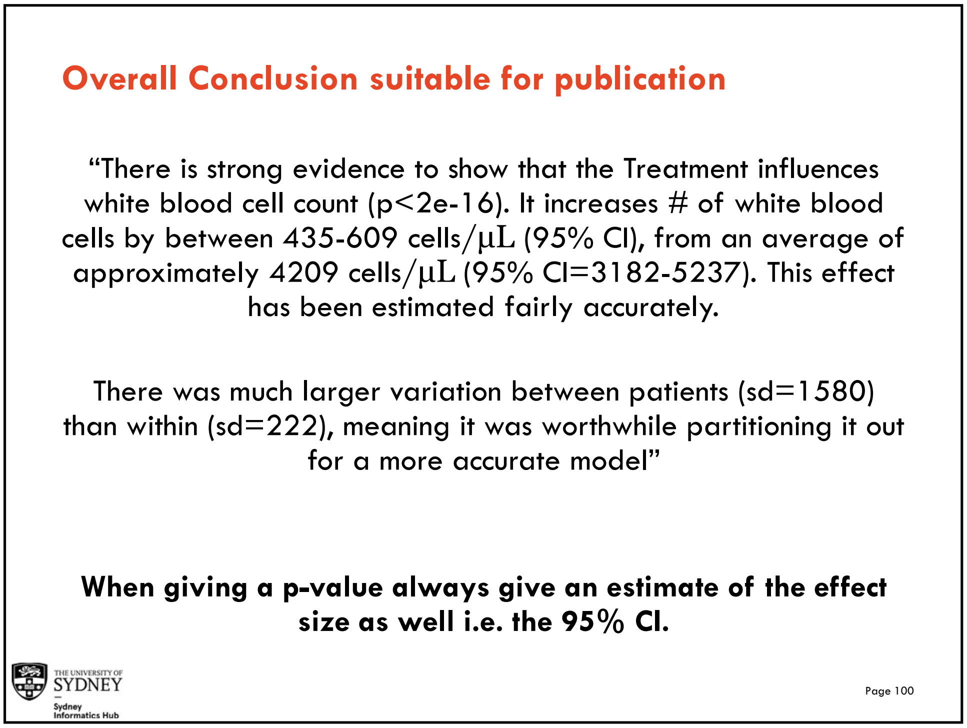


```
> summary(lm.mm2)
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: response ~ treatment + (1 | id)
   Data: data6

REML criterion at convergence: 1400.8

Scaled residuals:
     Min       1Q   Median       3Q      Max 
-2.91712 -0.52589  0.08103  0.65545  2.36502 

Random effects:
 Groups   Name        Variance Std.Dev.
 id       (Intercept) 2494845  1579.5  
 Residual               49198   221.8  
Number of obs: 100, groups:  id, 10

Fixed effects:
                   Estimate Std. Error      df t value Pr(>|t|)    
(Intercept)         4209.40     500.47    9.04   8.411 1.44e-05 ***
treatmentTreatment   521.98      44.36   89.00  11.767  < 2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:
            (Intr)
trtmntTrtmn -0.044
> confint(lm.mm2)
Computing profile confidence intervals ...
                       2.5 %    97.5 %
.sig01             1020.7097 2503.7810
.sigma              191.8871  257.1797
(Intercept)        3182.1446 5236.6612
treatmentTreatment  434.5836  609.3690
```



Step 5) Interpret Model Parameters and reach a conclusion

Parameter	Estimate	SE	T score	P value	95% Confidence Interval	
					Lower Bound	Upper Bound
Control (β_o)	4209	500	8	1.4e-5	3182	5237
Adjustment Treatment (β_1)	522	44	12	<2e-16	435	609
SD between patients	1580				1021	2504
SD within patients	222				192	257



Overall Conclusion suitable for publication

“There is strong evidence to show that the Treatment influences white blood cell count (p<2e-16). It increases # of white blood cells by between 435-609 cells/μL (95% CI), from an average of approximately 4209 cells/μL (95% CI=3182-5237). This effect has been estimated fairly accurately.

There was much larger variation between patients (sd=1580) than within (sd=222), meaning it was worthwhile partitioning it out for a more accurate model”

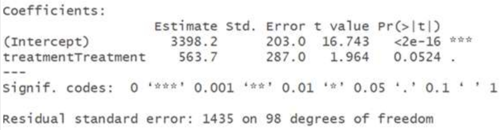
When giving a p-value always give an estimate of the effect size as well i.e. the 95% CI.

Was it worth fitting the more complex model?

If we fit a simple ANOVA model like we did previously it shows marginal support that the treatment has an impact (treatment p=0.052) while the random model has strong support (p < 2e-16). This is because the effect of treatment has been hidden by the noise in the data set (residual=1435), while the residual for the random model is much smaller (222) meaning it has more power. This is because the differences between subjects is included in the fixed effects residual, but is partitioned out in the random effects as the id-intercept SD (1580).

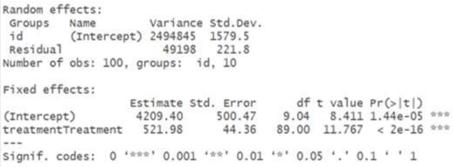
So fitting the more complex repeated measures model has shown us something the simpler ANOVA model cannot.

FIXED MODEL

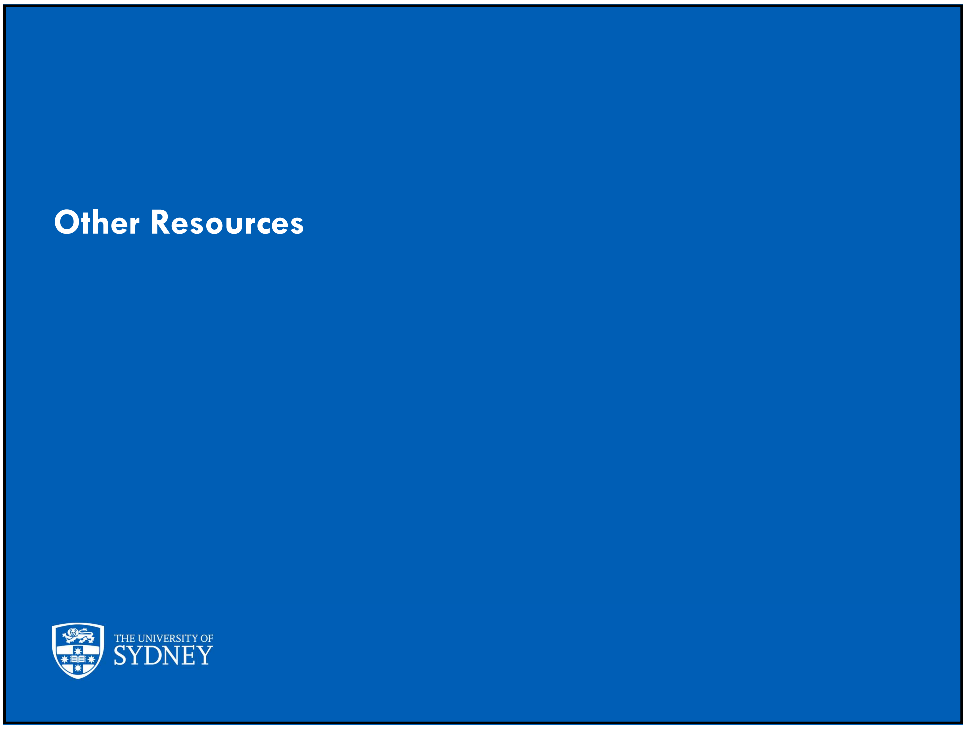


```
Coefficients:
                  Estimate Std. Error t value Pr(>|t|)
(Intercept)         3398.2      203.0  16.743   <2e-16 ***
treatmentTreatment   563.7      287.0   1.964   0.0524 .
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 1435 on 98 degrees of freedom
```

RANDOM MODEL



```
Random effects:
 Groups   Name        Variance Std.Dev.
 id       (Intercept) 2494845  1579.5
 Residual               49198   221.8
Number of obs: 100, groups:  id, 10

Fixed effects:
                   Estimate Std. Error      df t value Pr(>|t|)
(Intercept)         4209.40     500.47    9.04   8.411 1.44e-05 ***
treatmentTreatment   521.98      44.36   89.00  11.767  < 2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



Other Resources

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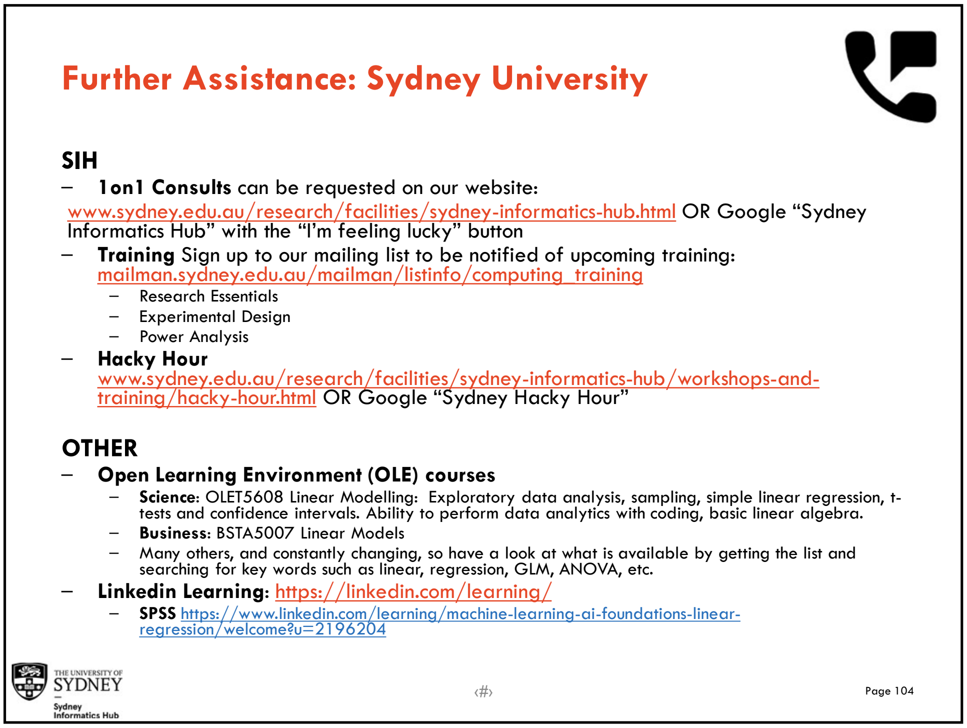

Further Assistance: Sydney University

SIH

- **1on1 Consults** can be requested on our website: www.sydney.edu.au/research/facilities/sydney-informatics-hub.html OR Google "Sydney Informatics Hub" with the "I'm feeling lucky" button
- **Training** Sign up to our mailing list to be notified of upcoming training: mailman.sydney.edu.au/mailman/listinfo/computing_training
  - Research Essentials
  - Experimental Design
  - Power Analysis
- **Hacky Hour** www.sydney.edu.au/research/facilities/sydney-informatics-hub/workshops-and-training/hacky-hour.html OR Google "Sydney Hacky Hour"

OTHER

- **Open Learning Environment (OLE) courses**
  - **Science:** OLET5608 Linear Modelling: Exploratory data analysis, sampling, simple linear regression, t-tests and confidence intervals. Ability to perform data analytics with coding, basic linear algebra.
  - **Business:** BSTA5007 Linear Models
  - Many others, and constantly changing, so have a look at what is available by getting the list and searching for key words such as linear, regression, GLM, ANOVA, etc.
- **Linkedin Learning:** https://linkedin.com/learning/
  - **SPSS** https://www.linkedin.com/learning/machine-learning-ai-foundations-linear-regression/welcome?u=2196204

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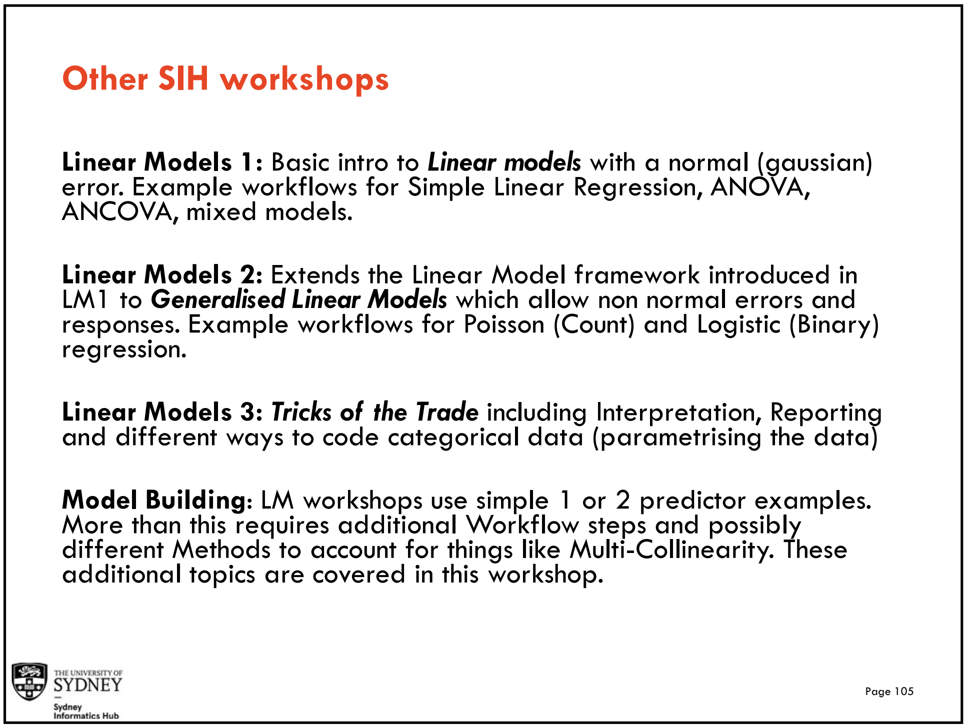

Other SIH workshops

Linear Models 1: Basic intro to ***Linear models*** with a normal (gaussian) error. Example workflows for Simple Linear Regression, ANOVA, ANCOVA, mixed models.

Linear Models 2: Extends the Linear Model framework introduced in LM1 to ***Generalised Linear Models*** which allow non normal errors and responses. Example workflows for Poisson (Count) and Logistic (Binary) regression.

Linear Models 3: ***Tricks of the Trade*** including Interpretation, Reporting and different ways to code categorical data (parametrising the data)

Model Building: LM workshops use simple 1 or 2 predictor examples. More than this requires additional Workflow steps and possibly different Methods to account for things like Multi-Collinearity. These additional topics are covered in this workshop.

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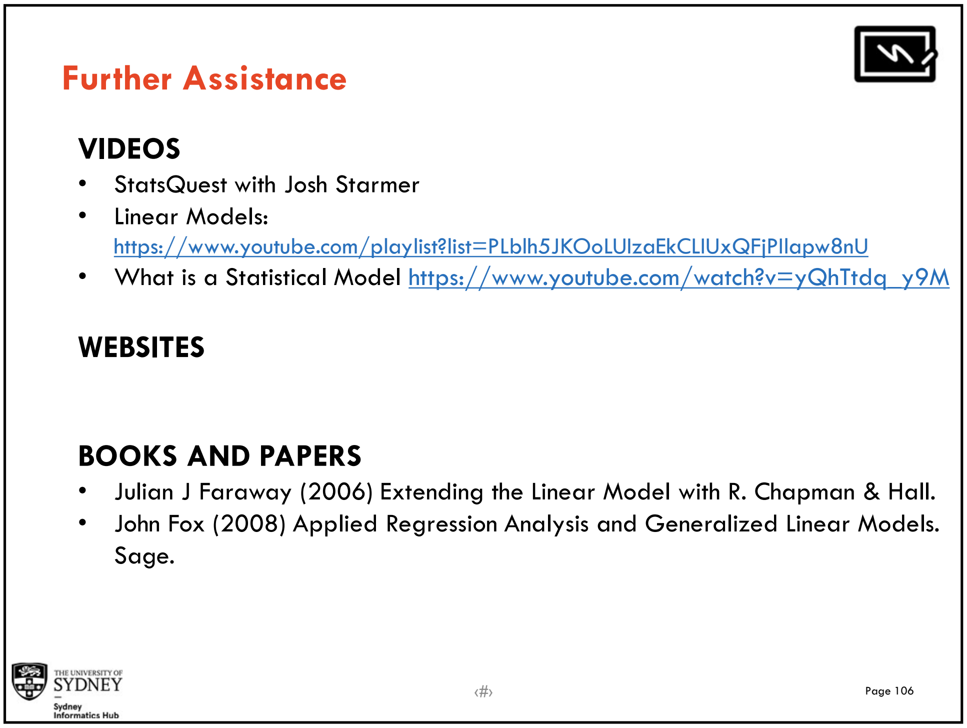

Further Assistance

VIDEOS

- StatsQuest with Josh Starmer
- Linear Models: https://www.youtube.com/playlist?list=PLblh5JKOoLUIzaEkCLIUxQFjPIlapw8nU
- What is a Statistical Model https://www.youtube.com/watch?v=yQhTtdq_y9M

WEBSITES

BOOKS AND PAPERS

- Julian J Faraway (2006) Extending the Linear Model with R. Chapman & Hall.
- John Fox (2008) Applied Regression Analysis and Generalized Linear Models. Sage.

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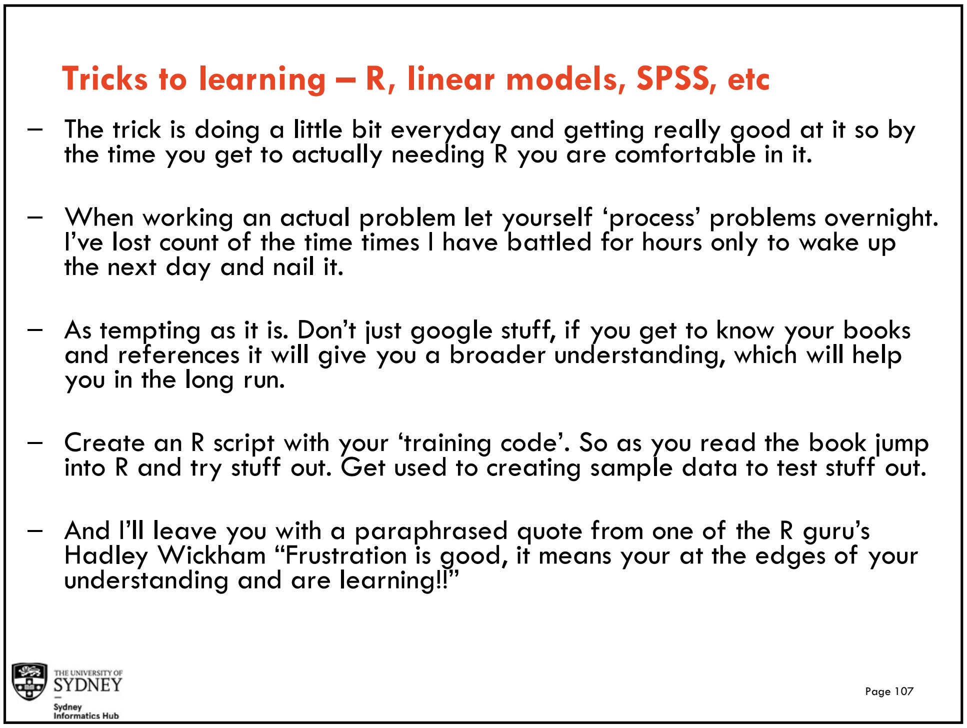

Tricks to learning – R, linear models, SPSS, etc

- The trick is doing a little bit everyday and getting really good at it so by the time you get to actually needing R you are comfortable in it.
- When working an actual problem let yourself ‘process’ problems overnight. I’ve lost count of the time times I have battled for hours only to wake up the next day and nail it.
- As tempting as it is. Don’t just google stuff, if you get to know your books and references it will give you a broader understanding, which will help you in the long run.
- Create an R script with your ‘training code’. So as you read the book jump into R and try stuff out. Get used to creating sample data to test stuff out.
- And I’ll leave you with a paraphrased quote from one of the R guru’s Hadley Wickham “Frustration is good, it means your at the edges of your understanding and are learning!!”

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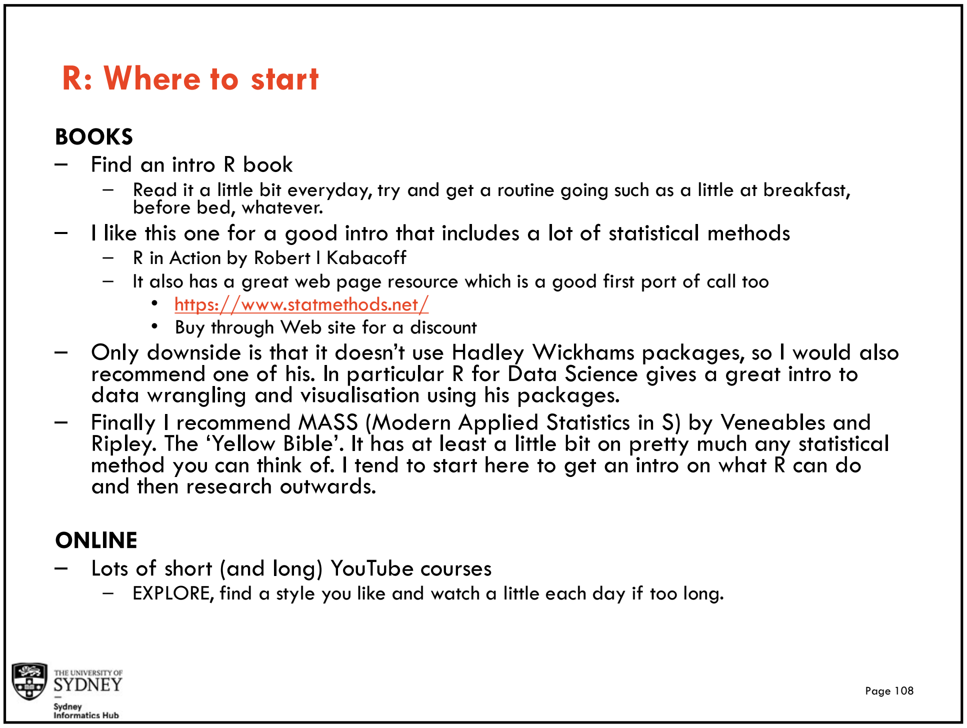

R: Where to start

BOOKS

- Find an intro R book
  - Read it a little bit everyday, try and get a routine going such as a little at breakfast, before bed, whatever.
- I like this one for a good intro that includes a lot of statistical methods
  - R in Action by Robert I Kabacoff
  - It also has a great web page resource which is a good first port of call too
    - https://www.statmethods.net/
    - Buy through Web site for a discount
- Only downside is that it doesn’t use Hadley Wickhams packages, so I would also recommend one of his. In particular R for Data Science gives a great intro to data wrangling and visualisation using his packages.
- Finally I recommend MASS (Modern Applied Statistics in S) by Veneables and Ripley. The ‘Yellow Bible’. It has at least a little bit on pretty much any statistical method you can think of. I tend to start here to get an intro on what R can do and then research outwards.

ONLINE

- Lots of short (and long) YouTube courses
  - EXPLORE, find a style you like and watch a little each day if too long.

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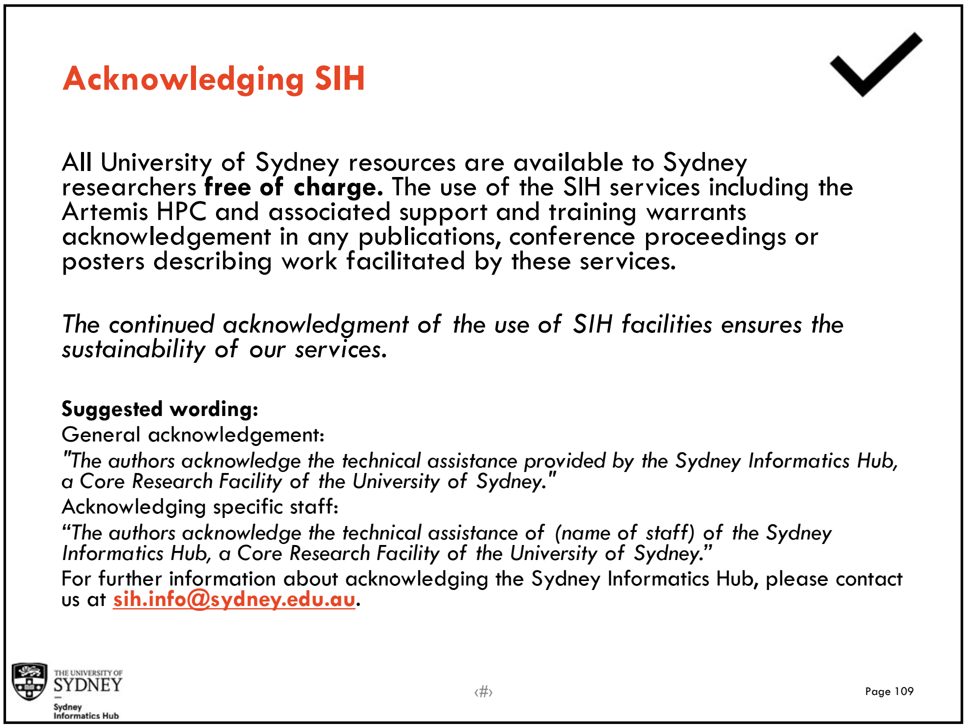

Acknowledging SIH

All University of Sydney resources are available to Sydney researchers **free of charge.** The use of the SIH services including the Artemis HPC and associated support and training warrants acknowledgement in any publications, conference proceedings or posters describing work facilitated by these services.

The continued acknowledgment of the use of SIH facilities ensures the sustainability of our services.

Suggested wording:
General acknowledgement:
"The authors acknowledge the technical assistance provided by the Sydney Informatics Hub, a Core Research Facility of the University of Sydney."
Acknowledging specific staff:
"The authors acknowledge the technical assistance of (name of staff) of the Sydney Informatics Hub, a Core Research Facility of the University of Sydney."
For further information about acknowledging the Sydney Informatics Hub, please contact us at sih.info@sydney.edu.au.

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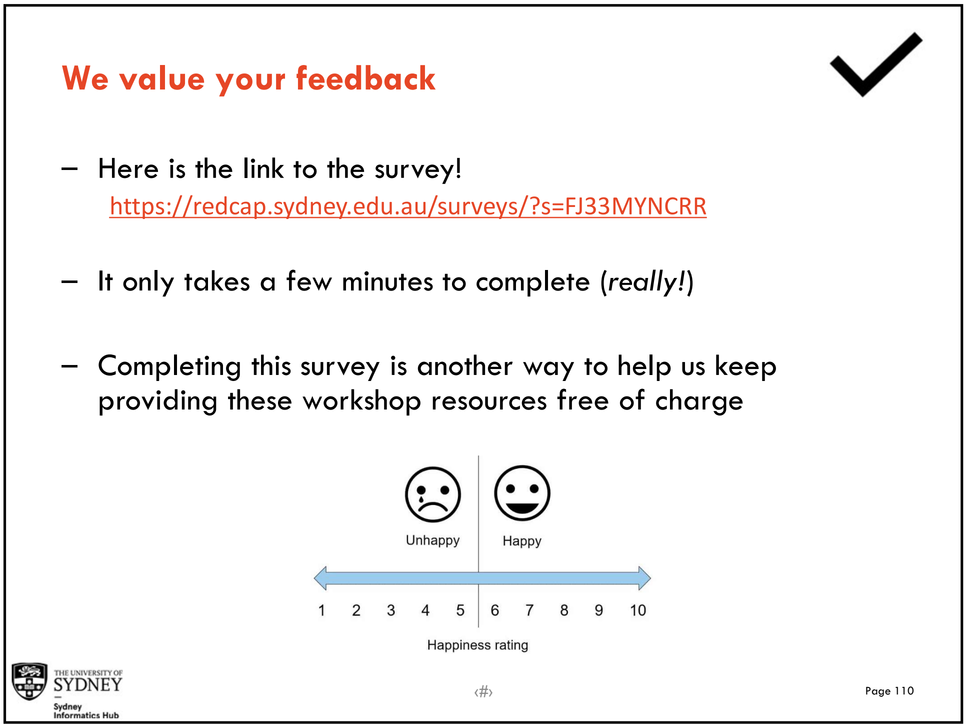

We value your feedback

- Here is the link to the survey!
  https://redcap.sydney.edu.au/surveys/?s=FJ33MYNCRR
- It only takes a few minutes to complete (*really!*)
- Completing this survey is another way to help us keep providing these workshop resources free of charge

Unhappy
Happy
1
2
3
4
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10
Happiness rating

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