Linear Models II: Logistic (binary) and Poisson (count) regression, and an introduction to Generalised Linear Models (GLM)

Presented by
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Core Research Facilities
The University of Sydney

1

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2

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

3

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

4

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)

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

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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7

CONTENTS: Generalised Linear Models II

First, we will explain the Generalised Linear Model Framework and how it is just an extension of the Simple Linear Framework introduced in Workshop I.

Statistical Workflows for:

– Logistic (binary) regression
– Poisson (count) regression

These workflows are software agnostic but also have 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().

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Page 8

8

Generalised Linear Models Framework

Simple Linear Models (workshop 1) vs Generalised Linear Models (workshop 2+)

Introducing the concepts of:

- Design Matrix
- Linear Predictor
- Data Distribution
- Link Function

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9

What are Generalised Linear Models?

ANOVA

Linear Regression

ANCOVA

Logistic (Binary) regression

Before After Control Impact (BACI) Studies

Count (Poisson) regression

Repeated measures

Randomised Control Trials (RCT's)

Plus Many More!!

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Page 10

10

A single unifying Theory

In Linear Models I we showed that although regression and ANOVA are often taught as different things, they aren't. Instead, it's much easier to understand them using a single unifying Linear Models theory.

This allows us to apply them using the same workflow.

In this workshops we extend this theory to allow non normal (gaussian) errors and responses. This extended theory is called:

Generalised Linear Models

The 3 elements of a GLM you need to know, and are the 1st topic of this workshop

When you ask software to do a GLM, it will ask you to specify the:

1. ***Deterministic part of the model*** i.e. relationship between Response (Y) and Predictors (X) ~ defined by the Design Matrix and Linear Predictor (Part 1 of a GLM)
2. ***Random/stochastic part of the model*** i.e. Responses distribution ~ e.g. is it normal (Part 2 of a GLM)
3. ***Link Function*** ~ which links the deterministic model with the random/stochastic model (Part 3 of a GLM)

We're gonna need some Equations

DON'T FREAK OUT!!!

Couple tricks with equations:

- They are a language.
  - Each symbol represents a concept, so learn the concept to learn the equation.
  - Then write the equation out in your native tongue
- If you don't get the concept that's fine. Just work on it a little bit each day. Like any language.

For example, this equation just means something called Y equals something called Beta Zero plus some Error.

$$Y_i = \beta_o + \varepsilon_i$$

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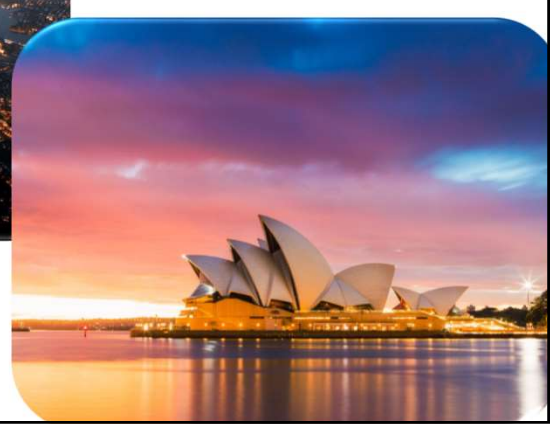
13

Don't get lost in the detail. Get the lay of the land at a *Conceptual* - big scale. And then come back and zoom into the detail when you have time.



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14

We are covering a lot in this first section, so don't worry if you get a little lost.

Just get the ***Big Picture***, remember where you get lost, and then come back and learn a little more each day.

If you can just get the take homes in these red boxes today that's a great start. The main concepts are:

- Design Matrix
- Linear Predictor
- Data Distribution
- Link Function

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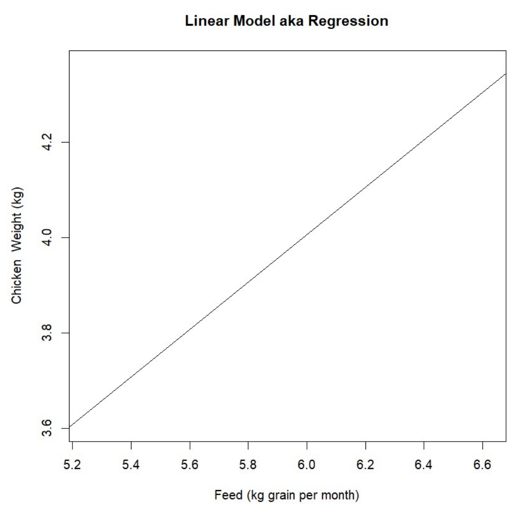
Simple Linear Model

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



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 (aka gradient) * X + Constant (aka Y intercept)

Y = mx + b

Statistical Equation for a line (puts the constant first)

$\hat{Y}_i = \beta_o + \beta_1 X_i$

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

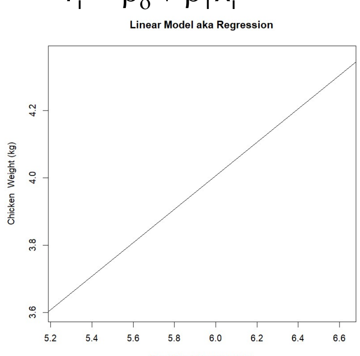
Another name for the Natural Variance is the "Error" of the model. Which is why we usually represent it as an ε in the model.

$\hat{Y}$ ~ The "hat" over the $\hat{Y}$ tells us that it's a **prediction** of Y for those specific predictor values for X.

Y ~ Is the **actual value** of Y, so it's the prediction + error.

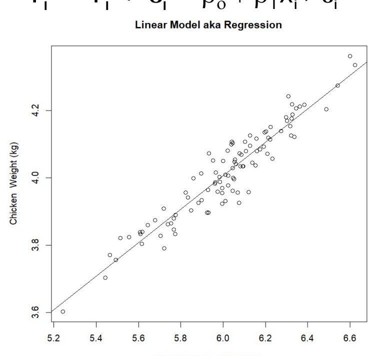
MODEL FOR A LINE

$\hat{Y}_i = \beta_o + \beta_1 X_i$



MODEL FOR OUR DATA

$Y_i = \hat{Y}_i + \varepsilon_i = \beta_o + \beta_1 X_i + \varepsilon_i$



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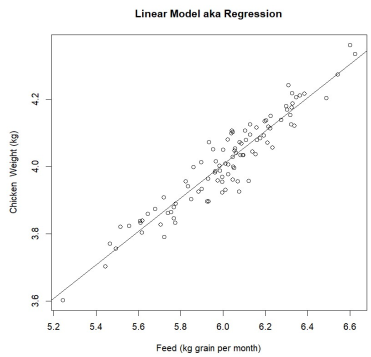
So let's look at all the different components of this equation so we can **generalise it to more complex models**. Such as:

- More than 1 continuous variable
- Categorical variables
- Non normal error

MODEL FOR OUR DATA

$Y_i = \hat{Y}_i + \varepsilon_i = \beta_o + \beta_1 X_i + \varepsilon_i$



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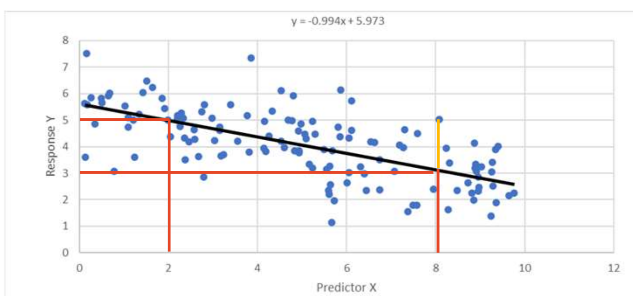
19



- The blue points are our data.
- The **black line** is the regression line we use to predict, it's our **model**
  - The red lines are some example predictions along the line. Notice that our prediction is ***conditional*** on what X is e.g. when X=2 our prediction is Y=5. When X=8 we predict Y=3. In other words the prediction of Y is **conditional** on X.
- The orange line is the error for the specific blue point X=8, Y=5. So although we predict Y=3, this particular point has Y=5. So an error of 2 above the line i.e. $Y = \hat{Y} + \varepsilon$ so $\varepsilon = Y - \hat{Y} = 5-3=2$.

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Page 20

20

Simple Regression – Numeric Statistical Model

$$Y_i = \beta_o X_{0i} + \beta_1 X_{1i} + \varepsilon_i$$

Actual Y value = Linear Prediction + Error/Natural Variation

Data			Design Matrix Parameters		Model Variables	
		Predictors				
Observation i	Response Yi	Continuous X1i	X0i	X1i	Prediction $\hat{Y}_i$	Error εi
1	4	4	1	4	4.6	-0.6
2	4	8	1	8	4.7	-0.7
3	6	1	1	1	5.1	0.9
4	3	9	1	9	2.1	0.9
5	2	1	1	1	2.9	-0.9
6	2	7	1	7	2.5	-0.5

Data **(the actual data you collect)**

Y_i ~ **Response** of Observation i

X_{1i} ~ **Predictor X_1** of Observation i

Design Matrix Parameters **(the parameters in your model i.e. the actual data you model)**

X_{oi} ~ design parameter for parameter β_0 (Constant/Y intercept)

X_{1i} ~ design parameter for β_1 (parameter X_{1i})

Model Variables **(variables the model calculates)**

$\hat{Y}_i$ ~ **Prediction** for Observation i

ε_i ~ **Error of** Observation i

β_0 ~ Constant/Y intercept parameter

β_{1i} ~ parameter for predictor 1

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Page 21

21

Simple Regression – Numeric Statistical Model

$$Y_i = \beta_o X_{0i} + \beta_1 X_{1i} + \varepsilon_i$$

Actual Y value = Linear Prediction + Error/Natural Variation

Data			Design Matrix Parameters		Model Variables	
		Predictors				
Observation i	Response Yi	Continuous X1i	X0i	X1i	Prediction $\hat{Y}_i$	Error εi
1	4	4	1	4	4.6	-0.6
2	4	8	1	8	4.7	-0.7
3	6	1	1	1	5.1	0.9
4	3	9	1	9	2.1	0.9
5	2	1	1	1	2.9	-0.9
6	2	7	1	7	2.5	-0.5

Take Home

1. We only indirectly model the data. ***What we actually model is the Design Matrix***, this is usually created in the background by the software.
2. You can fit ***fancy models*** by using a ***fancy design matrix***. Examples of parameters not in the data but are in the design matrix include:
   1. Intercept – so you can remove it to force the line through the origin e.g. calibrations.
   2. Polynomials e.g. add a quadratic term to fit a parabola curve.

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Page 22

22

Simple Regression – Numeric Statistical M

$$Y_i = \beta_o X_{0i} + \beta_1 X_{1i} + \varepsilon_i$$

Actual Y value = Linear Prediction + Error/Natura

Data			Design Matrix Parameters		Model Variables	
		Predictors				
Observation i	Response Yi	Continuous X1i	X0i	X1i	Prediction $\hat{Y}_i$	Error εi
1	4	4	1	4	4.6	-0.6
2	4	8	1	8	4.7	-0.7
3	6	1	1	1	5.1	0.9
4	3	9	1	9	2.1	0.9
5	2	1	1	1	2.9	-0.9
6	2	7	1	7	2.5	-0.5

Take Home

1. We only indirectly model the data. ***What we actually model is the Design Matrix***, this is usually created in the background by the software.
2. You can fit ***fancy models*** by using a ***fancy design matrix***. Examples of parameters not in the data but are in the design matrix include:
    1. Intercept – so you can remove it to force the line through the origin e.g. calibrations.
    2. Polynomials e.g. add a quadratic term to fit a parabola curve.

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Let's add another continuous predictor variable

Yellow represents the changes required for this to happen

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Multiple Regression

$$Y_i = \beta_o X_{0i} + \beta_1 X_{1i} + \beta_2 X_{2i} + \varepsilon_i$$

Actual Y value = Linear Prediction + Error/Natural Variation

Notice the predictions have changed and the errors are **overall** smaller (although some are individually larger). As expected when we add new parameters.

Data					Design Matrix Parameters			Model Variables	
	Predictors								
Observation	Response	Continuous	Continuous					Prediction	Error
i	Yi	X1i	X2i		X0i	X1i	X2i	$\hat{Y}i$	εi
1	4	4	12		1	4	12	4.4	-0.4
2	4	8	54		1	8	54	4.5	-0.5
3	6	1	87		1	1	87	5.3	0.7
4	3	9	96		1	9	96	3.2	-0.2
5	2	1	41		1	1	41	1.8	0.2
6	2	7	47		1	7	47	2.6	-0.6

Data (the actual data you collect)

Y_i ~ **Response** of Observation i

X_{1i} ~ **Predictor X_1** of Observation i

X_{2i} ~ **Predictor X_2 of Observation i**

Design Matrix Parameters (the parameters in your model i.e. the actual data you model)

X_{oi} ~ design parameter for parameter β_0 (Constant/Y intercept)

X_{1i} ~ design parameter for β_1 (parameter X_{1i})

X_{2i} ~ design parameter for β_2 (parameter X_{2i})

Model Variables (variables the model calculates)

$\hat{Y}_i$ ~ **Prediction** for Observation i

ε_i ~ **Error** of Observation i

β_0 ~ Constant/Y intercept parameter

β_{1i} ~ parameter for predictor 1

β_{2i} ~ parameter for predictor 2

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Multiple Regression

$$Y_i = \beta_o X_{0i} + \beta_1 X_{1i} + \beta_2 X_{2i} + \beta_3 X_{3i} + \varepsilon_i$$

Actual Y value = Linear Prediction + Error/Natural Variation

A new design matrix predictor is simply added for any new continuous predictors you want.

Just keep going!!

Data						Design Matrix Parameters				Model Variables	
	Predictors										
Obs	Response	Continuous	Continuous	Continuous						Prediction	Error
i	Yi	X1i	X2i	X3i		X0i	X1i	X2i	X3i	$\hat{Y}i$	εi
1	4	4	12	12		1	4	12	12	4.2	-0.2
2	4	8	54	54		1	8	54	54	4.3	-0.3
3	6	1	87	87		1	1	87	87	5.3	0.7
4	3	9	96	96		1	9	96	96	2.9	0.1
5	2	1	41	41		1	1	41	41	1.8	0.2
6	2	7	47	47		1	7	47	47	2.4	-0.4

Data (the actual data you collect)

Y_i ~ **Response** of Observation i

X_{1i} ~ **Predictor X_1** of Observation i

X_{2i} ~ **Predictor X_2** of Observation i

X_{3i} ~ **Predictor X_3 of Observation i**

Design Matrix Parameters (the parameters in your model i.e. the actual data you model)

X_{oi} ~ design parameter for parameter β_0 (Constant/Y intercept)

X_{1i} ~ design parameter for β_1 (parameter X_{1i})

X_{2i} ~ design parameter for β_2 (parameter X_{2i})

X_{3i} ~ design parameter for β_3 (parameter X_{3i})

Model Variables (variables the model calculates)

$\hat{Y}_i$ ~ **Prediction** for Observation i

ε_i ~ **Error** of Observation i

β_0 ~ Constant/Y intercept parameter

β_{1i} ~ parameter for predictor 1

β_{2i} ~ parameter for predictor 2

β_{3i} ~ parameter for predictor 3

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Multiple Regression

$$Y_i = \beta_o X_{0i} + \beta_1 X_{1i} + \beta_2 X_{2i} + \beta_3 X_{3i} + \varepsilon_i$$

Actual Y value = Linear Prediction + Error/Natural Variation

Data					Design Matrix Parameters				Model Variables	
		Predictors								
Obs	Response	Continuous	Continuous	Continuous					Prediction	Error
i	Yi	X1i	X2i	X3i	X0i	X1i	X2i	X3i	$\hat{Y}_i$	εi
1	4	4	12	12	1	4	12	12	4.2	-0.2
2	4	8	54	54	1	8	54	54	4.3	-0.3
3	6	1	87	87	1	1	87	87	5.3	0.7
4	3	9	96	96	1	9	96	96	2.9	0.1
5	2	1	41	41	1	1	41	41	1.8	0.2
6	2	7	47	47	1	7	47	47	2.4	-0.4

Data **(the actual data you collect)**

Y_i ~ **Response** of Observation i

X_{1i} ~ **Predictor X_1** of Observation i

X_{2i} ~ **Predictor X_2** of Observation i

X_{3i} ~ **Predictor X_3** of Observation i

Design Matrix Parameters **(the parameters in your model i.e. the actual data you model)**

X_{oi} ~ design parameter for parameter β_0 (Constant/Y intercept)

X_{1i} ~ design parameter for β_1 (parameter X_{1i})

X_{2i} ~ design parameter for β_2 (parameter X_{2i})

X_{3i} ~ design parameter for β_3 (parameter X_{3i})

Model Variables **(variables the model calculates)**

$\hat{Y}_i$ ~ **Prediction** for Observation i

ε_i ~ **Error of** Observation i

β_0 ~ Constant/Y intercept parameter

β_{1i} ~ parameter for predictor 1

β_{2i} ~ parameter for predictor 2

β_{3i} ~ parameter for predictor 3

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Page 27

27

So how do we add Categorical Variables??

Yellow represents the changes required for this to happen

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Page 28

28

Adding Categorical Variables (e.g. ANOVA)

$$Y_i = \beta_o X_{0i} + \beta_1 X_{1i} + \beta_2 X_{2i} + \varepsilon_i$$

Actual Y value = Linear Prediction + Error/Natural Variation

Data				Design Matrix Parameters			Model Variables	
		Predictors						
Obs	Response	Continuous	Categorical				Prediction	Error
i	Yi	X1i	X2i	X0i	X1i	X2i	$\hat{Y}_i$	εi
1	4	4	Non Smoking	1	4	0	4.6	-0.6
2	4	8	Smoking	1	8	1	4.2	-0.2
3	6	1	Non Smoking	1	1	0	5.1	0.9
4	3	9	Smoking	1	9	1	3.4	-0.4
5	2	1	Non Smoking	1	1	0	1.4	0.6
6	2	7	Non Smoking	1	7	0	2.2	-0.2

Data (the actual data you collect)

Y_i ~ **Response** of Observation i

X_{1i} ~ **Predictor X_1** of Observation i

X_{2i} ~ **Predictor X_2** of Observation i

Design Matrix Parameters (the parameters in your model i.e. the actual data you model)

X_{oi} ~ design parameter for parameter β_0 (Reference group = Non-Smoking)

X_{1i} ~ design parameter for β_1 (parameter X_{1i})

X_{2i} ~ design parameter for β_2 (parameter X_{2i} = smoking)

Model Variables (variables the model calculates)

$\hat{Y}_i$ ~ **Prediction** for Observation i

ε_i ~ **Error of** Observation i

β_0 ~ (Reference group = Non-Smoking)

β_{1i} ~ parameter for predictor 1

β_{2i} ~ parameter for smoking

Adding Categorical Variables (e.g. ANOVA)

$$Y_i = \beta_o X_{0i} + \beta_1 X_{1i} + \beta_2 X_{2i} + \varepsilon_i$$

Actual Y value = Linear Prediction + Error/Natural Variation

Data				Design Matrix Parameters			Model Variables	
		Predictors						
Obs	Response	Continuous	Categorical				Prediction	Error
i	Yi	X1i	X2i	X0i	X1i	X2i	$\hat{Y}_i$	εi
1	4	4	Non Smoking	1	4	0	4.6	-0.6
2	4	8	Smoking	1	8	1	4.2	-0.2
3	6	1	Non Smoking	1	1	0	5.1	0.9
4	3	9	Smoking	1	9	1	3.4	-0.4
5	2	1	Non Smoking	1	1	0	1.4	0.6
6	2	7	Non Smoking	1	7	0	2.2	-0.2

There are many different **parameterisations** (ways) to model categorical variables. The way I am showing you is called **Dummy** or **Treatment Coding.** Dummy coding works by picking 1 category as the **reference category**, this category is captured in the **constant/intercept parameter** and is always 'on'. We then adjust it when a different category is present by adding their specific parameter into the prediction equation/model.

This means that every other category other than the reference category has it's own design parameter which functions as an 'indicator variable" since:

- When X_2 = 1 it "turns on" β_2 since $\beta_2 X_{2i} = \beta_2 * 1 = \beta_2$
  - β_2 only comes into the model when $X_2 = 1$, i.e. when people smoke i.e. it is the extra effect of smoking compared to the baseline reference level of not smoking.
- When $X_2 = 0$ it "turns off" β_2 since $\beta_2 X_{2i} = \beta_2 * 0 = 0$
  - We only have β_0 when people don't smoke i.e. $X_2 = 0$, i.e. it is the baseline prediction when people don't smoke i.e. it's the reference level.

Adding Categorical Variables (e.g. ANOVA)

$$Y_i = \beta_o X_{0i} + \beta_1 X_{1i} + \beta_2 X_{2i} + \beta_3 X_{3i} + \varepsilon_i$$

Actual Y value = Linear Prediction + Error/Natural Variation

A new design matrix predictor is simply added for any new categorical levels you want.

Just keep going!!

Data				Design Matrix Parameters				Model Variables	
		Predictors							
Obs	Response	Continuous	Categorical					Prediction	Error
i	Yi	X1i	X2i	X0i	X1i	X2i	X3i	$\hat{Y}_i$	εi
1	4	4	Never Smoked	1	4	0	0	4.6	-0.6
2	4	8	Smoking	1	8	1	0	4.2	-0.2
3	6	1	Ex smoker	1	1	0	1	5.1	0.9
4	3	9	Smoking	1	9	1	0	3.4	-0.4
5	2	1	Never Smoked	1	1	0	0	1.4	0.6
6	2	7	Never Smoked	1	7	0	0	2.2	-0.2

Data (the actual data you collect)

Y_i ~ **Response** of Observation i

X_{1i} ~ **Predictor X_1** of Observation i

X_{2i} ~ **Predictor X_2** of Observation i

Design Matrix Parameters (the parameters in your model i.e. the actual data you model)

X_{oi} ~ design parameter for parameter β_0 (Reference group = Never Smoked)

X_{1i} ~ design parameter for β_1 (parameter X_{1i})

X_{2i} ~ design parameter for β_2 (parameter X_{2i} = Smoking)

X_{3i} ~ design parameter for β_2 (parameter X_{3i} = Ex Smoker)

Model Variables (variables the model calculates)

$\hat{Y}_i$ ~ **Prediction** for Observation i

ε_i ~ **Error of** Observation i

β_0 ~ (Reference group = Non-Smoking)

β_{1i} ~ parameter for predictor 1

β_{2i} ~ parameter for smoking

β_{3i} ~ parameter for Ex Smoker

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Page 31

31

Adding Categorical Variables (e.g. ANOVA)

$$Y_i = \beta_o X_{0i} + \beta_1 X_{1i} + \beta_2 X_{2i} + \varepsilon_i$$

Actual Y value = Linear Prediction + Error/Natural Variation

Data				Design Matrix Parameters			Model Variables	
		Predictors						
Obs	Response	Continuous	Categorical				Prediction	Error
i	Yi	X1i	X2i	X0i	X1i	X2i	$\hat{Y}_i$	εi
1	4	4	Non Smoking	1	4	0	4.6	-0.6
2	4	8	Smoking	1	8	1	4.2	-0.2
3	6	1	Non Smoking	1	1	0	5.1	0.9
4	3	9	Smoking	1	9	1	3.4	-0.4
5	2	1	Non Smoking	1	1	0	1.4	0.6
6	2	7	Non Smoking	1	7	0	2.2	-0.2

Linear Models 3 goes into more detail by:

- discussing ways other than dummy/treatment coding to model categorical variables, such as effects coding.
- having a worked example of how the deign matrix combines with the parameters to give the predictions.

32

What's the difference with multiple regression?

Virtually none. The underlying model is exactly the same!! The only changes are in the data:

1. The X predictor is continuous when adding a continuous variable aka multiple regression, while it's an indicator variable if adding a categorical variable.
2. Interpretation of the parameters differs.
3. But they are both still ***linear models.***

$$Y_i = \beta_o X_{0i} + \beta_1 X_{1i} + \beta_2 X_{2i} + \beta_3 X_{3i} + \varepsilon_i$$

Actual Y value = Linear Prediction + Error/Natural Variation

Take Home
Categorical ANOVA style models are the same as continuous style regression models. The only difference is in the design matrix.

Data					Design Matrix Parameters				Model Variables	
		Predictors								
Obs i	Response Yi	Continuous X1i	Continuous X2i	Continuous X3i	X0i	X1i	X2i	X3i	Prediction $\hat{Y}_i$	Error εi
1	4	4	12	12	1	4	12	12	4.4	-0.4
2	4	8	54	54	1	8	54	54	4.5	-0.5
3	6	1	87	87	1	1	87	87	5.3	0.7
4	3	9	96	96	1	9	96	96	3.2	-0.2
5	2	1	41	41	1	1	41	41	1.8	0.2
6	2	7	47	47	1	7	47	47	2.6	-0.6

Data				Design Matrix Parameters				Model Variables	
		Predictors							
Obs i	Response Yi	Continuous X1i	Categorical X2i	X0i	X1i	X2i	X3i	Prediction $\hat{Y}_i$	Error εi
1	4	4	Non Smoking	1	4	0	0	4.5	-0.5
2	4	8	Smoking	1	8	1	0	4.1	-0.1
3	6	1	Ex smoker	1	1	0	1	4.9	1.1
4	3	9	Smoking	1	9	1	0	3.4	-0.4
5	2	1	Non Smoking	1	1	0	0	1.2	0.8
6	2	7	Non Smoking	1	7	0	0	1.8	0.2

33

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Actual Y value = Linear Prediction + Error/Natural Variation

Take Home
Categorical ANOVA style models are the same as continuous style regression models. The only difference is in the design matrix

Data					Design Matrix Parameters				Model Variables	
		Predictors								
Obs i	Response Yi	Continuous X1i	Continuous X2i	Continuous X3i	X0i	X1i	X2i	X3i	Prediction $\hat{Y}_i$	Error εi
1	4	4	12	12	1	4	12	12	4.4	-0.4
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3	6	1	87	87	1	1	87	87	5.3	0.7
4	3	9	96	96	1	9	96	96	3.2	-0.2
5	2	1	41	41	1	1	41	41	1.8	0.2
6	2	7	47	47	1	7	47	47	2.6	-0.6

Data				Design Matrix Parameters				Model Variables	
		Predictors							
Obs i	Response Yi	Continuous X1i	Categorical X2i	X0i	X1i	X2i	X3i	Prediction $\hat{Y}_i$	Error εi
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4	3	9	Smoking	1	9	1	0	3.4	-0.4
5	2	1	Non Smoking	1	1	0	0	1.2	0.8
6	2	7	Non Smoking	1	7	0	0	1.8	0.2

34

Representing complex models in a single, simple, concise and generalisable way

Wouldn't it be great if we could represent any linear models study design e.g. ANOVA, regression, ANCOVA, BACI, etc.

Using the same notation?

That would give us a very easy framework to work within.

We wouldn't need to learn lots of different things, and could instead put lots of different analyses into the same 'compartment' in our brain!

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The design matrix can represent any model!

$Y_i = \beta_o X_{0i} + \beta_1 X_{1i} + \beta_2 X_{2i} + \beta_3 X_{3i} + \ldots + \varepsilon_i$

$= X\beta + \varepsilon_i$ ~ a shorter and simpler way to write any linear model

= linear/additive model

X = design matrix
~ the actual data modelled

β = vector of parameters

ε = vector of errors

Design Matrix Parameters		
X0i	X1i	X2i
1	4	12
1	8	54
1	1	87
1	9	96
1	1	41
1	7	47

β
β_o
β_1
β_2

Error εi
-0.4
-0.5
0.7
-0.2
0.2
-0.6

The design matrix can represent any model!

$\widehat{Y}_i = \beta_o X_{0i} + \beta_1 X_{1i} + \beta_2 X_{2i} + \beta_3 X_{3i} + \ldots$

$= X\beta$ ~ a shorter and simpler way to write any linear model

= linear/additive model

Let's remove the error to give us the predictive model. This is what the hat over the Y means i.e. it's the prediction of Y given (conditioned on) the X's i.e. it's the conditional expectation (average) of Y.

X = design matrix

~ the actual data modelled

β = vector of parameters

Design Matrix Parameters		
X0i	X1i	X2i
1	4	12
1	8	54
1	1	87
1	9	96
1	1	41
1	7	47

β
β_o
β_1
β_2

Page 37

37

The linear predictor can represent any model!

$\widehat{Y}_i = \beta_o X_{0i} + \beta_1 X_{1i} + \beta_2 X_{2i} + \beta_3 X_{3i} + \ldots$

$= X\beta$ ~ a shorter and simpler way to write any linear model

= linear/additive model

$= \eta_I$ ~ the linear predictor (the symbol is called eta). The conditional expectation (average) of Y on the data X.

X = design matrix

~ the actual data modelled

β = vector of parameters

The **Linear Predictor** (η_I) Part 1 of the 3 required for a GLM

Design Matrix Parameters		
X0i	X1i	X2i
1	4	12
1	8	54
1	1	87
1	9	96
1	1	41
1	7	47

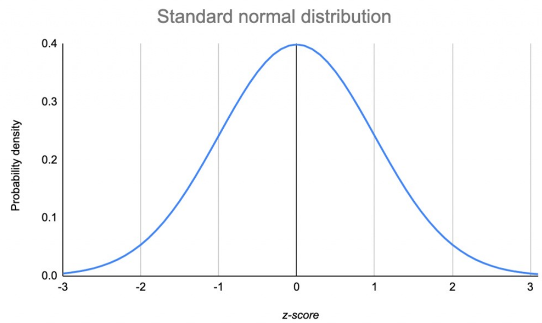
β
β_o
β_1
β_2

Page 38

38

So far we have assumed a Normal distribution

- Response is continuous
  - Ranges from –infinity to + infinity
- 2 parameters describes the curve
  - Mean = μ
  - Variance = σ^2
  - Variance independent of the mean i.e. different data sets with the same mean can have different variance.



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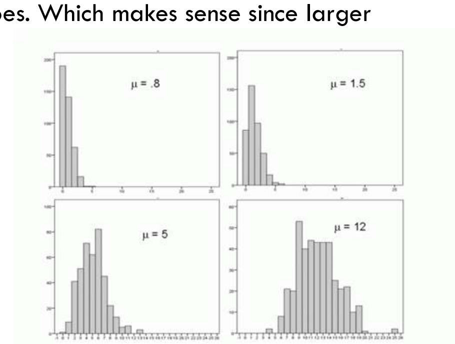
Page 39

39

BUT, what if it was different, say count data?

Could use the Poisson distribution instead

- Response is discrete
  - Often used for counts
  - Ranges from 0 to + infinity
- 1 parameter describes the curve
  - Mean = variance = λ (lamba) i.e. different data sets with same mean have to have the same variance
  - Variance gets bigger as mean does. Which makes sense since larger counts can have larger variance.



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40

Different Data Distributions

The **Data Distribution**
Part 2 of the 3
required for a GLM

Common Distributions

Normal for unbounded continuous data

Poisson for count, rate, positive integer and some log normal data

Binomial for binary data i.e. logistic regression

Adding Transformations using the Link function

So far we have established that $Y_i = \eta_i + \varepsilon_i$ can be used to efficiently represent all types of linear models.

But what if we also want to transform the response e.g. a very common transformation is to take its logarithm so we now have $\mathrm{Log}(Y_i) = \eta_i + \varepsilon_i$

This is done using the **link function** in a GLM.

The **Link Function**
Part 3 of the 3
required for a GLM

(A more formal way to represent it is $E(Y|X) = \mu = g^{-1}(\eta)$ where g is the link function.)

TAKE HOME
Link function allows us to effectively transform the response

Log links also allow us to change the additive linear predictor into a multiplicative model

$Y_i = \beta_o X_{0i} + \beta_1 X_{1i} + \beta_2 X_{2i} + \beta_3 X_{3i} + \ldots.. + \varepsilon_i$
$= \eta_I + \varepsilon_i$ = linear predictor + ε_i
= linear/additive model

$Y_i = \beta_o X_{0i} \times \beta_1 X_{1i} \times \beta_2 X_{2i} \times \beta_3 X_{3i} \ldots.. + \varepsilon_i$
= ***multiplicate model***

More info and examples to come. For now just take in that GLM's can use link functions, such as the log link, to 'convert' the linear predictor which is additive from an additive to a multiplicative model. This is how Poisson or Logistic regression become multiplicative, not additive, models.

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GLM components (so far – to be explained is greyed out)

Part 1 of the 3 required for a GLM

The **Linear Predictor** (η_I) is a ***deterministic*** additive/linear equation of predictors (X) and parameters (β) that will be used to predict the response ($\hat{Y}$), after linking with the data distribution. It tells us the expected value of the response Y is conditional on the data X.

The parameters (β) are defined by the ***Design Matrix*** (X).

$X\beta = \beta_o X_0 + \beta_1 X_1 + \beta_2 X_2 + \beta_3 X_3 + \ldots..$
$= \eta_I \sim$ **linear predictor (additive/linear model)**

Part 2 of the 3 required for a GLM

Different Data Distributions add the ***random/stochastic*** element of the model
e.g. $Y \sim N(\mu, \sigma^2)$

Part 3 of the 3 required for a GLM

The **Link Function** links Part 1 and 2 together by showing how the distributions average (Part 2) which is the model prediction can be predicted using a function of the Linear Predictor (Part 1) e.g. if the link function is $\mu = \eta = \beta_o + \beta_1 X$ then $Y_i \sim N(\beta_o + \beta_1 X_1, \sigma^2)$ = **Simple Linear Regression.** This also allows us to transform the response and make the model multiplicative.

So let's look at how these 3 things work together to let us model a wide range of data types

1. **Linear Predictor**
2. **Data Distribution**
3. **Link Function**

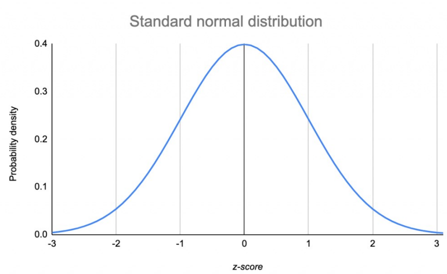
But first: some new notation so we can succinctly represent a GLM

If Y is normally distributed than we can represent it using this notation:

$Y_i \sim N(\mu, \sigma^2)$, where:

$\mu \sim$ average

$\sigma^2 \sim$ variance



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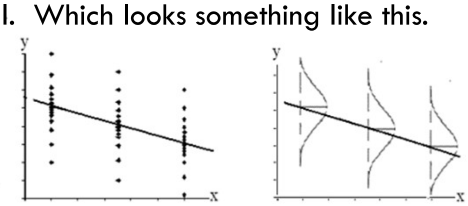
Let's use this new notation to represent a simple linear regression $Y_i = \beta_o + \beta_1 X_{1i} + \varepsilon_i$

In a simple linear regression Y is predicted using a model which is a line, and the error about this line is normal. Which looks something like this.



So using this notation we can say that

$Y_i \sim N(\mu, \sigma^2)$ where:

- **Y's average (μ)** comes from the model line which is $\mu = \beta_o + \beta_1 X_{1i.}$
    - Or in other words we predict Y's average (μ) for any combination of predictors (X) using our model i.e. Y's average (μ) **is conditional on the predictors (X).**
    - The variance (σ^2) is constant i.e. is not conditional on the predictors (X)

Succinctly we can say

We will use a **Linear Predictor** to model the ***deterministic*** relationship between Y and X:

$$\eta = \beta_o + \beta_1 X_1 = X\beta$$

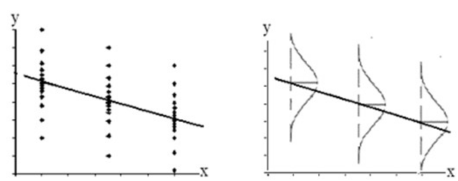
We want Y's ***random*** **Data Distribution** to be Normal:

$$Y_i \sim N(\mu, \sigma^2)$$

So we **Link** the deterministic with the random parts of the model by letting $\mathbf{E(Y|X) = \mu = \eta}$ to give us

$$\mathbf{Y_i \sim N(\beta_o + \beta_1 X_{1i}, \sigma^2)}$$

i.e. the **expectation of Y is conditional on X**



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The parameters (β) are defined by the ***Design Matrix*** **(X)**.

$$X\beta = \beta_o X_0 + \beta_1 X_1 + \beta_2 X_2 + \beta_3 X_3 + \ldots$$
$$= \eta_i \sim \text{linear predictor (additive/linear model)}$$

Part 2 of the 3 required for a GLM

Different Data Distributions add the ***random/stochastic*** element of the model
e.g. $\mathbf{Y \sim N(\mu, \sigma^2)}$

Part 3 of the 3 required for a GLM

The **Link Function** links Part 1 and 2 together by showing how the distributions average (Part 2) which is the model prediction can be predicted using a function of the Linear Predictor (Part 1) e.g. if the link function is $\mu = \eta = \beta_o + \beta_1 X$ then $Y_i \sim N(\beta_o + \beta_1 X_1, \sigma^2)$ **= Simple Linear Regression.** This also allows us to transform the response and make the model multiplicative.

Challenge Q: What do we change if the Error was Poisson instead of Normal?

We will use a **Linear Predictor** to model the relationship between Y and X:

$$\eta = \beta_o + \beta_1 X_1 = X\beta$$

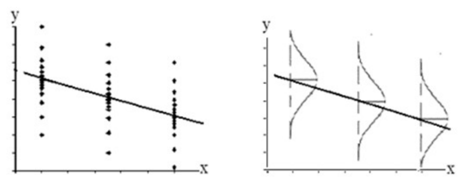
We want Y's **Data Distribution** to be Normal:

$$Y_i \sim N(\boldsymbol{\mu}, \sigma^2)$$

So we **Link** the above by letting **E(Y|X) = μ =** η to give us

$$\mathbf{Y_i \sim N(\beta_o + \beta_1 X_{1i}, \sigma^2)}$$

i.e. the **expectation μ of Y is conditional on X**



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Challenge Q: What do we change if the Error was Poisson instead of Normal?

We will use a **Linear Predictor** to model the relationship between Y and X:

$$\eta = \beta_o + \beta_1 X_1 = X\beta$$

We want Y's **Data Distribution** to be Poisson:

$$Y_i \sim P(\boldsymbol{\lambda})$$

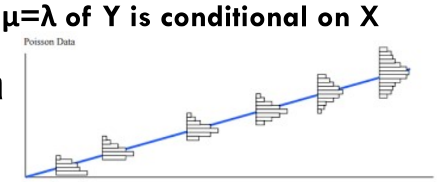
So we **Link** the above by letting **E(Y|X) = λ =** e^{η}, meaning $\eta = \log(\lambda)$ so we are using a Log link function, to give us

$$Y_i \sim P(e^{\beta_o + \beta_1 X_1})$$

i.e. the expectation μ=λ of Y is conditional on X

Note that the linear predictor (η) is linear, not Ŷ which is the log transform of (η)

η



Congratulations. You just developed Generalised Linear Models from 1st principles!

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So let's take a breath and tie everything we learnt in LM1 and so far in LM2 together into a concise summary you can refer back to

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Simple Linear Model (from LM1 workshops)

Y_i $= \mathbf{X}\beta + \varepsilon_i$

= Deterministic model + Random model

~ $N(\mu, \sigma^2)$ where $\mu = \mathbf{X}\beta$ so $N(\mathbf{X}\beta, \sigma^2)$ i.e. assumes a Normal error

~ Gives us a simple, single, unified way of fitting all types of continuous and categorical predictors so we can fit different models like simple linear regression, ANOVA, ANCOVA, BACI, RCT, Control/Treatment, etc. It does this by using a **design matrix X** with different design variables.

~ also known as *General* Linear Models – as opposed to *Genera**lised*** Linear Models which are the topic of this workshop.

Data				Design Matrix Parameters				Model Variables	
	Predictors								
Obs	Response	Continuous	Categorical					Prediction	Error
i	Yi	X1i	X2i	X0i	X1i	X2i	X3i	$\hat{Y}i$	εi
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5	2	1	Non Smoking	1	1	0	0	1.2	0.8
6	2	7	Non Smoking	1	7	0	0	1.8	0.2

55

Simple Linear Model vs Generalised Linear Model

Y_i $= \mathbf{X}\beta + \varepsilon_i$

= Deterministic model + Random model

~ $N(\mu, \sigma^2)$ where $\mu = \mathbf{X}\beta$ so $N(\mathbf{X}\beta, \sigma^2)$ i.e. assumes a Normal error

~ Gives us a simple, single, unified way of fitting all types of continuous and categorical predictors so we can fit different models like simple linear regression, ANOVA, ANCOVA, BACI, RCT, Control/Treatment, etc. It does this by using a **design matrix X** with different design variables.

~ also known as *General* Linear Models – as opposed to *Genera**lised*** Linear Models which are the topic of this workshop.

GENERALISED LINEAR MODEL (GLM)

Can fit ***all the same models*** as a Simple Linear Model since it uses the same design matrix within its Linear Predictor and can use a Normal distribution plus it:

1. ***Generalises*** the model so we can use **non normal errors/distributions** such as Poisson (for count data) and Binomial (for binary data).
2. **Adds** inbuilt response transformations via the **link** function.

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56

The 3 most common GLM's

Simple Linear Models such as simple linear regression and ANOVA
$Y_i \sim N(\mu, \sigma^2)$ where $E(Y|X) = \mu$, and an ***Identify Link of*** $\eta = \mu$ giving a mean function of $E(Y|X) = \mu = \eta$ hence our model is:

$$Y_i \sim N(X\beta, \sigma^2)$$

Poisson (count) Model ~ also used for rates and concentrations (refer to its example below)
$Y_i \sim Poisson(\lambda)$ where $E(Y|X) = \lambda$, and a ***Log Link of*** $\eta = log(\lambda)$ giving a mean function of $E(Y|X) = \lambda = e^{\eta}$ hence our model is:

$$Y_i \sim P(e^{X\beta})$$

Logistic (binary) Model
$Y_i \sim Binomial(p)$ where $E(Y|X) = p$, and a ***Logit Link of*** $\eta = logit(p) = ln\frac{p}{1-p}$ giving a mean function of $E(Y|X) = p = \frac{1}{1+e^{-\eta}}$ hence our model is:

$$Y_i \sim B(\frac{1}{1+e^{-X\beta}})$$

GLM components

Part 1 of the 3 required for a GLM

The **Linear Predictor** (η_l) is a ***deterministic*** additive/linear equation of predictors (X) and parameters (β) that will be used to predict the response ($\hat{Y}$), after linking with the data distribution. It tells us the expected value of the response Y is conditional on the data X.

The parameters (β) are defined by the ***Design Matrix*** **(X)**.

$$X\beta = \beta_o X_0 + \beta_1 X_1 + \beta_2 X_2 + \beta_3 X_3 + \ldots$$
$$= \eta_l \sim \text{linear predictor (additive/linear model)}$$

Part 2 of the 3 required for a GLM

Different Data Distributions add the ***random/stochastic*** element of the model
e.g. $Y \sim N(\mu, \sigma^2)$

Part 3 of the 3 required for a GLM

The **Link Function** links Part 1 and 2 together by showing how the distributions average (Part 2) which is the model prediction can be predicted using a function of the Linear Predictor (Part 1) e.g. if the link function is $\mu = \eta = \beta_o + \beta_1 X$ then $Y_i \sim N(\beta_o + \beta_1 X_1, \sigma^2)$ = **Simple Linear Regression.** This also allows us to transform the response and make the model multiplicative.

Logistic Regression

Binary Response e.g. yes/no, success/failure, 0/1

Workflow Suitable for:

- Continuous predictor

Logistic/Binary Regression

Used when we have a categorical response than can be 1 of 2 categories. We usually code them as:

1 = Success

0 = Failure

Tells us which predictors are positively and negatively correlated with more successes. To make the output easy to understand the trick is defining the success group.

Medical: We often define the disease as the success since we want to know what influences getting it i.e. risk factors. Conversely, we may want to look into preventative factors, so we would define those without the disease as the success.

Churn: Could be either the people who left or stayed, depending on who we want to focus on.

Loan Defaults: Defaulters would usually be the success group since we want to know why people default.

Similar to Survival Analysis

When deciding which to use consider the data available and Research Question:

Logistic Regression models the probability (chance) of an event occurring

Survival Analysis models the probability (chance) of an event occurring ***and the time to that event***

The main differences are that Survival Analysis:

1. Factors in time to the Event/Success and gives you survival curves. There is an important distinction between living for 6 months vs 6 years after diagnosis! Logistic treats them the same (unless time to death is explicitly added).
2. Can handle data where the event happens for everyone i.e. everyone dies.
3. Factors in patients lost to follow up (censoring)
4. Uses Hazard Ratios instead of Odds Ratio.
   - These are the ratio of 2 hazards. Hazards are the instantaneous rate of the event (e.g. death or failure) given an individual has survived up to that time (T), they are also the slope/tangent of the survival curve at time T. For a hazard ratio to be a consistent and hence good estimate of 2 hazards over a time interval they need to be proportional over this time period i.e. the slopes need to be parallel, which is why predator this assumption is often called the Parallel Lines assumption.
5. Naturally handles time varying covariates (since it naturally includes time to event while logistic regression does not).
   - Logistic regression factors in time as an additional predictor. A categorical predictor gives us different parameters/logit curves e.g. event occurred at 6 months vs 6 years, or continuous e.g. covariate adjustment parameter of Beta. Covariates that then vary by time can be added as interactions to the time predictor.

Refer to our Survival Analysis workshop for more information.

Model Fitting 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

Step 6) Reporting

Linear Models 3 and Model Building Workshops have more detail on many of these steps.

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.

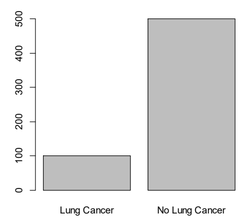
Step 1) Pick a suitable model to fit to the data via Exploratory Data Analysis (EDA).

Challenge Question: We have done a case control study. We got 100 people with lung cancer and 500 people without. How would you plot the response variable?

Our response has 2 options. There are no outliers or NA's.

So it's not appropriate for a Simple Linear Regression with a Normal error. No way the error will be normal with only 2 responses.

BUT it's a good contender for Logistic/Binary Regression.




```
> plot(cc1$"lung cancer")
```

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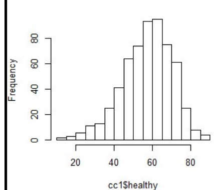
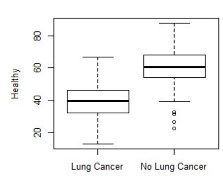
65

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

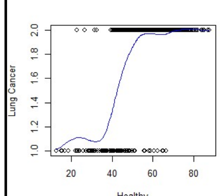
Now add the continuous predictor "healthy lifestyle" which is an index based on things like exercise, food, sleep, etc. It ranges from 0 = unhealthy to 100 = healthy. How might it be related to lung cancer?





All 3 plots tells us there are no outliers or other data problems with "Healthy".

The boxplot and scatterplot show us there is a relationship between healthy and lung cancer.



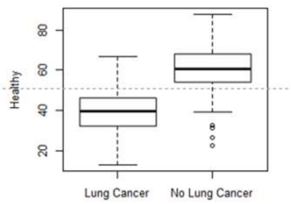

```
> windows()
> par(mfrow=c(2,2))
> hist(cc1$healthy, main="")
> plot(cc1$`lung cancer`, cc1$healthy, ylab="Healthy")
> plot(cc1$healthy, as.numeric(cc1$`lung cancer`), ylab="Lung Cancer", xlab="Healthy")
> lines(smooth.spline(cc1$healthy, as.numeric(cc1$`lung cancer`)), col="blue", ylab="Lung
Cancer",
  xlab="Healthy")
```

In vertical axis: 1 = Lung Cancer, 2 = No Lung Cancer. Had to convert to numbers and not label with the text in order to get the smoothed blue line.

Page 66

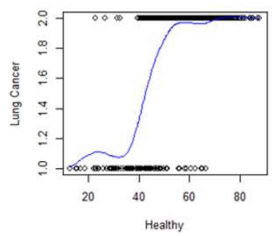
66

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



This plot show the health indices **average difference** between those with and without lung cancer. Its quantified using an ANOVA like we did in LM1.

It allows us to predict the health index score knowing if someone has lung cancer.



This plot shows the relationship between the health index and getting lung cancer. It is quantified using logistic regression.

It allows us to predict the chance of having lung cancer if we know their health score.

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Page 67

67

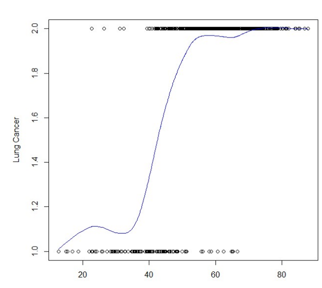
Step 1) Pick a suitable model to fit to the data via Exploratory Data Analysis (EDA).

Notice that the relationship between healthy and Lung Cancer **isn't linear.** It's more of an S shape.

This relationship is called a ***sigmoid*** function, and is what logistic regression fits.

But how do we fit this using a linear model?

The trick is the link function in a GLM. Which lets us fit non linear models.



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68

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

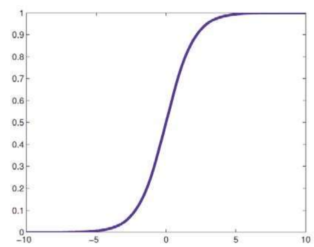
Logistic GLM might be a good fit, so lets try that

$Y_i \sim \text{Binomial}(\mu)$ where $\textbf{logit}(\mu) = \ln \frac{p}{1-p} = X\beta$ (since the probability of having lung cancer, p, is just the mean of the Y values, assuming 0,1 coding, which is often expressed as μ)

The **logit link** function lets us fit this sigmoid function.

(And makes it multiplicative model when we back transform to odd's ratios).

SIGMOID FUNCTION



Step 1) If we had categorical variables such as smoking

We also need to look for **Separation.**

Complete Separation occurs when we have cells that are entirely success or failures e.g. if we had included smoking perhaps all the smokers got lung cancer. This is an example of where smoking has ***separated*** the response. The model can not fit when this happens and is one common reason for logistic models not converging (since its effectively trying to divide by 0).

Separation often causes error messages like "failed to converge", warning messages like "! glm.fit: fitted probabilities numerically 0 or 1 occurred" or high parameter SE's.

Even if we don't have complete separation, marginal separation can still cause problems.

	Lung Cancer	No Lung Cancer
Smoker	100	0
Non Smoker	10	800

	Estimate	SE
Constant	7.9	0.06
Smoker	1000	597000

Step 1) If we had categorical variables such as smoking

Solution to separation can be merging/collapsing categories. Common problems are:

Age categories that are too fine so some have ***empty cells*** with no-one in them e.g. one would merge the last 3 columns to have a 75-85 category. One does need to be careful as it's a different age range, so some might merge them all into 10 year brackets.

	35-40	40-45	45-50	50-55	55-60	60-65	65-70	70-75	75-80	80-85
Success	100	45	35	25	26	31	27	15	8	0
Failure	10	64	46	24	24	28	32	13	6	4

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Step 1) If we had categorical variables such as smoking

Modelling lots of interactions and high order interactions between lots of variables increases the chance of empty cells, so its important to check sample sizes of all interactions before modelling them. High order interactions can be evaluated using tables like the below rather than the more usual 2x2 contingency table.

For example: if you did a survey of skiers in Japan you might have plenty of people with red or black hair, brown or black eyes, and who are Scottish or Japanese. But it would be rare to find a Japanese person with red hair and green eyes!

Hair Colour	Eye colour	Ethnicity	Count
Red	Green	Scottish	15
Red	Green	Japanese	0
Red	Black	Scottish	12
Red	Black	Japanese	2
Black	Green	Scottish	98
Black	Green	Japanese	104
Black	Black	Scottish	74
Black	Black	Japanese	98

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Step 2) Fit the Model

cc.model <- glm(lung.cancer ~ healthy, family=binomial(link= "logit", data=cc2)

Linear Predictor is	***lung.cancer ~ healthy***
Data Distribution is	***family=binomial***(link= "logit")
Link Function is	family=binomial(***link= "logit"***)

"Success" = Having Lung Cancer, meaning the parameters tell us what risk factors there are for getting cancer.

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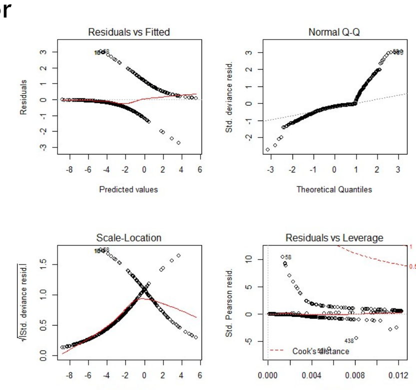
Step 3) Check Model Assumptions via Diagnostics: Residual Analysis

The standard residual plots don't help much here since we don't expect normal residuals and as we only have 2 responses we get these 2 lines in the residual plots.

However, they can be used to look for Outliers.

Dharma residuals are more useful and are in the R workflow which can be downloaded from our online library.




```
> windows()
> par(mfrow=c(2,2))
> plot(cc.model)
```

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Step 3) Check Model Assumptions via Diagnostics: Is there any Over Dispersion?

One of the problems we have is that the Binomial Distribution has no separate variance parameter.

The Normal distribution has 2 parameters. The mean (μ) and the variance (σ).

However, the Binomial Distribution only has 1 parameter: p~the probability of an event occurring. Its average and variance are both functions of this single parameter. But sometimes we have more variance than the distribution can handle.

There are some complications on how we handle this for logistic regression which are beyond the scope of this workshop. However we mention it here so you are aware.

Step 4) Goodness of Fit: Are any parameter SE's too high?

It's always a good idea to look at the parameter SE's to see if any are a lot higher than the others. This can be a sign of a variety of problems. At the very least they suggest the estimate for this parameter is very unstable. The below is for our model and doesn't suggest any problems.

```
# Some of the R output available from
> summary(cc.model)

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  7.98444    0.88840   8.987   <2e-16 ***
healthy     -0.19048    0.01856 -10.265   <2e-16 ***
```

BUT the below does might, notice SE is an order of magnitude larger than estimate i.e. times 10/add a zero. Often caused by separation, which we hopefully identified during the EDA. However marginal separation can be hard to identify, particularly if we are fitting a lot of 2 way interactions with a lot of cells.

```
Coeffects:
            Estimate  Std.  Error
(Intercept)  7.9844    88.840
Healthy     -0.19048   1.856
```

Step 4) Goodness of Fit: Are any parameter SE's too high?

As previously mentioned during the EDA stage (and copied below) a large SE can be a sign of **Separation.**

Complete Separation occurs when we have cells that are entirely success or failures e.g. if we had included smoking perhaps all the smokers got lung cancer. This is an example of where smoking has ***separated*** the response. The model can not fit when this happens and is one common reason for logistic models not converging (since its effectively trying to divide by 0).

Separation often causes error messages like "failed to converge", warning messages like "! glm.fit: fitted probabilities numerically 0 or 1 occurred" or high parameter SE's.

Even if we don't have complete separation, marginal separation can still cause problems.

	Lung Cancer	No Lung Cancer
Smoker	100	0
Non Smoker	10	800

	Estimate	SE
Constant	7.9	0.06
Smoker	1000	597000

Step 4) Goodness of Fit: Compare it to the NULL model

It's always worth comparing any model to the NULL model, which is the model without any predictors and only a constant/intercept.

In this case we have strong evidence that our model is outperforming the NULL model (P<2.2e-16).

The test used is a Likelihood Ratio Test (LRT), if the models are nested and have the same data. One drawback is that the LRT makes the asymptotic assumption that the chi-square distribution approximates the null distribution of likelihoods. In other words, at small sample sizes it may not be particularly accurate. As such the F test (which is s a specific type of LRT) might be better if the error is normal and sample sizes small - as it doesn't require the LRT asymptotic assumption since it's the actual ratio of 2 chi-squared variables. https://stats.stackexchange.com/questions/120309/low-sample-size-lr-vs-f-test and https://stats.stackexchange.com/questions/535709/anova-vs-likelihood-ratio-test-different-result

```
> null <- glm(lung.cancer ~ 1, data=cc2, family=binomial)
> anova(null, cc.model, test = "Chisq")
Analysis of Deviance Table

Model 1: lung.cancer ~ 1
Model 2: lung.cancer ~ healthy
  Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
1       599     540.67
2       598     292.26  1   248.41 < 2.2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Step 4) Goodness of Fit: What is it's (Pseudo) R-Squared?

Technically there is no R-Squared for a GLM, however there is an equivalent based on the % Deviance explained. This is one type of Pseudo R-Squared.

Which in this case is acceptable, at 45%

```
> # GOODNESS OF FIT: R-squared equivalent % Deviance explained
> (deviance.explained <- ((deviance(null)-deviance(cc.model))/deviance(null))*100)
[1] 45.94528
```

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Step 5) Interpret Model Parameters and reach a conclusion

For Simple Linear models we can simply interpret the parameters.

BUT in logistic regression since we used a logit link these are hard to interpret as they are on the logit scale.

The only really useful part of this 'raw' output is the p-value associated with the parameters. Which in this case shows strong evidence of being associated with healthy (p<2e-16).

```
# Some of the R output available from
> summary(cc.model)

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  7.98444    0.88840   8.987   <2e-16 ***
healthy     -0.19048    0.01856 -10.265   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> confint(cc.model) # 95% CI for the coefficients
Waiting for profiling to be done...
                 2.5 %     97.5 %
(Intercept)  6.3469356  9.8414159
healthy     -0.2294994 -0.1564947
```

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Step 5) Interpret Model Parameters and reach a conclusion - Using Odds Ratios (OR)

The parameters can be made more interpretable by taking their exponential since this turns them into ***odds ratios*** (which will be explained shortly).

Remember how the logit link used a log transform? Well, taking their exponential is the inverse of this, which puts them back into the original scale. And then some fancy math means we can also interpret them as odds ratios.

Taking the exponential is similar to taking something to the power10. But instead of 10 we use the constant e = exp = 2.718, which is the inverse of the natural logarithm function (ln) we used in the link function.

Don't overthink it!! You don't need to know why we use an exp, just accept and use it!

For an example, as our coefficient is -0.19 if we took it to the power 10 we would get $10^{-0.19048} = 0.65$, but instead we do $\mathbf{2.718}^{-0.19048} = \mathbf{e}^{-0.19048} =$ **exp**(-0.19048) = 0.83.

Step 5) Interpret Model Parameters and reach a conclusion - Using Odds Ratios (OR)

We get the below OR=0.83 for the continuous variable Health, which tells us that for each 1 point increase on the Health index the odds of getting lung cancer are 0.8 compared to the lower score (95%CI = 0.79-0.86).

So being healthy lowers the odds of getting lung cancer!

```
> exp(coef(cc.model)) # exponentiated coefficients
 (Intercept)      healthy
2934.9224129    0.8265662
> exp(confint(cc.model)) # 95% CI for exponentiated coefficients
Waiting for profiling to be done...
                 2.5 %       97.5 %
(Intercept) 570.7410272 1.879631e+04
healthy       0.7949314 8.551361e-01
```

Step 5) Interpret Model Parameters and reach a conclusion

Parameter	Estimate (raw)	SE (raw)	T score (raw)	P value (raw)	95% Confidence Interval Exp(β) i.e. odds ratio		
					Estimate	Lower Bound	Upper Bound
Constant / Control (β_o)	8.0	0.89	9.0	<2e-16			
Health index ($\beta 1$)	-0.19	0.019	-10	<2e-16	0.83	0.79	0.86

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Step 6) Reporting: Overall Conclusion suitable for publication

"There is strong evidence to show that being healthy is associated with lower odds of Lung Cancer ($p<2e-16$). For each 1point increase on the Health index the Odds of getting lung Cancer are 0.8 compared to the lower score (95%CI odds ratio = 0.79-0.86). This effect on lung cancer has been estimated very accurately [as 95% CI is quite narrow].

The model is an acceptable fit to the data with a pseudo R^2=45%. There were no outliers or unexplained structure.

The model fit was a GLM with binomial distribution and logit link function"

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

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So what exactly is an Odds Ratio (OR)?

It's best described with an example.

Say the OR for smoking on whether you get lung cancer is 3. This means the odds of getting lung cancer if you smoke is 3 times the odds of getting it if you don't smoke. In other words, ***an odds ratio is the ratio of two odds.***

And what is an "odds"? The odds of something happening is related to its probability, but isn't the same.

Say the ***probability/chance/risk*** of getting lung cancer if you smoke is 75%. Then the corresponding **odds** are p/(1-p)=75/25 = 3:1 = 3. These are obviously different numbers with different interpretations, which is why odds ratios can be used to comment on the odds of something occurring, not its probability, chance or risk.

You would have seen it in horse racing too e.g. if Phar Lap tends to win 19 out of 20 races than the odds of Phar Lap winning are 19:1 = 19/1 = 19. On the other hand, the probability of Phar Lap winning is 19/20 = 95%.

Risks report the # of events in relation to the *# of trials* i.e. # events vs # trials.

Odds report the # of events in relation to the *# of nonevents* i.e. # events vs # nonevents.

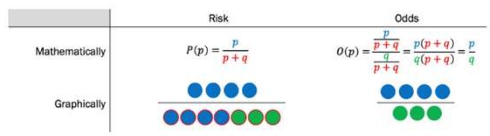

FIGURE 1: Probability (P) vs. Odds (O) where p=probability of success and q=probability of failure

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Figure from George A, Stead TS, Ganti L. What's the Risk: Differentiating Risk Ratios, Odds Ratios, and Hazard Ratios? Cureus. 2020 Aug 26;12(8):e10047. doi: 10.7759/cureus.10047. PMID: 32983737; PMCID: PMC7515812.

85

Odd Ratios (OR) are different to the Relative Risk (RR)

Relative Risk (RR) is the ratio (relative difference) of probabilities. The Odds Ratio (OR) is the ratio (relative difference) of odds. Meaning they have different interpretations ***so be careful what language you use when communicating results.***

If the **OR** of smoking on getting lung cancer is 3, then you need to say the **odds** of getting lung cancer if you smoke is 3 times the ***odds*** of getting it if you don't smoke.

If the **RR** of smoking on getting lung cancer is 3, then you need to say the **chance** of getting lung cancer if you smoke is 3 times the ***chance*** of getting it if you don't smoke.

Incorrectly interpreting ORs as RRs can exaggerate the impact as ORs underestimate the RR when both are <1 and overestimate it when >1.

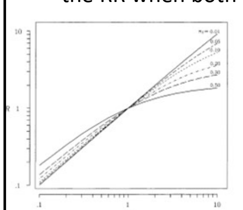

Fig. 6.1 Relationship between odds ratio O and relative risk R as a function of π_0, the background rate in the unexposed. Note that scale is logarithmic.

Gerald van Belle (2008) Statistical Rules of Thumb

Page 86

86

Expert Trick 1) Interpreting Odds Ratios (OR) as Relative Risks (RR) using the rare disease assumption

The medical literature commonly interprets odds ratios from logistic regression as relative risks.

This is because **when an event is 'rare' odds ratios approximate relative risks.** The plot below shows that when the incidence is 1% the OR and RR closely follow the 1:1 equivalence line, but become different very quickly as one moves away from 1 when the incidence is as low as 5% (plot is from Gerald van Belle (2008) Statistical Rules of Thumb).

So, although some authors say 10% is rare enough. I disagree and would suggest **1% is the maximum**. However, it is a subjective decision and if you are unsure then just report and interpret as an odds ratios.

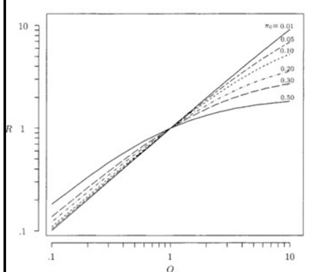

Fig. 6.1 Relationship between odds ratio O and relative risk R as a function of π_0, the background rate in the unexposed. Note that scale is logarithmic.

There are other complications as well e.g. this assumption usually can't be applied to case control studies meaning they always need to report odds ratios irrelevant to how small the incidence is. So before interpreting OR as RRs it's a good idea to read up on it, a good place to start is Gerald van Belle (2008) Statistical Rules of Thumb (which is where the plot on the left comes from).

Why OR underestimates the RR when both are <1 and overestimates it when >1

Because if we have p + q trials when we reduce p this means q has to increase. But this only impacts the numerator in the risk. While both the odds numerator and denominator are affected in opposite directions, so it falls faster. Similarly, if p increases the OR increases quicker.

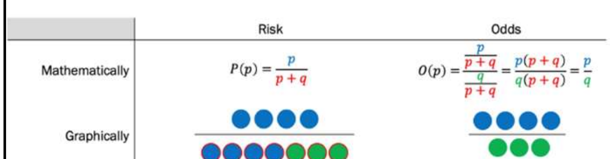

FIGURE 1: Probability (P) vs. Odds (O) where p=probability of success and q=probability of failure

George A, Stead TS, Ganti L. What's the Risk: Differentiating Risk Ratios, Odds Ratios, and Hazard Ratios? Cureus. 2020 Aug 26;12(8):e10047. doi: 10.7759/cureus.10047. PMID: 32983737; PMCID: PMC7515812.

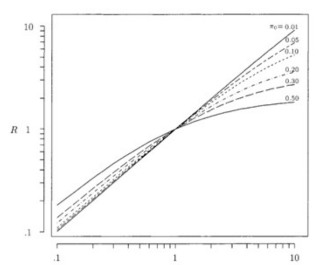

Fig. 6.1 Relationship between odds ratio O and relative risk R as a function of π_0, the background rate in the unexposed. Note that scale is logarithmic.

Gerald van Belle (2008) Statistical Rules of Thumb

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It’s a multiplicative model, not an additive one

Given the odds of getting lung cancer drop by 0.8 for a 1 point increase in health. What impact does a 2 point increase in health have?

Would it be 0.8 + 0.8 = 1.6 (additive)?

– Can’t be this, since it goes from dropping the odds of lung cancer (<1) to increasing them (>1)!

Or 0.8 * 0.8 = 0.64 (multiplicative)?

– This makes more sense as a 2 point increase in health leads to a lower chance of lung cancer than a 1 point increase.
– This is what the log link (transformation) does. It turns the additive linear predictor which is an additive model without a log link, into a multiplicative model when it has one.
– So to calculate the odds ratio for *k* intervals of difference in the health predictor it’s 0.8^k for this example or β^k in general e.g. if we wanted the odds ratio for a continuous predictor that moved from 5 to 10 it would be β^5.
  – Notice that this is for any difference in the predictor. The impact is the same if its 5 vs 10 or 100 vs 105, since both are a 5 interval difference.

Expert Trick 2: Interpreting fractional OR and when swapping the response events success/fail definition is helpful

Let’s continue the previous lung cancer example where smoking's OR was 3 – which means smokers have 3 times the odds of getting lung cancer than non-smokers.

If we changed the response reference category from having cancer to **not having cancer** than it makes sense for smoking’s OR to now be the reciprocal of what it was before i.e. 1/3=0.33 - since this now means that smoker’s have 1/3 = 33% the odds of **not** having lung cancer than non-smokers.

This is the same result, just expressed differently. Which makes sense since our conclusions shouldn’t differ based on the arbitrary decision on what to make the reference response category. Mathematically it shouldn’t affect the results.

The same thing occurs if one swaps the predictors event definitions around (but for slightly different reasons).

This is a handy trick to know since fractional odds ratios i.e. OR < 1, can be hard to interpret and communicate. So if you have a lot of hard to communicate OR < 1 just swap how you have defined the responses ‘success’ event and now they will all be greater than 1! (with the OR > 1 now less than 1).

You can also swap the response event, or predictor events, to make the interpretation easier. For example, double negatives when both are negative can be hard to interpret.

Interpreting fractional OR and when swapping the response events success/fail definition is helpful

Mathematically this happens for the response because the odds of an event happening is the reciprocal of the odds that it didn't happen i.e. if the odds(event A happening) = X than the odds(event A not happening) = 1/X.

For example, if we have a logistic regression where we define event A as the success, and this results in a predictors OR being 1/3=0.33

Then if we ***swap response events and make event A the failure*** each odds within the odds ratio is inverted within themselves making the OR it's reciprocal which is 1/0.33 = 3

On the other hand, if we swap the predictors then we are swapping the numerator and denominator odds in the odds ratio.

Expert Trick 3) Consider reporting absolute measures such as probabilities/risks, odds and % of sample too

ORs compare the ***relative*** change in the odds, but ignore the underlying ***absolute*** chance of an event happening. It's important to know both.

Example 1: Low absolute chance of event. Say eating avocados increases the odds of a rare cancer by 10 i.e. OR=10. ***But*** the baseline odds of getting the rare cancer is 0.0000000000000000000000000000001. Increasing the odds by 10 has little practical impact on the chance of getting cancer, so keep eating avocados! (Especially considering their other health benefits).

Example 2: Different ORs can have very different baseline chances. The below might show the % of people who got a dash of cabin fever during the COVID lockdowns of 2020. From 2 studies, one done in Melbourne (which had strict lockdowns) and 1 in Cairns Qld (who were largely unaffected)

- As you can see the odds ratio is the same, people with kids were more likely to be affected (I wonder why??).
- **However.** Far more people in Melbourne were affected than in Cairns, as expected.

Location	% of people who got Cabin Fever who had Children	% of people who got Cabin Fever who had no children	Odds(Children)	Odds(None)	OR Children vs None	p
Melbourne	75%	50%	3	1	3	0.003
Cairns	25%	10%	0.33	0.11	3	0.007

So, when reporting it can be useful to report both the underlying absolute %'s and their relative OR i.e.

- People with kids were more likely to exhibit signs of Cabin Fever than people with no kids (Melb-75% vs 50%; OR=3, p=0.003: Cairns-25% vs 10%; OR=3, p=0.007)

When reporting absolute measures such as probabilities/risks, % of sample and metrics based on them like RR can't be used, but odds and odds ratios are still OK

Before reporting absolute metrics such as probabilities/risks , sample %'s or metrics derived from them like relative risk we first need to decide if they are appropriate and useful metrics.

They ***may*** be useful if the study is an accurate representation of the overall population e.g. cross sectional studies.

They are ***not*** useful if the study is not an accurate representation of the overall population. In such cases odds and the odds ratio are still relevant, which is why logistic regression often focuses on odds ratios, since it's always applicable. For example:

– **Case-Control Studies:** are when we have a sample of cases e.g. a rare disease, and then collect a fixed number of controls e.g. those without the disease, to understand what the differences between the groups are and hence the risk factors for the disease. The # of controls collected is often fixed at 5 times the cases as this is optimal for minimising parameter standard errors. However, this means we can't estimate the chance of the disease since it's an artifact of the sampling (1/(1+5) = 1/6=0.17%) and not an accurate picture of its prevalence in the wider population. Meaning risks and relative risks can't be calculated, but odds and odds ratios can since they simply compare the difference between the cases and controls.

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When reporting more than 2 Categories

One has to be careful that the wording makes it clear what the reference category is. This is because the p value refers to the comparison to the reference category i.e. the category captured in the intercept, not comparisons between the other groups.

So assuming people with Kids were the reference category we might say: "Compared to people with no kids those with kids were more likely to get Cabin Fever (5+ kids-90% vs 50%; OR=9, p=0.003: 1-5 kids: 73% vs 50%; OR=2.7, p=0.007)".

So in this example all the p-values are for comparing to the "No Kids" group. The 2 groups with kids are not directly compared.

% of people who got Cabin Fever who have 5+ kids Children	% of people who got Cabin Fever who have 1-5 kids Children	% of people who got Cabin Fever who had no children	Odds (5+)	Odds (1-5)	Odds none	OR 5+ vs none	p	OR 1-5 vs none	p
90%	73%	50%	9	3	1.00	9.0	0.003	2.7	0.007

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Sample Size: Rule of 10

A common Rule of Thumb is that for stable results one needs 10 observations for each parameter.

This is modified for logistic regression.

Instead of 10 observations/parameter we need 10 events/parameter (or 10 non events if that is less common). E.g.

- A sample of 500 with 20 successes can have a model with 2 parameters
- A sample of 500 with 480 successes can still only have a model with 2 parameters (since we only have 20 failures).

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EDA for interactions with 2 continuous variables

Interactions with 2 continuous variables are not straight forward to fit. There are a number of complications one needs to consider.

Just one is what type of surface is a suitable fit, for example is a plane suitable (i.e. a sheet of paper), or are there nonlinear relationships that need to also be fit e.g. maybe its more concave?

The first step in assessing this is (as always) EDA, and for a continuous response a suitable data visualization is either a 3D scatterplot plot, or some variant such as a contour plot or heatmap.

However, this doesn't work as well with a binary response.

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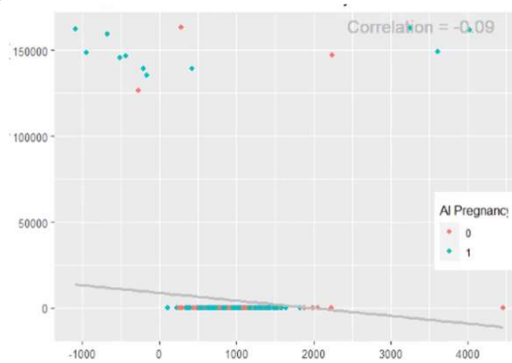
EDA for interactions with 2 continuous variables

An alternative is to a 2D plot, with the response colour coded. Below is a real-world example. This came to us in a consult, with the problem being the model would not converge. So as usual we started diagnosing the problem with EDA, which showed us that:

– Although the horizontal x axes continuous predictor is continuous there is no strong pattern with neither the red (failure of Artificial Insemination) or blue (success) symbols being more to the left or right. Making it hard to fit a sigmoid curve and hence logistic regression.

– The more likely reason for the convergence problem though is the vertical axis. The large gap in the middle with no data makes it hard to fit a continuous interaction as a surface. This variable is actually more binary i.e. 0 vs very high.



Poisson (count) Regression

Discrete Positive Integer Response e.g. 0, 1, 2, 3, 4.

Workflow Suitable for:

- Positive Integers
- Counts
- Rates
- Some Log Normal data
- Before After Control Impact design (BACI)

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99

Poisson (count) Regression

Uses the Poisson distribution which assumes the data is from the set of Natural Numbers i.e. the non-negative integers 0, 1, 2, 3, 4, etc. So it's a ***good distribution for counts***.

Can also be used to ***model rates***. This is done by adding an **offset** variable to the model. This variable divides the count by something to turn it into a rate. For example:

- Cell **concentrations** are actually cell counts divided by volume of blood/plasma/etc. So rather than model the concentration assuming a Normal error which often fails we can instead model the counts as a Poisson using the volume as the offset i.e. cell concentration = $\frac{cell\ count}{volume}$.
- We might have the count of fish caught, and want to divide it by the size of the net so it has no impact on the analysis (otherwise big nets would simply have higher counts which is obvious and not helpful). This is done by adding the net size in m^2 as an offset so we convert the count of fish caught to the amount of fish caught/m^2 of net.

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100

Changes to dingo diet caused by human interaction, and its implications on conservation.

Dingos are an important predator in Australian Landscapes. The meso-predator theory states that increasing them decreases cat/fox numbers and reduces pressure on small natives currently under threat of extinction.

A mine in the Tanami desert had 2 garbage tips which they fenced off. This gave us the opportunity to investigate how this affects dingo feeding behaviour.

4 sites were selected: the 2 mine sites, 1 site that was a long way away from the tips and one that was an intermediate distance away. Scats were collected Before and After the tips were fenced and the # of different types of animals and rubbish found in them were counted.

This gave us a Before, After, Control, Impact (BACI) design. ***Which has good causal interpretation.***

Newsome T, Chris H, Wirsing A (2020) Restriction of anthropogenic foods alters a top predator diet and intraspecific interactions

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101

Model Fitting 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

Step 6) Reporting

Linear Models 3 and Model Building Workshops have more detail on many of these steps.

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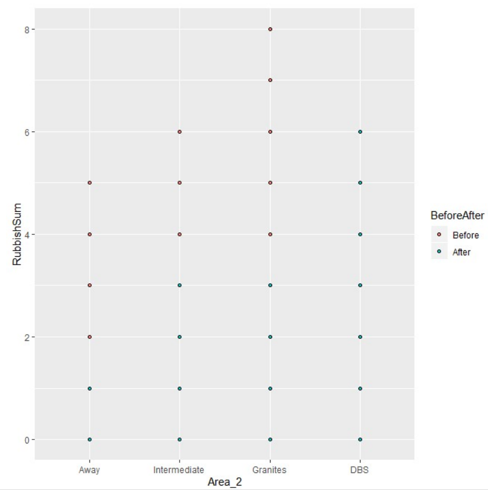
Page 102

102

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

So here is a plot for each of the 4 sites. But it's not very good since all the scats are overlayed on each other.

EG: all the Away Scats that had 1 piece of rubbish in them are being plotted at the same point.




```
> windows()
> ggplot(data = data, aes(x=Area_2, y=RubbishSum,
fill=BeforeAfter)) + geom_point(pch=21)
```

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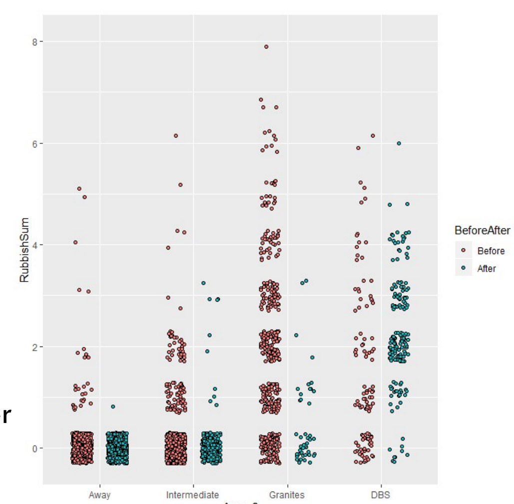
103

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

- To fix this I add a jitter - to the **plot only, not the data we model.**
- Now I can see that the number of scats with rubbish in them has dropped after the fences were installed. Except at DBS for some reason?
- The reason was that they broke through the fence wasn't, so they all went over there!!




```
> windows()
> ggplot(data = data, aes(x=Area_2, y=RubbishSum, fill=BeforeAfter))
+ geom_point(pch=21,
position=position_jitterdodge(jitter.width=0.4, jitter.height=0.3))
```

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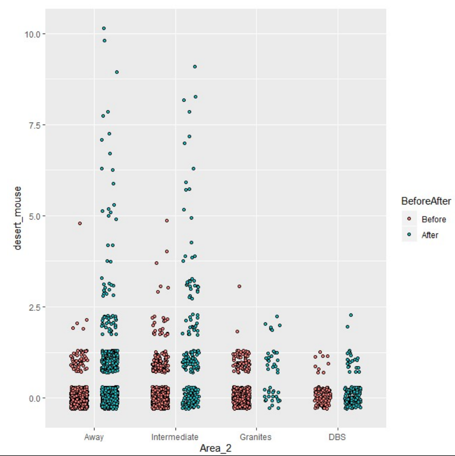
Page 104

104

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

– The model I will show you is for the Desert mouse




```
> windows()
> ggplot(data = data, aes(x=Area_2, y=desert_mouse,
fill=BeforeAfter)) + geom_point(pch=21,
position=position_jitterdodge(jitter.width=0.4, jitter.height=0.3))
```

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105

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

Poisson GLM might be a good fit, so let's try that meaning:

$Y_i \sim \text{Poisson}(\lambda)$

$\sim$ mean=variance= λ

We link the linear predictor ($X\beta$) to λ using the log link i.e. $\log(\lambda)=X\beta$ since that is the conventional model. (NB: this makes a multiplicative model when we back transform to rates).

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Page 106

106

Step 2) Fit the Model

desert_mouse.p1 <- glm(desert_mouse~Area_2*BeforeAfter, family=poisson(link="log"), data=data)

Linear Predictor is	***desert_mouse~Area_2*BeforeAfter***
Data Distribution is	***family=poisson***(link="log")
Link Function is	family=poisson(***link="log"***)

Step 3) Check Model Assumptions via Diagnostics: Zero Inflation

Sometimes we get count data with far too many zeros for the Poisson distribution to handle. This is called Zero Inflation.

It often happens if there are effectively 2 processes occurring:
1. Whether the event occurs
2. If it does occur, how often it does

Simplistically fitting 2 models is an older way around this (called 2 step/stage or hurdle models). These fit a binomial (logistic) model to whether the event occurs, and then a Poisson if it does. The modern approach is to use Zero Inflated Poisson (ZIP) and Zero Inflated Negative Binomial (ZINB) models that effectively combine these 2 models into a single model fit.

Step 3) Check Model Assumptions via Diagnostics: Zero Inflation

A rough test for this is to simulate the number of zeros we expect based on the overall average and then compare it to what we have. If it is very different we may need some type of ZIP model.

Below shows we may have more zero's than the theoretical distribution. But I have seen much worse and this is only rough since it's actually the conditional theoretical distribution we should be comparing to. So it isn't bad enough to be overly worried about.

Theoretical Distribution

```
    0     1     2     3     4
69.25 25.13  4.96  0.60  0.06
```

Actual Distribution

```
    0     1     2     3     4     5     6     7     8     9    10
75.87 18.60  2.89  1.18  0.38  0.35  0.24  0.17  0.17  0.07  0.07
```

```
> mean(data$desert_mouse)
> test.0i.theory <- rpois(mean(data$desert_mouse), n=10000)
# better to use proportion with large N since it will be stable. count of 0's at low n will not be.
> prop.table(table(test.0i.theory))*100
> round(prop.table(table(data$desert_mouse))*100,2)
```


Step 3) Check Model Assumptions via Diagnostics: Overdispersion

For the same reasons explained in logistic regression Poisson distributions can be over dispersed i.e. there is too much variance for the single parameter in the Poisson distribution to handle.

We test this using a function from http://bbolker.github.io/mixedmodels-misc/glmmFAQ.html#overdispersion. There is ongoing research on this topic so more recent information and solutions may be available here.

This function tests whether the dispersion parameter is different to 1, which is what a Poisson distribution assumes. It tells us that although there is statistically significant overdispersion it is not very large at only 1.6, so not worth worrying about. What is considered too large is domain specific and subject to ongoing research, I have seen cutoffs from 1.10 – 5 used.

Common ways to deal with this are:

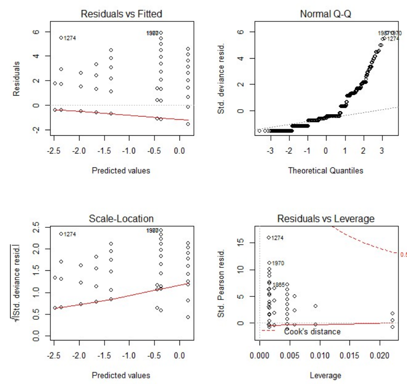
1. **Distributional Regression.** 2 distributions are commonly used:
   1. **Negative Binomial** distribution - fits a more suitable distribution with an extra dispersion parameter, there are a variety of R packages (including gamlss.dist) that fit this model and is usually available in other software such as SPSS. Very commonly used.
   2. **Generalised Poisson** distribution - fit in R using the gamlss.dist package and the GPO distribution, harder to fit in other software.
2. Fit an **individual level random effect using a GLMM** (this tricks the model into adding an extra variance parameter).
3. **Quasi-Poisson** can also be used. Given the above alternatives there is some debate on how useful it is due to the difficultly in applying inferential methods such as likelihood ratio test, AIC, etc. http://bbolker.github.io/mixedmodels-misc/glmmFAQ.html

```
> is_overdispersed(desert_mouse.p1) #
       chisq        ratio          rdf             p
4.467379e+03 1.557663e+00 2.868000e+03 9.576844e-74
```

Step 3) Check Model Assumptions via Diagnostics: Residuals

- No obvious influential outliers
- No systematic patterns we need to account for
  - The discrete lines are caused by the 8 combinations of treatments i.e. 4 sites before and after = 8
- Residuals aren't normal, but nor do we expect them to be. They're Poisson!
- Dharma residuals are more useful and are in the R workflow which can be downloaded from our online library.

```
# Standard plots
> windows()
> par(mfrow=c(2,2))
> plot(rubbish.p1)
```



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111

Step 4) Goodness of Fit: Compare to NULL model

It's a much better fit than the NULL model.

```
> anova(null, desert_mouse.p1, test = "Chisq")
Analysis of Deviance Table

Model 1: desert_mouse ~ 1
Model 2: desert_mouse ~ Area_2 * BeforeAfter
  Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
1      2875     3477.5
2      2868     2743.8  7   733.69 < 2.2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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Page 112

112

Step 4) Goodness of Fit: What is it's Pseudo R-Squared?

Technically there is no Pseudo R-Squared for a GLM, however there is an equivalent based on the % Deviance explained.

Which in this case is acceptable, at 57%

```
> (deviance.explained <- ((deviance(null)-deviance(rubbish.p1))/deviance(null))*100)
[1] 57.37869
```

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Step 5) Interpret Model Parameters and reach a conclusion

For Simple Linear models we can simply look at the parameter estimate summary and CI's. BUT in Poisson regression these are hard to interpret as they are still on the log scale (which was our link function).

The only really useful part of this 'raw' output is the p-value associated with the parameters. Which in this case shows strong evidence of Intermediate and Granites being different from Away (Intercept), Before/After and the interactions (which means the Before/After effect differs between sites) – since p values are so small.

```
Coefficients:
                                   Estimate Std. Error z value Pr(>|z|)    
(Intercept)                         -2.3638     0.1240 -19.057  < 2e-16 ***
Area_2Intermediate                   1.0033     0.1475   6.802 1.03e-11 ***
Area_2Granites                       0.7043     0.1679   4.194 2.74e-05 ***
Area_2DBS                           -0.1119     0.3557  -0.314 0.753150    
BeforeAfterAfter                     1.9915     0.1331  14.960  < 2e-16 ***
Area_2Intermediate:BeforeAfterAfter -0.4518     0.1671  -2.704 0.006842 ** 
Area_2Granites:BeforeAfterAfter     -0.7715     0.2550  -3.025 0.002483 ** 
Area_2DBS:BeforeAfterAfter          -1.4796     0.4129  -3.583 0.000339 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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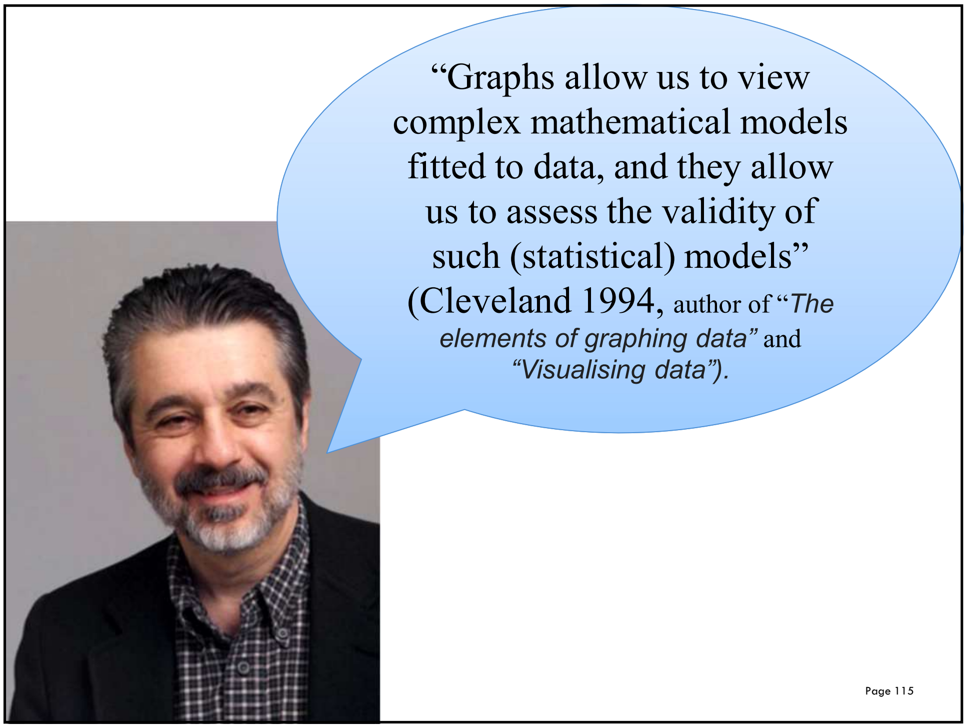

Page 115

115

Step 6) Reporting: Overall Conclusion suitable for publication

"The model is a good fit to the data with a pseudo R^2=57%. There were no outliers or unexplained structure.

The model fit was a GLM with Poisson distribution and log link function. There was no evidence of over dispersion or zero inflation."

But as it's a complex design with a lot going on we will use a plot to report the patterns and effects.

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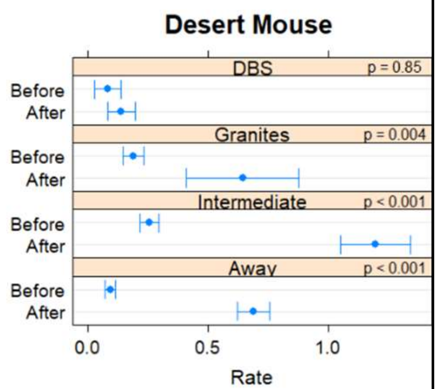
Page 116

116

Step 6) Reporting: Overall Conclusion suitable for publication

So far our examples have had few predictors and easy interpretation, so the words I've been giving you have been sufficient.

More complex designs with more predictors often require novel reporting methods. And charts are a great way to do that.

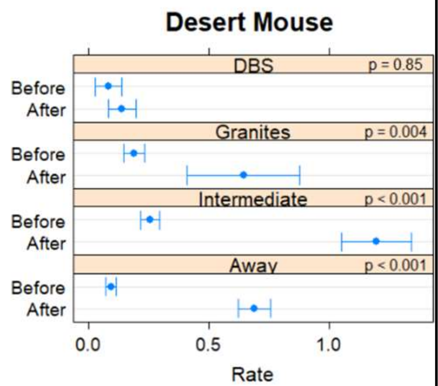


117

Step 6) Reporting: Overall Conclusion suitable for publication

We actually used this chart. Where the p-value at the top right is the specific t-test comparing Before vs After for each site, adjusted for multiple comparisons using Tukeys. The response has been adjusted to the response scale. The interpretation is:

- DBS, where dingos could still access garbage, is the only site where there is no evidence of dingos eating more Desert Mouse after the tips were fenced. This provides strong evidence that anthropocentric food availability can effect dingos diet and the wider Tanami Ecology.
- Interestingly, even at the sites far Away there is very strong evidence of a difference after the tips were fenced with scats having Desert Mouse in them increasing to a rate of [95%CI: 0.6-0.8] from [95% CI: 0.07-0.12] before the tip was fenced. There is strong evidence these rates have changed (p<0.001).



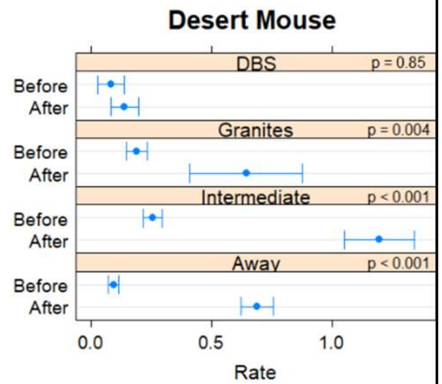
118

Step 6) Reporting: Overall Conclusion suitable for publication

This type of chart can be used for any GLM.

Not just Poisson.

This is the power of GLM's, similar charts work for all of them. So what you learn for one type of data you can easily apply to other types.



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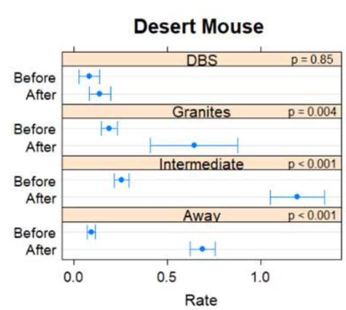
Step 6) Reporting R code

```
?pmmeans
(desert_mouse.p1.mm1 <- pmmeans(desert_mouse.p1, ~BeforeAfter|Area_2,
transform="response"))


# Chart
windows()
plot(desert_mouse.p1.mm1, main="desert_mouse")

# P-values
(desert_mouse.p1.mm2 <- pmmeans(desert_mouse.p1, specs=c( "BeforeAfter", "Area_2"),
transform="response"))
(desert_mouse.pw <- summary(pairs(desert_mouse.p1.mm2)))
```



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121

Other Resources

122

Further Assistance: Sydney University

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- **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: https://signup.e2ma.net/signup/1945889/1928048/
  - Research Essentials
  - Experimental Design
  - Power Analysis
- **Online library.** Useful links and the most recent version of all our workshops.
  - https://sydney-informatics-hub.github.io/stats-resources/
- **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

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: Shows how to build interpretable models and analyse data to extract insightful & impactful patterns which enable you to make the impactful discoveries that expand our knowledge, and how to craft engaging research stories to communicate those discoveries.

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.

Linear Models 3: How to build interpretable models and analyse data to extract insightful & impactful patterns, and craft an engaging research story

Statistical analysis is more than just building the best predictive model, it should also enable you to make impactful discoveries that expand our knowledge. Constructing engaging narratives about your research is also invaluable as you look to connect with your field, the community and funding bodies. To do this you need to build interpretable models, test hypotheses, uncover insightful & impactful patterns, and present results in insightful, intuitive and memorable ways. In this workshop we explore tips and tricks to make your research do just that. Topics covered will be:

– ***Building impactful real-world recommendations and guidelines*** – i) why we need to understand both stated and model derived importance, ii) how Quadrant Analysis uses both variable performance and importance to develop impactful real-world recommendations and guidelines.
– ***Reporting tricks that extract insightful & impactful patterns and craft engaging stories*** – i) establishing the importance of a predictor/risk factor, ii) confidence vs prediction intervals, iii) applying and correcting for multiple comparisons, iv) testing different hypothesis using different model parameterisations of the design matrix, v) interpreting categorical predictors - dummy vs effects coding and estimated marginal means, plus other reporting and interpretation tricks.
– ***Building interpretable models*** – it's quite common for researchers to incorrectly use model parameters to establish variables 'impact' or 'importance' . We show how multi-collinearity prevents this interpretation, and how to assess and then fix it so parameters can be used to identify important predictor/risk factors and other insightful patterns.
– ***Mixed models*** – extend the Linear Model 1 intro to: i) better explain how mixed models work, ii) use them to test population wide hypotheses outside your sampled groups, and iii) use a random slope (with examples of the patterns it can explain and hypotheses it can test).
– ***Using data visualisation to report complex nonlinear models graphically and aid pattern extraction***

125

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
  - Logistic Regression: https://www.youtube.com/watch?v=yIYKR4sgzI8
- Zedstatistics, longer videos than StatsQuest. https://www.youtube.com/c/zedstatistics

WEBSITES

- R GLMM FAQ https://bbolker.github.io/mixedmodels-misc/glmmFAQ.html

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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‹#› Page 126

126

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 you're 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
  - A series of short videos on **Logistic Regression** https://www.youtube.com/playlist?list=PLblh5JKOoLUKxzEP5HA2d-Li7IJkHfXSe

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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:
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We value your feedback

- We will email you a link to the survey shortly
- 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