Linear Models 3: Advanced Topics, Tips and Tricks

Presented by
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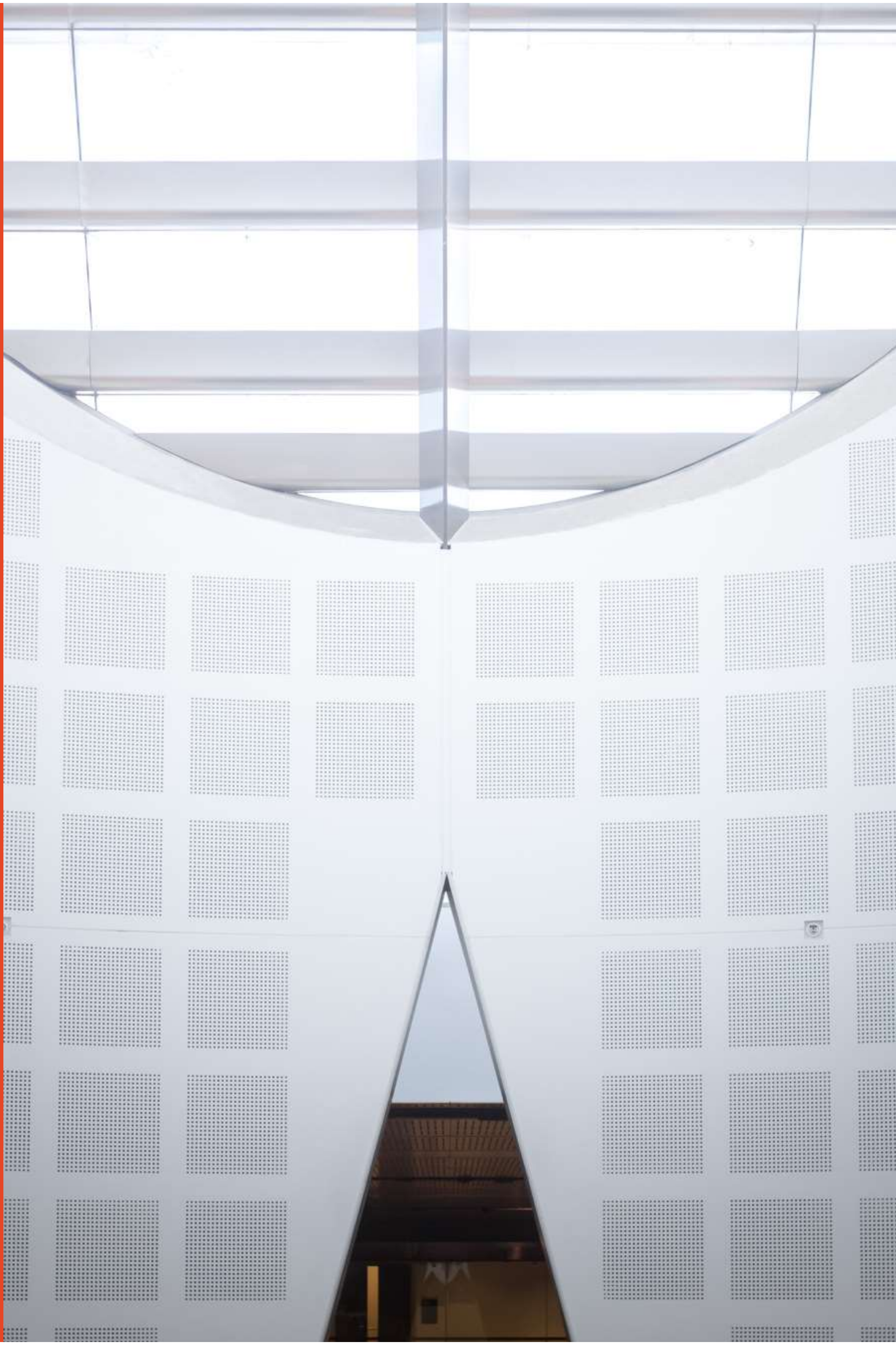

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Suggested wording:

General acknowledgement:

"The authors acknowledge the technical assistance provided by the Sydney Informatics Hub, a Core Research Facility of the University of Sydney."

Acknowledging specific staff:

“The authors acknowledge the technical assistance of (name of staff) of the Sydney Informatics Hub, a Core Research Facility of the University of Sydney.”

For further information about acknowledging the Sydney Informatics Hub, please contact us at sih.info@sydney.edu.au.

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

After the workshop

These slides should be used after the workshop as reference material and include workflows

- 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 Workflows

- Why do we need a research workflow?

  - As researchers we are motivated to find answers *quickly*

  - But we need to be *systematic* 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?

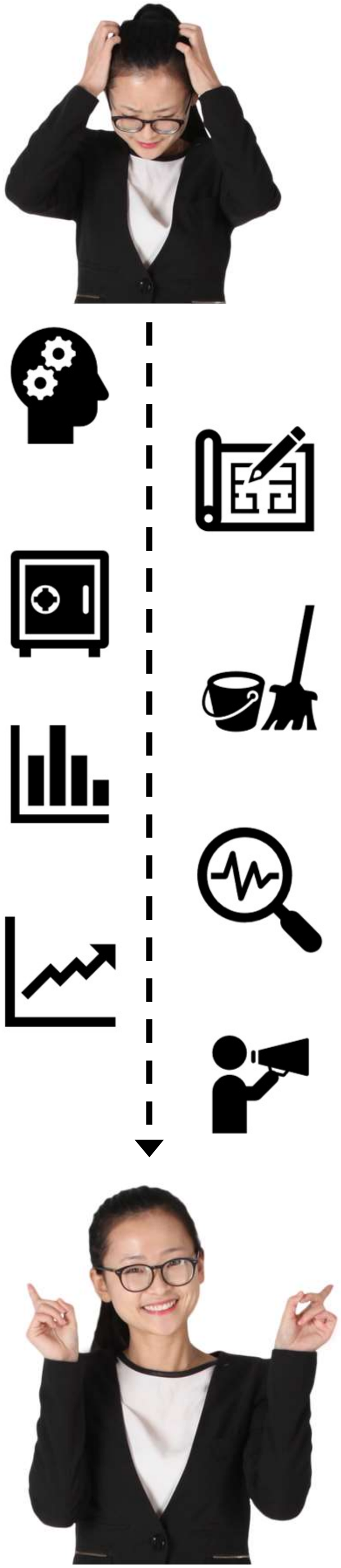
  - The process of doing a statistical analysis follows the same general "shape".

  - 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**



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

- Parametrising the model
- Mixed Models

Step 3) Check Model Assumptions via Diagnostics: Residual Analysis

Step 4) Goodness of Fit: Plots and Statistics

Step 5) Interpret and Report Model Parameters to reach a conclusion and build Knowledge

- Estimated Marginal Means vs Parameter contrasts, Confidence and Prediction Intervals, Multiple Comparisons

Step 6) Reporting

Linear Models 1 and 2 and Model Building Workshops have more detail on many of these steps.

A Conversation is better than a Presentation

So please speak up and ask questions!

People think differently. So I may need to explain things in 2 or 3 different ways!

Experimental Design Tips

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What are Linear Models?

Linear Regression

ANOVA

ANCOVA

Logistic regression

Before After Control Impact (BACI) Studies

Count regression

Randomised Control Trials (RCT's)

Repeated measures

Plus Many More!!

Predictors don't need to be normally distributed

Remember, it's the model error we assume to be normally distributed. Not the response or the predictors.

Its often better if the predictors aren't normally distributed. Some common design methods are:

1. **Uniform and random** since this efficiently samples the space, avoids bias due to unknown structures and a gives well structured variance. However it may lead to clusters of points or miss focal points which is not ideal e.g. 3 random samples over a 6 month period or for a 100 point measure of sweetness would miss the beginning and end which might be focal points.

2. **Equally Spaced Categories between the minimum and maximum.** Note that although common this is not always ideal since if there is some structure it may sit between the equally spaced points, so be careful e.g. minimum, average/midpoint, maximum over a 3 month period or 100 point measure of sweetness. However maybe the 'turning point' for unimodal sweetness is at 70.

Predictors don’t need to be normally distributed

3. **Equally Spaced Intervals/Bins that are randomly sampled.** This combines the above two methods and avoids the problems of both. We first create equally spaced intervals/bins (rather then points) along the predictors range and then randomly sample within those bins. This ensure each bin has the same # of points so no clusters, but introduces some randomness within each bin so we don’t accidently miss patterns that would match regularly spaced points e.g. split the 6 month timeline and 100 point measure of sweetness into 3 intervals (0-2, 2-4, 4-6 months/0-33, 33-67,67-100) and sample within them.

4. **Intervals/Bins designed to focus on areas of interest that are randomly sampled.** combines all of the above 3 e.g. for the 6 month time period we may need the 0 and 6 month times and then randomly sample between. For the measure of sweetness we might know there a ‘sweet spot’ between 60-80 which is where the unimodal curve is maximum so randomly sample within the intervals 0-60, 60-80, 80-100.

Predictors don’t need to be normally distributed

Other considerations

- The **Equally Spaced method usually gives categorical data,** while the others continuous which often gives more interesting information e.g. one can fit a curve to continuous data rather than simply compare categories.
- **Continuous data can be binned into categorical data if an ANOVA style method** is preferred. But it’s much harder/impossible to turn categorical data into continuous data. Meaning continuous data gives us more options.
- When sampling in a continuous fashion we **need enough sample for the range to be well sampled,** if not then it may be better to sample within specific categories such as min, average/midpoint, max.
- **What is the data your analytical method requires** e.g. formal timeseries methods assume equally spaced data, ANOVA requires categorical data, curve fitting continuous, etc.
- **Random sampling allows for much stronger causal inference,** since it removes bias.

More on Experimental Design and Sample Size

Experimental Design Workshop

- Far too many researchers think they know all they need to in this area, when they don't. We commonly see designs that could be **substantially improved for stronger causal inference and results -** leading to **publication in higher impact journals** (amongst other benefits).
- **If you don't thoroughly understand the things I have been talking about then you could benefit from this workshop** e.g. randomisation leads to stronger causal inference, the same data but different ED has different causal inference, what is causal inference!!
- Even if you have already collected your data it is well worth attending since it may improve your write up and analysis e.g. we had a client who didn't realise they had a Before/After Control/Impact (BACI) design which allowed them to make **much stronger causal inferences** than the simple observational study they thought they had.

Sample and Power Workshop

- Shows the steps and decisions researchers need to make when designing experiments to **ensure sufficient sample** e.g. power, minimum required to fit the necessary model, stability, etc.
- And **how much power the study has** i.e. does it have sufficient power to detect the effects you expect to see, or is your study a complete waste of time and resources.

Interpret and Report Model Parameters to reach a conclusion

- Estimated Marginal Means vs Parameters
- Confidence vs Prediction Intervals
- Multiple Comparisons

Our **Goal** is to **Build Models that answer our Research Questions and expand our Knowledge** (this is what statisticians focus on)

Not just build the best predictive model (which is what machine learning methods usually focus on)

Very different processes are used for those 2 goals

If all you want is the ‘best predictive model’ then model building is rather straightforward.

1. Pick a fit metric and method to maximise it, usually penalised for complexity e.g. cross validation on the correct answer

2. Try out all models with lots of different variable combinations to find the best fit

3. Maybe do some model averaging at the end

The problem with these methods is that their models are rarely interpretable

For a few reasons:

1) The **model and model parameters may not be easily extracted**

2) Even if the model gives model parameters they often **can't be easily interpreted due to multicollinearity.** Which they usually sweep under the carpet and ignore, rather than explicitly deal with.

3) The modelling process and models created **don't test specific research questions and scientific hypotheses.**

A statistical workflow for answering specific research questions is covered in our Model Building Workshop. It also covers ways to handle multicollinearity as does our Multivariate Workshop.

Case Study: How multicollinearity effects model building, interpretation and reporting

Let's assume there is a segment of coffee drinkers who only care about 2 things: **coffee taste** and **sweetness.** And we give them some coffee with honey in it.

We measure the following variables on a 100 point continuous scale (which is not ideal as explained in Surveys 1: but makes this example easier to explain)

- Response
  - overall Liking
- Predictors
  - coffee taste
  - sugar (measures sweetness)
  - honey (also measures sweetness)

Notice that we **don't measure the underlying sweetness latent variable directly, instead we use sugar and honey.**

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

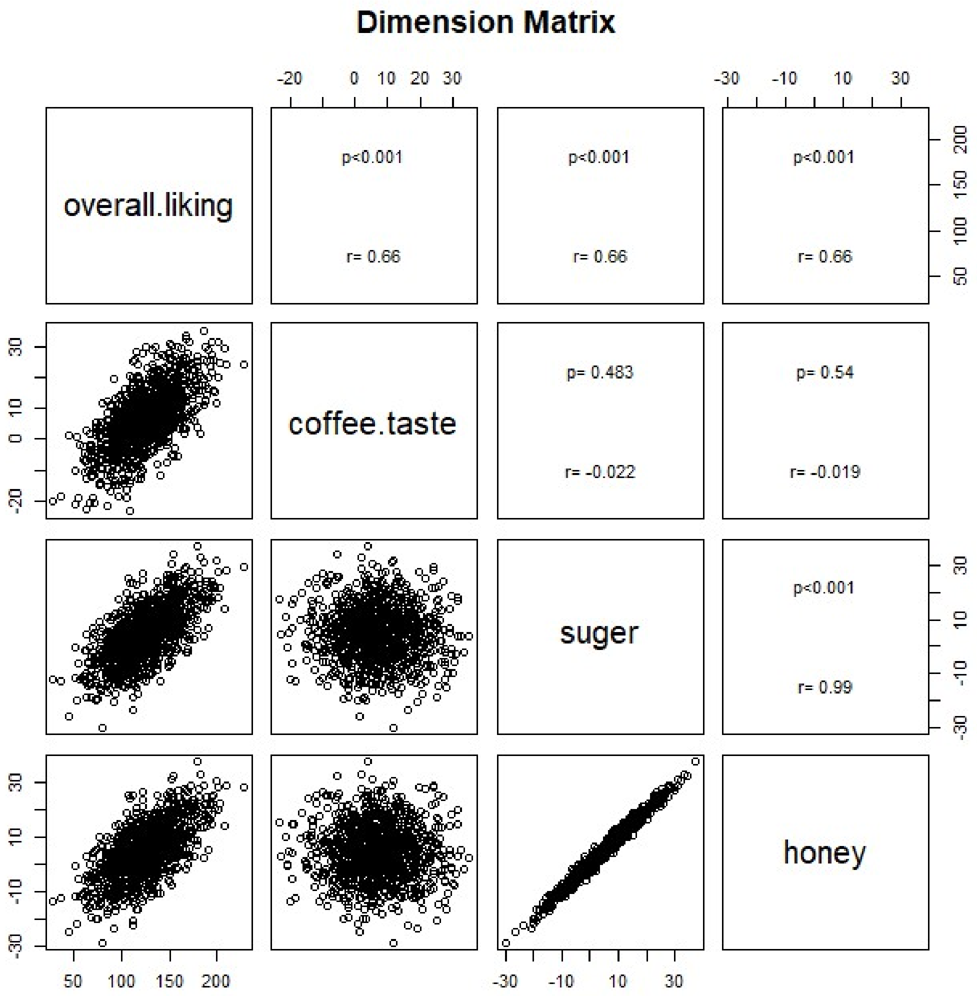
Step 5) Interpret Model Parameters and reach a conclusion

Step 6) Reporting

Linear Models 1 and 2 and Model Building Workshops have more detail on many of these steps.

EDA (Exploratory Data Analysis) – We notice that

- overall liking is correlated to all of them.
- coffee taste and sugar/honey aren't correlated.
- sugar and honey are strongly correlated.



Result of throwing all predictors into a model

```
Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)  102.26398    0.41754 244.918  < 2e-16 ***
coffee.taste   1.97621    0.03194  61.882  < 2e-16 ***
sugar          1.04067    0.22551   4.615 4.45e-06 ***
honey          0.93778    0.22635   4.143 3.72e-05 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 10.16 on 996 degrees of freedom
Multiple R-squared:  0.8833, Adjusted R-squared:  0.883
F-statistic:  2514 on 3 and 996 DF,  p-value: < 2.2e-16
```

One might conclude that coffee taste has about twice the impact of sugar and honey since it's parameter is about 2 while theirs are about 1

Of course we would also note that:

- All of them have very small p-values so there is a lot of evidence this effect is real.
- It's a good fit to the data with an R2 of 88% and very small p-value.
- NB: I'm not showing the GoF and checking assumptions/diagnostic tests, but they should be done!!

Results when we look at each predictor separately

```
             Estimate Std. Error t value Pr(>|t|)
Intercept)  115.87806    0.78309  147.98   <2e-16 ***
sugar         1.92209    0.06982   27.53   <2e-16 ***

Multiple R-squared:  0.4316,    Adjusted R-squared:  0.431
F-statistic: 757.8 on 1 and 998 DF,  p-value: < 2.2e-16
```

```
                Estimate Std. Error t value Pr(>|t|)
Intercept)     111.93985    0.85530  130.88   <2e-16 ***
coffee.taste     1.93462    0.07048   27.45   <2e-16 ***

Multiple R-squared:  0.4302,    Adjusted R-squared:  0.4296
F-statistic: 753.4 on 1 and 998 DF,  p-value: < 2.2e-16
```

```
             Estimate Std. Error t value Pr(>|t|)
Intercept)  115.90691    0.78094  148.42   <2e-16 ***
honey         1.93387    0.06997   27.64   <2e-16 ***

Multiple R-squared:  0.4336,    Adjusted R-squared:  0.433
F-statistic:   764 on 1 and 998 DF,  p-value: < 2.2e-16
```

But now we conclude that coffee taste, sugar and honey all have the same impact?! Since: their parameters are all the same, about 2!!

Of course we would also note that:

- All of them have very small p-values so there is a lot of evidence this effect is real.
- They're a good fit to the data with an R2 of about 43% and very small p-value.
- NB: I'm not showing the GoF and checking assumptions/diagnostic tests, but they should be done!!

So which model is right? What’s happened?

Because we simulated the data we know that the underlying sweetness and coffee taste dimensions have the same impact, which in both cases is a gradient (slope) of 2.

So the information we want to get from this analysis is that:

1. There is an underlying sweetness dimension that we are capturing twice. Once with honey and once with sugar.
2. That sweetness and coffee taste have the same impact on overall liking.

The **statical work flow tells us this** by using:

- EDA (Exploratory Data Analysis) to show that sugar and honey are highly correlated and measuring the same underlying variable. A bit of thought would suggest this is sweetness, and that if we want to understand the unique effect of this we should have only 1 of them in a model. So we need to decide which of them to use as a ***proxy*** for sweetness.
- Individual models show that the marginal/independent effect of each of them is about the same. Which is the ***correct interpretation if we want knowledge.***
- We might also look at the models with coffee taste and honey or sugar to understand their combined effect. This confirms that they have the same effect as coffee taste, and tells us they are operating independently.

```
             Estimate Std. Error t value Pr(>|t|)
(Intercept)  102.26709    0.42091  242.96   <2e-16 ***
coffee.taste   1.97865    0.03219   61.47   <2e-16 ***
sugar          1.96569    0.03193   61.57   <2e-16 ***
```

```
             Estimate Std. Error t value Pr(>|t|)
(Intercept)  102.36156    0.42123  243.01   <2e-16 ***
coffee.taste   1.97306    0.03225   61.18   <2e-16 ***
honey          1.97199    0.03211   61.41   <2e-16 ***
```

So which model is right? What’s happened?

Simply going for a model fit with all 3 variables needs to ‘share’ the effect of sweetness between sugar and honey, which is why their parameters are halved and suggest that honey and sugar have halve the effect of coffee taste.

This highlights the problem with interpreting models with more than 1 predictor. They ***need to be interpreted in the context (at the same time) as all the others, which is very difficult when there is multicollinearity and more than 2 or 3 predictors.***

Which is why it is impossible for anyone to interpret machine learning “best fit” model parameters independently in the presence of multicollinearity. One shouldn’t even try unless multicollinearity has been assessed, and ideally found to be negligible.

However interpretation is possible if we follow a statistical workflow and/or other analysis that accounts for multicollinearity. Which is why we should always follow this workflow:

1. First check to see if there is any multicollinearity to see if this is even a problem using EDA (Exploratory Data Analysis) plots, compare SS1 to SS3, Variance Inflation Factors (VIF’s), etc. Note that the pairwise plots we used only identify pairwise correlations, VIF’s find higher dimensionality multicollinearity.
   - This is another reason good EDA (Exploratory Data Analysis) is so important. Since it removes multicollinearity right from the beginning and allows for simple interpretation at the end.
2. If multicollinearity is a problem consider ***starting simple and getting complex*** so you can identify where parameter interpretations change and you need to start factoring in the multicollinearity.

(NB: These methods are covered in more detail in our Model Building Workshop)

Reproducibility Crisis: Instrument and Design Bias

Imagine for a moment that we have 2 researchers, both doing the preceding experiment. But they use these 2 different designs and instruments, the different being how they measure the sweetness latent variable:

- Researcher 1: captures both honey and sugar
- Researcher 2: captures only honey

If they used our statistical workflow both researchers would come to the same conclusion i.e. there is a sweetness latent variable which has about the same impact as coffee taste.

But if they simply fitted a machine learning ‘best model’ they would disagree i.e.

- Researcher 1 would incorrectly conclude that honey and sweetness have half the impact of coffee taste
- Researcher 2 would correctly conclude that honey has the same impact as coffee taste

I feel this is one of the biggest problems and mistakes researchers make.

  - And is 1 reason for the Reproducibility Crisis.

So Remember

Predictors can only be interpreted **independently** if they are **independent.**

If they are **dependant** (correlated) they need to be interpreted **dependant** on each other (in the context of each other).

*Another way of saying this is that if there is **multicollinearity** predictors need to be interpreted in the **context** of each other.*

To do this one needs to:

1. Determine how dependant they are
2. Where they are dependant

Basic Reporting – Refresher From LMI and II

Parameter	Estimate	SE	T score	P value	95% Confidence Interval	
					Lower Bound	Upper Bound
Constant / Intercept (β_o)	102	0.42	243	<2e-16	101	103
Coffee taste	2.0	0.03	62	<2e-16	1.92	2.04
sugar	2.0	0.03	62	<2e-16	1.90	2.01
Model Fit is => $Y_i = \beta_o + X_i\beta_1 + X_i\beta_1 + \varepsilon_i$ => Overall Liking = 1.03 + 2*Coffee taste + 2*sugar + $\mathcal{E}_i$						

"There is strong evidence to show that Overall Liking is associated with both Coffee Taste (p<2e-16) and sugar (p<2e-16). With a 1 point increase in Coffee Taste associated with an increase in liking of between 1.92-2.04. Sugar had a very similar effect of between 1.90-2.01. This correlation on liking has been estimated very precisely.

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

Notice

1. **When giving a p-value always give an estimate of the effect size as well** i.e. the 95% CI.
2. I have **shied away from causal language** since this type of study is often observational rather than experimental. This is an example of how **the same statistical analysis and results** can have **very different casual interpretations based solely on the Experimental design.** For more info on how your experimental design determines how strong of a causal link your analysis provides refer to our **Experimental Design Workshop.**

Basic Reporting – Workflow that accounts for multi-collinearity

Parameter	Estimate	SE	T score	P value	95% Confidence Interval	
					Lower Bound	Upper Bound
Constant / Intercept (β_o)	102	0.42	243	<2e-16	101	103
Coffee taste	2.0	0.03	62	<2e-16	1.92	2.04
sugar	2.0	0.03	62	<2e-16	1.90	2.01
Model Fit is => $Y_i = \beta_o + X_i\beta_1 + X_i\beta_1 + \varepsilon_i$ => Overall Liking = 1.03 + 2*Coffee taste + 2*sugar + ε_i						

"There is strong evidence to show that Overall Liking is associated with both Coffee Taste (p<2e-16) and sugar (p<2e-16). With a 1 point increase in Coffee Taste associated with an increase in liking of between 1.92-2.04. sugar had a very similar effect of between 1.90-2.01. This correlation on liking has been estimated very precisely.

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

As this was a multivariable model multicollinearity was investigated using a scatterplot matrix during the EDA (Exploratory Data Analysis) phase of the analysis. This showed that coffee taste and sugar were not correlated, meaning their effect on Overall liking can be treated as independent of each other. This was confirmed by comparing the conditional multivariable models coefficients with the marginal models to ensure they were similar.

Furthermore this EDA phase also showed that the sugar and honey variables were highly correlated, suggesting they represent an underlying Sweetness dimension. For this reason honey was dropped from the analysis."

Basic Reporting – Workflows that accounts for multi-collinearity

1) Showing that honey and sugar represent the same underlying Sweetness dimensions and only 1 of them is needed:

   I. Show that if one replaces sugar with honey in all models they are approximately the same (or vice versa)

   II. That adding honey to a model with sugar (or vice versa) does not improve the model fit using appropriate methods such as no increase in R2 or the Likelihood Ratio Test.

2) Create a Sweetness factor from sugar and honey using Multivariate methods such as Principle Components or Factor Analysis and use that instead of either of them (refer to Multivariate Workshop for how to do this).

A more realistic example and workflow

Our goal was to understand the drivers of coffee overall liking.

To do this we asked 200 people to make a coffee in their standard way and then collected 30 sensory variables about their coffee such as sweetness, amount of sugar added, honey, bitter, coffee taste, milky, white colour, etc (full list appendix 1).

EDA (Exploratory Data Analysis) scatterplots and correlation showed substantial multicollinearity between these 30 sensory variables. Factor analysis suggested 4 main non correlated drivers: coffee taste, bitter, sweetness and milky. The 30 sensory variables were split into these 4 dimensions, in each block all were correlated with r>0.8.

2 models were fit using this data:

1. The sensory variable from each block with the highest correlation with coffee overall liking was retained. Leaving us with sweetness, coffee taste, milky flavour, bitterness.
   - This model should give us our **best fit** from a model that is easily interpreted.
2. The sensory variable that we could most easily adjust was retained. Leaving us with amount of sugar, amount of milk added, amount of coffee added, bitterness.
   - This one is useful since it suggests **an experimental design we might use to show causality. And what we might actually do to impact liking.**

Rcode to create data

```
sweetness <- rnorm(1000, mean=5, sd=10) # Latent variable
coffee.taste <- rnorm(1000, mean=6, sd=10) # Latent variable
sugar <- sweetness + rnorm(1000, mean=0, sd=1)
honey <- sweetness + rnorm(1000, mean=0, sd=1)
bitter <- -1*sweetness + rnorm(1000, mean=0, sd=1)

error <- rnorm(1000, mean=100, sd=10)

overall.liking <- 2 + 2*sweetness + 2*coffee.taste + error

sens <- data.frame(overall.liking, coffee.taste, sweetness, sugar,
honey, bitter, error)
```

Rcode for EDA (Exploratory Data Analysis) and Analysis

EDA (Exploratory Data Analysis)

```
panel.cor <- function(x, y, digits=2, cex.cor)
{
  usr <- par("usr"); on.exit(par(usr))
  par(usr = c(0, 1, 0, 1))
  r <- cor(x, y)
  txt <- format(c(r, 0.123456789), digits=digits)[1]
  test <- cor.test(x,y)
  Signif <- ifelse(round(test$p.value,3)<0.001,"p<0.001",paste("p=",round(test$p.value,3)))
  text(0.5, 0.25, paste("r=",txt))
  text(.5, .75, Signif)
}

windows()
pairs(sens[c(1,2,4,5)], main="Dimension Matrix", upper.panel=panel.cor)
graphics.off()
```

Analysis

```
lm.coffee <- lm(overall.liking~coffee.taste, data=sens)
(s.lm.coffee <- summary(lm.coffee))

lm.sugar <- lm(overall.liking~sugar, data=sens)
(s.lm.sugar <- summary(lm.sugar))

lm.honey <- lm(overall.liking~honey, data=sens)
(s.lm.honey <- summary(lm.honey))

lm.coffee.sugar <- lm(overall.liking~coffee.taste+sugar, data=sens)
(s.lm.coffee.sugar <- summary(lm.coffee.sugar))

lm.coffee.honey <- lm(overall.liking~coffee.taste+honey, data=sens)
(s.lm.coffee.honey <- summary(lm.coffee.honey))

lm.sugar.honey <- lm(overall.liking~sugar+honey, data=sens)
(s.lm.sugar.honey <- summary(lm.sugar.honey))

lm.coffee.sugar.honey <- lm(overall.liking~coffee.taste+sugar+honey, data=sens)
(s.lm.coffee.sugar.honey <- summary(lm.coffee.sugar.honey)
```

Reporting the “Importance” of Predictors

People often want to calculate the “importance” of predictors. There are many ways to do this. 2 common ways use the regression coefficients and the R-squared (R^2) from a linear regression. They often give similar results.

The regression coefficient method simply divides each regression parameter by their sum and then multiples by 100. To give a % importance score.

Both can be misleading so use with care, **neither are recommended.** ***Better to talk about them in terms of the relative difference in their parameters i.e. relative importance*** e.g.

– Example 1: Coffee taste and sugar have a similar association with Liking

– Example 2: Coffee taste has 3 times the association as sugar

Example 1 Parameter	Estimate	Importance
coffee taste	1.93	50%
sugar	1.92	50%
Total	3.85	

Example 2 Parameter	Estimate	Importance
Coffee taste	6.0	75%
sugar	2.0	25%
Total	8	

Reporting the “Importance” of Predictors

One of the problems with most, if not all, importance scores is that multicollinearity throws them out too. From the previous example we get the below:

- The **multivariable model is effected by multicollinearity** and makes it look like sugar and honey have half the effect of coffee taste. Which technically they do in the model, but the underlying sweetness dimension has the same effect so this leads to poor conclusions i.e. knowledge.
- While the marginal models show them to have equal effects. Which technically they do, but we aren’t really capturing that sugar and honey both represent the same sweetness dimension, so best to not have both of them.

Another problem is that the **multivariable importance’s differ between studies with different variables.** While the **marginal parameters will remain the same and be directly comparable.**

Multivariable model Parameters	Estimate	Importance
Coffee taste	1.98	50%
Sugar	1.04	26%
Honey	0.94	24%
Total	3.96	

Marginal Model Parameters	Estimate	Importance
Coffee taste	1.93	33%
Sugar	1.92	33%
Honey	1.93	33%
Total	5.78	

Reporting the “Importance” of Predictors

Be careful of methods that claim to ‘account’ for multicollinearity. Some deal with it by sweeping it under the carpet, do that enough times and you’ll wind up with a mound you’ll trip over!

For instance, Shapley Values gives similar values to the multivariable model importance, so doesn’t account for multicollinearity in a way that enables knowledge building.

Shapley Values

- are also known Shapley regression, Shapley Value analysis, LMG, Kruskal analysis, and dominance analysis, and incremental R-squared analysis. https://www.displayr.com/shapley-value-regression/
- similar to a method often used in machine learning known as Relative Weights. https://www.displayr.com/shapley-vs-relative-weights/
- Are the average expected marginal contribution of one product after we’ve looked at all possible combinations

Multivariable model Parameters	Estimate	Importance	Shapley Values
Coffee taste	1.98	50%	0.50
Sugar	1.04	26%	0.25
Honey	0.94	24%	0.25
Total	3.96		

Marginal Model Parameters	Estimate	Importance
Coffee taste	1.93	33%
Sugar	1.92	33%
Honey	1.93	33%
Total	5.78	

Categorical Predictors

Confidence vs Prediction Intervals

Multiple Comparisons

Estimated Marginal Means

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Categorical predictor tests and p-values

Categorical predictors with more than 2 levels have different types of tests, and p-values associated with them.

1. ANOVA table
2. Parameter Estimates

Consider hair colour as a predictor for # of freckles. We often see the following 2 types of tables with p-values.

ANOVA TABLE: tells us that there is an overall association between Hair Colour and freckles (p<2.2e-16). In general we look at this one first to determine if there is an overall/familywise/global effect and report as such.

BUT it doesn't describe the association very well, which is what the parameters do.

Parameter	Degrees of Freedom (DF)	Sum of Squares (SS)	Mean (MS)	F value	P value
Hair Colour	3	84943183	28314394	286624	<2.2e-16
Residuals/Error	396	39119	99		

Categorical predictor tests and p-values

The **PARAMETER TABLE** describes the association. It tells us that:

- Our **reference category of Black Hair has about 8 freckles** (p=2.08e-15), and in general most black haired people have between 6-10 freckles (95% CI).
- And that compared to our Black Haired reference level:
  - **Blondes have on average 91** more (p<2.2e-16), and this precisely estimated between 88-94 (95% CI)
  - There is **no evidence that Brown haired** folk have a different amount since P>0.05. Although **one might say there is some weak evidence** of about 3 more since p=0.06.
  - **Redheads tend to have just over 1000 more freckles!!** (since its estimate is 1092, p=2.22e-16, 95% CI=[1089, 1094])

Parameter	Estimate	SE	T score	P value	95% Confidence Interval	
					Lower Bound	Upper Bound
Constant (Black)	8	0.99	8.3	2.08e-15	6	10
Blonde	91	1.4	64.6	<2.2e-16	88	94
Brown	3	1.4	1.9	0.0627	-0.1	5
Red	1092	1.4	776	<2.2e-16	1089	1094

Categorical predictor tests and p-values

But there is a bit of a problem with using parameters to describe and report the associations. Can anyone see what it is? Hint: what if we wanted to focus on redheads?

It only describes the difference from the black haired folk it doesn't (effectively):

– **Tell us the overall # of freckles we expect each hair type to have overall.** (This can be done by ***predicting*** the number each should have and putting a ***confidence or prediction interval*** around it.)

– **Compare to other hair types** e.g. Redheads to all other hair types. This is done using ***Multiple Pair Wise Comparisons*** or changing the ***Parametrisation*** so a different hair colour is used as the reference level.

Parameter	Estimate	SE	T score	P value	95% Confidence Interval	
					Lower Bound	Upper Bound
Constant (Black)	8	0.99	8.3	2.08e-15	6	10
Blonde	91	1.4	64.6	<2.2e-16	88	94
Brown	3	1.4	1.9	0.0627	-0.1	5
Red	1092	1.4	776	<2.2e-16	1089	1094

Predicting the # of freckles we expect each hair type to have

There are 2 common ways to do this:

1. **Confidence Intervals** estimate the number of freckles **all the people** in a hair type have e.g. the average number of freckles all redheads have is between 1098-1102.
2. **Prediction Intervals** estimate the number of freckles **an individual** can expect to have e.g. the number of freckles we can expect an individual redhead to have is between 1081-1120.
   - They are wider than confidence intervals since we expect an average to be less variable than individual data.

Hair Colour	Point Estimate	95% Confidence Interval		95% Prediction Interval	
		Lower Bound	Upper Bound	Lower Bound	Upper Bound
Black	8	6	10	-11	28
Blonde	99	97	101	79	119
Brown	11	9	13	-9	30
Red	1100	1098	1102	1081	1120

Multiple Comparisons

The **parametrisation** we've used makes black haired people the **reference group**. So the parameters tell us the difference between other levels compared to this reference group.

But what if we want to compare other groups e.g. red with blond?

This is where we do **multiple comparisons** which compare all possible pairwise comparisons of the levels.

Notice that we made 6 different comparisons.

```
contrast         estimate    SE  df t.ratio  p.value
1 black - blonde   -90.850 1.406 396  -64.634 <.0001
2 black - brown     -2.624 1.406 396   -1.867 0.2441
3 black - red    -1092.028 1.406 396 -776.911 <.0001
4 blonde - brown    88.226 1.406 396   62.767 <.0001
5 blonde - red   -1001.178 1.406 396 -712.277 <.0001
6 brown - red    -1089.404 1.406 396 -775.045 <.0001

P value adjustment: tukey method for comparing a family of 4
estimates
```

Say we made 20 such (unadjusted) multiple comparisons and they all had p=0.05. If we concluded that all of them showed a real difference in the population how many would we expect to be wrong (on average)?

A) None
B) 1 Correct
C) 5
D) Can’t tell

A p-value of 5% means we make the wrong decision to reject the null hypothesis of no effect and accept there is one 5% or 1 in 20 times. Since we made 20 comparisons with a p-value of 5% we expect to come to the wrong conclusion 1 in 20 times (on average).

And we don’t know which one is likely wrong either!

So how do we fix this?

Correcting for Multiple Comparisons

We effectively **adjust the p-value cut off to keep the family wide error rate of all comparisons at 5%.**

The simplest method is called **Bonferroni** and simply divides the family wide p-value we want by the # of comparison we make.

$$\text{New Bonferroni p-value} = \frac{\text{family wide p−value}}{\text{\# of comparisons}}$$

$$\text{E.G.: New Bonferroni p-value} = \frac{0.05}{20} = 0.0025$$

Correcting for Multiple Comparisons

Unfortunately Bonferroni is overly conservative i.e. it makes the adjusted p-value unnecessarily small, making it harder to find statistically significant results worth reporting.

To fix this there are other multiple comparisons that are less conservative, the one we used is Tukey's which assumes we are comparing all possible means.

```
contrast        estimate    SE  df t.ratio  p.value
1 black - blonde   -90.850 1.406 396  -64.634 <.0001
2 black - brown     -2.624 1.406 396   -1.867 0.2441
3 black - red    -1092.028 1.406 396 -776.911 <.0001
4 blonde - brown    88.226 1.406 396   62.767 <.0001
5 blonde - red   -1001.178 1.406 396 -712.277 <.0001
6 brown - red    -1089.404 1.406 396 -775.045 <.0001

P value adjustment: tukey method for comparing a
family of 4 estimates
```

Which multiple comparison to use?

We want the one which is the **least conservative** since that makes it easier to find statistically significant results we can report.

This table ranks some common methods from least to most conservative by showing the Critical Value t score above which something is significant. The higher the critical score the harder it is to get a statistical significant difference.

(Assumes Family wise alpha = 0.05, 4 groups with N=6 so 20 error DF. Gerard E. Dallal http://www.jerrydallal.com/LHSP/mc.htm. This order may not hold for all cases.)

Test	Critical Value	Assumed # of comparisons
Uncorrected t-test Least Significant Difference (LSD) i.e. the fancy way of saying no correction performed.	2.09	NA
Duncan new multiple range test (MRT) (as it's a stepwise procedure we must assume testing homogeneity of all 4 groups. Has a lot of critics.)	2.22	6
Dunnett - each level compared to a control, ideal in medical studies **if** comparison to control is all that is needed and not between treatments	2.54	3
Bonferroni (3 comparisons done, for reference to Dunnett)	2.63	3
Tukey HSD (commonly used since covers all pairwise comparisons)	2.80	6
Bonferroni (6 comparisons done, for reference to Tukey HSD)	2.93	6
Scheffe	3.05	6+

Bonferroni Correction

$$\text{Adjusted p-value} = \frac{\text{family wide p-value}}{\text{\# of comparisons}}$$

$$\text{E.G.: New Bonferroni p-value} = \frac{0.05}{20} = 0.0025$$

PROS

– Easy to calculate

– Can be used to make Confidence Intervals

– Few assumptions so can be applied when other methods can't

  – Can be applied across different models

CONS

– Not very accurate and is overly conservative i.e. we will miss quite a few real differences

– As number of comparisons increases the cut off p-value gets very, very small very, very quickly making it difficult to find significant results

Tukey HSD (Honestly Significant Difference)

LSD i.e. unadjusted, uses a critical value assuming only 2 groups are being compared.

Tukeys HSD adjusts this to all possible pairwise comparisons.

PROS	CONS
– Easy to calculate – Can be used to make Confidence Intervals	– Assumes all multiple pair-wise comparisons are being made, which makes it overly conservative if this isn't being done

Scheffe

Scheffes uses a t-score assuming all possible comparisons are being made, so not just pairwise comparisons but contrasts like the average of 2 things = the average of another 2 things.

Used to be very popular

PROS	CONS
– Easy to calculate – Can be used to make Confidence Intervals – Covers any set of comparisons we want to do	– Assumes all comparisons are being made, which makes it overly conservative if this isn’t being done

Dunnet

Uses a t-score assuming groups are being compared to a single control.

PROS	CONS
– Easy to calculate – Can be used to make Confidence Intervals – Accurate when applicable	

Duncans new multiple range test (MRT)

Uses a completely different approach to the previous methods. Finds **homogenous groups**, rather than looking for differences.

Based on the [Student]-Newman-Keuls Procedure but with greater power. This is a complex algorithmic procedure.

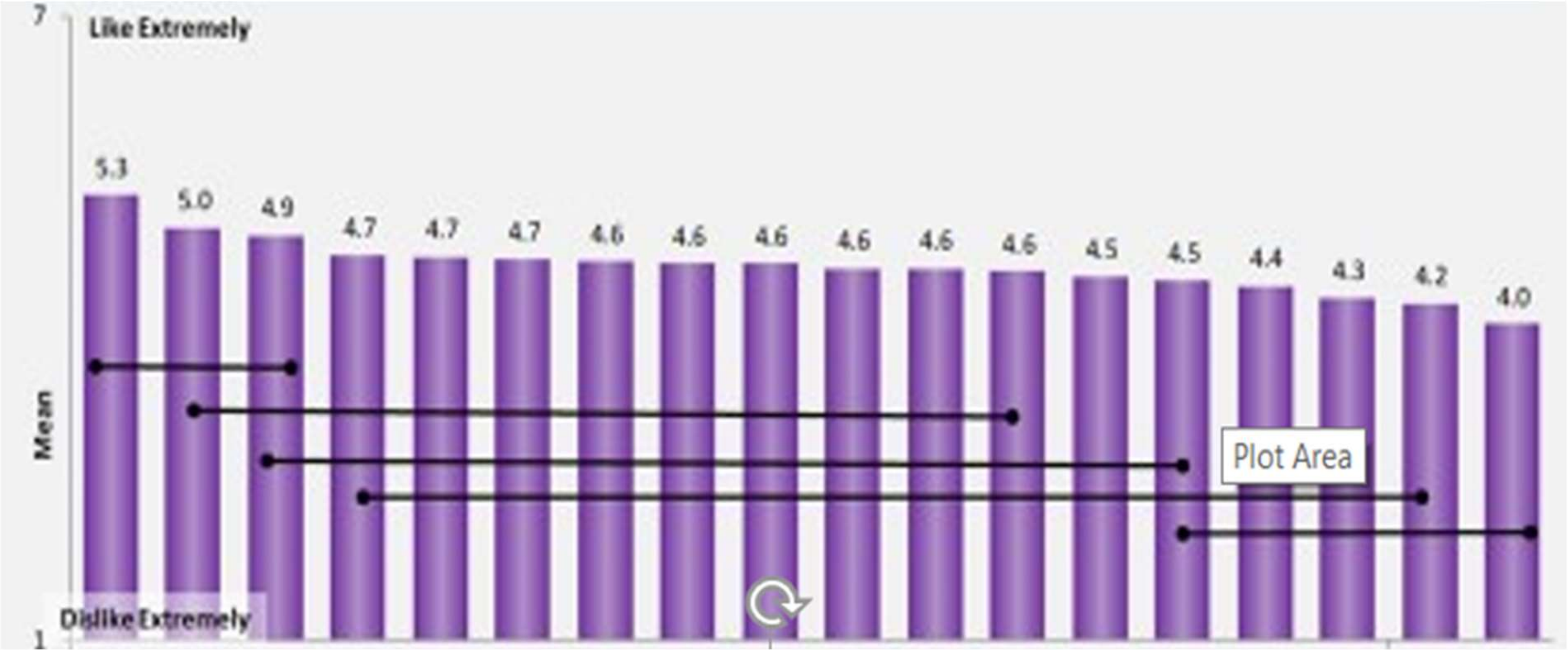
PROS

- Least conservative i.e. more significant differences so more to talk about. But some say too liberal.
- Useful if we want to find homogenous groups.
- A quick way of doing fuzzy clustering.
- An efficient way to summarise lots of groups in 1 slide.

CONS

- Can't be used to make Confidence Intervals that match the test results
- Has some (a lot?) of critics so may get criticized at the review stage if not used in your domain

Homogenous Subset Example



Bars linked with a black line from a homogenous group i.e. there is no significant difference.

NB: Forgive the lack of a horizontal axis, this was a real world test, so names were removed to retain commercial confidentiality.

Hypothesis testing vs Screening/Exploratory analysis

There is considerable debate about when Multiple Comparisons should be used, preferences can be quite domain specific.

One generally **always tests 'within model and/or factor' comparisons, but rarely between model comparisons** i.e. also known as correcting for multiple ***testing*** to distinguish it from multiple ***comparisons*.** For example: if we had a single model for freckles with 2 predictors: hair colour (4 options) and eye colour (4 options) we would generally correct each predictor for multiple comparisons independently i.e. assume 6 comparisons were being done for each. We wouldn't sum up the total comparison and correct for 12. Similarly if we ran 2 different models each with a different predictor we would correct each one independently.

1 useful distinction I often make is the difference between Hypothesis Testing vs Screening/Exploratory Analysis.

Hypothesis testing

- Requires corrections for Multiple Comparisons, e.g. Bonferroni, Tukey, Holmes, False Discovery Rate. For more information on correcting for multiple comparisons refer to Linear Models III.

- Is when we are testing apriori theories developed from previous research or modelling and are the focus of the paper. Usually only a few are made.
- Often used to make important decisions with minimal or no supporting evidence.
- EXAMPLE: Randomised clinical trials to evaluate 3 vaccines, Comparing a new formulation to the existing product, Land management Trials.

Screening/Exploratory Analysis i.e. Screening lots of tests for possibly interesting pattern.

– Often doesn't correct for all multiple comparisons being done.
– Is when we do lots of tests looking for unknown associations or interesting patterns.
– Often used to suggest future research.
– If used to make decisions must be in conjunction with other information e.g. other studies, qualitative work, prior expert knowledge.
– EXAMPLE: Pharmacological study on 1000's of off the shelf medications impact on covid to identify those worth moving into better randomised clinical trials , analysing a survey with lots of questions and splits, driver analysis between numerous sensory/hedonistic variables and liking, data mining.

Surveys

Surveys often consider analyses of each question a different test, so we don't correct for multiple testing.

We also consider different splits of the same variable as different tests e.g. if comparing different medical treatments between genders, age and BMI we don't correct for all of them at the same time. **Instead of using strict hypothesis testing we take the view that these p-values are used to screen** all the different comparisons being done to see what might be worthwhile incorporating into the story and to generate hypotheses to be tested in future research.

We do however often correct for comparisons between different categories within a single variable e.g. if we had 4 age groups that's 6 different pairwise comparisons which we would usually correct for. Sometimes though we can have so many different categories to make even this problematic as correcting for multiple comparisons in the normal ways usually means nothing is worthwhile reporting.

As such we can also report both. For instance, if one was comparing some statements to a benchmark one can use colour, font and/or asterisk's to signify whether something has a p-value <0.05 **with and without correcting for multiple comparisons (MC)**.

The basic idea is that **as we are more sure of those corrected for multiple comparisons we bring more attention to them.**

Method	**P<0.05** **No MC correction**	**P<0.05** **MC correction**
Colour	Light Red	Dark Red
Asterisk	*	**
Bold or not	Not Bold	**Bold**

Significance testing, colour coding and screening

Example 1 - Colour

Importance of Animal Welfare on purchase decisions	% who agree
Australian Average (Benchmark)	**50%**
Vegetarian	**90%**
Byron Bay	60%
Low Socio Economic Band	**20%**
Sydney	53%

Example 2 - No colour so can be used in more journals

Importance of Animal Welfare on purchase decisions	% who agree
AUSTRALIAN AVERAGE (BENCHMARK)	50%
Vegetarian	90% **
Byron Bay	60% *
Low Socio Economic Band	20% **
Sydney	53% *

Reporting more than 1 categorical predictor: Estimated Marginal Means (EMMs)

Reporting more than 1 categorical predictor present some challenges.

Let’s extend our example to include the factor SUN with 2 levels

1. Bronzed Bondi Beach Bathers (BBBB)
2. Goths

Reporting more than 1 categorical predictor: Estimated Marginal Means (EMMs)

The first table we look at is below, this tells us that we don’t need the interaction. So let’s rerun it without.

```
 Df    Sum Sq  Mean Sq     F value Pr(>F)
hair         3 41701428 13900476 1.3958e+05 <2e-16 ***
sun          1 53843550 53843550 5.4065e+05 <2e-16 ***
hair:sun     3       48       16 1.5910e-01 0.9238
Residuals 392    39039      100
```

Main Effects Model ANOVA table. Shows there is strong evidence that both predictors are associated with # of freckles since p<2.2e-16

```
Df    Sum Sq  Mean Sq F value     Pr(>F)
hair         3 41701428 13900476  140474 < 2.2e-16 ***
sun          1 53843550 53843550  544129 < 2.2e-16 ***
Residuals 395    39087       99
```

Reporting more than 1 categorical predictor: Estimated Marginal Means (EMMs)

So let’s look at the parameters. And now we may run into a bit of a problem interpreting them.

Things are a little more complicated now…. So let’s come back to that.

```
Estimate Std. Error  t value Pr(>|t|)
(Intercept)  808.529      1.133  713.519   <2e-16 ***
hairblonde    90.850      1.407   64.579   <2e-16 ***
hairbrown      2.624      1.407    1.865   0.0629 .
hairred     1092.276      1.472  741.903   <2e-16 ***
sunGoth     -800.621      1.085 -737.651   <2e-16 ***
```

Reporting more than 1 categorical predictor: Estimated Marginal Means (EMMs)

And talk about the predictions confidence intervals first. When we have 2 predictors we might want to look at the predictions for all the different combinations as below.

BUT we also often want **an 'overall' effect for BBBB and Goth?**

```
sun  hair     emmean    SE  df lower.CL upper.CL
BBBB black   808.529 1.133 395  806.301   810.76
Goth black     7.907 1.133 395    5.679    10.13
BBBB blonde  899.378 1.133 395  897.150   901.61
Goth blonde   98.757 1.133 395   96.529   100.98
BBBB brown   811.153 1.133 395  808.925   813.38
Goth brown    10.531 1.133 395    8.303    12.76
BBBB red    1900.805 1.394 395 1898.064  1903.55
Goth red    1100.184 1.001 395 1098.216  1102.15
```

Reporting more than 1 categorical predictor: Estimated Marginal Means (EMMs)

And talk about the predictions confidence intervals first. When we have 2 predictors we might want to look at the predictions for all the different combinations as below.

BUT we also often want **an 'overall' effect for BBBB and Goth?**

To do this we can take the simple average of all the hair colours for BBBB i.e. from the previous slide (808.5 + 899.4 + 811.2 + 1900.9)/4 = 1105

```
sun   emmean      SE  df lower.CL upper.CL
 BBBB 1105.0 0.8194 395     1103   1106.6
 Goth  304.3 0.6602 395      303    305.6
```

And also use these averages for the pairwise comparisons i.e. 1105 – 304.3 = 800.7 (the difference from the 800.6 below is just rounding errors)

```
 contrast    estimate    SE  df t.ratio p.value
 BBBB - Goth    800.6 1.085 395 737.651 <.0001
Results are averaged over the levels of: hair
```

Reporting more than 1 categorical predictor: Estimated Marginal Means (EMMs)

We calculate the overall effect of hair colours in a similar way, we just average over BBBB and Goth.

```
 hair    emmean     SE  df lower.CL upper.CL
 black    408.2 0.9948 395    406.3    410.2
 blonde   499.1 0.9948 395    497.1    501.0
 brown    410.8 0.9948 395    408.9    412.8
 red     1500.5 1.0854 395   1498.4   1502.6
```

And use these averages for the pairwise comparisons

```
  contrast          estimate    SE  df t.ratio  p.value
 black - blonde   -90.850 1.407 395  -64.579 <.0001
 black - brown     -2.624 1.407 395   -1.865 0.2448
 black - red     -1092.276 1.472 395 -741.903 <.0001
 blonde - brown    88.226 1.407 395   62.714 <.0001
 blonde - red    -1001.427 1.472 395 -680.196 <.0001
 brown - red     -1089.652 1.472 395 -740.121 <.0001
Results are averaged over the levels of: sun
P value adjustment: tukey method for comparing a
family of 4 estimates
```

But the EMM is different to the data's mean. And that's why we use model averages not data averages.

One might expect a good model to replicate the data, right? A naïve person might think the best estimate for the # of freckles a redhead has is to average the number of freckles from our sample.

So why then does the EMM for red hair differ so much from the data average??

It's because the sample size is skewed towards Goths, if we take the average EMM for Red-Goth and Red-BBB and weight it by the sample size we get the Data Average = 1100 * 0.9 + 1901*0.1 = 1180.

So an EMM let's us **remove the effect of our sample and get a clean read assuming all categories had equal sample size.**

Average Freckles	EMM	Data Average
Black	408	408
Blonde	499	499
Brown	411	411
Red	**1501**	**1180**

Sample Size	BBB	Goths
Black	50	50
Blonde	50	50
Brown	50	50
Red	**10**	**90**

But the EMM is different to the data's mean. And that's why we use model averages not data averages.

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So an EMM let's us **remove the effect of our sample and get a clean read assuming all categories had equal sample size.**

Which is a **good thing if our sample is not a good representation of the overall population.** In this instance it would have made it look like being a red head didn't have as much impact on freckles as it does.

But a bad thing if our sample does represent the population. Which is why EMMs can be weighted using different inputs.

EMMs can also incorporate continuous variables

There are a number of ways to do but we usually include it’s contribution to the prediction at a single point, often it’s average Other options are:

– A different value for each contributing category (often the average for that category). e.g. if we added age to our example we might use a different age for each hair*sun combination (its specific average) rather than the overall average.

Examples of when EMMs are better than data

- We want an estimate of the # of freckles by hair colour, **after correcting for other variables** such as Sun.

- We want to estimate the impact of a new medical treatment, **after removing the effects of other covariates.** Particularly useful if the covariate distribution in our sample data doesn't match the population.

References

- Vignettes from the R package emmeans https://cran.r-project.org/web/packages/emmeans/index.html

R code: Freckles = Hair Example

```
# ____ Simulate data---------------
hair <- factor(c(rep("black", 100), rep("blonde", 100), rep("red", 100), rep("brown", 100)))

freckles.hair <- NA
freckles.hair <- ifelse(hair=="black", 10, freckles.hair)
freckles.hair <- ifelse(hair=="blonde", 100, freckles.hair)
freckles.hair <- ifelse(hair=="brown", 10, freckles.hair)
freckles.hair <- ifelse(hair=="red", 1100, freckles.hair)
table(freckles.hair)

set.seed(485)
error <- rnorm(length(hair), 0, 10)
freckles <- freckles.hair + error

df.hair <- data.frame(hair, freckles, freckles.hair, error)


# _____BASIC LINEAR MODEL (ANOVA) --------------------------------------
lm.hair <- lm(freckles ~ hair, data=df.hair)
anova(lm.hair)
summary(lm.hair)


# _____Prediction vs confidence intervals-------------
# https://rpubs.com/aaronsc32/regression-confidence-prediction-intervals
pred.hair <- data.frame(hair=factor(levels(df.hair$hair)))
?predict
predict(lm.hair, newdata=pred.hair, interval='confidence')
predict(lm.hair, newdata=pred.hair, interval='prediction')
```

R code: Freckles = Hair Example

```
# ____MULTIPLE COMPARISONS ----------------------------------------------
--------
# METHOD 1: GLHT()  ---------------------------------------------
(hair.posthoc <- glht(lm.hair, linfct=mcp(hair="Tukey")))
summary(hair.posthoc)

# METHOD 2: EMMEANS() -----------------------------------------------------
?emmeans


hair.emm <- emmeans(lm.hair, specs="hair")
summary(hair.emm) # same as prediction
predict(lm.hair, newdata=pred.hair, interval='confidence') # same as
emmeans


pairs(hair.emm) # same as glht()
summary(hair.posthoc) # same as emmeans
```

Parametrising the Model

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What does Parametrising the Model mean?

All **linear models have a set of parameters that need to be defined** for the software to estimate our model and **give us the knowledge that we seek** e.g. fixed effects parameters in the design matrix, random part of the model if there is one, distribution (normal, poisson, binomial, etc)

1 of the most basic are the parameters in the equation and design matrix. There is often **more than 1 way to define and calculate these parameters**. How we do so determines how we interpret the parameters we get at the end.

Which influences how we interpret and report our results.

And the knowledge we get from our analysis.

Simple Regression – Numeric Statistical Model

Quick Refresher from Linear Models 2

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

Prediction = Linear Predictor + Error/Natural Variation

Data			Design Matrix Parameters		Model Variables	
		Predictors				
Observation	Response	Continuous			Prediction	Error
i	Yi	X1i	X0i	X1i	$\hat{Yi}$	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
3	3	9	1	9	2.1	0.9
4	2	1	1	1	2.9	-0.9
5	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

B_o ~ Constant/Y intercept parameter

$\beta_{1\,i}$ ~ parameter for predictor 1

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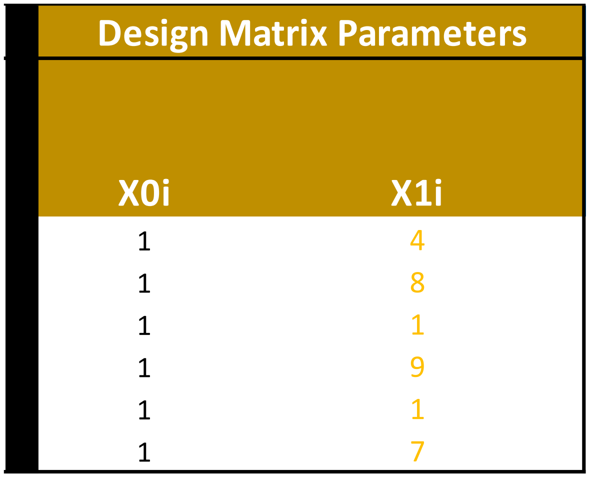
The Design Matrix is an important part of our model Parametrisation

It defines the **fixed effects** part of our model Parametrisation

And is directly used in the software's calculations



Design Matrix Parameters	
X0i	X1i
1	4
1	8
1	1
1	9
1	1
1	7

Multiple Regression Parametrisation

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

Prediction = Linear Predictor + 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
3	3	9	96	96	1	9	96	96	2.9	0.1
4	2	1	41	41	1	1	41	41	1.8	0.2
5	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

B_o ~ Constant/Y intercept parameter

$\beta_{1\,i}$ ~ parameter for predictor 1

β_{2i} ~ parameter for predictor 2

β_{3i} ~ parameter for predictor 3

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No Intercept Parametrisation

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

Prediction = Linear Predictor + Error/Natural Variation

Forces the line through the origin. Can be useful if you know this should happen.

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

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

B_o ~ Removed

$\beta_{1\,i}$ ~ parameter for predictor 1

β_{2i} ~ parameter for predictor 2

β_{3i} ~ parameter for predictor 3

Other important parts of Model Parametrisation

Equation

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

Is usually defined in the software e.g.

```
    R> lm(response ~ predictor, data=data)
```

Note that the `~ predictor` defines the design matrix

Other important parts of Model Parametrisation

Transformations on the response and predictors e.g.

$\text{Log}(Y_i) = \beta_o X_{0i} + \beta_1 X_{1i} + \varepsilon_i$

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

There are generally 2 ways to do this:

1. Use the raw variable and include the transformation in the model equation e.g.

```
R> lm(log(response)~predictor, data=data)
```

   – Usually the **preferred option** since doing it within the equation modelled means the software knows the response has been transformed and can pass this on to other functions, such as emmeans() in R.

2. Transform the variable and include it in the model equation e.g.

```
R> log.response <- log(response)
R> lm(log.response ~predictor, data=data)
```

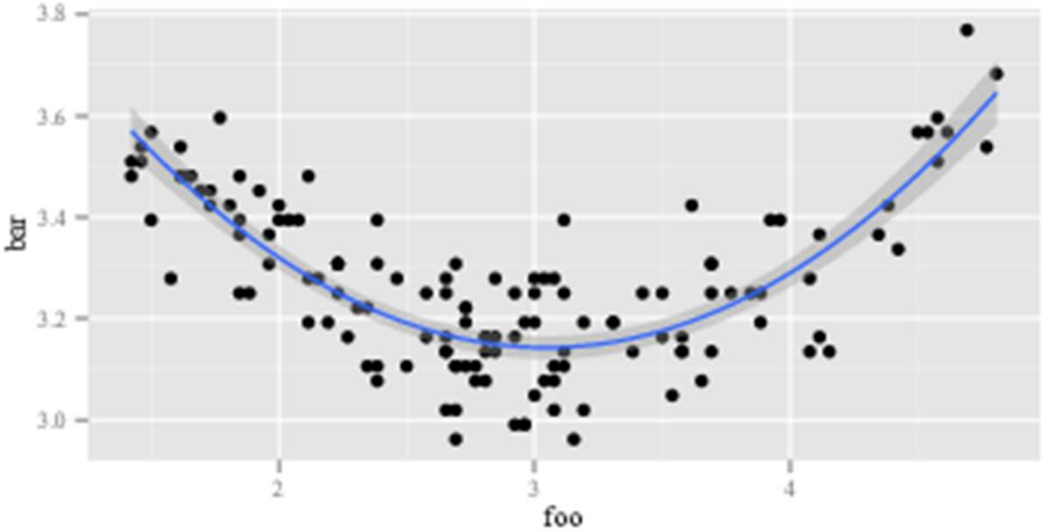
Other important parts of Model Parametrisation

Quadratic and other functions e.g.

```
lm(log.response~predictor+I(predictor^2),
data=data)
```

This above uses the raw variable and tells the equation to square it in the design matrix. Which as mentioned in the previous slide is generally preferred over calculating it and entering the squared variable beforehand i.e.

```
R> predictor.sq <- predictor^2
R> lm(response ~ predictor + predictor.sq,
data=data)
```



Model Building has more info on this

Other important parts of Model Parametrisation

General Linear Mixed Models

- The **link** function (this is where we would usually transform the response rather than log it beforehand)
- The **distribution** e.g. normal, poisson, binomial, etc

Mixed Models

Need to define the random effects parameters e.g. this example defines a nested design with id nested in class. And a fixed effect design matrix of 2 parameters: intercept and time. The response is score.

```
R>lme(data=mixed.int3, fixed=score~time, random= ~ 1|class/id)
```

Categorical Predictor Interpretation

Is particularly influenced by the type of parametrisation used.

Recall our freckles = Hair + Sun model

Below are the results we get which I said we'd come back to.

In order to interpret it we need to recognise that it used **Dummy Coding parametrisation with Black haired BBBB's as the reference.**

```
             Estimate Std. Error  t value Pr(>|t|)
(Intercept)  808.529      1.133  713.519   <2e-16 ***
hairblonde    90.850      1.407   64.579   <2e-16 ***
hairbrown      2.624      1.407    1.865   0.0629 .
hairred     1092.276      1.472  741.903   <2e-16 ***
sunGoth     -800.621      1.085 -737.651   <2e-16 ***
```

Categorical Variables (e.g. ANOVA)

Quick Refresher from Linear Models 2

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

Prediction = Linear Predictor + Error/Natural Variation

Data				Design Matrix Parameters			Model Variables	
	Predictors							
Obs	Response	Continuous	Categorical				Prediction	Error
i	Yi	X1i	X2i	X0i	X1i	X2i	$\hat{Yi}$	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
3	3	9	Smoking	1	9	1	3.4	-0.4
4	2	1	Non Smoking	1	1	0	1.4	0.6
5	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

B_o ~ (Reference group = Non-Smoking)

$\beta_{1\,i}$ ~ parameter for predictor 1

β_{2i} ~ parameter for smoking

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Categorical Variables (e.g. ANOVA)

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

Prediction = Linear Predictor + Error/Natural Variation

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

There are many different **parameterisations** (ways) to add categorical variables. The way I am showing you is called **Dummy** or **Treatment Coding.** Linear Models 3 discusses other ways such as effects 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" either:

1. Turning the variable on/including it in the equation when it is a 1 (since $\beta_2 X_{2i} = \beta_2 * 1 = \beta_2$)
2. Turning the variable off/excluding it in the equation when it is a 0 (since $\beta_2 X_{2i} = \beta_2 * 0 = 0$)

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Categorical Variables (e.g. ANOVA)

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

Prediction = Linear Predictor + 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
3	3	9	Smoking	1	9	1	3.4	-0.4
4	2	1	Non Smoking	1	1	0	1.4	0.6
5	2	7	Non Smoking	1	7	0	2.2	-0.2

There are many different **parameterisations** (ways) to add categorical variables. The way I am showing you is called **Dummy** or **Treatment Coding.** Linear Models 3 discusses other ways such as effects 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.

How to Dummy Code Categorical Variables in the Design Matrix

1. Create the X0 reference variable by assigning a 1 to it for all levels.
2. For each categorical variable decide which level is the reference (for Hair it's black and for Sun its BBB). Then for all other levels assign them a parameter in the design matrix that works as it's indicator variable i.e. it turns on when that level is present and is interpreted as effect/difference compared to the reference (tables below).

Hair	X0 Constant Black	X1 Blonde	X2 Brown	X3 Red
Black	1	0	0	0
Blonde	1	1	0	0
Brown	1	0	1	0
Red	1	0	0	1

Sun	X0 Constant BBBB	X4 Goth
BBBB	1	0
Goth	1	1

Dummy Coding Categorical Variables in the Design Matrix

1. Create the X0 reference variable by assigning a 1 to it for all levels.
2. For each categorical variable decide which level is the reference (for Hair it’s black and for Sun its BBB). Then for all other levels assign them a parameter in the design matrix that works as it’s indicator variable i.e. it turns on when that level is present and is interpreted as effect/difference compared to the reference (tables below).
3. Combine the tables to give the final design matrix

Hair	Sun	X0	X1	X2	X3	X4	Predict
		Constant Black BBB	Blonde	Brown	Red	Goth	# Freckles
Black	BBBB	1	0	0	0	0	X0
Blonde	BBBB	1	1	0	0	0	X0 + X1
Brown	BBBB	1	0	1	0	0	X0 + X2
Red	BBBB	1	0	0	1	0	X0 + X3
Black	Goth	1	0	0	0	1	X0 + X4
Blonde	Goth	1	1	0	0	1	X0 + X1 + X4
Brown	Goth	1	0	1	0	1	X0 + X2 + X4
Red	Goth	1	0	0	1	1	X0 + X3 + X4

Dummy Coding Categorical Variables in the Design Matrix

$$Freckles_i = \beta_o X_{0i} + \beta_1 X_{1i} + \beta_2 X_{2i} + \beta_3 X_{3i} + \beta_4 X_{4i} + \varepsilon_i$$

```
    Beta(β)         Estimate Std. Error  t value Pr(>|t|)
X0=(Intercept)   808.529       1.133  713.519   <2e-16 ***
X1= Hairblonde     90.850       1.407    64.579   <2e-16 ***
X2= hairbrown       2.624       1.407     1.865   0.0629 .
X3= hairred      1092.276       1.472   741.903   <2e-16 ***
X4= sunGoth      -800.621       1.085 -737.651   <2e-16 ***
```

Hair	Sun	X0 Constant Black BBB	X1 Blonde	X2 Brown	X3 Red	X4 Goth	Predict # Freckles COPY OVER THE PARAMETERS
Black	BBBB	1	0	0	0	0	808 + 0 + 0 + 0 + 0 = 808
Blonde	BBBB	1	1	0	0	0	808 + 91 + 0 + 0 + 0 = 899
Brown	BBBB	1	0	1	0	0	808 + 0 + 3 + 0 + 0 = 811
Red	BBBB	1	0	0	1	0	808 + 0 + 0 + 1092 + 0 = 1900
Black	Goth	1	0	0	0	1	808 + 0 + 0 + 0 – 801 = 7
Blonde	Goth	1	1	0	0	1	808 + 91 + 0 + 0 – 801 = 98
Brown	Goth	1	0	1	0	1	808 + 0 + 3 + 0 – 801 = 10
Red	Goth	1	0	0	1	1	808 + 0 + 0 + 1092 – 801 = 1099

Dummy Coding Categorical Variables in the Design Matrix

$\text{Freckles}_i = \beta_o X_{0i} + \beta_1 X_{1i} + \beta_2 X_{2i} + \beta_3 X_{3i} + \beta_4 X_{4i} + \varepsilon_i$

```
   Beta(β)        Estimate Std. Error  t value Pr(>|t|)
X0=(Intercept)  808.529      1.133  713.519   <2e-16 ***
X1= Hairblonde    90.850      1.407    64.579   <2e-16 ***
X2= hairbrown      2.624      1.407     1.865   0.0629 .
X3= hairred     1092.276      1.472   741.903   <2e-16 ***
X4= sunGoth     -800.621      1.085  -737.651   <2e-16 ***
```

So we interpret this as saying

Our reference category of Black Hair and BBBB has about 808 freckles (p<2.08e-16) and compared to this

- Blondes have 91 more (p<<2.2e-16)
- There is no evidence that Brown haired folk have a different amount since P>0.05. Although one might say there is some weak evidence of about 3 more since p=0.06)
- Being a Redhead likely has a **big impact** since they tend to have 1000 more freckles!! (p<2.22e-16)
- And being a Goth also has a **big impact** since that is associated with a drop in the number of freckles by 800!!

NB: don’t forget we would also usually report the 95% CI’s for all these point estimates.

Always remember this is framed against an arbitrary reference level. Impact of changing Sun’s reference level from BBB to Goth

Changing the reference level changes the way we look at the data. It doesn’t change the overall interpretation but it does change our focus which makes answering specific Research Questions easier or harder.

Reference is Hair:Black, Sun:BBB.

This parametrisation suggests that **Goths reduce** the # of freckles by 800

```
     Beta(β)  Estimate Std. Error  t value Pr(>|t|)
Intercept)  808.529      1.133  713.519   <2e-16 ***
Hairblonde    90.850      1.407   64.579   <2e-16 ***
hairbrown      2.624      1.407    1.865   0.0629 .
hairred     1092.276      1.472  741.903   <2e-16 ***
sunGoth     -800.621      1.085 -737.651   <2e-16 ***
```

Reference is Hair:Black, Sun:Goth

This parametrisation suggests that **BBBB’s increase** the # of freckles by 800.

The **overall effect is the same,** but we are just looking at it from a different angle. And maybe one that is **more relevant to our research question?**

```
     Beta(β)  Estimate Std. Error  t value Pr(>|t|)
(Intercept)    7.907      1.133   6.978 1.27e-11 ***
hairblonde    90.850      1.407  64.579  < 2e-16 ***
hairbrown      2.624      1.407   1.865   0.0629 .
hairred     1092.276      1.472 741.903  < 2e-16 ***
sunBBBB       800.621      1.085 737.651  < 2e-16 ***
```

Always remember this is framed against an arbitrary reference level. Impact of changing Hairs reference level from Black to Red

If we wanted to focus on the difference compared to redheads then lets make them the reference level. BUT notice how this changes our interpretation!

Reference is Hair:Black, Sun:Goth

```
     Beta(β)   Estimate Std. Error  t value Pr(>|t|)
Intercept)  808.529      1.133  713.519   <2e-16 ***
Hairblonde    90.850      1.407   64.579   <2e-16 ***
hairbrown      2.624      1.407    1.865   0.0629 .
hairred     1092.276      1.472  741.903   <2e-16 ***
sunGoth     -800.621      1.085 -737.651   <2e-16 ***
```

Reference is Hair:Redhead, Sun:Goth

By focusing on redheads we see some changes. All the parameters

- are now strongly significant <2e-16
- and have negative effects

The **overall effect is the same,** but we are just looking at it from a different angle. And maybe one that is **more relevant to our research question?**

Estimate Std. Error t value Pr(>|t|)

```
     Beta(β)   Estimate Std. Error  t value Pr(>|t|)
(Intercept)  1900.805      1.394  1363.4   <2e-16 ***
hairblack   -1092.276      1.472  -741.9   <2e-16 ***
hairblonde  -1001.427      1.472  -680.2   <2e-16 ***
hairbrown   -1089.652      1.472  -740.1   <2e-16 ***
sunGoth      -800.621      1.085  -737.7   <2e-16 ***
```

Its common to make the control the refence level. Since then its easy to understand how treatments differs from it.

The family wise ANOVA table never changes though!

Since the model is the same, we've just changed how the categorical variable is parametrised

```
> # Reference level is HAIR:Black & SUN:BBBB
> anova(lm.hair.sun)
Df    Sum Sq  Mean Sq F value    Pr(>F)
hair        3 41701428 13900476  140474 < 2.2e-16 ***
sun         1 53843550 53843550  544129 < 2.2e-16 ***
Residuals 395    39087       99

> # Reference level is HAIR:Black & SUN:Goth
> anova(lm.hair.sun3.0)
Df    Sum Sq  Mean Sq F value    Pr(>F)
hair        3 41701428 13900476  140474 < 2.2e-16 ***
sun         1 53843550 53843550  544129 < 2.2e-16 ***
Residuals 395    39087       99

> # Reference level is HAIR:red & SUN:BBBB
> anova(lm.hair.sun4.0)
Df    Sum Sq  Mean Sq F value    Pr(>F)
hair        3 41701428 13900476  140474 < 2.2e-16 ***
sun         1 53843550 53843550  544129 < 2.2e-16 ***
Residuals 395    39087       99
```

Common ways to Parametrise Categorical Variables

Dummy Coding/Treatment coding

- Useful when we have a control or some natural reference group we want to compare other treatment levels to since each parameter is interpreted as the difference from this control/reference group.
- Most common.
- Constant by itself represents the base reference level for all factors.
- Can't calculate an effect for each level since the reference level for each factor is confounded with all the other reference levels.

Effects Coding

- Useful if there is no natural reference group since we can calculate the effect of each level. So likely better for our freckles example.
- Constant by itself represents the 'grand mean' which is the average effect overall factor levels.
- Each parameter is that levels change from the 'grand mean'. The missing level can be calculated from the other levels.

Reporting complex non linear effects

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Reporting complex non linear effects

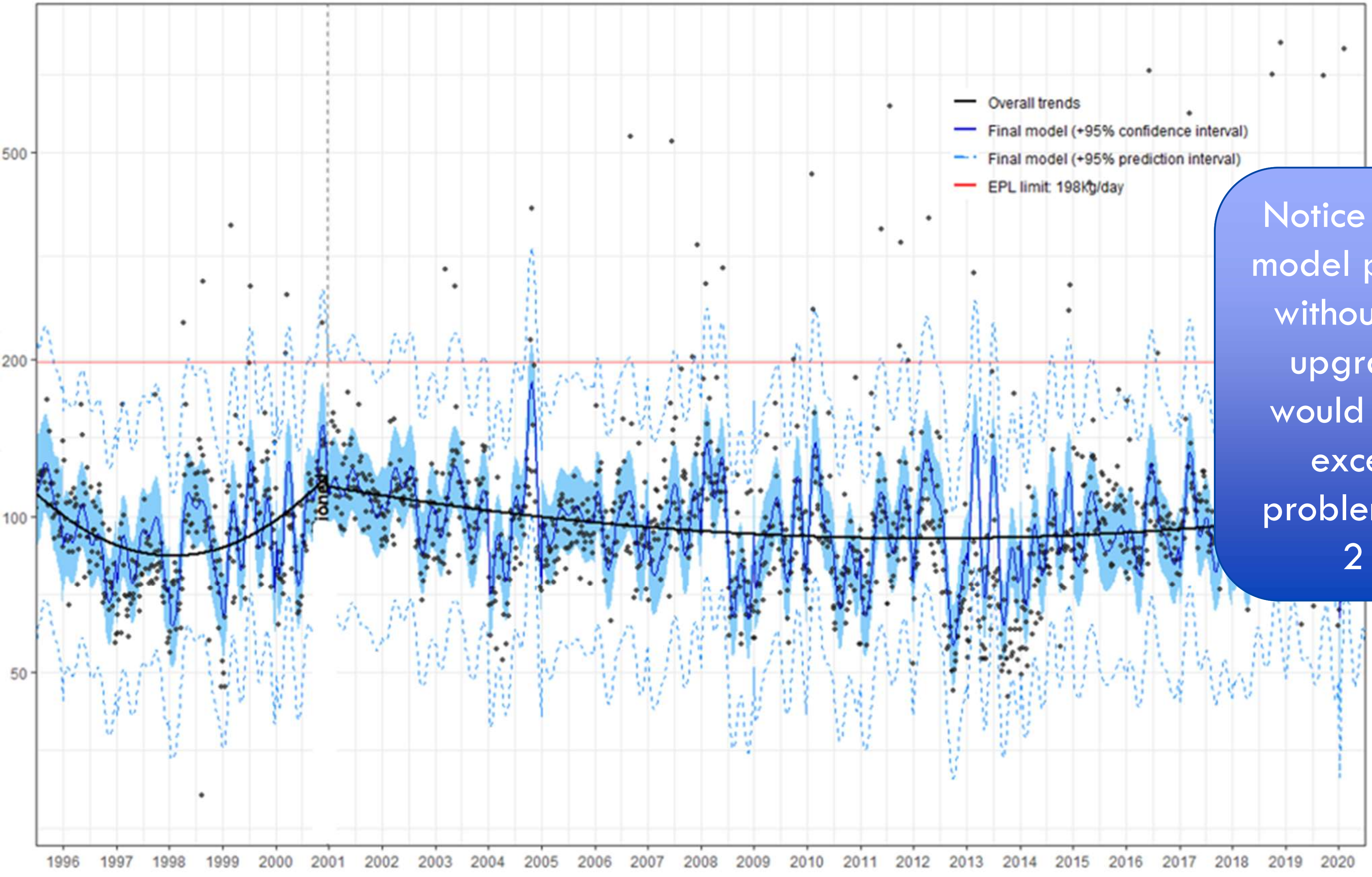
These comments refer to the plot on the next slide:

- This is a model I built to capture the effect of a water treatment plant upgrade on a analyte of interest (such as nitrogen, phosphorus, dissolved oxygen, etc). The analyte is not shown as the analysis was confidential.
- The horizontal dotted line is the plant upgrade.
- The green line captures the overall trend.
- The blue line factors in seasonal trends.
- Notice the difference between the confidence and prediction intervals.
  - **Confidence intervals** show where we expect the modelled average i.e. the blue line, to be after considering sample variance and model uncertainty.
  - **Prediction intervals** show were we expect individual observations to be i.e. the grey points. They are often used when we want to predict an actual point in the future, rather than the average. They are wider since they factor in the extra variance associated with a single observation, rather than the average of observations.

Reporting complex non linear effects

When reporting simple linear effects like ANOVA or regression a table representing the effect and it’s CI is often sufficient. But when reporting non linear effects or complex models

– plots or
– Estimated Marginal Means are often easier.



Notice how the 1st model predicts that without the plant upgrade there would have been exceedance problems in about 2 years.

More on Mixed Models

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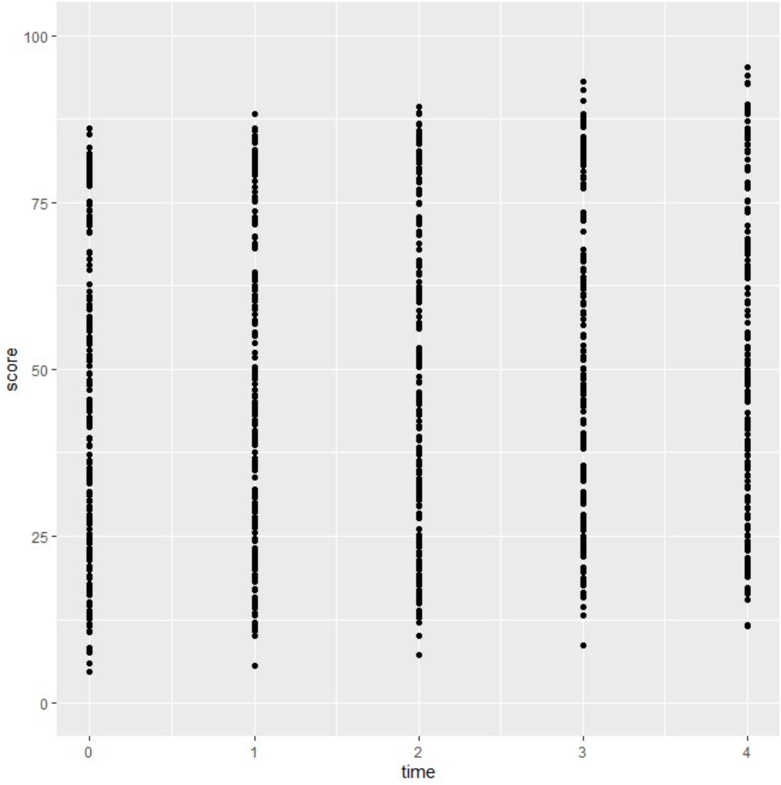
Random Intercepts

Let's say we wanted to understand the effect of teaching on some skill. And we had 5 classes with 40 people in each and 5 time points.

Here's the data a normal regression would model.



Random Intercepts

And here’s the data a mixed effects model that nests student in class would model.

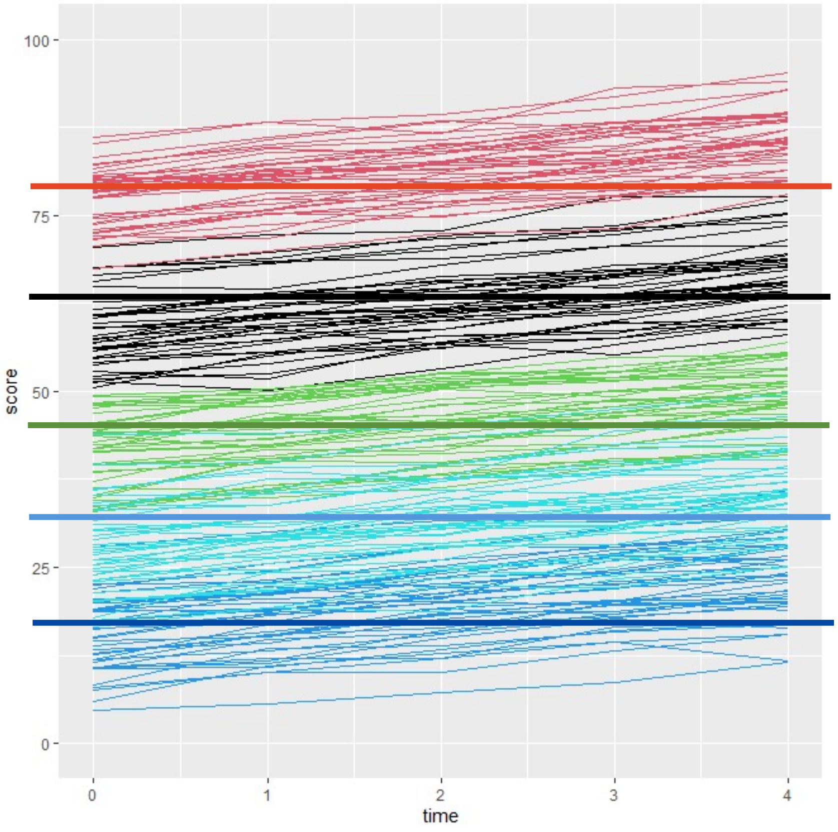
Notice how there is more structure in this model. How it groups:

- Each students data together via the **lines**
- Each classes data together via the **colours**

A random intercept model factors this information in by

- **Adjusting** each **classes** intercept from the base B0 y intercept
  - Notice the 5 different lines, 1 for each class.
  - It then captures this adjustment by calculating the variance for these 5 points.

- **Adjusting** each **person’s** intercept from their classes y intercept
  - It then captures this adjustment by calculating the variance for each individuals adjustment.



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"Graphs allow us to view complex mathematical models fitted to data, and they allow us to assess the validity of such (statistical) models" (Cleveland 1994, author of *The elements of graphing data and Visualising data*).

Including Random Effects: gives us more precise and sensitive models

Because they **increase the signal to noise ratio, by reducing the noise.** Which allows us to **detect smaller signals, with greater precision.**

They do this by partitioning out different types of variance/error/noise by adjusting the intercept for different parameters e.g. class and ID. We then capture this adjustment as a variance and remove it from the model.

This can often be the difference between finding publishable results or not. As the example in our LM1 workshop showed i.e. the fixed effect model did not detect a difference between treatments, while the mixed effect model did since by giving each patient a random intercept it removed the between patient noise/variance.

This is another reason why understanding and **developing a great Experimental Design is so important.** It allows us to identify and remove noise leading to better results. (Refer to our Experimental Design for more info).

NB: they are not always more accurate, in that the parameter estimates may stay the same. They are more precise though as their SE's are reduced, leading to smaller p-values.

Including Random Effects: Understanding the relative source of variance/noise/error

	Variance Point Estimate	95% CI Lower Bound	95% CI Upper Bound
Difference **between Classes**	25	12	50
Difference **between Individual**	5	4.5	5.4
Error/noise/change/difference **within each Individual**	1	1.0	1.1

Another benefit is that we get estimates of the different sources of variance. So in our example we can tell that class accounted for about 5 times more difference in the scores than individuals or the individuals change over time.

If we wanted to improve results this might prompt us to investigate why the classes are so different.

While if this were a quality control exercise such estimates are used to design better processes by determining which elements introduce the most difference from batch to batch.

Including Random Effects: Answering Population Level Research Questions

	Variance Point Estimate	95% CI Lower Bound	95% CI Upper Bound
Difference **between Classes**	25	12	50
Difference **between Individual**	5	4.5	5.4
Error/noise/change/difference **within each Individual**	1	1.0	1.1

If we had included **Class as a fixed effect** we can only answer the question if these 5 classes differ. It **tells us nothing about the wider population.**

But by including as a random effect we instead ask the **RQ: do all classes differ in the entire population**

And our answer is **yes, there is evidence they do.**

This is an often overlooked advantage of Random Effects.

Including Random Effects: Answering Population Level Research Questions

	Variance Point Estimate	95% CI Lower Bound	95% CI Upper Bound
Difference **between Classes**	25	12	50
Difference **between Individual**	5	4.5	5.4
Error/noise/change/difference **within each Individual**	1	1.0	1.1

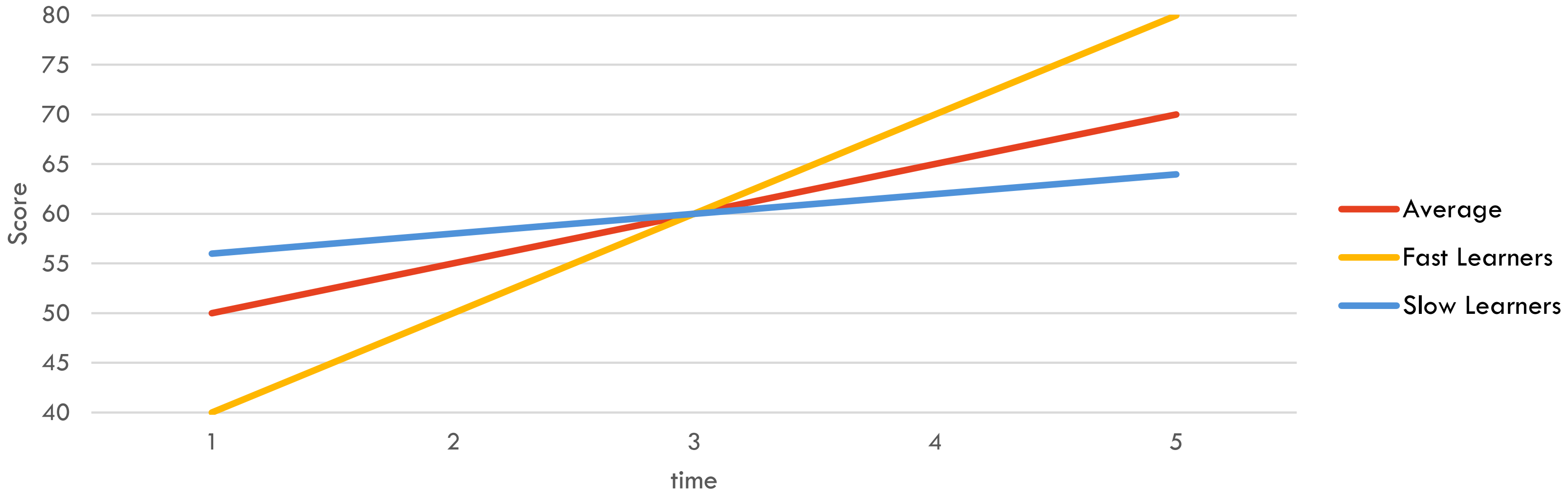
It also tells us that the variance between Classes has been poorly estimated since the CI is so wide 12-50.

So future studies that want to measure this effect more accurately should increase the number of classes.

Random Slopes

Are similar to random intercepts, except they allow the slope to differ for each individual.

Which is useful when we want to understand the overall ‘average’ trend over time, after accounting for the different learning abilities of students. Another way of putting this is that peoples learning differs not just in their error but systematically i.e. their slope differs from an underlying average slope.



Random Slopes: Answering Population Level Research Questions

Adding a Random Slope lets us test the **Population Level Question**

There is little variation from the average trend **so most students learn at similar rates.**

Vs

There is a lot of variation from the average trend **which suggests students learn at quite different rates.** And perhaps this is worthy of further study to understand why, so we can apply these learnings to all students?

References

GLMM FAQ by Ben Bolker (can't recommend this highly enough!! Just start here with any question before you even google it)
https://bbolker.github.io/mixedmodels-misc/glmmFAQ.html

1:25

Other Resources

THE UNIVERSITY OF
SYDNEY

Further Assistance at Sydney University

SIH

– **1on1 Consults** can be requested on our website:
www.sydney.edu.au/research/facilities/sydney-informatics-hub.html OR Google "Sydney Informatics Hub" with the "I'm feeling lucky" button
– **Training** Sign up to our mailing list to be notified of upcoming training: 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**
– **Linkedin Learning:** https://linkedin.com/learning/
  – **SPSS** https://www.linkedin.com/learning/machine-learning-ai-foundations-linear-regression/welcome?u=2196204

A reminder about Acknowledging SIH

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

Suggested wording:

General acknowledgement:

"The authors acknowledge the technical assistance provided by the Sydney Informatics Hub, a Core Research Facility of the University of Sydney."

Acknowledging specific staff:

“The authors acknowledge the technical assistance of (name of staff) of the Sydney Informatics Hub, a Core Research Facility of the University of Sydney.”

For further information about acknowledging the Sydney Informatics Hub, please contact us at sih.info@sydney.edu.au.

We value your feedback

✓

- We aim to help HDR students and researchers in a wide range of fields across different faculties
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- 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

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