Course introduction

Michael Noonan

December 29, 2020

Biol 520C: Statistical modelling for biological data

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Course Overview



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 $Course\ Website:\ https://noonanm.github.io/Biol520C/index.html$





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- Emphasis on statistical best practices.
- How to use open source software (R) to apply these analyses.





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- Methods for handling ad hoc, corner cases.





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- Lectures will cover the core concepts of the course. Lecture slides
 will be posted on the course website the evening prior to the lecture.
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 lectures. All lectures will be recorded and made available to you.
- The practicals use structured tutorials to guide you on the use of the open-source software program R for applying the methods learned in the lectures to data. The lectures and practicals are designed to be complementary and not all the material in the practicals will be covered in the lectures and vice versa.





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The course web page on github will host the practicals, and the various datasets associated with each practical. Lectures will be given on Mondays and Tuesdays. After the Tuesday lecture, we will have covered all of the material that is needed to complete the week's practical assignment material which is due before the start of the following Tuesday lecture (to be submitted online).



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Grading: Each practical assignment is worth a total of 3% of your total grade. Of this, 1% is given for submitting the tutorial on time, irrespective of whether or not the answers are correct (participation). The remaining 2% comes from the answers provided. Late practicals will be accepted, but will only be worth a maximum of 2%.

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- **Appendix:** The appendix material should include an R markdown document that details every step of the analyses. (30%)

Papers 1 and 2 cont.



Datasets: To complete these assignments, you will have access to a number of pre-selected datasets. You can opt to use your own data to complete these assignments if you prefer, and are encouraged to do so, but you must seek instructor approval. If you intend on using your own data, it is recommended that you discuss this with me as early as possible.

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Late Assignments: You are to submit Paper 1 by the end of the day on Feb. 27th, and paper 2 by the end of the day on Apr 17th. Late papers will have 10% deducted per day that they are overdue, and will receive a grade of zero if more than 10 days late without a valid excuse.





Prior to submitting their papers to the instructor, students will be required to give a 10-minute presentation to the class.



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Lecture outline



Week/Dates	Lecture Topics
1 - Jan 10-16	Course introduction; Regression refresher
2 - Jan 17-23	Probability theory; Likelihood; Maximum likelihood
3 - Jan 24-30	Mult. linear regression; Param inter.; Interpreting residuals
4 - Jan 31-Feb 6	Mixed effects models; Model Selection; Information criterion
5 - Feb 7-13	Model Selection; Model averaging; Independent Project Work
6 - Feb 14-20	Mid-term break, no lectures
7 - Feb 21-27	Student presentations (10%) & Term paper 1 due (25%)
8 – Feb 28-Mar 6	Heteroskedasticity; Temporal autocorrelation
9 – Mar 7-13	Spatial Autocorrelation; Phylogenetic inertia
10 - Mar 14-20	Logistic and Poisson regression
11 - Mar 21-27	Non-linear modelling; Deterministic functions;
	Stochastic simulation and power analysis
12 - Mar 28-Apr3	Course Overview; Independent Project Work
13 - Apr 4-10	No lecture on Monday; Student presentations (10%)
14 - Apr 11-17	Student presentations (10%) & Term paper 1 due (25%)

Design- vs. Model-based Inference





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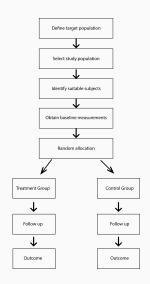


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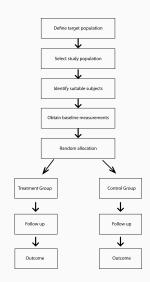
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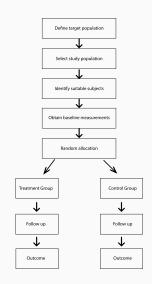


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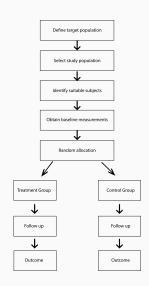


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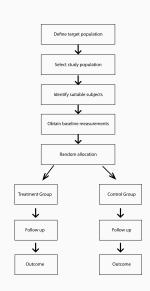


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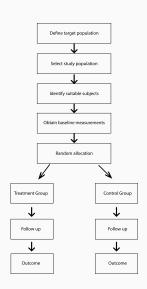


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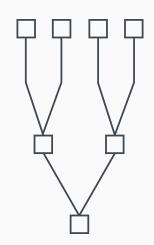


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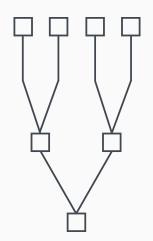
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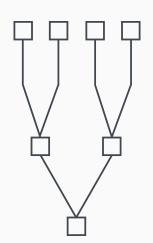
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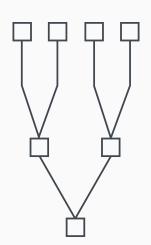
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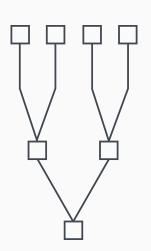
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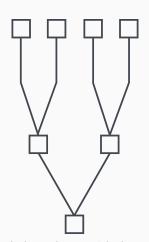
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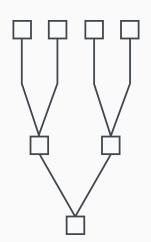
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Core of design-based inference is confronting single hypotheses with data



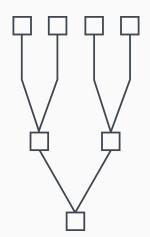
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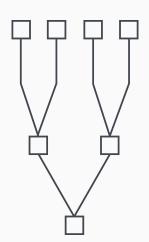
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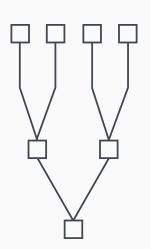
- i) Clear, distinct hypotheses
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Platt's decision tree is based on:

- i) Clear, distinct hypotheses
- ii) Unambiguous outcomes
- iii) A relationship between statistical significance and biological relevance





Many biological processes have long time-scales.







Humpback whales (*Megaptera novaeangliae*) can live for 50+ years. Source: David Valencia

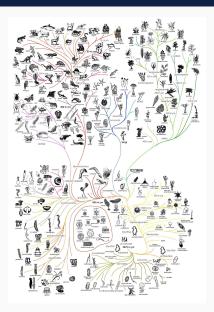




Humpback whales (Megaptera novaeangliae) can live for 50+ years. Source: David Valencia



Bristlecone pines (*Pinus longaeva*) live for thousands of years. Source: wired.com



Source: Chris King



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Many biological systems have very poor reproducibility.

Poor reproducibility



Source: Tom and Pat Leeson



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How can you design a controlled experiment in a wild population?



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Source: Wikipedia

In 1988 the wild pop. of black footed ferrets (Mustela nigripes) was down to 18 ind.



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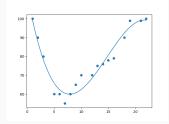


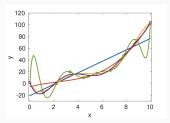
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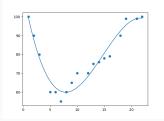
What do you do if a power analysis says you need 20 animals?

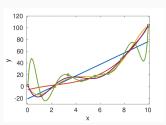






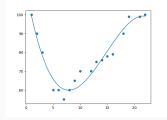
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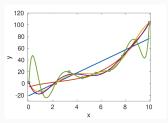






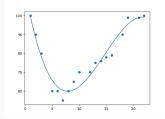
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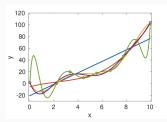






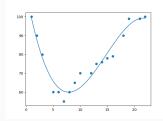
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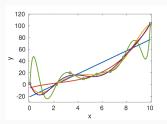






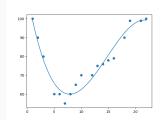
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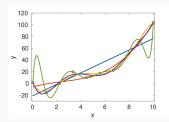






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What is modelling?





Hypothesis:



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 $Model \neq Hypothesis$





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Hypothesis: Body mass M increases with age L

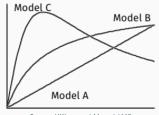


A single hypothesis can be represented by multiple models.

Hypothesis: Body mass M increases with age L

Models:

- M = aL Model A: Body mass is proportional to age
- $M = \frac{AL}{1+bL}$ Model B: Body mass saturates as age increases
- M = aLe^{-bL} Model C: Body mass increases and then decreases as age increases



Source: Hillborn and Mangel 1997





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Models help us understand which parameters and processes are important, and which ones are not.

No model is completely correct.





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Don't fall in love with a model, the important thing is the system





Complex models provide more numerical precision



Complex models provide more numerical precision, but simple models are more interpretable.



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Short answer: Let the data tell you.

Long answer: There are methods for this that we'll cover in later lectures.

Components of a model





Models are comprised of two main components:



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Deterministic part: Describes the shape of the relationship (i.e., your hypothesis).



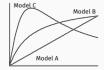
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• Model A: M = aL

• Model B: $M = \frac{AL}{1+bL}$

• Model C: $M = aLe^{-bL}$





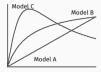
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Stochastic part: Describes the randomness of the process (i.e., captures the noise in a system).





Deterministic models



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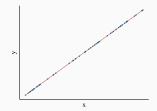




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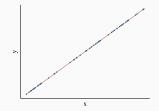
Stochastic models



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Stochastic models

 Some components are uncertain and characterised by probability distributions



• No components are uncertain

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Stochastic models

- Some components are uncertain and characterised by probability distributions
- Outcome is variable



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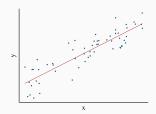
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Stochastic models

- Some components are uncertain and characterised by probability distributions
- Outcome is variable

•
$$y_i = \beta_0 + \beta_1 x_i + \varepsilon_i$$



References

Platt, J.R. (1964). Strong inference. science, 146, 347-353.