

How predictable is extinction?

Forecasting species survival at million-year timescales

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Foundational assertion of conservation paleobiology

By studying the **past**,
we can better predict the **future**.

What are we predicting?

Extinction is **hard** to predict, but is **important** to conservation decisions.

Predicting extinction

- ▶ A taxon with a **greater than average** global geographic range is likely to **survive for longer** than a taxon with **less than average** global geographic range.

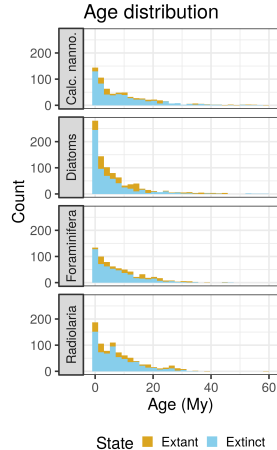
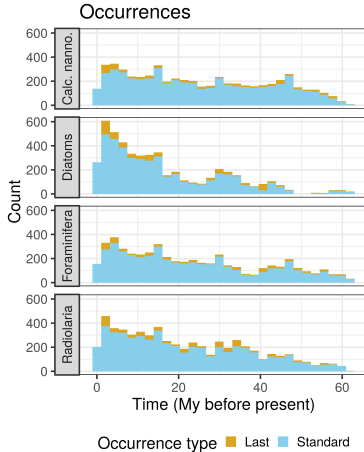
Predicting extinction

- ▶ A taxon with a **greater than average** global geographic range is likely to **survive for longer** than a taxon with **less than average** global geographic range.
- ▶ A taxon's global geographic range can change over time.

Predicting extinction

- ▶ A taxon with a **greater than average** global geographic range is likely to **survive for longer** than a taxon with **less than average** global geographic range.
- ▶ A taxon's global geographic range can change over time.
- ▶ What happens to extinction risk as a taxon changes geographic range? How is extinction risk impacted if that taxon's global geographic range has recently **increased** or **decreased**?

Data being analyzed: Neptune database



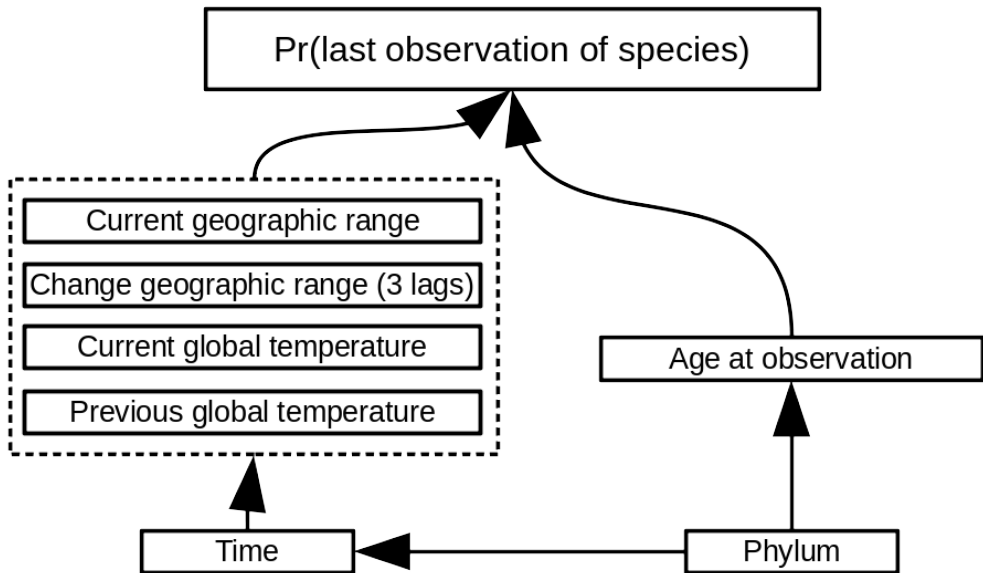
(UCL)

Global occurrences from Deep Sea Drilling Program and Ocean Drilling Project. – Lazarus. 1994. Math. Geo.; Spencer-Cervato. 1999. Palaeo. Elec.

How we're analyzing the data

- ▶ Encoding the past
 - ▶ Change in geographic range between current observation and previous observation.
 - ▶ Average global temperature at time of previous observation (Mg/Ca elemental ratio).
 - ▶ Age in millions of years at time of observation.
- ▶ Explore model adequacy using posterior predictive distribution.
- ▶ Estimate out-of-sample predictive performance using k -fold cross-validation.

A conceptual model for predicting extinction

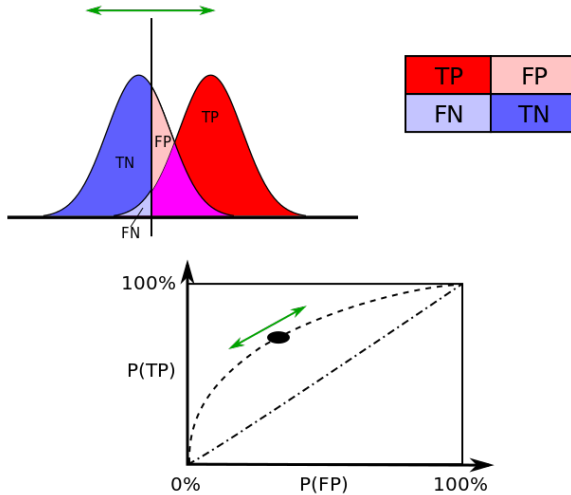


Measuring performance: confusion matrix

		True condition	
Total population		Condition positive	Condition negative
Predicted condition	Predicted condition positive	True positive, Power	False positive, Type I error
	Predicted condition negative	False negative, Type II error	True negative

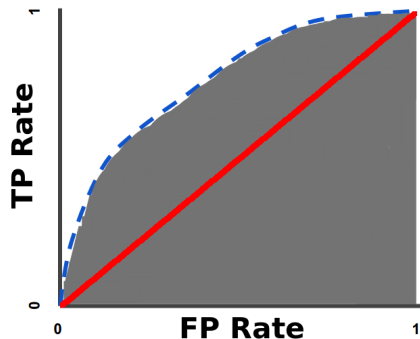
(wikimedia)

Measuring performance: Receiver Operating Characteristic



(wikimedia)

Measuring performance: AUC ROC

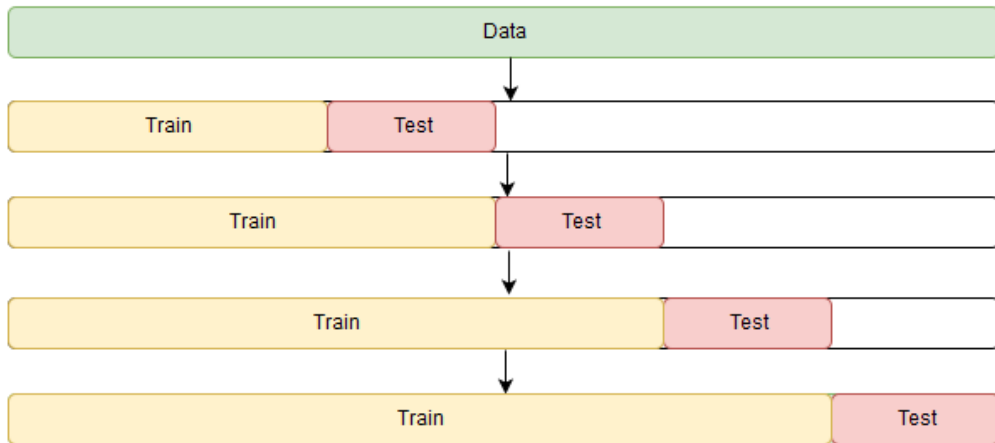


(<https://goo.gl/91nEpM>)

The area represents the probability of correct ranking of a random “extant” - “extinct” pair.

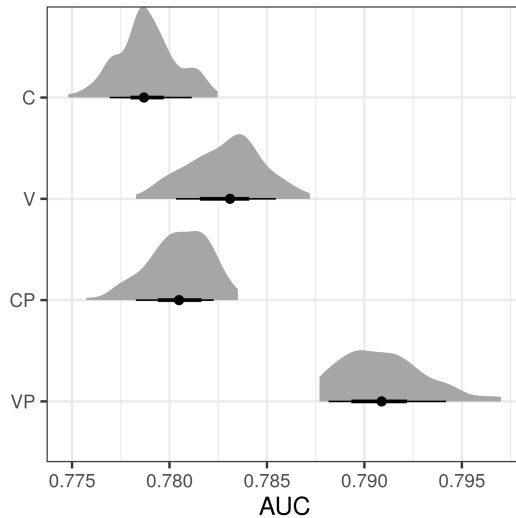
$$\text{AUC} = \begin{cases} 0.5 & \text{non discrimination} \\ 0.6 - 0.7 & \text{poor} \\ 0.7 - 0.8 & \text{acceptable/fair} \\ 0.8 - 0.9 & \text{excellent/good} \\ > 0.9 & \text{outstanding} \end{cases}$$

Measuring performance: k -fold cross-validation



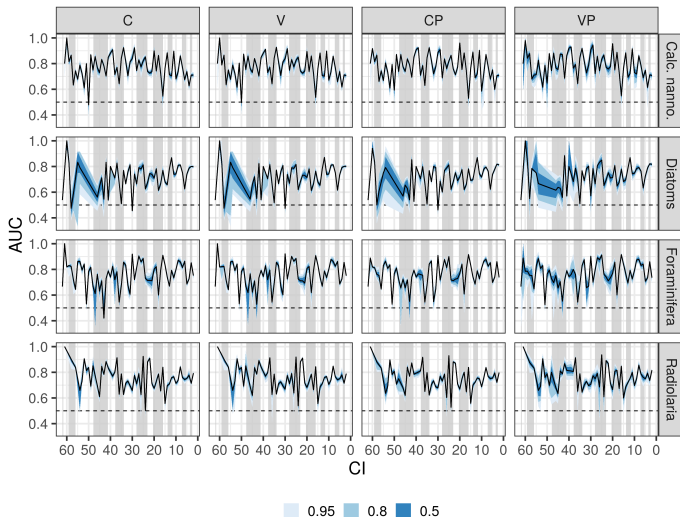
(Ken Williams, <https://goo.gl/qLcfL8>)

In-sample predictive performance, full dataset

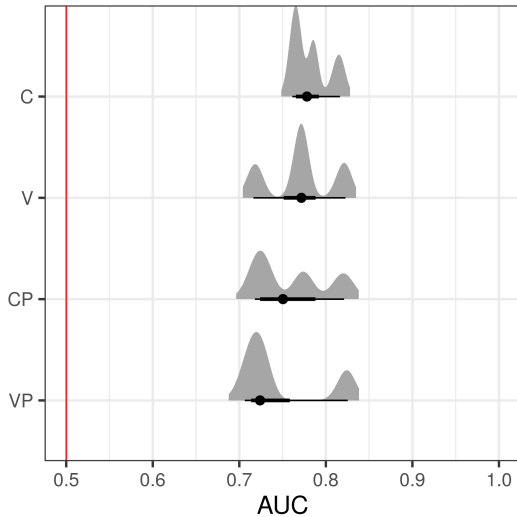


AUC = 0.7-0.8 acceptable/fair

In-sample predictive performance, by time and taxa

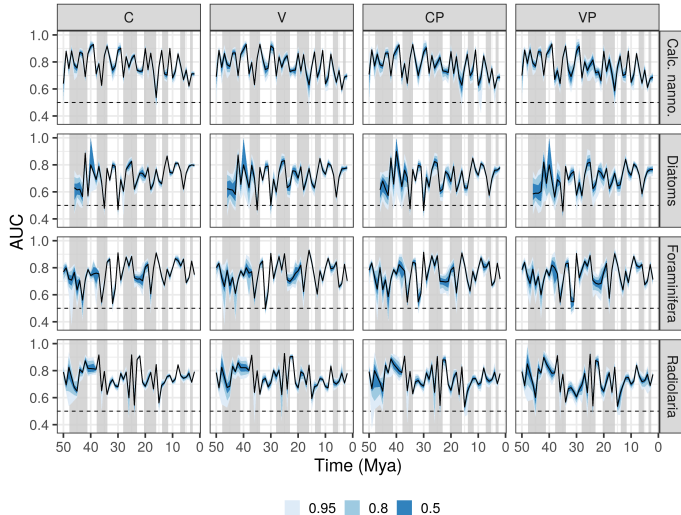


Cross-validation results, full dataset



AUC = 0.7-0.8 acceptable/fair

Cross-validation results, by time and taxa



Summary

- ▶ The past matters. . .
 - ▶ Our best supported model includes either our historical covariates or allows all effects to vary over time.
- ▶ But not that much. . .
 - ▶ Models only average/fair expected out-of-sample performance.
- ▶ Allowing effects to vary over time is probably preferable to historical covariates – measures and accounts for variation which is important when predicting extinction in novel environments.
- ▶ Mechanisms behind changes to geographic range operate at sub-million year scales. Perhaps their effects are weak/masked at million (or greater) year scales.

Activities Chromium Web Browser Thu 12:42 Analytical Paleobiology - Chromium

Analytical Paleobiology x +

https://psmits.github.io/paleo_book/index.html

Short-Course on Analytical Paleobiol...

Preface

1 Managing and Processing Data Fro...

1.1 Objectives

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1.6 Binning observations

1.7 Sharing data

1.8 Summary

2 Introduction to Bayesian data analy...

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2.5 Terms and theory

2.6 Bayes' Theorem

2.7 But how does it work?

2.8 Working with samples

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3 Introduction to linear regression

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3.4 Adding a predictor to the mix

Analytical Paleobiology

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Preface

This book is a series of tutorials on data analysis with examples drawn from paleobiology, macroevolution, and macroecology. Each chapter of this book can act as a 2-hour tutorial, with each lesson building on the previous ones.

I emphasize Bayesian data analysis approaches throughout this text. Parameter inference is done using the [brms](#) package which is a flexible tool for implementing [Stan-based](#) models in R.

This book uses the [tidyverse](#) collection of R packages with a particular emphasis on [dplyr](#), [ggplot2](#), and [purrr](#). Other [tidyverse](#) packages are used as necessary (e.g. [modelr](#)). Management and processing of posterior estimates, as well as some aspects of visualization, is done using the [tidybayes](#) package. The [pacman](#) package is used throughout to ensure that all packages are both installed and loaded into namespace. The [here](#) package is used to ensure safe file paths. I attempt to stick to the [tidyverse style guide](#) as much as possible.

A lot of material in this book is derived from material and examples presented in [Statistical Rethinking](#) by Richard McElreath, [Bayesian Data Analysis 3](#) by Gelman et al., and [Data Analysis Using Regression and Multilevel/Hierarchical Models](#) by Gelman and Hill.

Additionally, some of the code used in this book is derived from [this rewriting](#) of [Statistical Rethinking](#).

This textbook was made possible by my postdoctoral funding provided by [Seth Finnegan](#) during my

https://psmits.github.io/paleo_book/index.html

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GitHub

psmits.github.io/ **trident**



@PeterDSmits

