Analyzing paleoecological data: Best practices and current resources

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Learning Objectives

Workshop participants will learn:

- Key elements of paleoecological data
- how to use APIs (Application Programming Interface) for Neotoma and other databases
- how to use the neotoma R package to write scripts to retrieve Neotoma data directly into R for further analysis

Agenda

- ▶ 1 1:30pm: Getting started
 - Introductions
 - Getting set up for the day
- ▶ 1:30 2:00pm: Overview of paleoecological data
- ▶ 2:00 2:30pm: Neotoma web explorer
- 2:30 300pm: Intro to API and JSON queries
- ▶ 3:00 4:00pm: R Neotoma

Getting started

Resources

- Following along today
 - Intro/Background slides can be viewed through this link: https://speakerdeck.com/jessicablois/ analyzing-paleo-data-intro-slides
 - The primary workshop document can be viewed through this link: https://cdn.rawgit.com/NeotomaDB/Workshops/ master/SVP2016/R/Workshop_SVP2016_v0.1.html # Need to update!!
- All slides and materials are on GitHub
 - ► The Neotoma Paleoecology Database https://github.com/NeotomaDB
 - ► The Workshops section https://github.com/NeotomaDB/ Workshops/tree/master/SVP2016

Getting started

Installations

- Download and install R (available at https://cran.r-project.org/)
- Download and install RStudio Desktop (https: //www.rstudio.com/products/rstudio/download3/)
- 3. Install the following R packages: RJSONIO, RCurl, neotoma
 - Open up R Studio, then type: install.packages('RJSONIO', 'RCurl')
 - Install the neotoma package:

```
install.packages('devtools')
devtools::install_github("ropensci/neotoma")
```

Paleoecological data and the Neotoma Paleoecology Database

We will discuss different types of paleo data in the context of Neotoma www.neotomadb.org, a database that houses different data from the more recent periods of Earth history

What is Neotoma?

- ▶ Neotoma is a database consortium: www.neotomadb.org
- Organized around proxy types
 - historically, brought together several major databases or datasets (i.e. FAUNMAP, COHMAP)
 - moving towards direct entry of individual data files
- ► The different databases use a common, extendable platform to ensure compatibility across proxy types
- Each proxy community can develop own standards, e.g. for taxonomy

The Neotoma ecosystem

- Faunal data
 - FAUNMAP, FAUNMAP2 (in progress)
 - MIOMAP (with Tony Barnosky)
 - ► ANTIGUA (South America megafaunal dates, in progress, with Tony Barnoksy and Emily Lindsey)
 - MQMD (Mexico, in progress, with Joaquin Arroyo Cabrales)
- Pollen and plant macros
- Packrat midden database
- Ostracodes, Diatoms
- Isotopes (coming online soon)
- ▶ Use neotoma::get_table("datasettype") to see all 25 available types

Scope and strengths of Neotoma

- Pliocene to present, global
- Chronology tools and storage
- Multiproxy
- Active development community
- Curated database -> high quality data

Curated database

- Each proxy group has a set of data stewards, led by one or a few lead stewards
- ► Anyone can deposit data into Neotoma
- ▶ Before going 'live', data need to be validated by a data steward

Key elements of paleoecological data

- Fundamental message: need to know the taphonomy of your study system in order to accurately infer biogeographic patterns across space and time
 - Occurrence records and taxonomy
 - Orienting occurrences in space
 - Orienting occurrences in time
- Some key references
 - Behrensmeyer AK, Kidwell S, Gastaldo R. 2000. Taphonomy and paleobiology. Paleobiology. 26(sp4):103–47
 - ▶ Jackson ST. 2012. Representation of flora and vegetation in Quaternary fossil assemblages: known and unknown knowns and unknowns. Quaternary Science Reviews. 49:1–16

Occurrence records and taxonomy

- Each occurrence is associated with a taxonomic identification
- Paleo data are often, though not always, less precise taxonomically than present-day data
- Different proxy types are recorded in different ways
 - Vertebrate data: MNI/NISP/Presence
 - ▶ Pollen data: originally counts per total pollen count, usually converted to relative abundance

Spatial precision

- lat-long coordinates, similar to present-day data
- ▶ Different proxy types, different taxa, and different depositional environments record different levels of spatial precision
 - ▶ Plant macrofossils vs pollen
 - Cave deposits vs fluvial deposits

Example: Fossil pollen from lake sediments

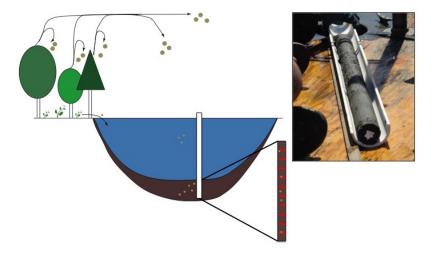


Figure 1:

Temporal precision

- Every occurrence is associated with an inference about the time the organism died
- ► There are different dating methods, each with their own assumptions and associated strengths and weaknesses
- ► Different proxy types and depositional environments will be associated with different amounts of time-averaging

Dataflow

Getting data out of Neotoma

- Focus of this workshop!
 - Neotoma Explorer
 - API
 - R
 - Database snapshots (housed at www.neotomadb.org/snapshots)

Key caveats*

- Errors or omissions in the data
- Updates to the data may not be stored in the database
 - new dates, changes in taxonomy, etc.
- "Garbage in, garbage out"
 - Many of the original databases like FAUNMAP and COHMAP convened a group of experts to assess various aspects of data quality. We need to keep applying that same lens to new datasets
 - Data without associated metadata can only go so far
 - Note: What is considered "good metadata" changes through time!
- When in doubt, record and store as much information as possible.



^{*}for Neotoma and all other databases!

Major activities

- Adding new data (MIOMAP, ANTIGUA, MQMD)
- ► Integration with other databases: PBDB/Neotoma cross-database searches
- DOIs: assign datasets individual DOIs (will satisfy NSF data access guidelines)
- Embargos: tools for embargoing data.
 - will allow users to enter and validate data, get a DOI for paper submission, then data go 'live' when the paper is published
- Governance and Sustainability
 - Recently formed a leadership structure
 - Formalized bylaws and policy
- Education and outreach
 - ▶ Partnerships with SERC, Flyover Country, etc.



Questions and Discussion

- ► Thoughts, questions??
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