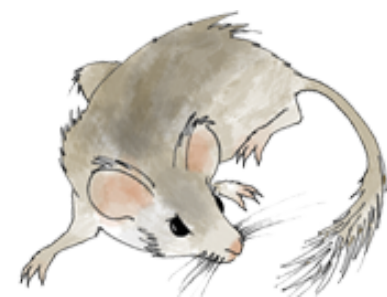


Neotoma2 R

EPD Workshop

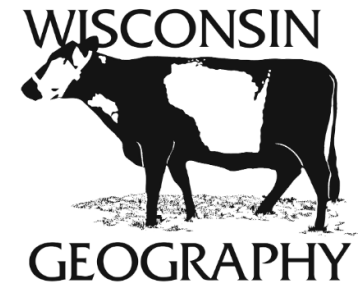
June 2nd, 2022

Prague, Czechia



The Team!

- Simon Goring University of Wisconsin - Madison
- Socorro Dominguez University of Wisconsin - Madison
- Steve Crawford Penn State University
- Jonathan Nichols Penn State University



R in your Browser:

<https://bit.ly/3FW0Qrh>

Introduce yourselves in the following link:

<https://docs.google.com/presentation/d/1j3SXPLE7O29lgK9nsx6HO76oaLFRI5THD9xY0j2kQrusp/sharing>

The Database

The Neotoma Database contains all the data

- Schema: <https://open.neotomadb.org/dbschema>
- Manual: <https://open.neotomadb.org/manual>



Created by Lance Weisser
from Noun Project

But we want to use it ourselves!

How Do We Get Data?



Created by Dan Hetteix
from Noun Project



Created by Candy Design



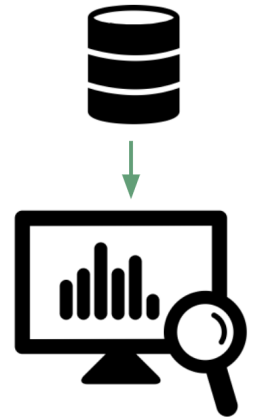
Created by Lance Weisser
from Noun Project

How Do We Get Data (*DB Snapshot*)

- Database snapshot: <https://neotomadb.org/snapshots>
- Using PostgreSQL RMDBS
 - Restore the Snapshot
 - Connect to the Database (pgAdmin, dBeaver, others)

or

- R/Python with the DB directly (RPostgreSQL, psycopg2)



Created by Dan Hetteix
from Noun Project

How Do We Get Data (*API*)

Using the Application Program Interface (API)

<https://api.neotomadb.org>

Structured (JSON) data, using URLs as “commands” for data:

<https://api.neotomadb.org/v2.0/data/datasets/17473>

Dataset information for Lake Allie, a Diatom Surface Sample

Where is the API used?

- Tilia uses the [Tilia API](#) for data input & output.
- Explorer uses the [Neotoma API](#) for data input.
- The Landing Pages use the [Neotoma API](#) for page information.
- The Neotoma “State of the Database” pages use the API (and SQL).



Created by Dan Hetteix
from Noun Project



Created by Candy Design



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from Noun Project

How Do We Get Data (*R Package*)

Neotoma through the R package `neotoma2`

- Pre-defined functions to access & manipulate data
- Connect with other existing R packages

To try `neotoma2` from Binder: <https://bit.ly/3FW0Qrh>

To install, you need the `devtools` package as well.

```
install.packages('devtools')  
devtools::install_github('NeotomaDB/neotoma2')
```



Created by Candy Design



Sites

<https://open.neotomadb.org/dbschema/tables/sites.html>

—



Collection Units

<https://open.neotomadb.org/dbschema/tables/collectionunits.html>

—



Datasets

<https://open.neotomadb.org/dbschema/tables/datasets.html>

—



S4 Object Structure

