Finding Field Station Data for Research Use

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Searching programmatically...

...by using the iDigBio search API
What is an API?

Application Programming Interface

An organization has a system that external users can interact with.
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What is an API useful for?

An API facilitates programmatic data access, which enables...

→ Automating data retrieval
→ Documenting procedures within your code
→ Running analyses in a way that is reproducible
→ Bringing data from different sources together, e.g. via:
  ◆ multiple APIs
  ◆ multiple downloaded datasets
  ◆ your own data
  ◆ any combination of the above

And, you can bring your own programming language!
For example...

Retrieve the data ➔ Clean the data ➔ Bring in more data ➔ Do the analysis ➔ Visualize the analysis

See a full example at https://github.com/mgaynor1/CURE-FL-Plants
What is an endpoint?

An endpoint is an address, often a URL, where you can find a particular API

https://maps.googleapis.com/maps/api/directions/
Let me ask Google Maps for directions

https://maps.googleapis.com/maps/api/geocode/
Let me ask Google Maps to find a place on a map

https://search.idigbio.org/v2/search/
Let me ask iDigBio to look for certain specimen records

https://search.idigbio.org/v2/download/
Let me ask iDigBio to download certain specimen records
How do I talk to an API?

You talk to an API by making a request, either through a user interface or programmatically, e.g. via R or Python.

Please search for these terms and return the results

Please count how many results match my query

Please download this file
What does a request look like?

You can talk to an API by making a request, often including parameters, to an endpoint.

```
https://search.idigbio.org/v2/search/records?rq={"genus": "acer"}
```
What does a request look like?

You can talk to an API by making a request, often including parameters, to an endpoint.
What is an API useful for?

An API facilitates programmatic data access, e.g. using the iDigBio API in R

```
# Load package to access iDigBio API
library(ridigbio)

# Retrieve records for specimens identified as being in the genus Acer and
# collected in Utah
data <- idig_search_records(rq = list(genus = "acer",
                                     stateprovince = "utah"),
                             fields = c("uuid",
                                         "institutioncode",
                                         "collectioncode",
                                         "catalognumber",
                                         "stateprovince",
                                         "county",
                                         "locality",
                                         "geopoint"),
                             limit = 1000)

# Begin data cleaning and analysis...
```
Resources to learn more

iDigBio office hours: an informal drop-in session where anyone is welcome to bring their questions or ideas about using tools such as the iDigBio API to work with biodiversity occurrence data.

Every 2nd and 4th Wednesday of the month at 3:30pm Eastern, next is October 14th

- Focus on using the R language
- Often will do code demos but experience is not required or expected
Thank you!

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