A Simple Model Workflow

```
# Run this cell if you want to follow along
options(warn = -1)
suppressMessages(library(neotoma2))
suppressMessages(library(sf))
suppressMessages(library(geojsonsf))
suppressMessages(library(dplyr))
suppressMessages(library(ggplot2))
suppressMessages(library(leaflet))
```

Goals

- 1. Geographic search for sites
- 2. Collect datasets
- 3. Filter for time/space/etc.
- 4. Get full download
- 5. Analyze & plot

Search for Sites

```
get_sites()
```

- Site names: sitename='Lait%'
- Location: loc=c()
- Altitude: altmin, altmax

```
In [ ]:
    laitSites <- neotoma2::get_sites(sitename = "%Lait%")
    laitSites</pre>
```

```
In [ ]:
    laitSites <- neotoma2::get_sites(sitename = "%Lait%")
In [ ]:
    neotoma2::plotLeaflet(laitSites)</pre>
```

Location loc=c()

Location loc=c()

```
In [ ]:
```

```
In [ ]:
```

```
czBbox = c(12.4, 48.64, 18.91, 50.99)
cz_sites <- neotoma2::get_sites(loc = czBbox)
neotoma2::plotLeaflet(cz_sites)</pre>
```

summary()

```
In [ ] :
    neotoma2::summary(cz_sites) %>%
    DT::datatable(data = ., rownames = FALSE)
```

Search for Datasets

```
get_datasets()
```

- Datasettype: datasettype='Diatom surface sample'
- Location: loc=c()
- Altitude: altmin, altmax

```
In [ ]:

cz_datasets <- neotoma2::get_datasets(cz_sites, all_data = TRUE, verbose = FALSE)

datasets(cz_datasets) %>%
    as.data.frame() %>%
    DT::datatable(data = .)
```

filter()

filter()

```
In [ ]:
    cz_pollen <- cz_datasets %>%
        neotoma2::filter(datasettype == "pollen")
    neotoma2::summary(cz_pollen) %>% DT::datatable(data = .)
```

Remember that the order in which packages are loaded makes a difference.

```
Error in UseMethod("filter"):

no applicable method for 'filter' applied to an object of class "sites"
```

The previous error message means that a different package is trying to run filter()

Pulling the Data

get_downloads()

• Done after the preliminary filtering

```
In [ ]:
```

```
## This line is commented out because we've already run it for you.
## cz_dl <- cz_pollen %>% get_downloads(all_data = TRUE)
cz_dl <- readRDS('data/czDownload.RDS')</pre>
```

```
In [ ]:
    ## This line is commented out because we've already run it for you.
    ## cz_dl <- cz_pollen %>% get_downloads(all_data = TRUE)
    cz_dl <- readRDS('data/czDownload.RDS')

In [ ]:
    allSamp <- samples(cz_dl)
    head(allSamp, n = 2)</pre>
```

taxa()

```
In [ ]:
    neotomatx <- neotoma2::taxa(cz_dl) %>%
    unique()

DT::datatable(data = head(neotomatx, n = 10), rownames = FALSE)
```