Taking the Pulse of Natural History Collections During COVID-19 Series: Where are we now?

September 16: Collections' perspectives

John Bates, The Field Museum

Emily Braker, University of Colorado Boulder

Brian Atkinson, The University of Kansas

Mare Nazaire, California Botanic Garden

iDigBio is funded by grants from the National Science Foundation's Advancing Digitization of Biodiversity Collections Program [DBI-1115210 (2011-2018) and DBI-1547229 (2016-2021)]. Any opinions, findings, and conclusions or recommendations expressed in this material are those of the author(s) and do not necessarily reflect the views of the National Science Foundation. © 2011-2019 iDigBio

The Field Museum in the time of Covid-19

The New Museum “Normal”

- Decreased attendance
- Budget shortfalls
- Staff reductions
- Salary reductions
- Frozen searches

- Little collections access
- Reduced lab access
- No fieldwork
- Working from home
- Zoom fatigue
- Reopening strategies

The Field Museum: 126 years of Biodiversity collections and research


The scientists are now taking questions
PRITZKER LABORATORY FOR MOLECULAR SYSTEMATICS AND EVOLUTION
EXIT
2 EXTRACT
STEP 3 AMPLIFY


NITR NITROGEN
1830HE-190


BUFFALO

Expertise

The “New” Museum

- Working from home (the upside)
- Honest discussions of I.D.E.A.
- Virtual Meetings (global access)
- Virtual Educational Activities (broader local and regional access)
- Virtual interactions with donors (no need to drive to the museum)
- Realizing the benefits of digitization

Issues of societal concern.

Closed for the pandemic, the Field Museum of Natural History hosted a socially-distanced blood drive in its empty, cavernous halls. SCOTT OLSON/GETTY IMAGES

Shuttered natural history museums fight for survival amid COVID-19 'heartbreak'

By Elizabeth Pennisi | May 28, 2020 , 8:55 PM

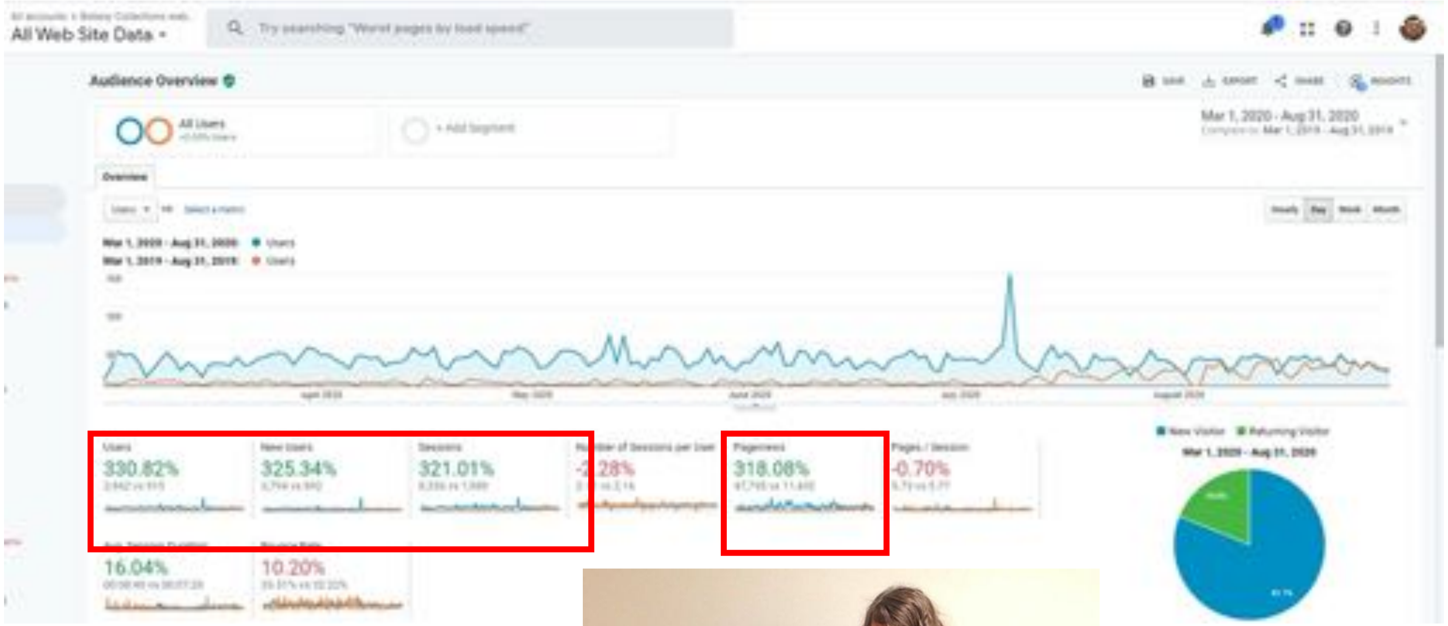
Inclusion, Diversity, Equity, and Accessibility: So much to do

¿Cómo pueden surgir especies por cambios en el comportamiento migratorio?

Valentina Gómez-Bahamón


Zoom Meeting
Speaker View
Ellen Woodward
John Bates
Lesley de Souza
petra sierwald
Nigel & Lesley
Amy Rosenthal
Michael Goulding
Ken Kaye
Mark Bouman
Diana "Tita" Alvira
Doug Stotz, Field Museum (he...
Unmute
Stop Video
Participants 11
Chat
Share Screen
Record
Reactions
Leave

Field Museum Botany: Increased access of the web site



All Web Site Data

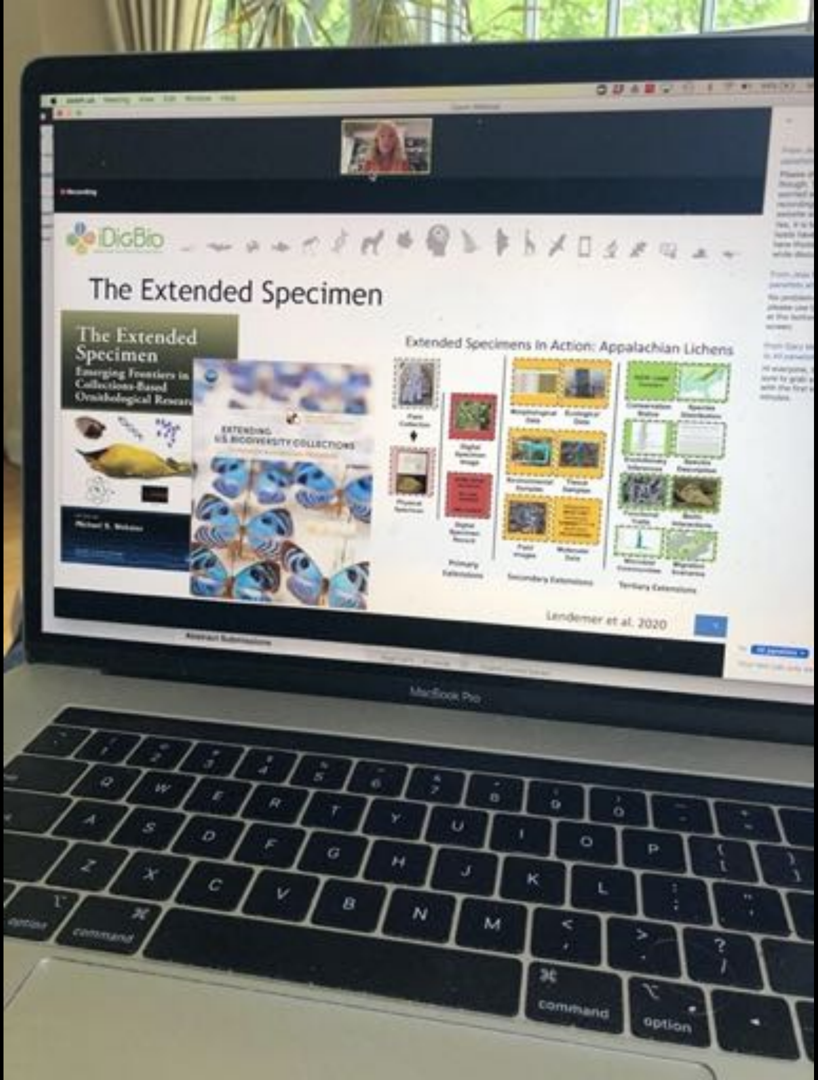
Audience Overview

All Users

Mar 1, 2020 - Aug 31, 2020

Users	New Users	Sessions	Number of Sessions per User	Pageviews	Pages / Session
330.82%	325.34%	321.01%	-2.28%	318.08%	-0.70%

Avg. Session Duration	Bounce Rate
16.04%	10.20%

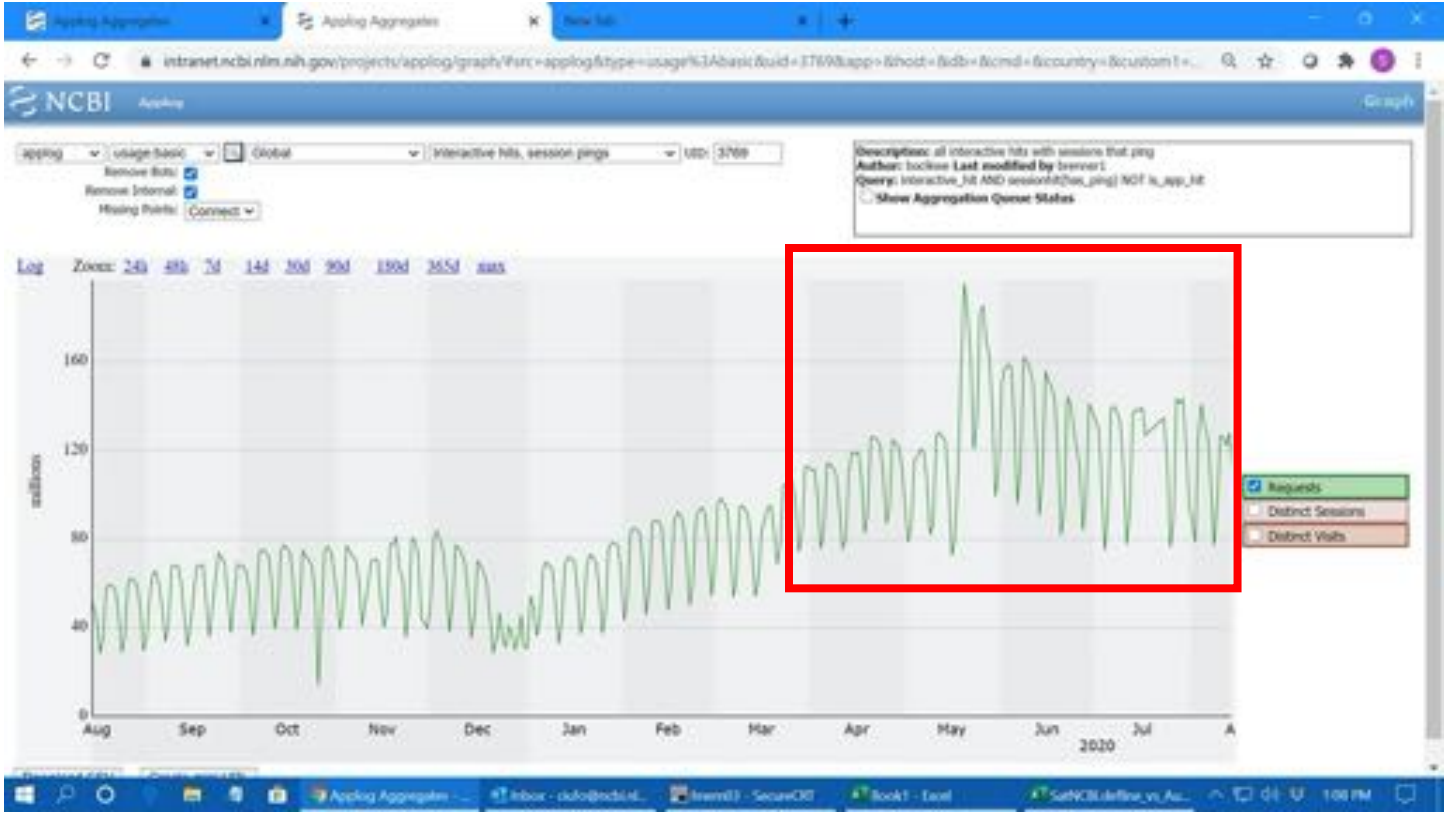


iDigBio
The Extended Specimen
The Extended Specimen
Emerging Frontiers in Collections-Based Ornithological Resear
Michael S. Webster
EXTENDING U.S. BIODIVERSITY COLLECTIONS
Extended Specimens in Action: Appalachian Lichens
Primary Extensions
Secondary Extensions
Tertiary Extensions
Lendemer et al. 2020
MacBook Pro

The Extended specimen: Genotype

Long-term archival of genetic resources available at multiple facilities (thousands/millions of specimens) for scientific research

GenBank sequence downloads for the last 12 months



applog usage basic Global Interactive hits, session pings UID: 3769

Remove Bots: ☑

Remove Internal: ☑

Missing Points: Connect

Description: all interactive hits with sessions that ping

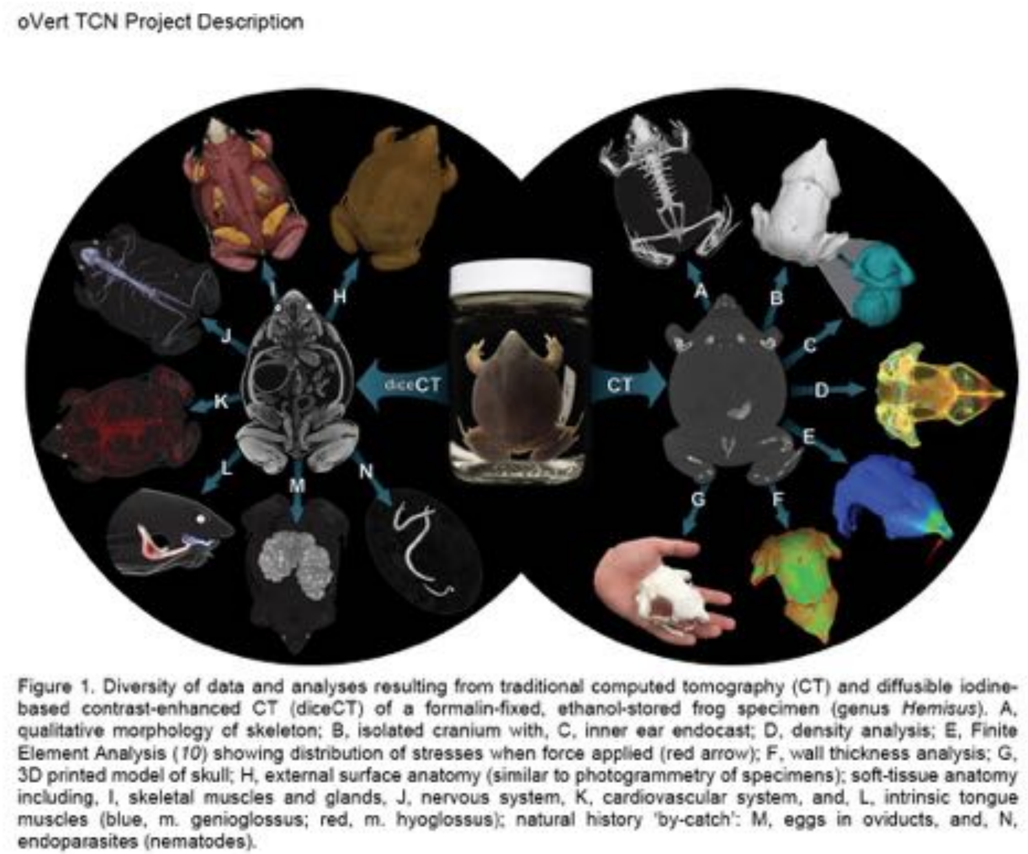
Author: [illegible] **Last modified by** [illegible]

Query: interactive_hit AND sessionhit(has_ping) NOT is_app_hit

☐ **Show Aggregation Queue Status**

The extended specimen realized: phenotype

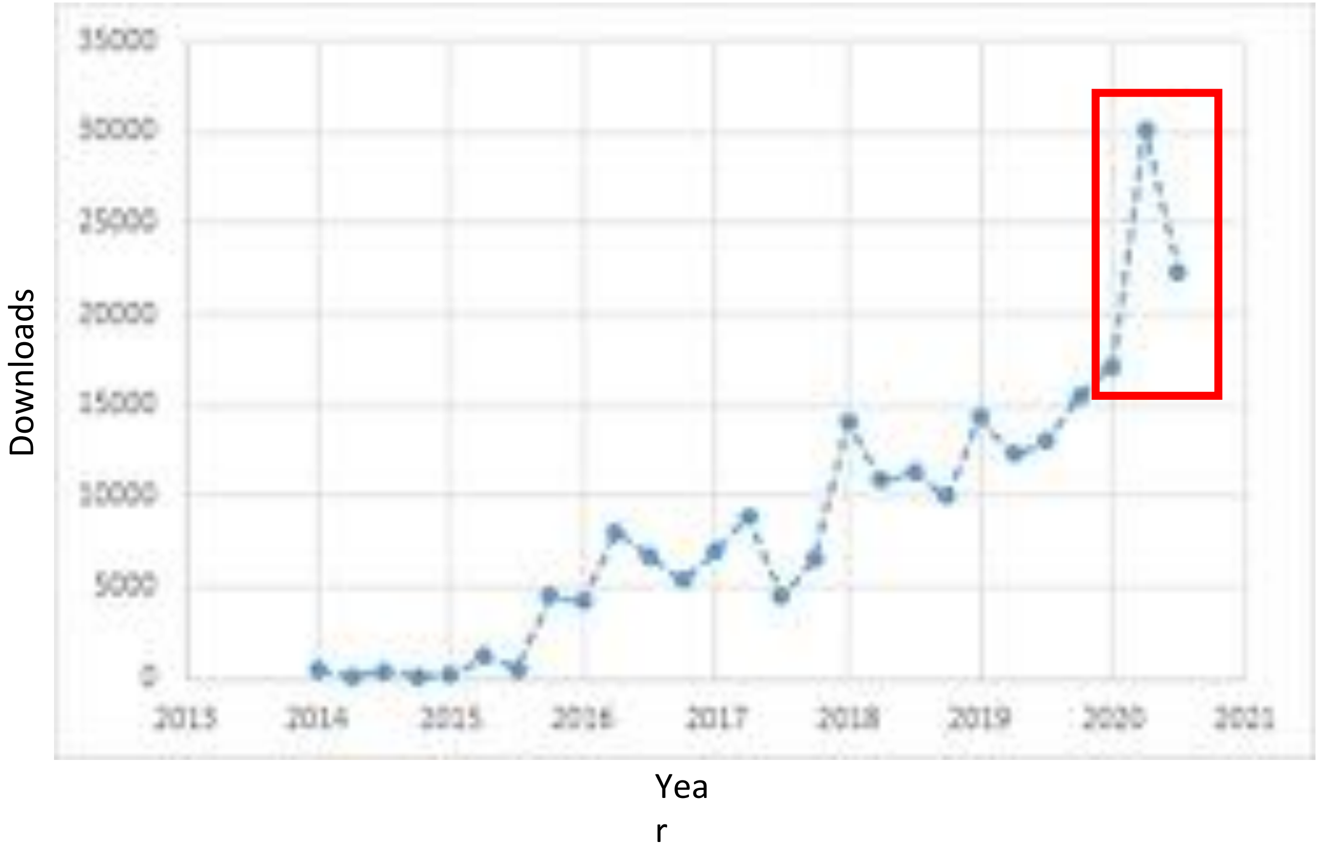
NSF supported CT-scanning of vertebrates



oVert TCN Project Description

Figure 1. Diversity of data and analyses resulting from traditional computed tomography (CT) and diffusible iodine-based contrast-enhanced CT (diceCT) of a formalin-fixed, ethanol-stored frog specimen (genus *Hemisus*). A, qualitative morphology of skeleton; B, isolated cranium with, C, inner ear endocast; D, density analysis; E, Finite Element Analysis (*10*) showing distribution of stresses when force applied (red arrow); F, wall thickness analysis; G, 3D printed model of skull; H, external surface anatomy (similar to photogrammetry of specimens); soft-tissue anatomy including, I, skeletal muscles and glands, J, nervous system, K, cardiovascular system, and, L, intrinsic tongue muscles (blue, m. genioglossus; red, m. hyoglossus); natural history 'by-catch': M, eggs in oviducts, and, N, endoparasites (nematodes).

Quarterly downloads of Morphosource 3-D specimen data



Our “New” Museum

- Working from home if you can
- Virtual Meetings (global access)
- Virtual Educational Activities
  (broader local and regional access)
- Virtual interactions with donors
  (no need to drive to the museum)
- Continued digitization
- Beyond discussions of I.D.E.A.

NSC ALLIANCE

BIODIVERSITY
COLLECTIONS NETWORK

FIELD MUSEUM

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Museum of Natural History
UNIVERSITY OF COLORADO **BOULDER**

COVID Operations and Interim Outcomes

VERTEBRATE COLLECTIONS

University of Colorado Museum of Natural History

Museum of Natural History
UNIVERSITY OF COLORADO **BOULDER**

- Boulder, Colorado
- Student population ~35,000
- 5 million natural history specimens
  - Anthropology
  - Botany
  - Diatoms
  - Entomology
  - Paleontology
  - Zoology
- 50,000 visitors annually. Audiences:
  - K-12
  - University students
  - General public
- Museum and Field Studies (MFS) Graduate Program

University of Colorado **Boulder**

PROTECT OUR HERD

Current campus operating mode = **EXPANDED**

- Limited in-person research and teaching
- Online course offerings
- Remote work for noncritical staff
- Infrastructure mitigation - HVAC improvements
- Formal 'return to campus' request process
- Daily online health assessment
- Limited COVID testing (dorms, waste streams)

Mandatory mask wearing, social distancing, enhanced custodial and sanitation practices

HAVE YOU COMPLETED YOUR DAILY HEALTH FORM?

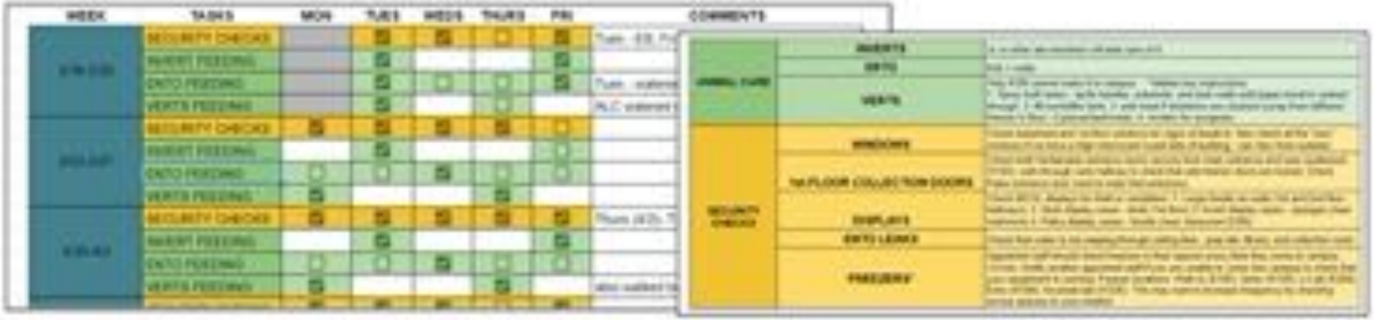
colorado.edu/daily-health-form

Collections Operations (March – August 2020)

- **Museum closure**
- **Remote work**
- **Tiered furloughs, anticipated budget cuts**
- **Critical In-House Functions (collections):**
    - Building security
    - Collections checks
    - Caring for live organisms

Museum Collections (MCOL) Building

Dermestid tank



Preparation for Return to Campus

- Campus COVID Task Force coordination
- PPE and cleaning supply distribution
- Directional & safety signage
- Building security – after-hours campus police sweeps due to extended class schedule (7am-10pm)

Vertebrate Collections – Current Operations

- Hybrid mode: In-house and remote tasks
- Hiatus on visiting researchers and volunteers
- Reduced occupancy: 1 person per room
- Increased sanitation practices

Positive Outcomes

I. Priority Reshuffling: *Rise of the backburners*

- **Collections Policy revision**

- **Data improvement projects**
  - Georeferencing
  - Taxonomy updates
  - Data Linkages:
    - Citations
    - GenBank sequences
    - Exchanged materials
  - Media Linkages:
    - Ledger pages
    - Field notes

27 ledgers and 40+ field notebooks scanned

UCM:Mamm:8166

Marmota flaviventris luteola

On Smith Trail, near Coon Creek, 2 miles W of Creste

North America, United States, Colorado, Gunnison County

11 July 1902 (1902-07-11)

Identified by Edward R. Warren on 1902

Nature of ID: features

Confidence: high

Remarks: Former nature_of_id: type specimen

collector

Edward R. Warren

collector number: ERW 35

USNM: National Museum of Natural History, Smithsonian Institution

Citations

voucher of Marmota flaviventris luteola in Warren 1906

holotype of Marmota flaviventris luteola, page 16 in Howell 1914

Links

GBIF Occurrence

II. Increased Collaboration

- Collections Managers
    - Sharing strategies
    - Continuity of Operations Planning (COOP)
    - Collaborative student training

- Institutional
    - Virtual Exhibits
    - MFS virtual tours and panel discussion
    - Museum Unlocked podcast
    - Gallery space for in-person classes

Museum gallery Mammalogy Lab – gloves required, traffic guides on floor, socially distanced lab stations

III. Opportunistic Continuity Tools

- Video Tutorials
  - Zoom recordings
  - Annotated specimen prep videos
- COOP – Hotspot Maps
- Remote Work – possible, even for collections people!

Hotspot Map

Lessons & Tips

- Consider collaborative training opportunities
- Video conferencing
    - Regular check-ins with remote staff
    - Record - Good for current and future technicians
    - Even when in person, database training is easier over Zoom (for social distancing)
- Scan archives! University collections may be able to partner with libraries
- Invest in laptops for staff when possible
- **Adaptability**

iDigBio
Integrated Digitized Biocollections

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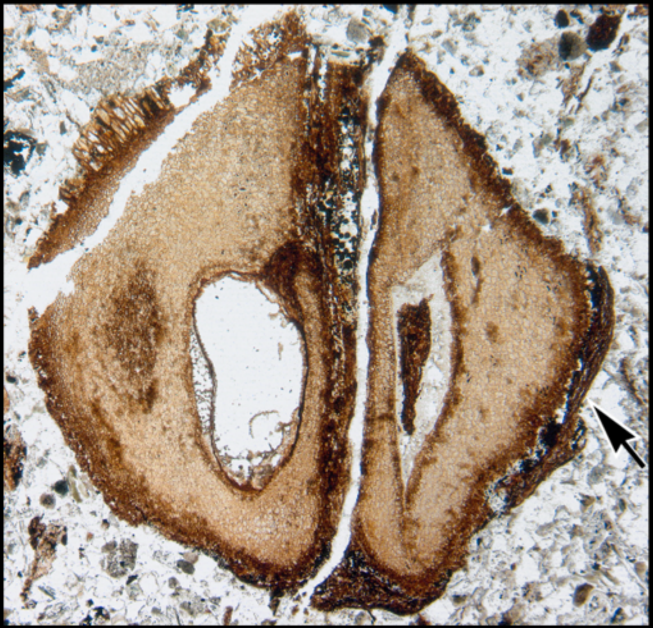
COVID-related operations from the perspective of a faculty curator teaching classes with a virtual lab

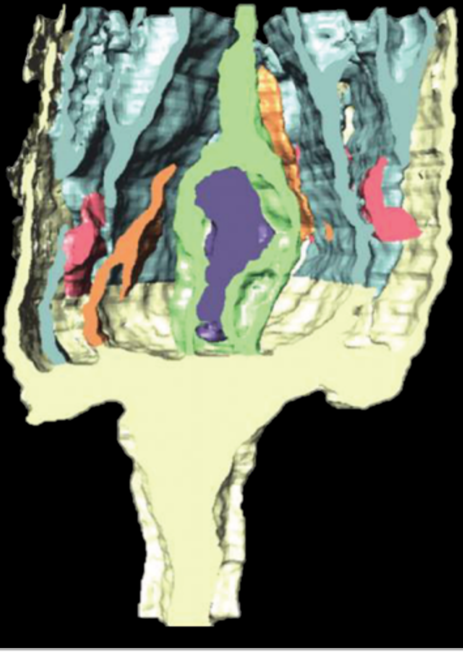
Brian Atkinson
Asst. Professor, Ecology and Evolutionary Biology Department

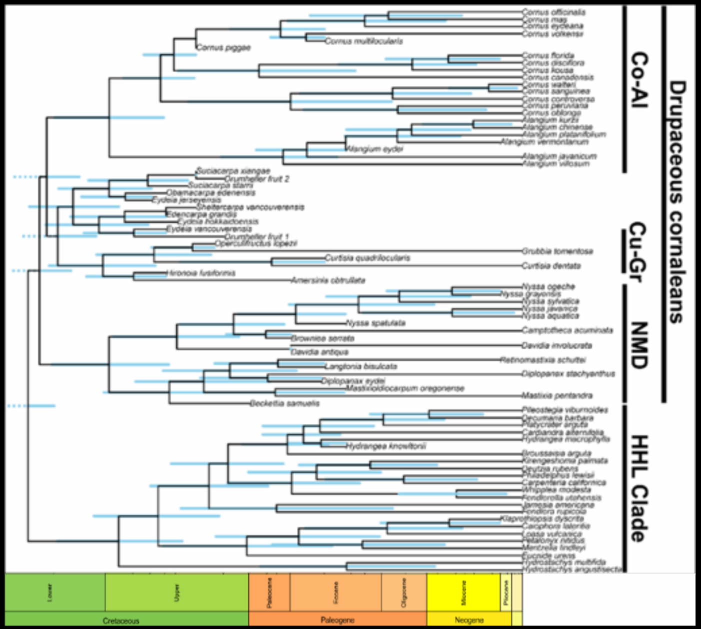
Curator, Division of Paleobotany, Biodiversity Institute
University of Kansas
Email: brian.atkinson@ku.edu

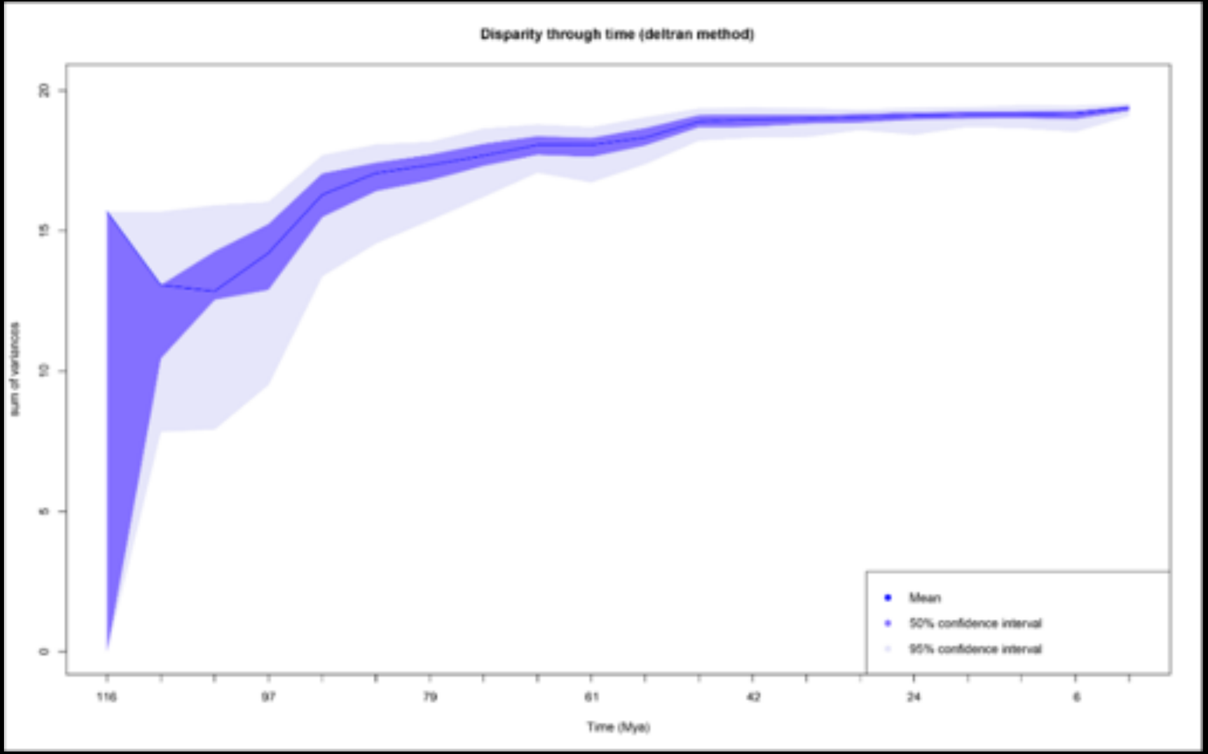
Break down of this report:

a. Introductions: myself, KU Paleobotany personnel, research, and collections
b. Status of KU Paleobotany before and during covid
c. Teaching a lab based course in a virtual format
d. Outlook






Cornus officinalis
Cornus mas
Cornus eyceana
Cornus volkensii
Cornus multilocularis
Cornus piggae
Cornus florida
Cornus disciflora
Cornus kousa
Cornus canadensis
Cornus walteri
Cornus sanguinea
Cornus controversa
Cornus peruviana
Cornus oblonga
Alangium kurzii
Alangium chinense
Alangium platanifolium
Alangium vermontanum
Alangium eydei
Alangium javanicum
Alangium villosum
Suciacarpa xiangae
Drumheller fruit 2
Suciacarpa starrii
Obamacarpa edenensis
Eydeia jerseyensis
Shelltercarpa vancouverensis
Edencarpa grandis
Eydeia hokkaidoensis
Eydeia vancouverensis
Drumheller fruit 1
Operculifructus lopezii
Grubbia tomentosa
Curtisia quadrilocularis
Curtisia dentata
Hironoia fusiformis
Amersinia obtrullata
Nyssa ogeche
Nyssa grayensis
Nyssa sylvatica
Nyssa javanica
Nyssa aquatica
Nyssa spatulata
Camptotheca acuminata
Browniea serrata
Davidia involucrata
Davidia antiqua
Retinomastixia schultei
Langtonia bisulcata
Diplopanax stachyanthus
Diplopanax eydei
Mastixioidiocarpum oregonense
Mastixia pentandra
Beckettia samuelis
Pileostegia viburnoides
Decumaria barbara
Platycrater arguta
Cardiandra alternifolia
Hydrangea macrophylla
Hydrangea knowltonii
Broussaisia arguta
Kirengeshoma palmata
Deutzia rubens
Philadelphus lewisii
Carpenteria californica
Whipplea modesta
Fendlerella utahensis
Jamesia americana
Fendlera rupicola
Klaprothiopsis dyscrita
Caiophora lateritia
Loasa vulcanica
Petalonyx nitidus
Mentzelia lindleyi
Eucnide urens
Hydrostachys multifida
Hydrostachys angustisecta
Co-Al
Cu-Gr
NMD
HHL Clade
Drupaceous cornaleans
Lower
Upper
Paleocene
Eocene
Oligocene
Miocene
Pliocene
Cretaceous
Paleogene
Neogene


Disparity through time (deltran method)
sum of variances
0
5
10
15
20
116
97
79
61
42
24
6
Time (Mya)
Mean
50% confidence interval
95% confidence interval

Active field program along the western coast of North America and Antarctica


Kelly Matsunaga
Asst. Professor &
Curator

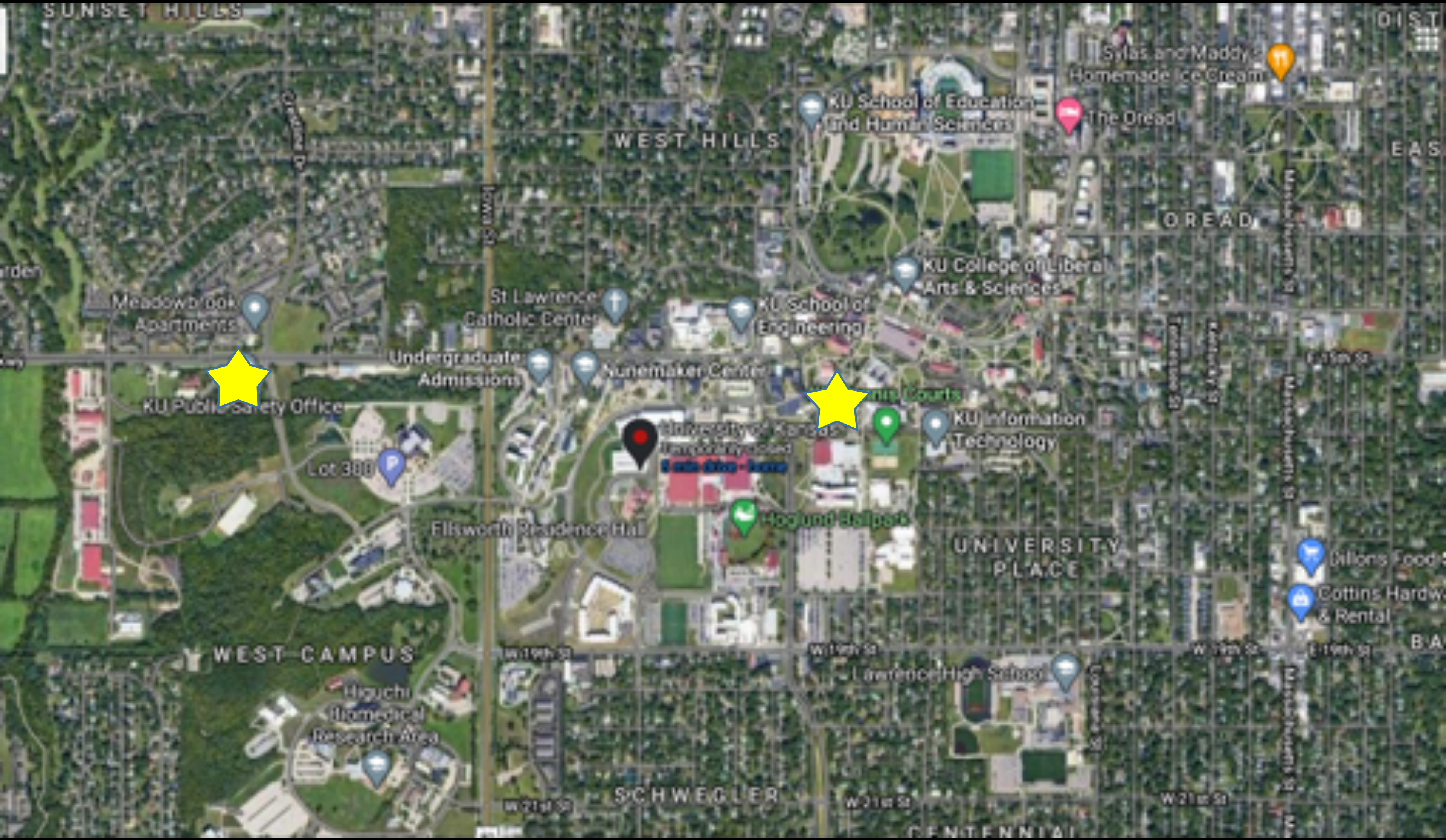

Kelly Pfeiller
PhD student


Ben Perry
Undergraduate


Anna Krause
Undergraduate


Keana Tang
Masters student


Rudolph Serbet
Collections Mngr


SUNSET HILLS
WEST HILLS
KU School of Education and Human Sciences
The Oread
Sylas and Maddy's Homemade Ice Cream
OREAD
Crestline Dr
Iowa St
KU College of Liberal Arts & Sciences
St Lawrence Catholic Center
KU School of Engineering
Meadowbrook Apartments
Undergraduate Admissions
Nunemaker Center
Tennis Courts
KU Information Technology
KU Public Safety Office
University of Kansas
Temporarily closed
Lot 300
Ellsworth Residence Hall
Hoglund Ballpark
UNIVERSITY PLACE
Tennessee St
Kentucky St
Massachusetts St
E 13th St
Dillons Food
Cottins Hardware & Rental
WEST CAMPUS
W 19th St
E 19th St
Lawrence High School
Louisiana St
Higuchi Biomedical Research Area
SCHWEGLER
W 21st St
CENTENNIAL

Collection and Research Strengths:

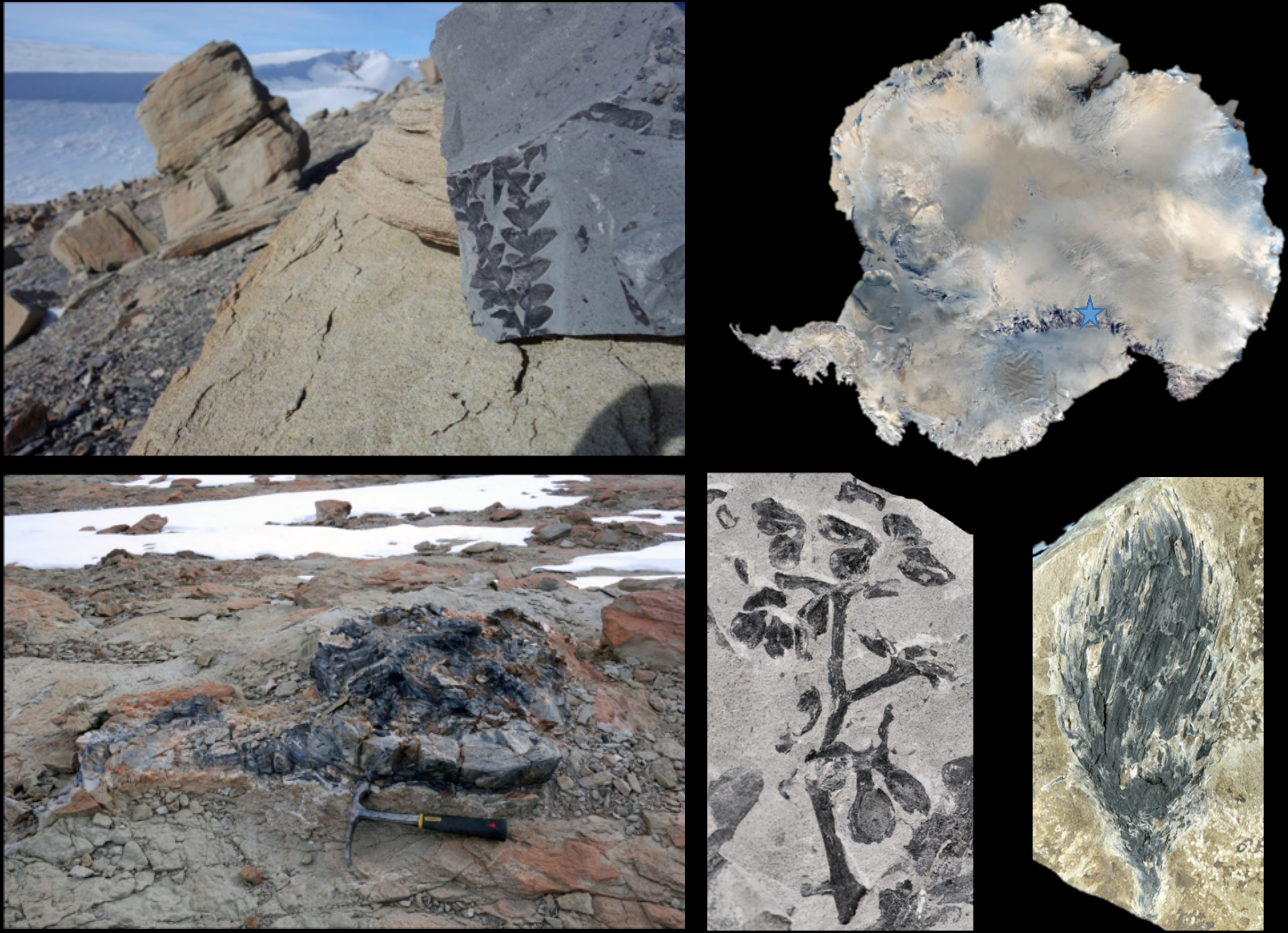
400,000 specimens: Pre-Cambrian-Recent

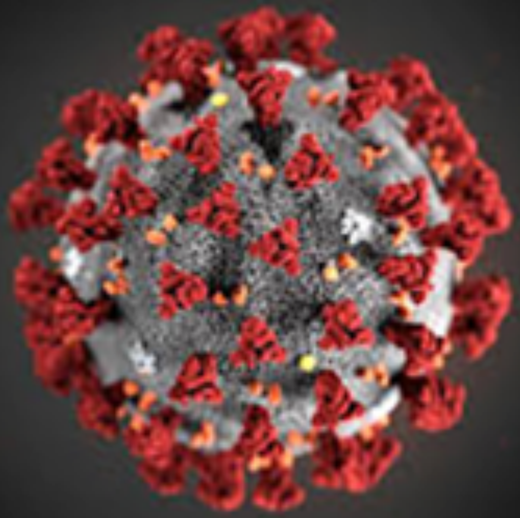
Largest North American repository for Antarctic fossil plants (>35,000 specimens, Permian-Jurassic)

NSF Sanctioned Repository for Antarctic fossil plants

Anatomically preserved plants from crucial time intervals

Currently digitizing our specimens via Specify





COVID-19, the Novel Corona Virus

News and information for the ERA-EDTA community and kidney patients.

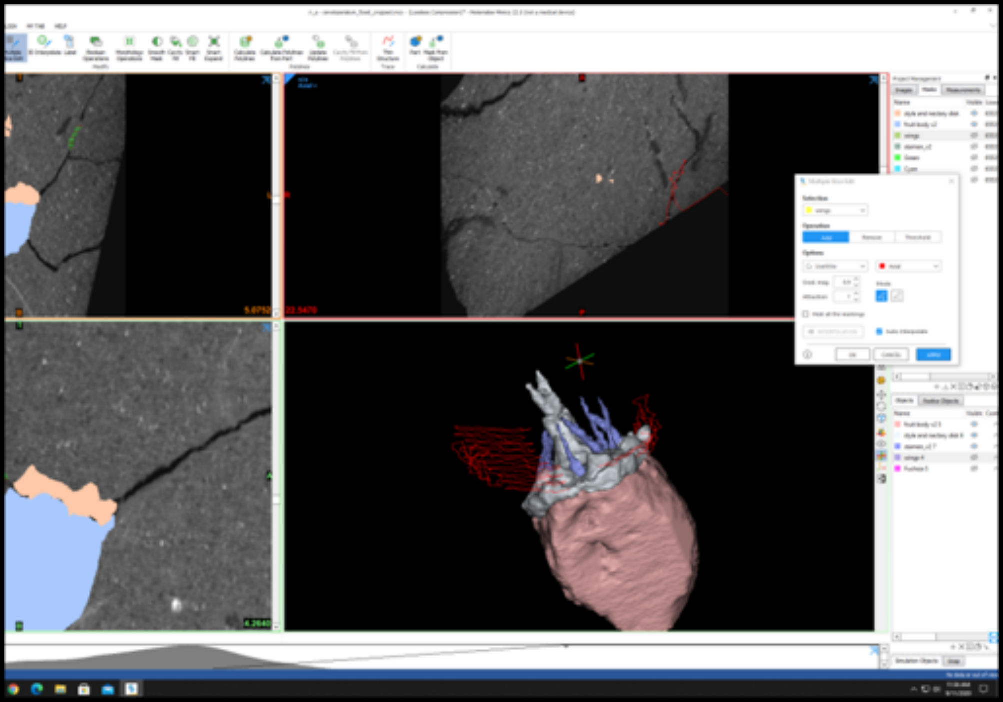
Managing a research program and collection in the middle of a pandemic???

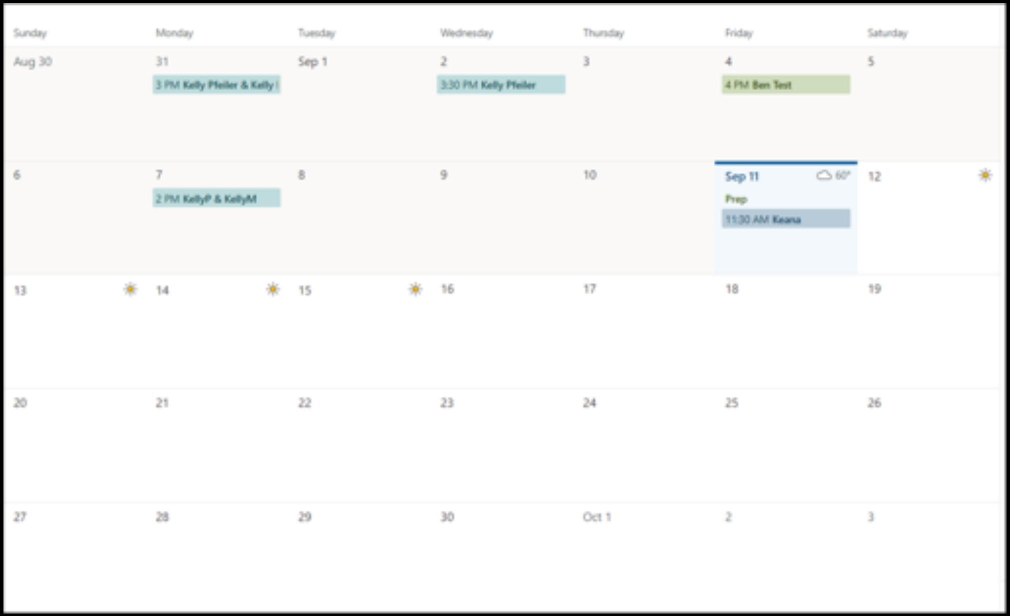
Research within the division:
Everyone has scopes at home

Remote access to fast computers for Ct-imaging processing

Dedensifying the lab

Collections management:
Loans are still out and normal operations have resumed





Sunday	Monday	Tuesday	Wednesday	Thursday	Friday	Saturday
Aug 30	31 3 PM Kelly Pfeiler & Kelly	Sep 1	2 3:30 PM Kelly Pfeiler	3	4 4 PM Ben Test	5
6	7 2 PM KellyP & KellyM	8	9	10	Sep 11 60° Prep 11:30 AM Keana	12
13	14	15	16	17	18	19
20	21	22	23	24	25	26
27	28	29	30	Oct 1	2	3

Teaching

Diversity and History of Organisms (lecture and lab)

Co-taught: Myself (everything except Metazoa); Rich Glor (Metazoa)

Lab has traditionally been a hands-on specimen based experience

Ray Troll

KU Undergraduate Biology Program
College of Liberal Arts & Sciences

Students learn critical skills in biology laboratory courses.

Teaching a biodiversity class in the middle of a pandemic???

Phylogenetic Tree Literacy

Given the current situation and a prioritization of safety. What do we want the students to walk away with this year?

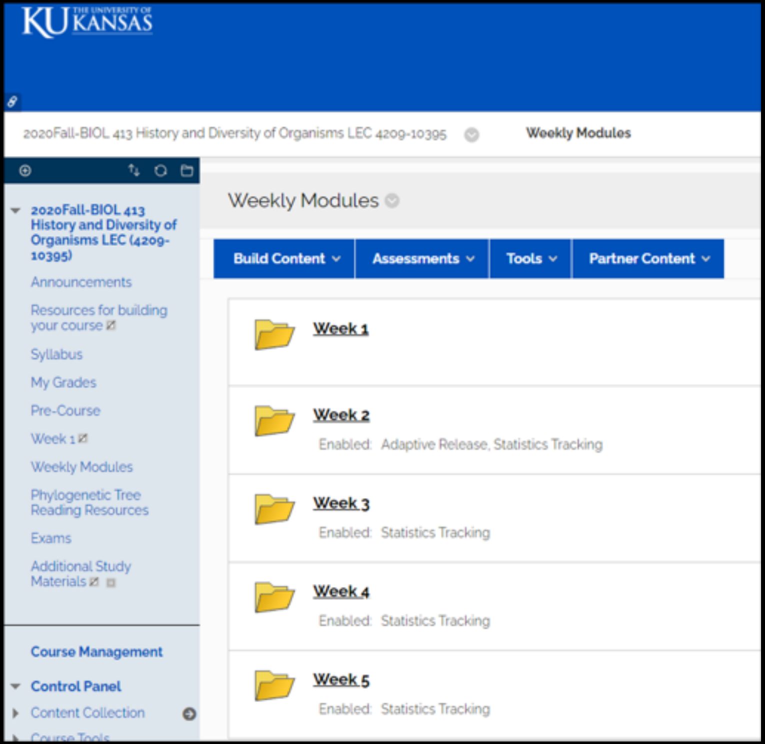
Richard Glor
Professor &
Curator

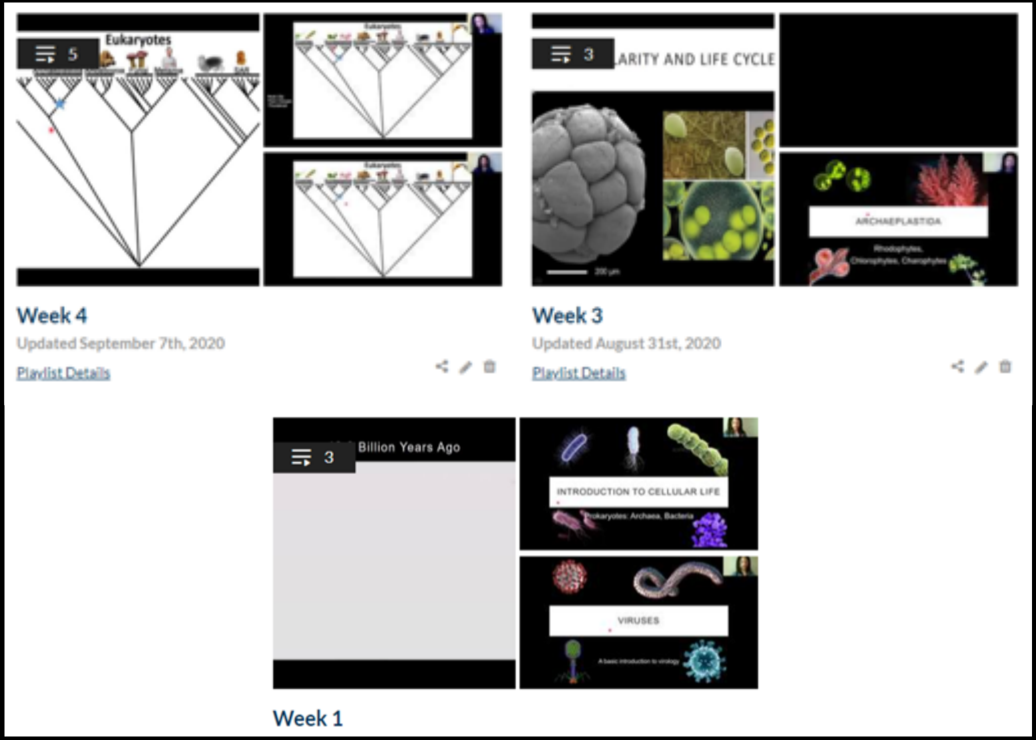
Walter Tapondjou
PhD Student &
Graduate TA

Keana Tang
PhD Student &
Graduate TA

Anna Krause
Undergrad Rschr.
& Undergrad TA

Asynchronous pre-recorded lectures
Synchronous recitations, 2 sections per week
Open book exams (24 hrs to take exam)

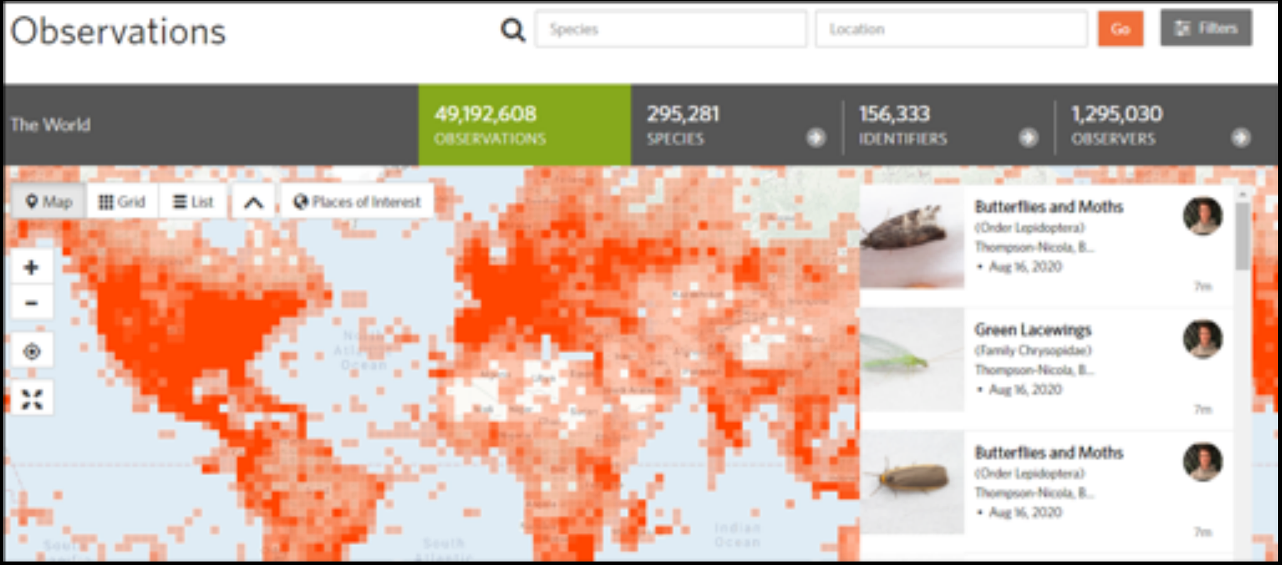




Online labs:

Tree thinking exercises using iTOL

Hopefully: diversity surveys via iNaturalist



The World

49,192,608 OBSERVATIONS

295,281 SPECIES

156,333 IDENTIFIERS

1,295,030 OBSERVERS

Butterflies and Moths (Order Lepidoptera) Thompson-Nicola, B... • Aug 16, 2020 7m

Green Lacewings (Family Chrysopidae) Thompson-Nicola, B... • Aug 16, 2020 7m

Butterflies and Moths (Order Lepidoptera) Thompson-Nicola, B... • Aug 16, 2020 7m

Lab 1: Viruses & the Three Domains

Introduction

This week's lab explores phylogenetic trees for viruses and the three major domains of non-viral life. In Part 1, you will do some basic tree reading excercises to investigate the origins of our current pandemic. One important goal of these exercises is to help you better understand monophyly, paraphyly and polyphyly, and their evolutionary implications. By the end of these exercises you should be able to interpret important phylogenetic data about the origins of COVID-19 better than some authors who have published on this topic. In Part 2, you will use a series of exercises to explore a tree for the three major domains of non-viral life (Archaea, Eukaryota and Bacteria). You will use this tree to gain experience with important basic tree concepts like most recent common ancestors (MRCAs), tree rooting, and tree support. Finally, you will learn how to map traits onto your tree and identify different types of homologous traits (e.g., synapomorphies, autapomorphies and symplesiomorphies).

Goals

Exploring the tree of life
Use phylogenetic trees to trace the origin of covid-19 and examine relationships between the three domains of life (Archaea, Eukaryota and Bacteria)

Concepts
Visualization and interpretation of different types of phylogenetic trees; monophyly, paraphyly, and polyphyly; mrcas; homology, autapomorphy, synapomorphy and symplesiomorphy

Part 1: COVID cobras and pandemic pangolins: using phylogenetic trees to trace the zoonotic origins for SARS-CoV-2

Background: The Spanish flu of 1918, ebola, SARS, and now COVID-19, all result from viruses that jumped to humans from another animal species. These infectious agents are known as **zoonoses** (s: zoonose). Determining the sources **zoonoses** is critical to understanding how pathogens evolve, and potentially stopping zoonotic transfers from occurring in the first place. Phylogenetic trees are one of the main tools that scientists use to identify the sources for zoonotic viruses. The simplest approach is to build a phylogenetic tree that includes the human virus together with related viruses from other species of animals; this allows scientists to identify the likely source species as the one hosting the virus that is most closely related to human pathogen. In this manner, the Spanish flu of 1918 has been traced to birds (Hoag 2014) and Middle Eastern Respiratory Syndrome (MERS) to domesticated dromedary camels (Wong et al. 2020).

Two recent global outbreaks of Sudden Acute Respiratory Syndrome caused by coronaviruses – first SARS and now COVID-19 – appear to have emerged initially at live animal markets in Asia, where a remarkably diverse range of animal species are regularly bought and sold. SARS, which killed

Snakes could be the source of the Wuhan coronavirus outbreak

Snakes Could Be the Original Source of the New Coronavirus Outbreak in China

The new coronavirus outbreak in China may have originated in snakes

Fig 1. Headlines from January 2020 suggesting that SARS-CoV-2 jumped to humans from snakes.

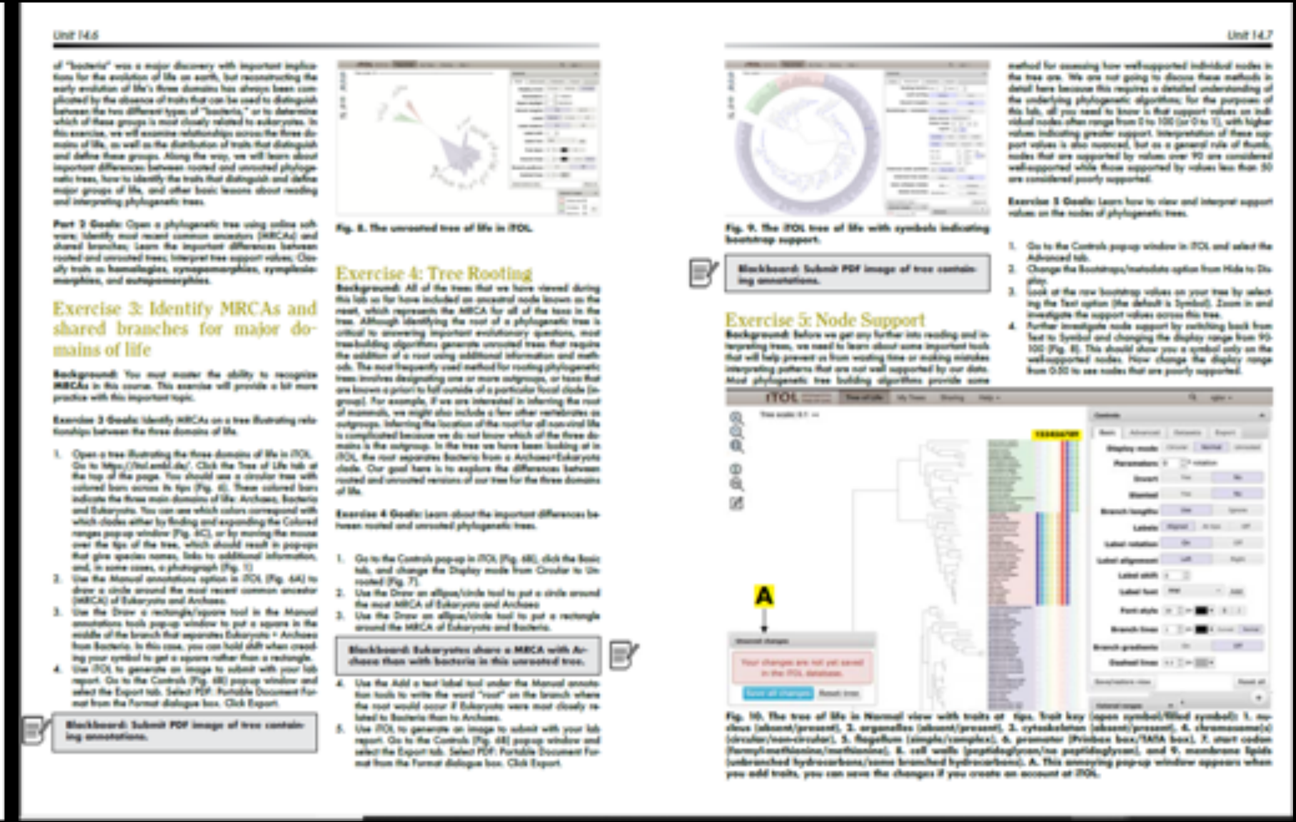


Fig. 8. The unrooted tree of life in iTOL.

Exercise 3: Identify MRCAs and shared branches for major domains of life

Exercise 4: Tree Rooting

Blackboard: Submit PDF image of tree containing annotations.

Blackboard: Submit PDF image of tree containing annotations.

Exercise 5: Node Support

Reconstructing the history of traits that can be gained and lost using **parsimony** is not difficult, but does require us to learn a simple algorithm known as **Fitch parsimony**. **Fitch parsimony** was invented as a solution to solving parsimony questions a half century ago and remains widely used today. In this lab you will use **Fitch parsimony**'s signature downpass/uppass algorithm to infer the evolutionary history of a game-changing evolutionary innovation: photosynthesis (Fig. 2). For details on using Fitch parsimony, see Box 1 below.

Goals: Learn how to use **Fitch parsimony** to reconstruct trait evolution.

Exercise 1: Good idea! I'll take it!

Background: One important goal of this week's lab is to learn how to reconstruct the evolution of traits that may exhibit **reversible evolution** via **Fitch parsimony**. A secondary goal is to learn more about another explanation for why a trait might be scattered across the tree of life. Last week, we learned that complex multicellularity evolved repeatedly in distantly related groups via **convergent evolution**, and always from ancestors that had themselves independently evolved simple multicellularity.

A second way that organisms in different parts of the tree can obtain similar traits is via **horizontal transfer**, or, put another way STEALING (Fig. 3)! We will define **horizontal transfer** broadly as any instance where one organism ac-

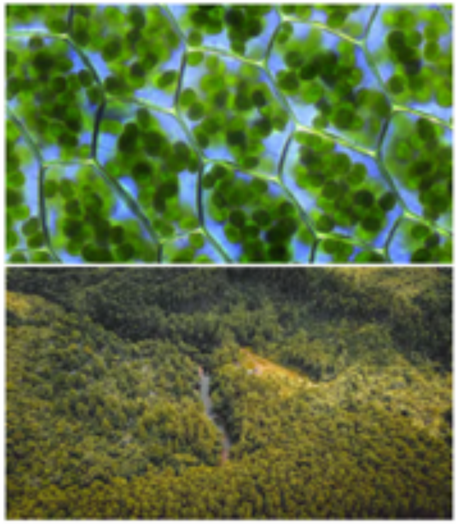


Fig 2. "The world is green," is a well-known truism among ecologists, and concisely captures the success of photosynthetic organisms. It is also a good mic drop line if you hear anyone disrespecting plants.

Box 1: Reconstructing Evolution of Reversible Traits Using Fitch Parsimony

The goal of **parsimony** is to reconstruct the evolutioary scenario(s) with the fewest possible evolutionary changes. In the case of relatively small trees, where traits change infrequently, or where changes are **irreversible**, it is often possible to infer the most parsimonious solution "by eye" without the aid of any specific rules or algorithms (this is what you did last week with multicellularity). In many real world scenarios, however, we need to apply simple algorithms designed to efficiently identify the most parsimonous solution. The purpose of this box is to explain how to apply the **Fitch parsimony** algorithm.

The **Fitch parsimony** algorithm works by stepping through the tree one node at a time and making decisions about possible ancestral states that ensure the most parsiminious solution(s). The algorithm involves two steps. First, you complete an **downpass**, where possible ancestral states are reconstructed from the tips down to the root. During this **downpass**, the ancestral state at some internal nodes may be reconstructed as **ambiguous**, meaning that the node could be either a photosynthetic or non-photosynthetic. Second, you complete an **uppass** by working backwards from the root to the tips to resolve ambiguous nodes inferred during the **downpass**. During both the **downpass** and **uppass**, character states are reconstructed following two simple rules. Once you have completed the downpass and uppass, you can assign trait changes to branches in your tree.

Rule 1: If the descendants of an ancestral node share any common traits, assign those shared states to the ancestral node. Here are a few examples of how this rule is applied: (A) if your downpass starts with two descendents that are both photosynthetic, you would assign photosythesis to the ancestor. (B) If one descendent is classified as ambiguous (i.e., either photosynthetic or non-phosynthetic) and the other as photosynthetic, you would assign photosynthesis to the ancestor. (C) if both descendents are classified as ambiguous, the ancestor would also be classified as ambiguous.

Rule 2: If the descendents of an ancestral node do not share traits in common traits, assign both of the possible states to the ancestor. For example, if one descendent has photosynthesis and the other does not, you would reconstruct the ancestor as ambiguous. For every node where you apply Rule 2, you will ultimately infer a trait change along one of the two descendent branches.

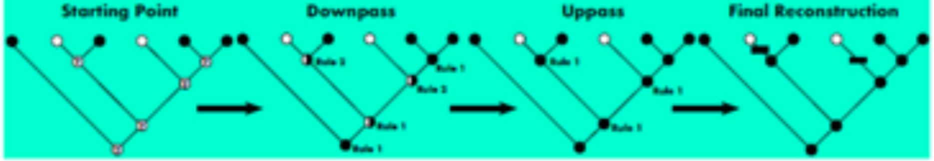


Figure 2. A sample of bryophyte diversity. The top two images show the liverwort, *Marchantia*. At the top right, we can see the elongated archaegonia(phores) that contain the egg and eventually the sporophyte. The bottom image shows an expansive moss gametophyte bearing small unbranched sporophytes.

carried by the wind (rather than water as seen in their aquatic and marine algal relatives). In some cases, such as in the liverworts (Marchantia) the **gametophyte** grows specialized structures that raise the female sex organs (archaegonia) and and their short-lived **sporophytes**.

Before going any further, we need to mention that land plants are divided into two main groups: the **bryophytes** and the **polysporangiophytes** (vascular plants are the only survivors of this later group). **Bryophytes** are characterized by having a sporic life cycle with alternation of generations where the **gametophyte** is the dominant multicellular form (Fig 1); in this group, the **sporophyte** is simple, short lived, unbranched, and has only one sporangium. **Polysporangiophytes** (polysporangio- "multiple sporangia" –phyte "plant"), meanwhile, are characterized by having a sporic life cycle with **alternation of generations** where where the **sporophyte** is the dominant multicellular form. In this case the **sporophyte** is long lived, complex, branched, and has multiple sporangia (see Fig 2). As **polysporangiophytes** began to become more abundant and diversify, competition and natural selection drove increases in height that allowed plants to disperse their **spores** further (stay tuned for Part 2) and obtain more sunlight than competitors.

Recent major changes to the **embryophyte** tree of life have major implications for our understanding of early land plant evolution (Fig 3). Historically, **bryophytes** were thought to be **paraphyletic** with respect to **polysporangiophytes**. In fact, the latest edition of the Raven textbook includes this arrangement. However, within the past few years (like basically yesterday), new molecular phylogenetic studies have converged on a phylogeny where **Bryophytes** are a **monophyletic** group, or clade. In this lab, we will consider the implications of these new results for understanding trait evolution along the **embryophyte** tree of life, and by extension, how we study the traits that lead to the success of land plants.

Part 1 Goal: Analyze the evolution of the sporic life cycle and **alternation of generations** across two phylogenetic hypotheses for Embryophytes.

Exercise 1a: Evolution of Alternative Generations Under the Classic Tree

Background: Our first goal is to evaluate how the two different life history strategies involving **alternation of generations** - **gametophyte** and **sporophyte** dominant - evolved under the classic phylogenetic hypothesis – where bryophytes are paraphyletic. To do this we will use parsimony to reconstruct the evolution of the two alternative life histories on a phylogenetic tree that includes broad sampling of major embryophite lineages.

Exercise 1b Goals: Reconstruct evolution of **alternation of generations** under the classic phylogenetic hypothesis involving paraphyly of bryophytes.

1. Open iTOL and upload the tree file – Lab4_Exercise1a_Tree1.new (Fig. 4). This file is a simple text document that contains a NEWICK formatted tree. Note: this lab includes several files with similar names, please be sure to carefully read and check the entire file name(s) to avoid the trouble that results from carelessly picking the wrong one (one of your instructors may have made this mistake while testing the lab).
2. Download and save the file that contains annotations for seven major clades of embryophytes – Lab4_Exercise1a_MajorClades.txt. Drag and drop this file into the iTOL window. You should see shaded boxes that indicate the following seven clades of embryophytes: mosses, hornworts, liverworts, lycophytes, ferns, gymnosperms, and angiosperms. You can view the names associated with each of these clades using the Datasets tab in the Controls window of iTOL (Fig. 4).
3. Download and save the file that contains data on whether the gametophyte is dominant or whether the sporophyte is

Figure 3. Two of the new studies - de Sousa et al. 2018 and Harris et al. 2020 - that recover monophyly of Bryophytes.

Reflections teaching during Covid:

Class enrollment is virtually the same as compared to previous years

KU undergraduate biology program enrollment is up

Overall students have appreciated the flexibility in our class format and are learning

Rich and I are happy to share our lab material

Outlook:

Specimen based research will continue

Fieldwork will resume next summer and beyond

Grant proposals focusing on collections based work are being written

Taking the Pulse of Natural History Collections During COVID-19 Series: Where are we now?

September 16: Collections’ perspectives

John Bates, The Field Museum

Emily Braker, University of Colorado Boulder

Brian Atkinson, The University of Kansas

Mare Nazaire, California Botanic Garden

iDigBio is funded by grants from the National Science Foundation's Advancing Digitization of Biodiversity Collections Program [DBI-1115210 (2011-2018) and DBI-1547229 (2016-2021)]. Any opinions, findings, and conclusions or recommendations expressed in this material are those of the author(s) and do not necessarily reflect the views of the National Science Foundation.

California Botanic Garden’s Collections and COVID: Creating the Silver Lining

Mare Nazaire, Herbarium Administrative Curator
Chair, Collections Committee

COVID-19: Challenges

- Budget constraints
- Reduced staffing
- No volunteers
- No fieldwork
- Delays: collecting permits
- Non-essential tasks on hold
- Staggered schedules
- Inside vs. outside work

Living Collection

Seed Collection

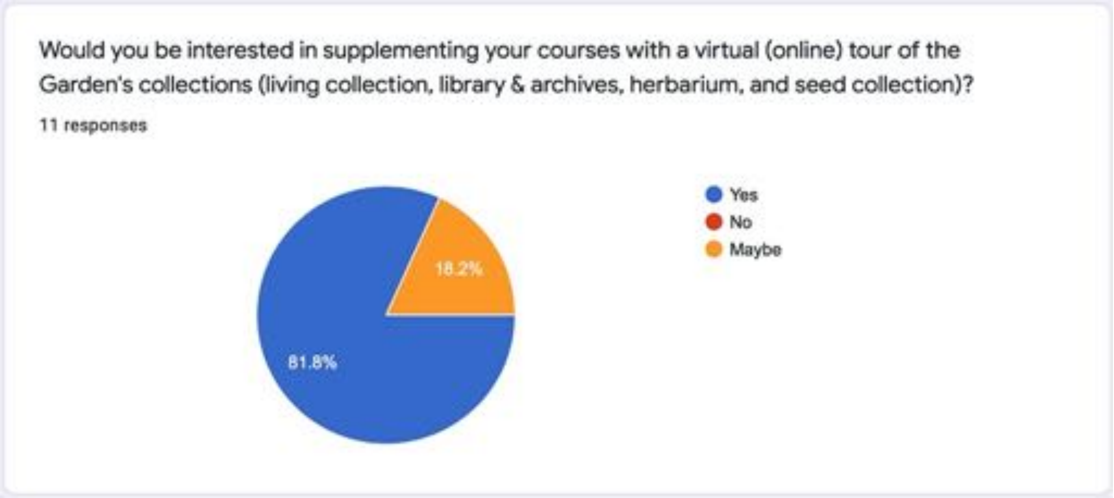
Library & Archives

Herbarium

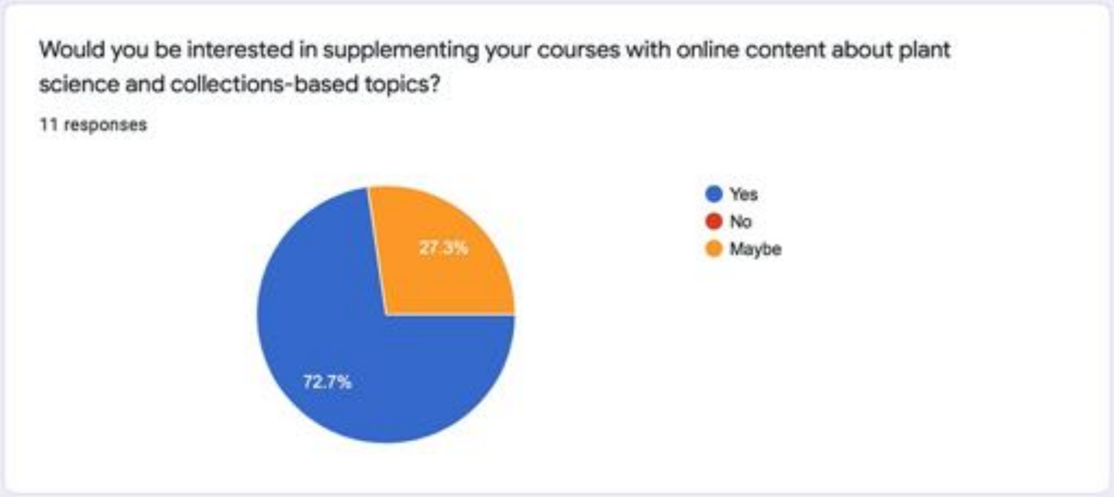

CANELLACEAE
DEGENERIACEAE
EUPOMATIACEAE
HERNANDIACEAE


EXIT

How do we connect students to collections when they cannot visit in person?


Would you be interested in supplementing your courses with a virtual (online) tour of the Garden's collections (living collection, library & archives, herbarium, and seed collection)?

11 responses


Would you be interested in supplementing your courses with online content about plant science and collections-based topics?

11 responses

Surveyed the academic community:

- Previous visitation and tours
- Determine interest in virtual tours
- Determine interest in supplementing coursework

The Collections Connection
Educational module:

Plants in a changing world: California Diversity, Species Distributions, and Climate Change

This work is supported by the Hispanic-Serving Institution's Education Grants Program, grant no. 2015-38422-24058/project accession no. 1007104, from the USDA National Institute of Food and Agriculture.

Home >> Collections >> Search Criteria >> **Specimen Records**

Dataset: RSA VascularPlants
Taxa: Encelopsis covillei (Encelopsis argophylla var. grandiflora, Helianthella covillei)
Search Criteria: has images; excluding cultivated/captive occurrences

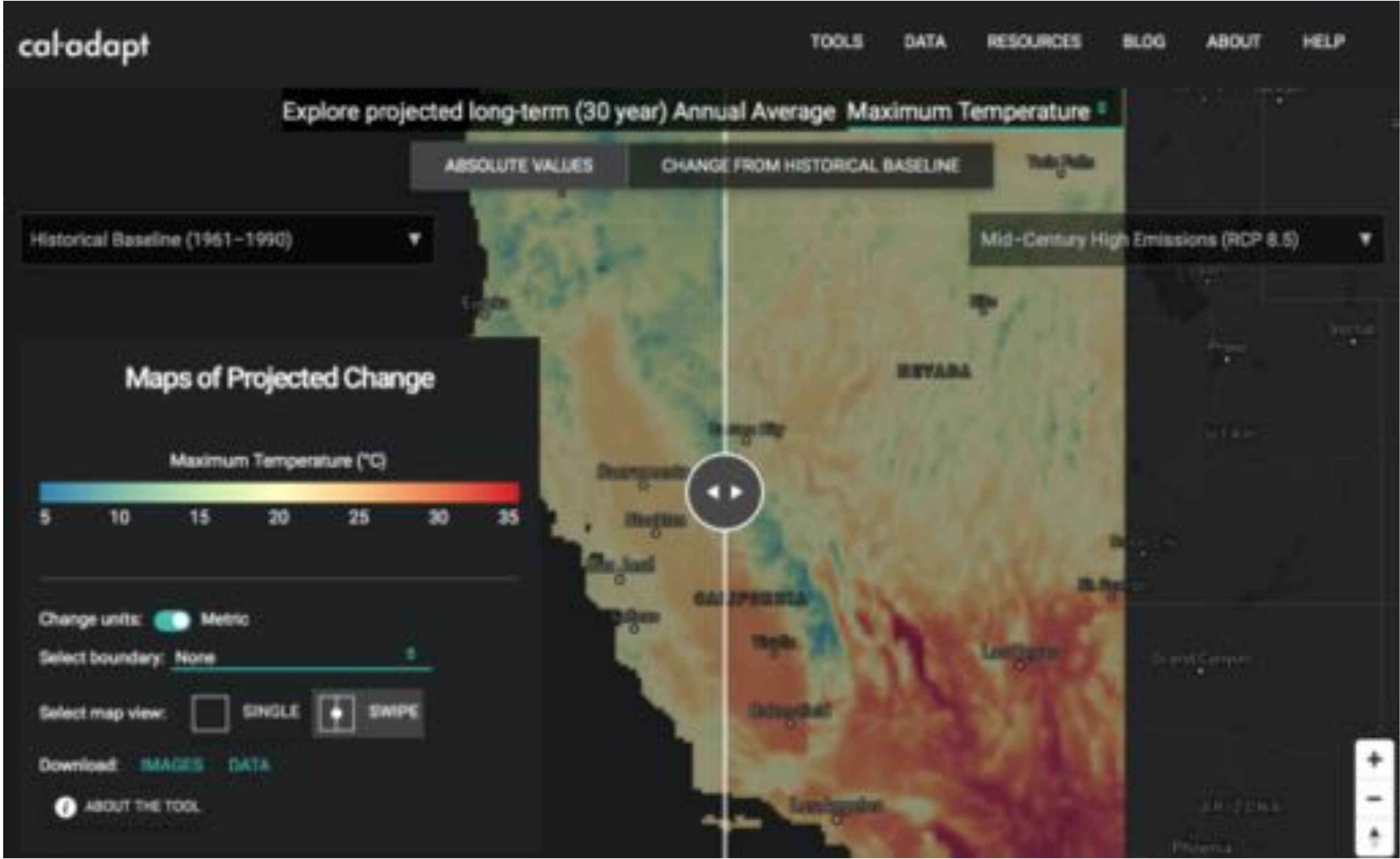
1 Page 1, records 1-1 of 1

RSA - California Botanic Garden Herbarium

RSA VascularPlants

Encelopsis covillei (A. Nels.) Blake
RSA0081889 B. C. Tschopp s.n. 1957-04-14
United States, California, Inyo County, Surprise Canyon, [Ballarat Quadrangle], 36.11081 -117.150669, 762m
Full Record Details

1 Page 1, records 1-1 of 1



Explore projected long-term (30 year) Annual Average Maximum Temperature

Historical Baseline (1961–1990) ▼

Mid-Century High Emissions (RCP 8.5) ▼

Maps of Projected Change

Change units: Metric

Select boundary: None

Select map view: ☐ SINGLE ☑ SWIPE

For more info:
https://www.calbg.org

Break-out room discussion

What are the top three positive outcomes experienced by collections as we adapt to new COVID-aware workplace guidelines?

bit.ly/idigbio-poll

Break-outs (15 minutes) • Review (5 minutes) • Discussion

Taking the Pulse of Natural History Collections During COVID-19 Series: Where are we now?

September 17: Moving Forward: Communities Response and Opportunities for the Future: Presentations and Panel Discussion/Q&A

Speakers: Rob Gropp, Pam Soltis, Scott Miller, Roland Roberts

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Please help by providing feedback about this webinar series!

Survey link:

https://ufl.qualtrics.com/jfe/form/SV_aVL7wEfLYUXcbFb

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