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Motivation: the Taxonomic Impediment

Example: Kenai NWR LTEMP, $t_1$

Example: the global biodiversity crisis
Setting: Kenai National Wildlife Refuge
Setting: Kenai National Wildlife Refuge
A broad conservation mandate

to conserve fish and wildlife populations and habitats in their natural diversity...

fish and wildlife = any member of the animal kingdom including without limitation any mammal, fish, bird, amphibian, reptile, mollusk, crustacean, arthropod or other invertebrate
Stressors: climate, development, exotic species

→ novel species assemblages, trophic mismatch, and potential extinctions
Long Term Ecological Monitoring Program, $t_1$

- Collaborative effort with USDA FIA program
- 259 permanent plots at 5-km intervals
- Plants, birds, and arthropods inventoried
1,106 species:
- 80 birds
- 256 invertebrates (15,136 specimens!)
- 324 vascular plants
- 297 lichens
- 149 bryophytes
Problem: the Taxonomic Impediment

Morphological identification is impractical for monitoring.
Humans Causing Fast Changes

Earth in Sixth Major Extinction

As most kids probably know, dinosaurs came to a sudden end about 65 million years ago. Did you know that there have been four other super-big, or mass, extinctions of life on Earth?

Most scientists believe we are in the middle of a sixth mass extinction. But this time, the extinction isn’t being caused by an asteroid or volcanoes. Its causes can be traced to us.

To find out more about this event, The Mini Page talked with Michael Brett-Surman from the Smithsonian National Museum of Natural History.

What is a mass extinction?

When a species, or type of life, becomes extinct, it means there are no more members of that species alive.

Extinctions are normal. Usually, there is a steady rate of extinctions during every million years. Life forms evolve and change. Some species can’t change and can’t handle new conditions, and so they disappear.

The most famous mass extinction was at the end of the Cretaceous Period, when six out of seven of all dinosaur groups were wiped out, along with half of all life. There is evidence that a giant asteroid hit the Earth then.

The ages of Earth

Each time there is a mass extinction, a new age begins on Earth. As older species die out, other species suddenly have no competition. They begin to fill in the Earth’s habitats.

Over millions of years, newer types of life develop. Diversity increases again. The makeup of the planet changes yet again.

Let’s explore Earth’s earlier mass extinctions.

End of the Ordovician

The Ordovician (or-doh-VIH-shun) Period ended about 445 million years ago. Most life lived in the oceans at this time. Experts believe more than 50 percent of life was wiped out at the end of this age.

One reason for the extinctions might have been a drop in sea level. Huge
Linnaean taxonomy: species described per year

2000-2009 average: 18,000 species/yr.\textsuperscript{a}

\textsuperscript{a}http://www.esf.edu/species/documents/sosretro.pdf
Described and estimated global biodiversity

8.7M Estimated

1.7M Described

The rise of molecular systematics

DNA barcoding

The technologies

A homeschool example
DNA Barcoding

DNA Barcoding: growth of boldsystems.org


http://v4.boldsystems.org/
Technologies: sequencing cost

Cost per Raw Megabase of DNA Sequence

from $5,300 to 1.4¢!

Graphic from http://www.genome.gov/sequencingcosts/.
Technologies: portable DNA sequencer

$1,000 portable DNA sequencer

Technologies: consumer-ready kit

$35 consumer-ready DNA-based identification kit

Image from https://pbs.twimg.com/media/CVy48OZUAAEfFJ-.jpg:large.
Homeschool test: willow gall midges

*Rabdophaga rosaria* 
gall midge adult (4 mm)

“Willow rose” induced by *Rabdophaga rosaria*
on *Salix barclayi*

*Cross section showing the orange larva*

*Beaked gall induced by* 
*Rabdophaga rigidae*

*Stem swelling induced by* 
*Rabdophaga salicis* on *Salix barclayi*

*Bud gall induced by* 
*Rabdophaga sp.* on *Salix sitchensis*

Watercolors from *Willows of Southcentral Alaska* by Dominique Collet, 2002
Homeschool test: results
Biomonitoring by molecules

Next generation metagenomic sequencing

Building an Alaska library

NGS Test drive: Tetlin NWR 2014
Next generation metagenomic sequencing
Alaska library: specimens (UAM & USFWS)

Alaska library: specimen localities

Alaska DNA barcode library: status

- 8,421 terrestrial arthropod species known from Alaska
- 4,020 (47%) of Alaska species now on BOLD
- 1,464 Alaska species sequenced by UAM & USFWS

![Bar chart](image)

- Insecta: 3522 of 7411
- Arachnida: 494 of 905
- Chilopoda: 3 of 31
- Diplopoda: 1 of 9
Tetlin NWR 2014: design
Tetlin NWR 2014: field methods

- Extensive remote-sense and vegetation data collected at 27 sites
- 2 sweep net samples at each site
Tetlin NWR 2014: molecular methods

Research and Testing Laboratory → Galaxy

samples → sequencing → paired-end read merger → dereplication → clustering → VSearch search → identifications

Sequences from BOLD

Alaska vicinity COI reference library
Tetlin NWR 2014: results

- 84 Latin names at various levels of taxonomic resolution
- 53 species names
- 118 BINs
- 1–9 species per plot
- 2–13 BINs per plot

Most common species: *Ochlerotatus communis*

Tetlin NWR 2014: results

First collection date (2014) of the Blackberry Skeletonizer (*Schreckensteinia festaliella*) from Alaska.

Image by Peter Buchner ([https://commons.wikimedia.org/wiki/File:Schreckensteinia_festaliella01.jpg](https://commons.wikimedia.org/wiki/File:Schreckensteinia_festaliella01.jpg))
Conclusion

↑ Power and availability of sequencing technology

↓ Cost

→ DNA sequencing is the future of inventory and monitoring for insects, fungi, soil biota, freshwater plankton, diet...
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- **Dominique Collet** *(willow gall midges: ideas and advice)*