

Biomonitoring by molecules: the future of conservation

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Outline

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Example: the global biodiversity crisis

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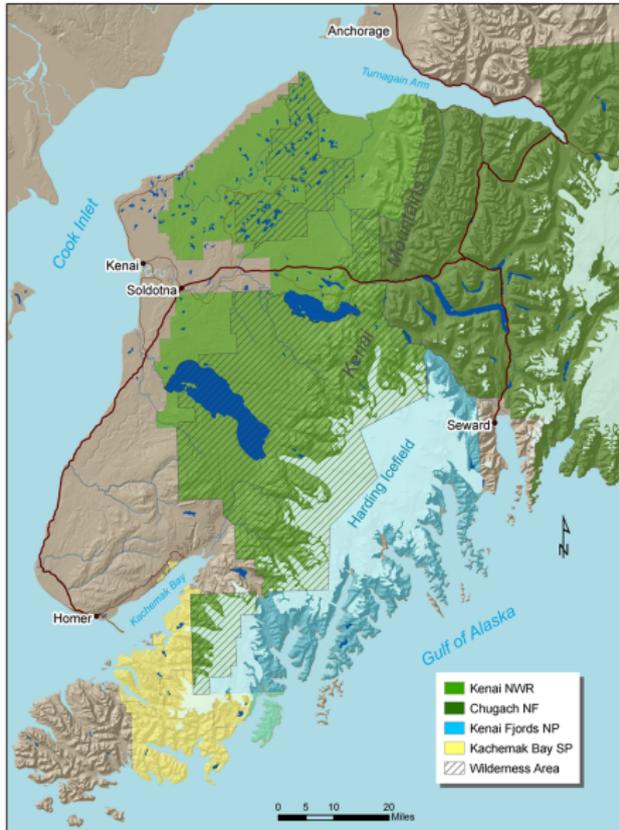
Motivation: the Taxonomic Impediment

Example: Kenai NWR LTEMP, t_1

Example: the global biodiversity crisis



Setting: Kenai National Wildlife Refuge



Setting: Kenai National Wildlife Refuge



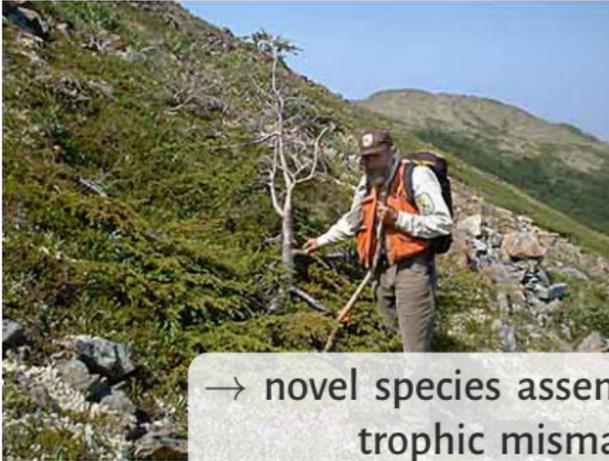
A broad conservation mandate

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

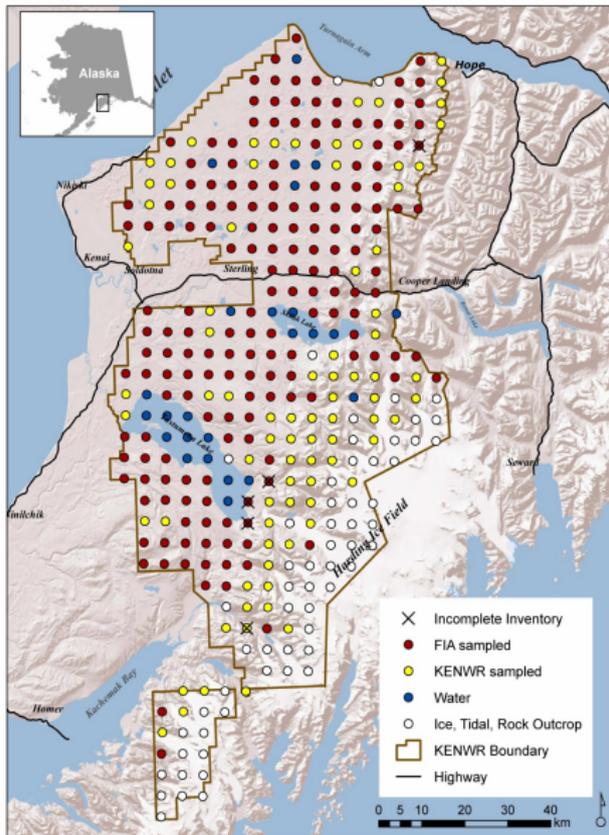
Stressors: climate, development, exotic species



→ novel species assemblages,
trophic mismatch,
and potential extinctions



Long Term Ecological Monitoring Program, t_1



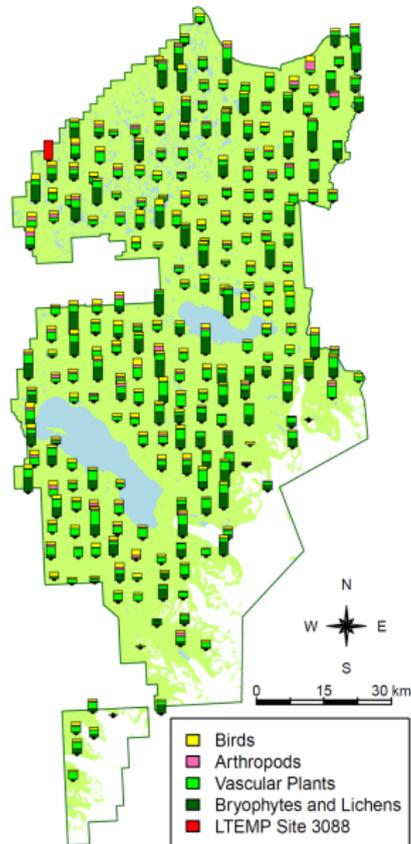
- ▶ Collaborative effort with USDA FIA program
- ▶ 259 permanent plots at 5-km intervals
- ▶ Sampled 2004, 2006, 2008
- ▶ Plants, birds, and arthropods inventoried



Long Term Ecological Monitoring Program, t_1

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*.



The Mini Page

Betty Debnam, Founding Editor and Editor at Large



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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



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.

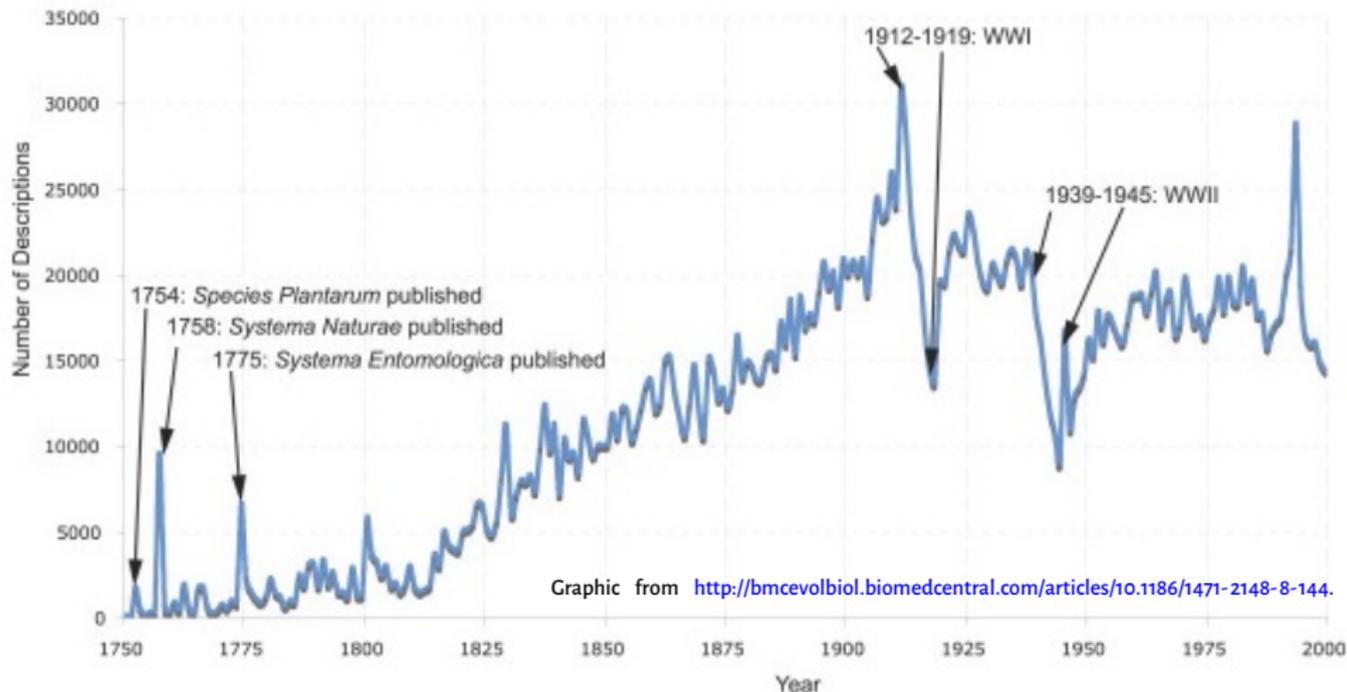
End of the Ordovician

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

art by Don Dink, courtesy NASA

Linnaean taxonomy: species described per year



2000-2009 average: 18,000 species/yr.^a

^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

Thunnus albacares



Thunnus maccoyii



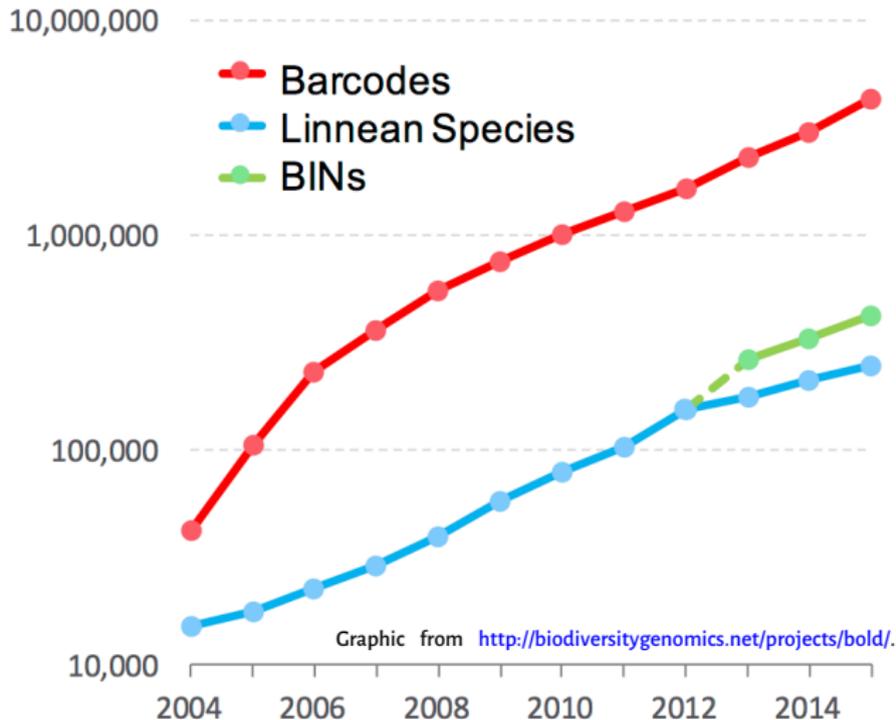
Lutjanus purpureus



Lutjanus campechanus



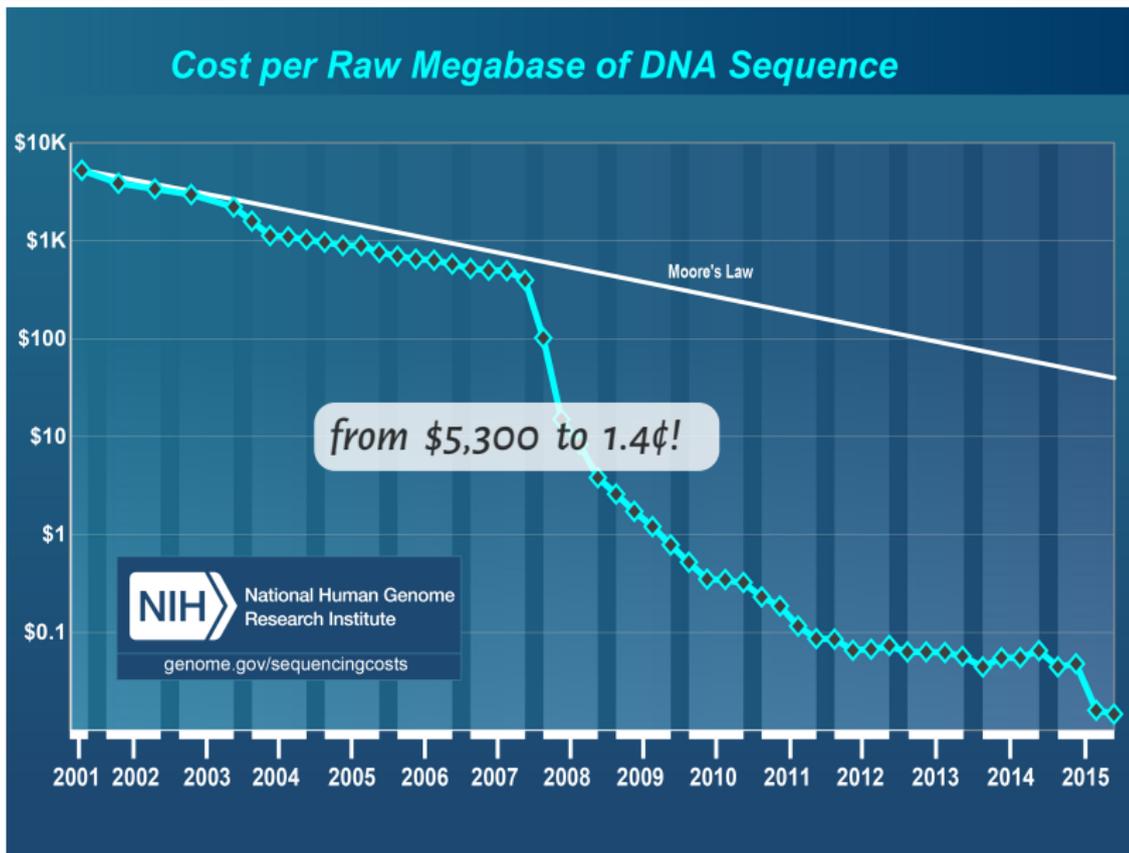
DNA Barcoding: growth of boldsystems.org



4.7M sequences, 693K species as of 18.Feb.2016^a

^a<http://v4.boldsystems.org/>

Technologies: sequencing cost



Technologies: portable DNA sequencer



\$1,000 portable DNA sequencer

Technologies: consumer-ready kit



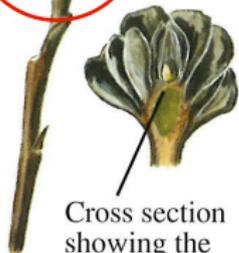
\$35 consumer-ready DNA-based identification kit

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



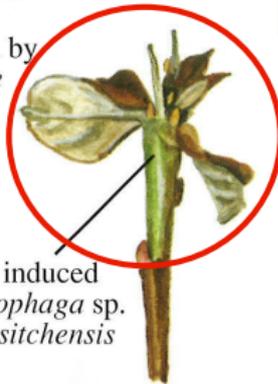
Stem swelling
induced by
Rabdophaga
salicis on *Salix*
barclayi



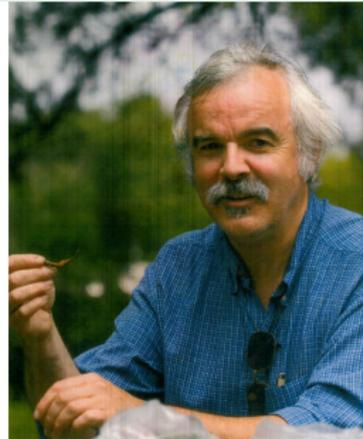
Beaked gall induced by
Rabdophaga rigidae



Cross section
showing the
orange larva



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



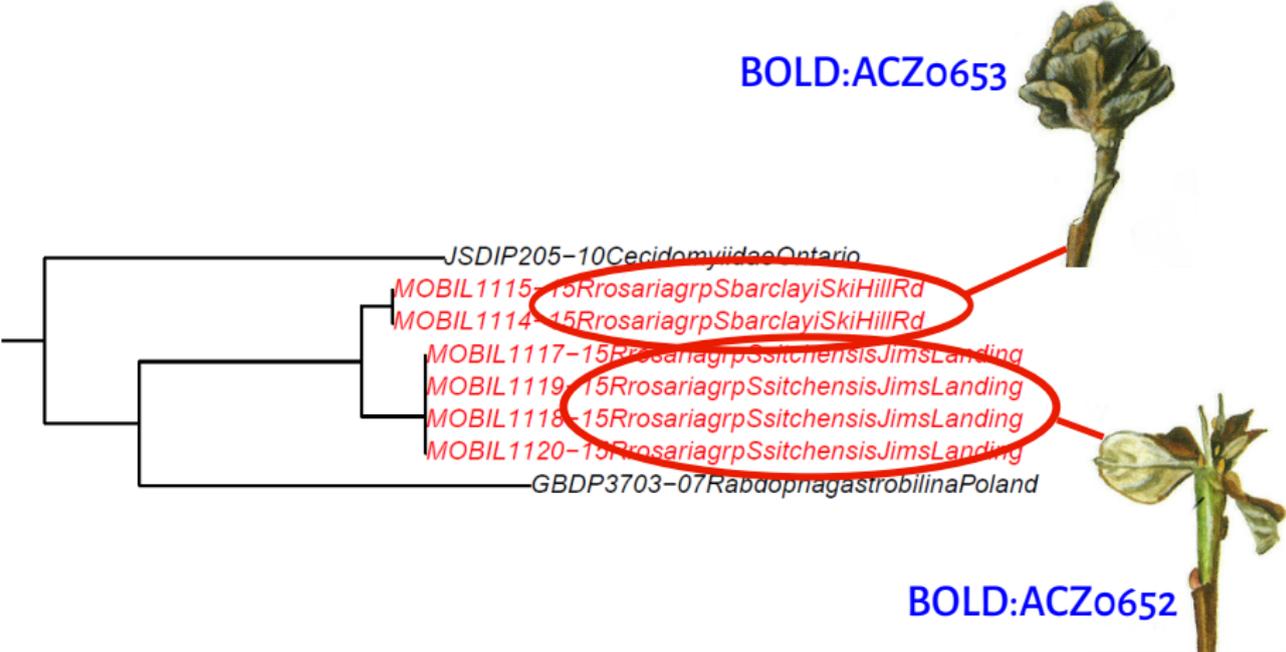
Dominique Collet







Homeschool test: results



Barcode Compliant
Members: 0
Founding Record

NEAREST NEIGHBOR (NN) DETAILS:

<u>Nearest BIN URI:</u>	BOLD:ACZ0652	<u>Average Distance:</u>	0% (p-dist)
<u>Member Count:</u>	4	<u>Maximum Distance:</u>	0% (p-dist)
<u>Nearest Member:</u>	MOBIL1117-15	<u>Distance Variance:</u>	0% (p-dist)
<u>Nearest Member Taxonomy:</u>	Arthropoda, Insecta, Diptera, Cecidomyiidae		

TAXONOMY:

Phylum: Arthropoda [2]

Class: Insecta [2]

Order: Diptera [2]

Family: Cecidomyiidae [2]

Subfamily:

Genus:

Species:

Add Tags & Comments Comments: Associated Tags: No Tags

TREE RECONSTRUCTION OF BIN & NEAREST NEIGHBOR:

No tree is generated when there are less than 3 or more than 1000 public records.

COLLECTION LOCATION:

Countries: United States - [2]

DATA MANAGERS:

Public Data: Private Data:
Megan A. Milton - [2]

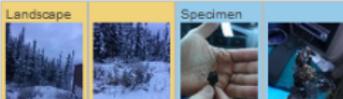


MOBIL1115-15 (Cecidomyiidae)

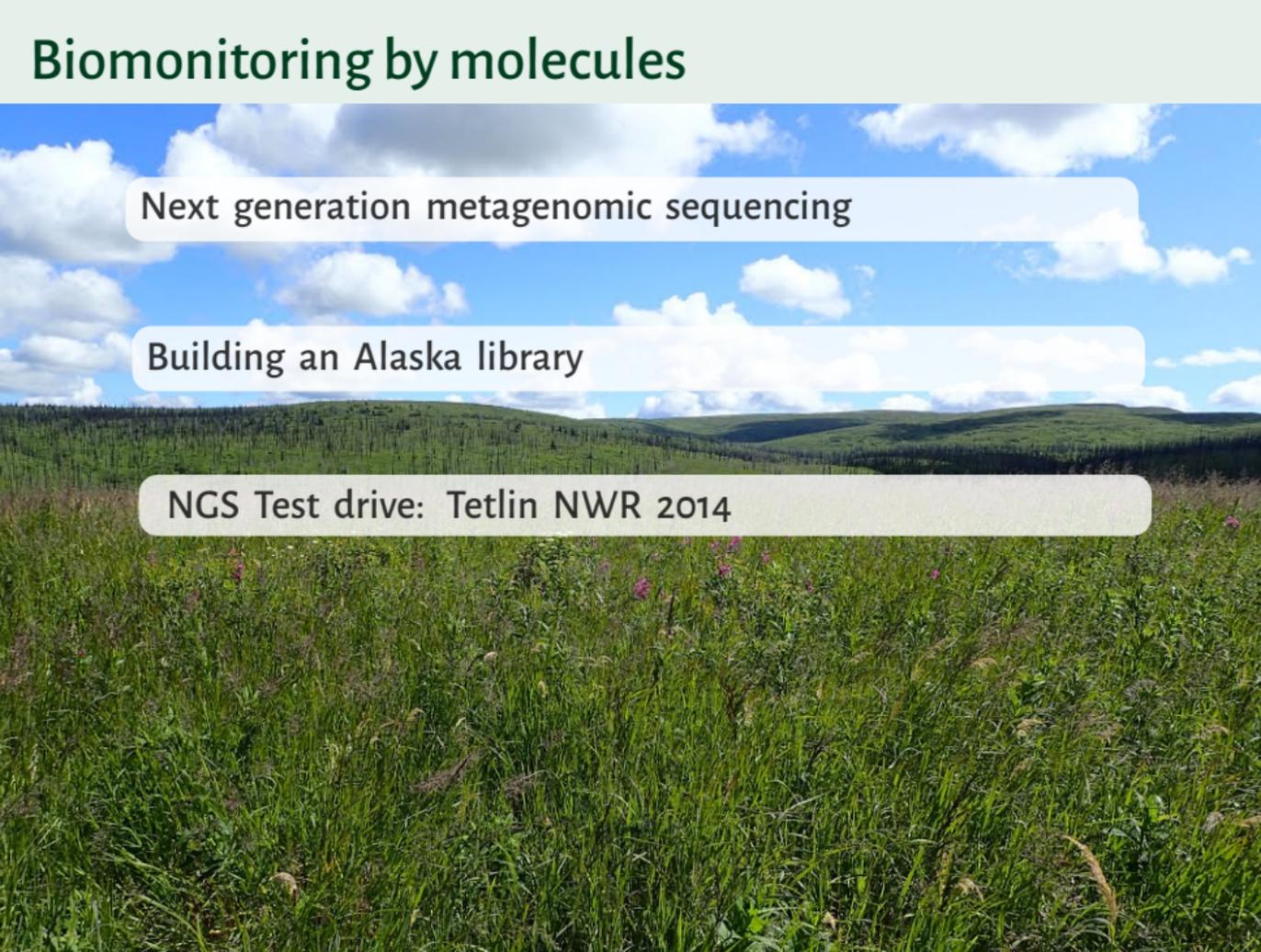
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**Collection Sites:**

Biomonitoring by molecules

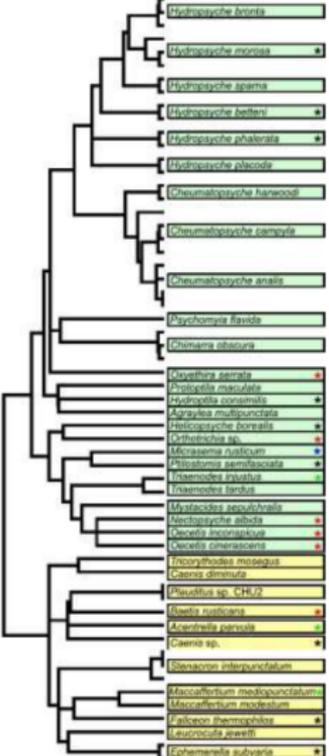


Next generation metagenomic sequencing

Building an Alaska library

NGS Test drive: Tetlin NWR 2014

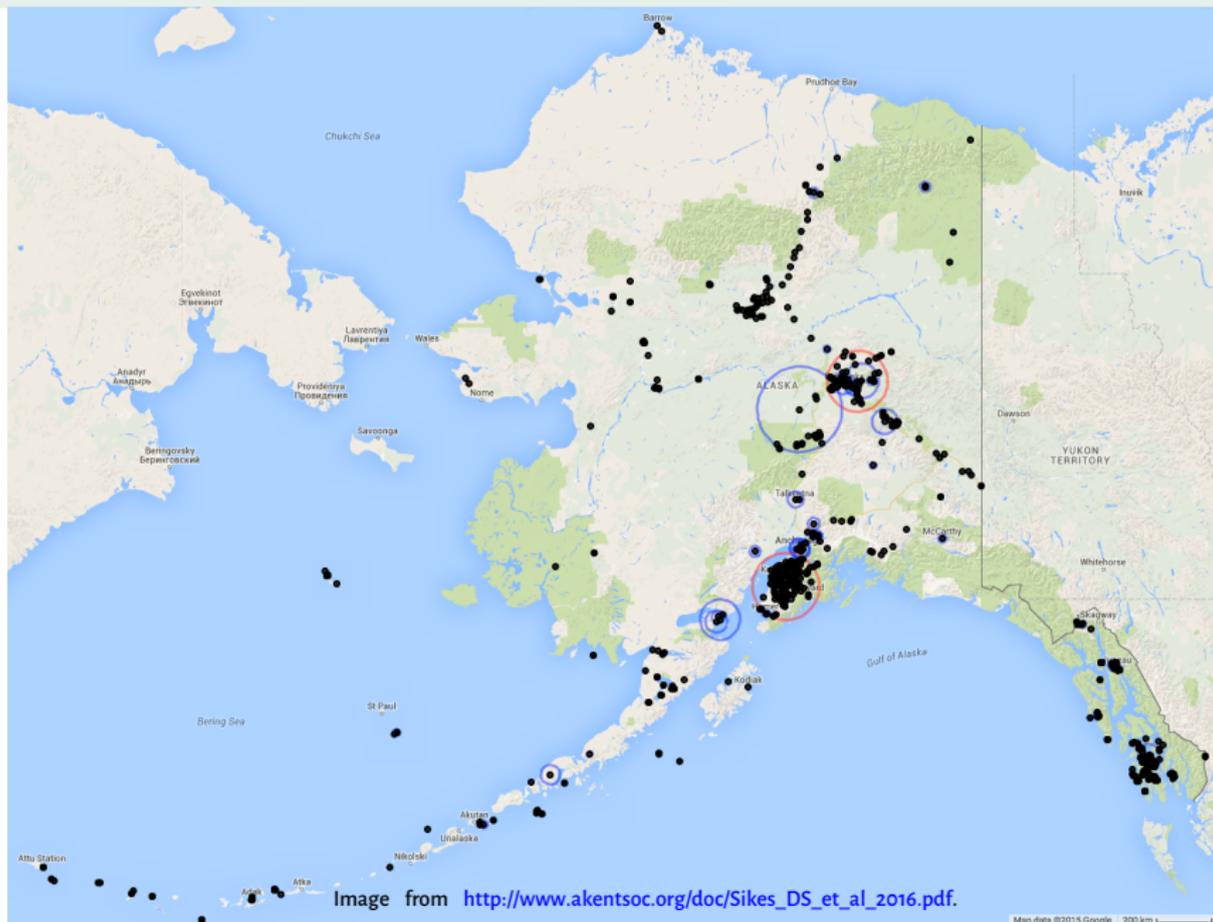
Next generation metagenomic sequencing



Alaska library: specimens (UAM & USFWS)

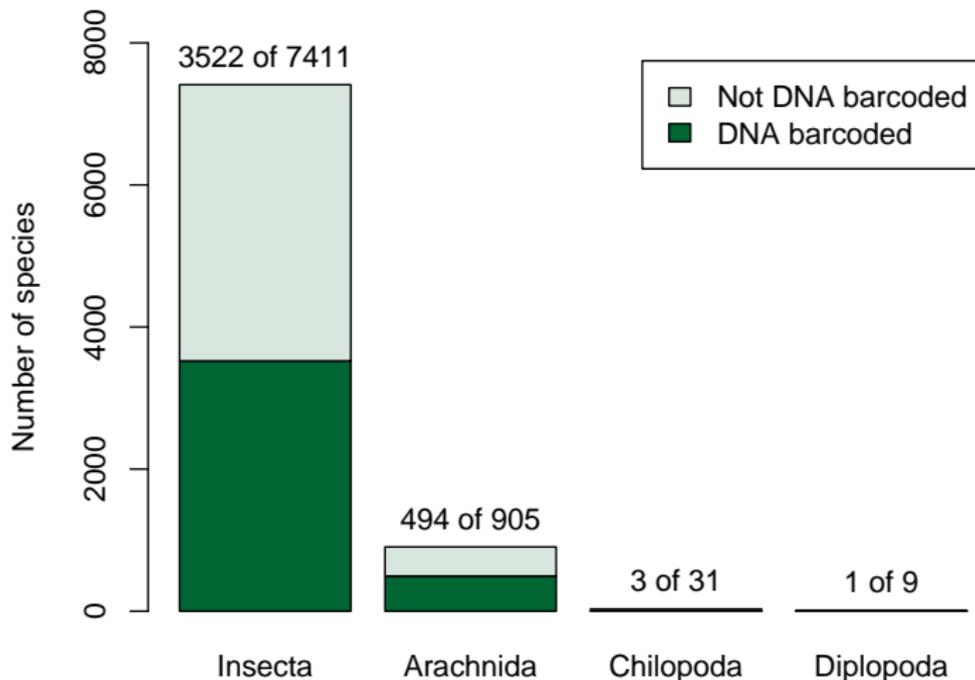


Alaska library: specimen localities

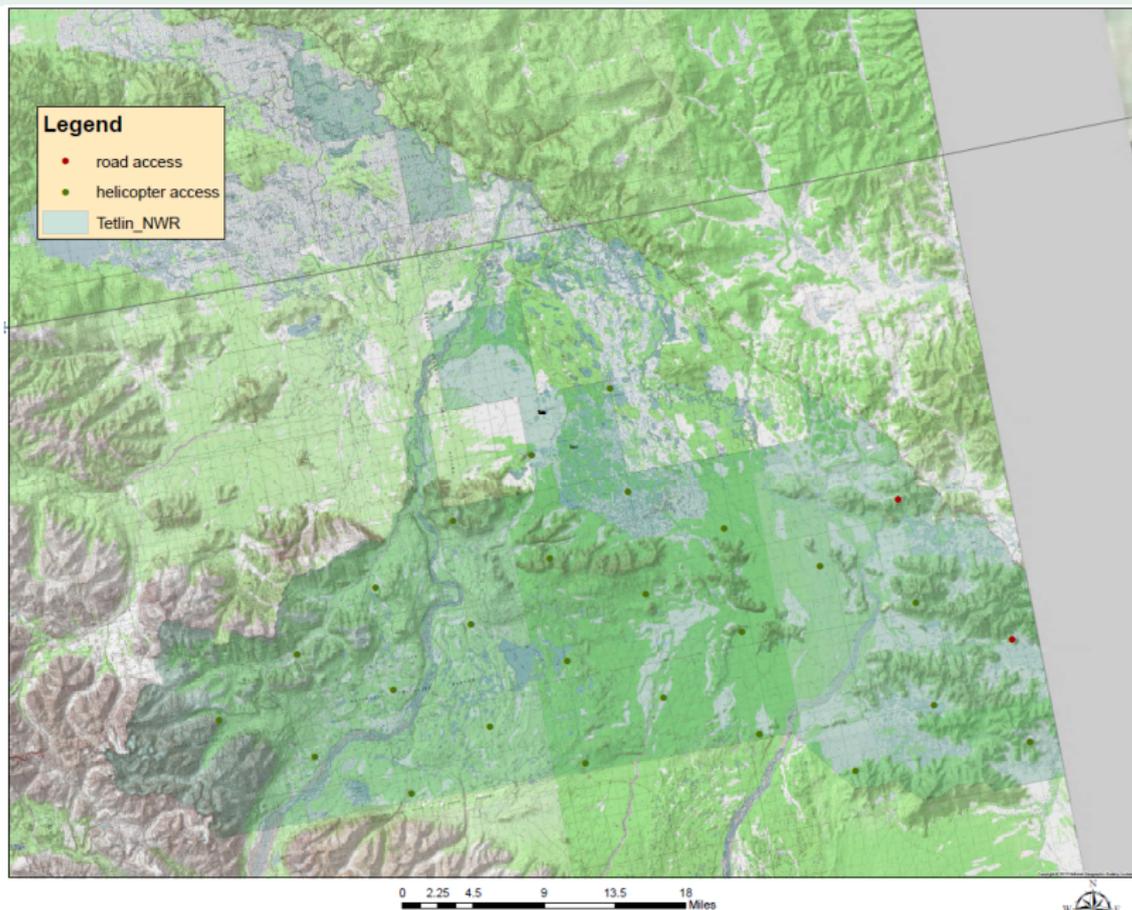


Alaska DNA barcode library: status

- ▶ 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**



Tetlin NWR 2014: design



Tetlin NWR 2014: field methods

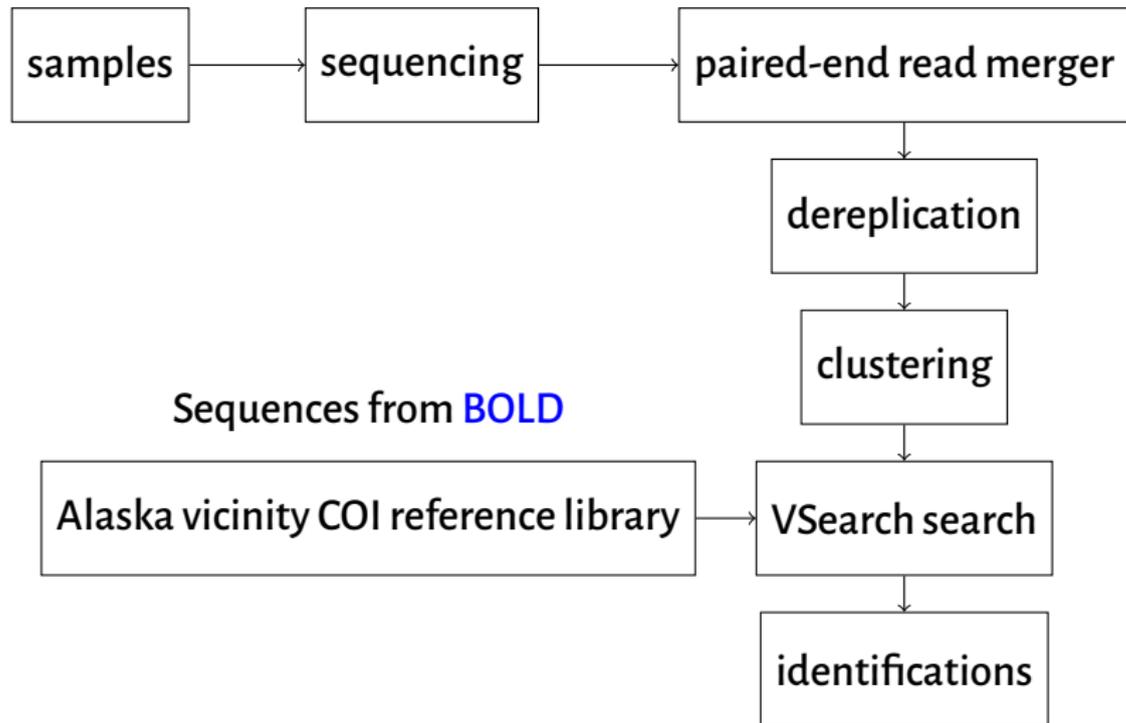


- ▶ Extensive remote-sense and vegetation data collected at 27 sites
- ▶ 2 sweep net samples at each site

Tetlin NWR 2014: molecular methods

Research and Testing Laboratory

Galaxy



Tetlin NWR 2014: results

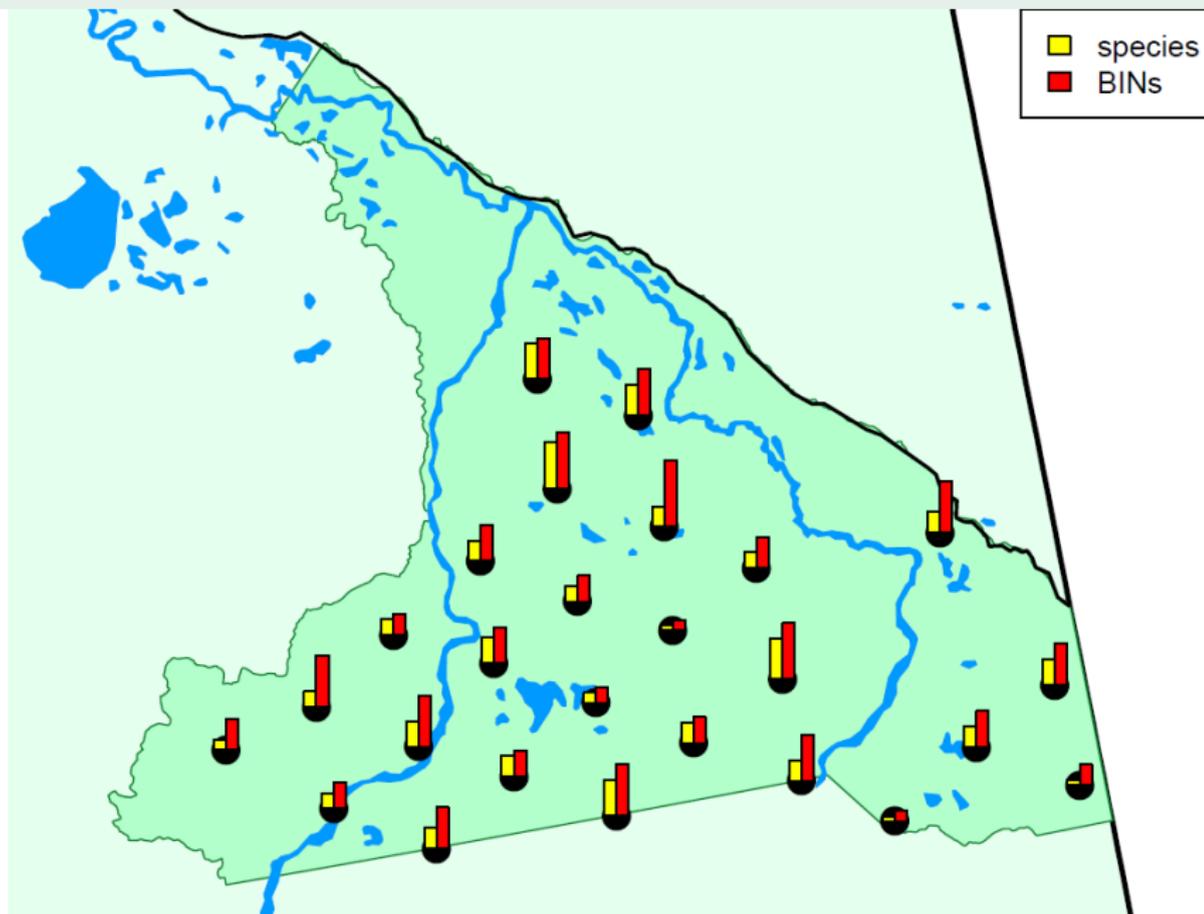
- ▶ 84 latin names at various levels of taxonomic resolution
- ▶ 53 species names
- ▶ **118 BINs**
- ▶ 1–9 species per plot
- ▶ 2–13 BINs per plot



Image from <http://www.commanster.eu/commanster/Insects/Flies/SuFlies/Ochlerotatus.communis.html>.

Most common species:
Ochlerotatus communis

Tetlin NWR 2014: results



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)

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...*

Acknowledgments

- ▶ **USFS Forest Inventory and Analysis program** (*sample frame design, field work, data on Kenai NWR & Tetlin NWR*)
- ▶ **Derek Sikes** and others, **University of Alaska Museum** (*Alaska regional arthropod DNA barcode library contributions*)
- ▶ **USFWS Alaska Regional Inventory and Monitoring program** (*funding for Tetlin NGS sequencing and Alaska regional arthropod DNA barcode library*)
- ▶ **Research and Testing Laboratory** (*sequencing*)
- ▶ **Dominique Collet** (*willow gall midges: ideas and advice*)