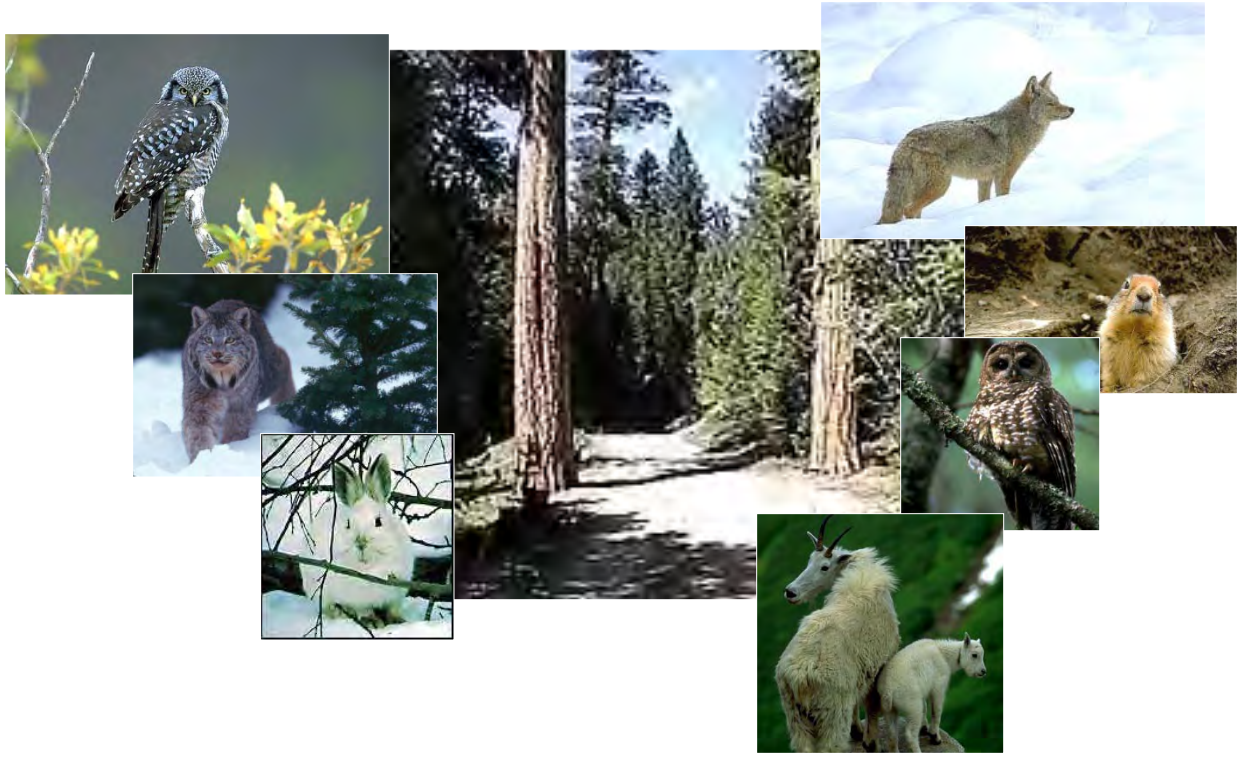
Efficient, reliable multi-species monitoring

Kevin S. McKelvey, Michael K. Schwartz, Michael K. Young, and Samuel A Cushman



A) Plan ~ what you think will happen

B) Inventory/monitoring ~ what actually happened

New Plan ~ based on (B), what you think will happen

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Why haven't we done more?

Science has not provided appropriate direction

Presence/absence sampling + genetic patterns

Genetics helps presence/absence

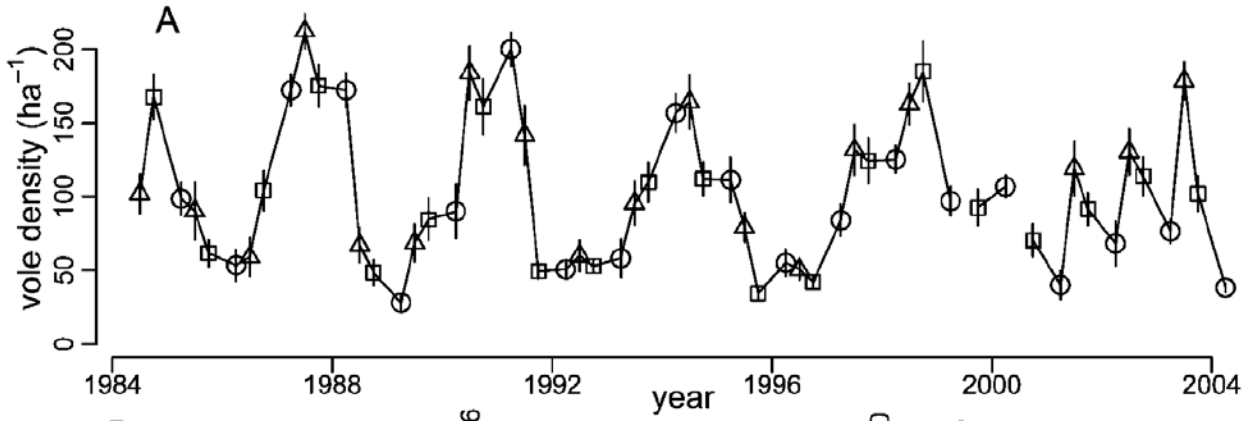
Mammals, birds and fish

Population size over time—gold standard

Difficult to impossible across large areas

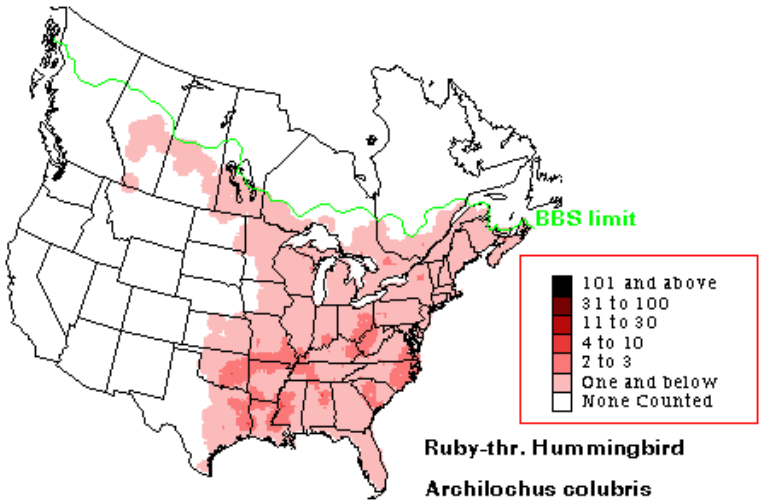
- Repeated captures
- Large proportion of the population

In many cases, not useful



From: Bierman et al. 2006

Indices based on organisms



Increasingly viewed as unreliable

Indirect indices

Habitat surrogates-- We manage habitat and monitor elements

We create more…

And hope for…

But…

≠

Indirect indices

Species surrogates

Without this

You can’t maintain this

But…

≠

Growing consensus -> presence/absence data

Explosion of statistical methodolgies

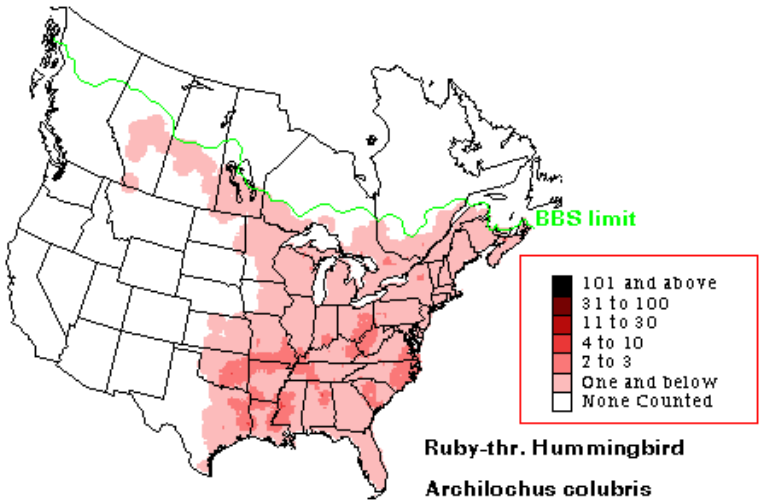
Area occupied = range/distribution

Focus on **where** population is expanding or declining

Hard to expand range while population decreases

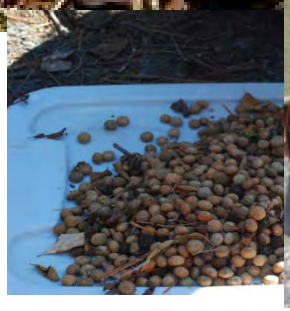
Spatial understandings link to management

Indices based on organisms



Much better for P/A!

Genetic Approaches to P/A



Non-invasive and eDNA

Chicago Sanitary and Ship Canal – Aquatic Nuisance Species Dispersal Barrier

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Overview: Fishes, including Asian carp, release DNA into

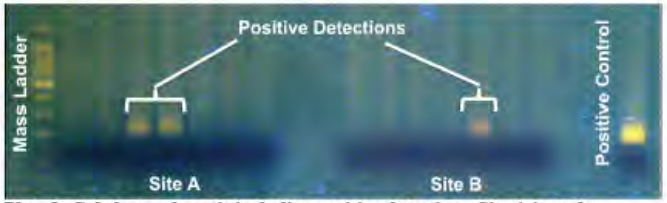


Plate 1: Gel electrophoresis including positive detections. Site A is at the confluence of the CSSC and the Des Plaines River in the Brandon Road pool and Site B is near a power plant in the Dresden Island Pool where water temperature exceeded 90F.

How will this improve our current monitoring?

The eDNA approach to surveillance will allow greater geographic coverage throughout the CSSC and connected waterways, and is

Presence/Absence has problems:

Sensitivity to change

Habitat fragmentation
Population fragmentation
Corridors

Spatial genetic patterns

Genetic patterns fill these gaps

Collection of spatial genetic data often virtually free
Generally less demanding than P/A

Analysis

Cost halving every 2 years

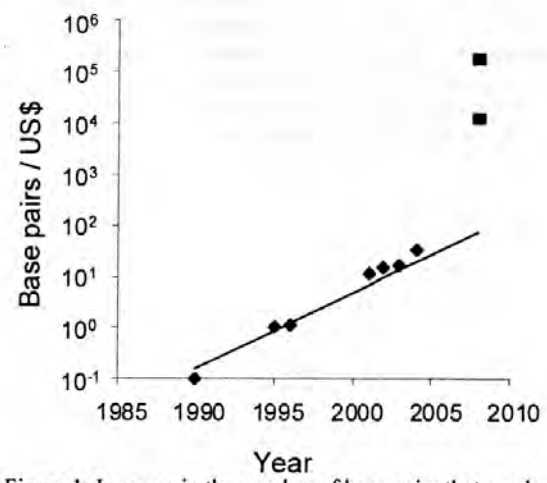


Figure 1: Increase in the number of base pairs that can be sequenced for one US dollar. Until recently, sequencing costs declined (and number of basepairs/US$ increased) exponentially, halving about every two years. Recent developments in pyrosequencing and related techniques allowed a massive leap in efficiency. Further leaps are likely to occur in the near future (see text). Data from (Shendure et al., 2004, Kurzweil, 2005, Mardis, 2008).

From: Hauser and Seeb 2008

Sensitive to movement/fragmentation

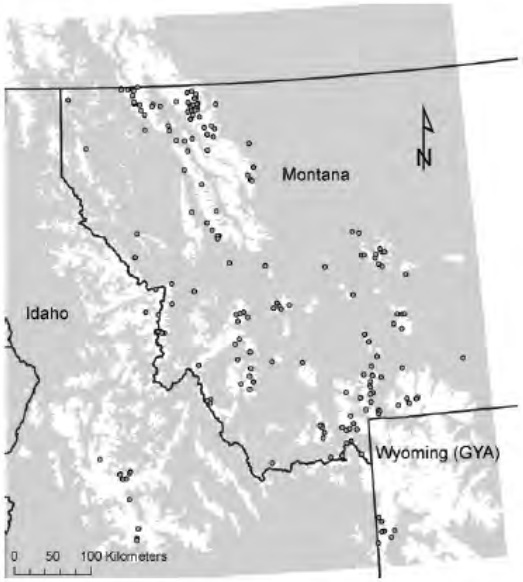
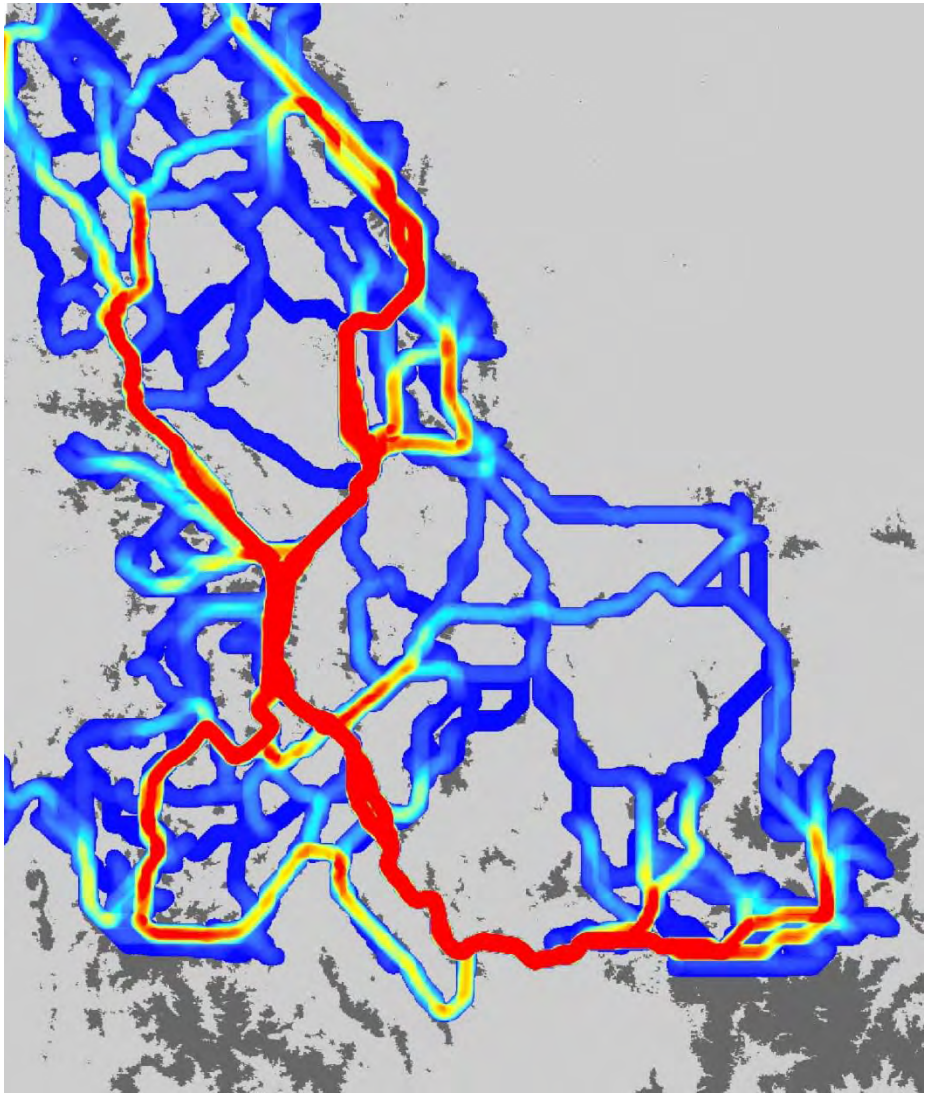


FIG. 1. Map of the northern U.S. Rockies. The white areas are locations of the spring snow cover bioclimatic envelope (J. P. Copeland et al., *unpublished manuscript*), whereas the gray areas do not have spring snow cover. Circles are locations of samples collected between 1989 and 2006. GYA stands for the Greater Yellowstone Area.



210 wolverines

Empirical corridor map

Schwartz et al. 2009

Conclusion

Past approaches (abundance/surrogates) don't provide solutions

Presence/Absence + Spatial genetics in many cases will

Genetic costs halving every 2 years

New genetic methods
- massively parallel sequencing
- eDNA