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Genetic methods for monitoring aquatic invasive species

A case study in rapid evolution

John Darling
Center for Environmental Measurement & Modeling
US Environmental Protection Agency

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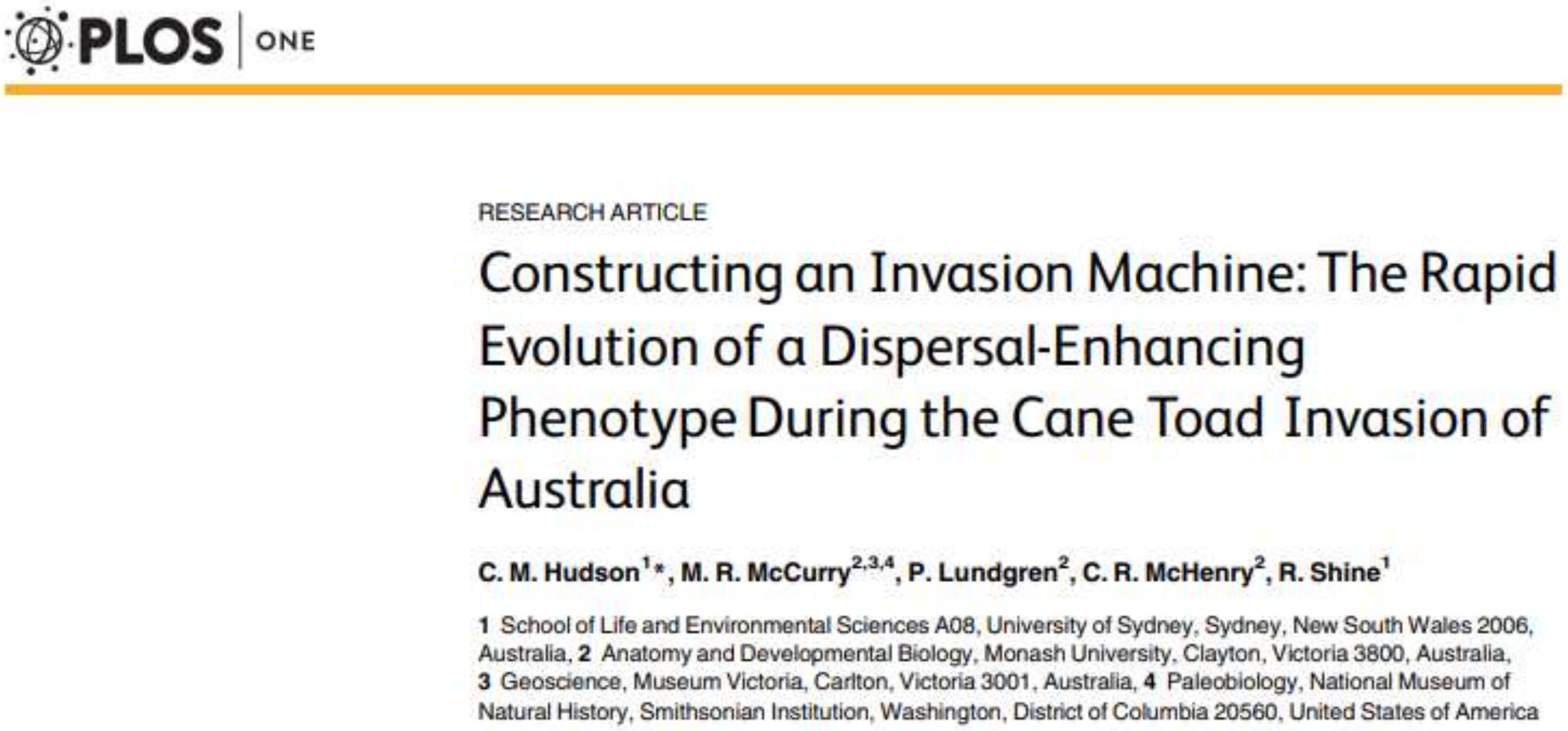

PLOS | ONE

RESEARCH ARTICLE

Constructing an Invasion Machine: The Rapid Evolution of a Dispersal-Enhancing Phenotype During the Cane Toad Invasion of Australia

C. M. Hudson[1]*, M. R. McCurry[2,3,4], P. Lundgren[2], C. R. McHenry[2], R. Shine[1]

1 School of Life and Environmental Sciences A08, University of Sydney, Sydney, New South Wales 2006, Australia, **2** Anatomy and Developmental Biology, Monash University, Clayton, Victoria 3800, Australia, **3** Geoscience, Museum Victoria, Carlton, Victoria 3001, Australia, **4** Paleobiology, National Museum of Natural History, Smithsonian Institution, Washington, District of Columbia 20560, United States of America

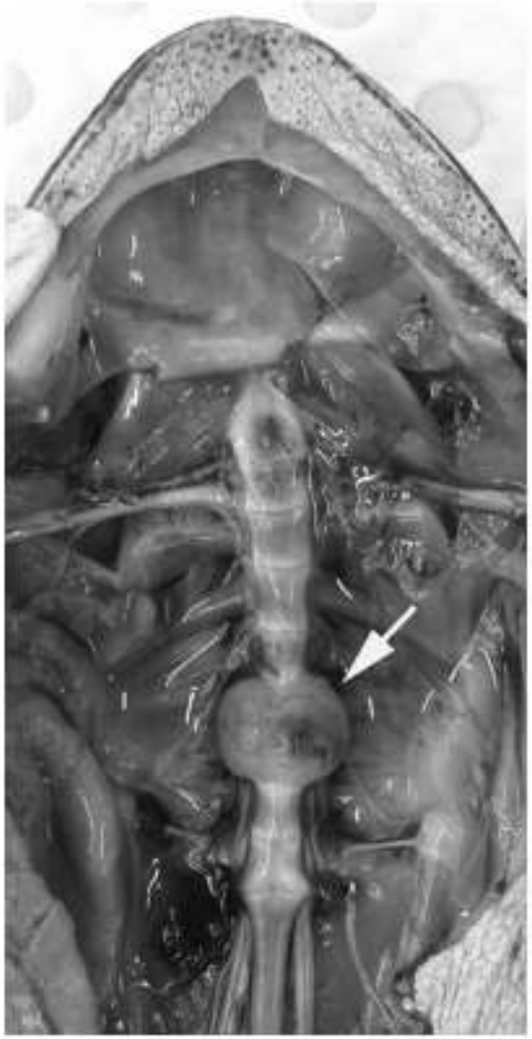

Fig. 1. Dissection of an adult cane toad with viscera removed showing ventral view of spinal column. Note the marked enlargement of bodies of vertebrae 7 and 8 with fusion of intervertebral joint.

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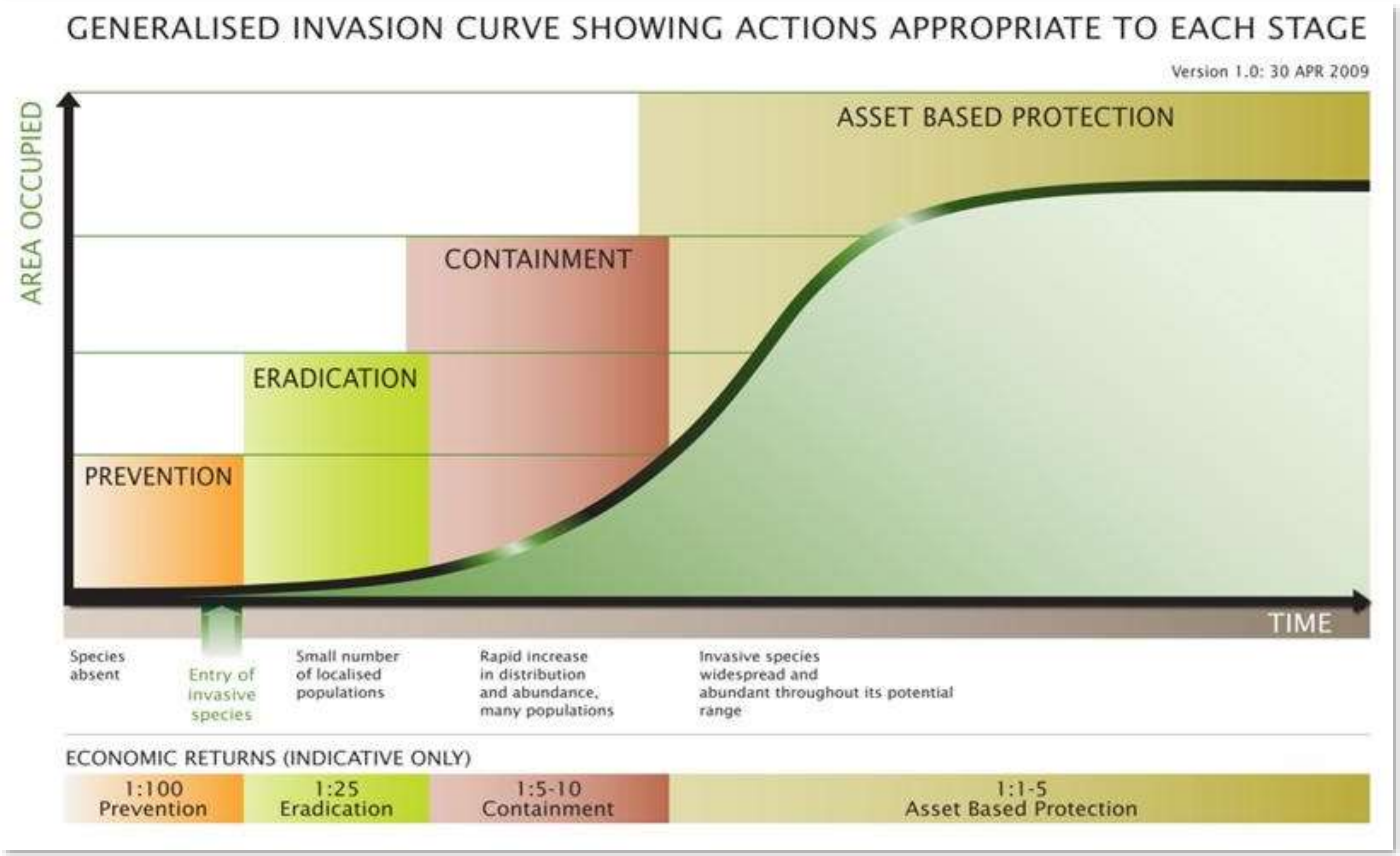
What kinds of tools do we need?

THE PROBLEM OF DETECTION

The Problem of Detection



GENERALISED INVASION CURVE SHOWING ACTIONS APPROPRIATE TO EACH STAGE

Version 1.0: 30 APR 2009

Department of Primary Industries, Australia

The Problem of Detection

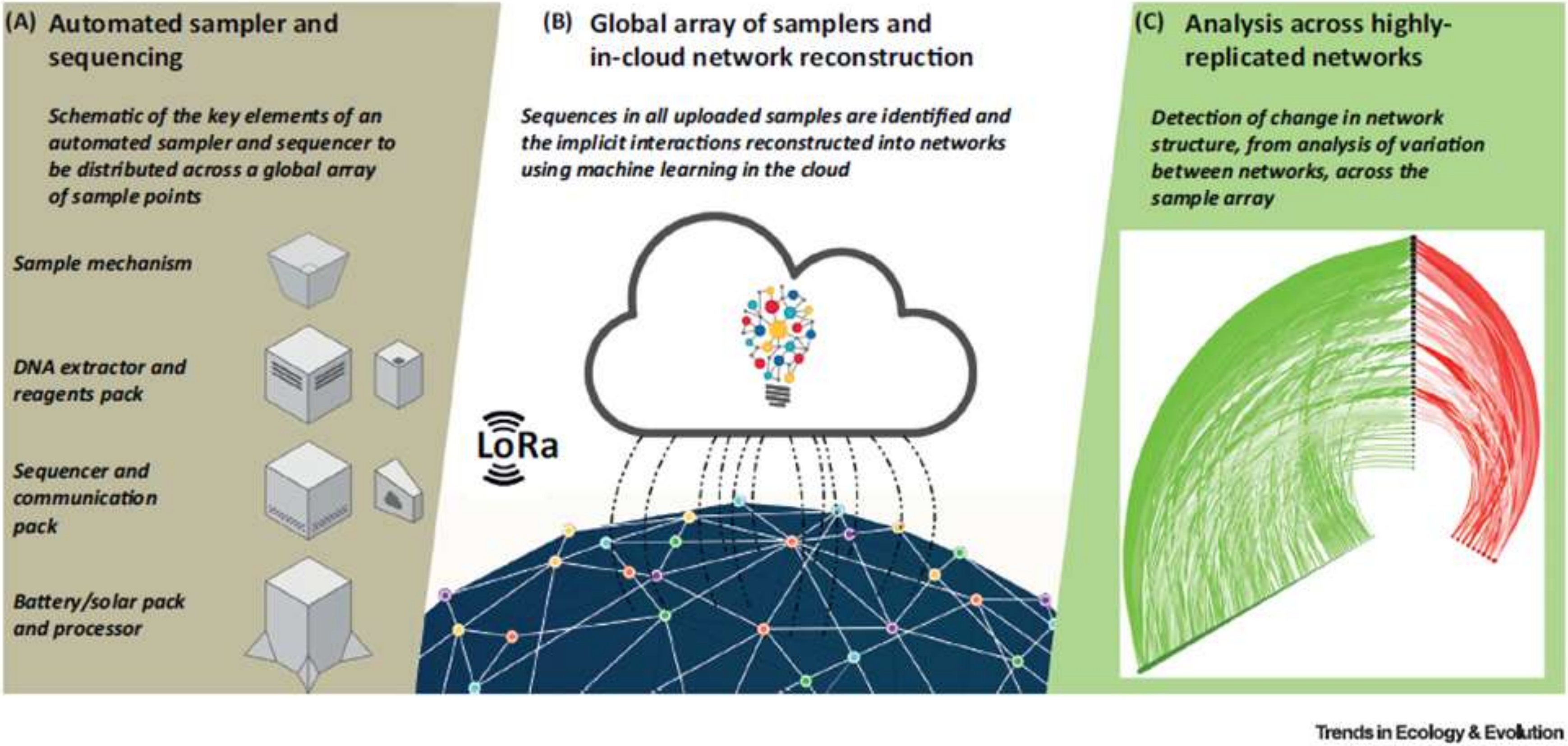
More sensitive

Faster

Less expensive

More easily deployable

Science? Or science fiction?



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Schematic of the key elements of an automated sampler and sequencer to be distributed across a global array of sample points

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Detection of change in network structure, from analysis of variation between networks, across the sample array

Trends in Ecology & Evolution

Bohan et al. 2017. *Trends in Ecology and Evolution*

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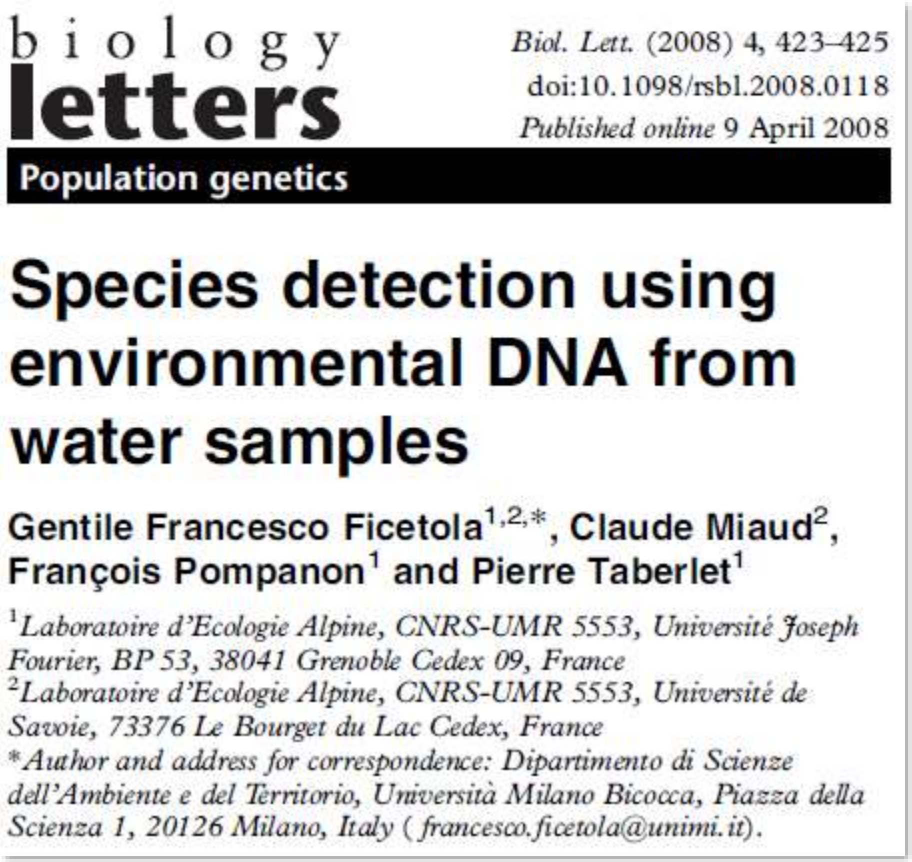
A conceptual breakthrough enabling “sight-unseen” detection

ENVIRONMENTAL DNA



biology letters

Biol. Lett. (2008) 4, 423–425
doi:10.1098/rsbl.2008.0118
Published online 9 April 2008

Population genetics

Species detection using environmental DNA from water samples

Gentile Francesco Ficetola[1,2,*], Claude Miaud[2], François Pompanon[1] and Pierre Taberlet[1]

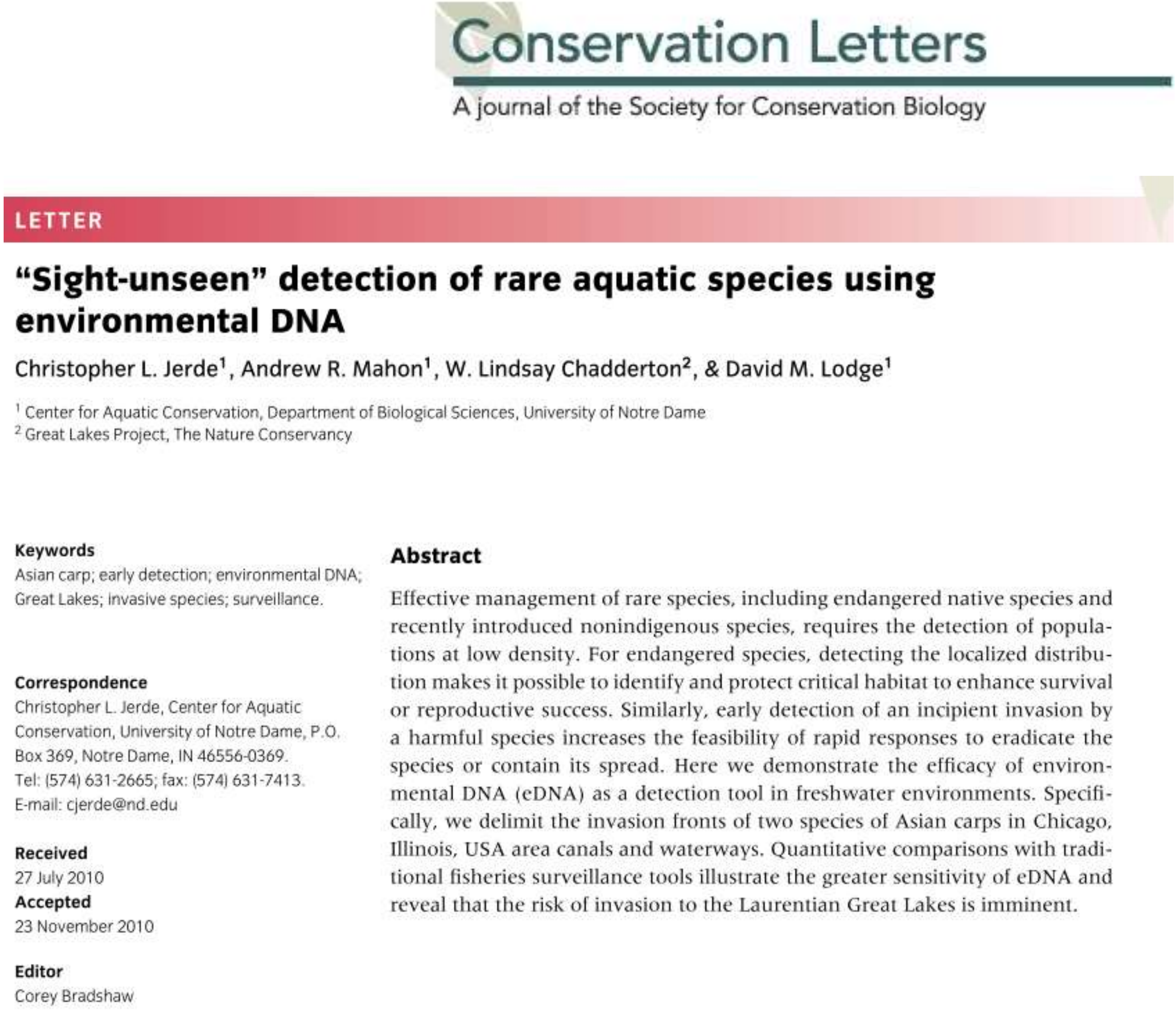
[1]*Laboratoire d'Ecologie Alpine, CNRS-UMR 5553, Université Joseph Fourier, BP 53, 38041 Grenoble Cedex 09, France*
[2]*Laboratoire d'Ecologie Alpine, CNRS-UMR 5553, Université de Savoie, 73376 Le Bourget du Lac Cedex, France*
**Author and address for correspondence: Dipartimento di Scienze dell'Ambiente e del Territorio, Università Milano Bicocca, Piazza della Scienza 1, 20126 Milano, Italy (francesco.ficetola@unimi.it).*

Environmental DNA

noun

also eDNA

DNA present in the environment that can be collected and extracted without the isolation of the target organism(s)



Conservation Letters
A journal of the Society for Conservation Biology

LETTER

“Sight-unseen” detection of rare aquatic species using environmental DNA

Christopher L. Jerde[1], Andrew R. Mahon[1], W. Lindsay Chadderton[2], & David M. Lodge[1]

[1] Center for Aquatic Conservation, Department of Biological Sciences, University of Notre Dame
[2] Great Lakes Project, The Nature Conservancy

Keywords
Asian carp; early detection; environmental DNA; Great Lakes; invasive species; surveillance.

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Received
27 July 2010
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Editor
Corey Bradshaw

Abstract

Effective management of rare species, including endangered native species and recently introduced nonindigenous species, requires the detection of populations at low density. For endangered species, detecting the localized distribution makes it possible to identify and protect critical habitat to enhance survival or reproductive success. Similarly, early detection of an incipient invasion by a harmful species increases the feasibility of rapid responses to eradicate the species or contain its spread. Here we demonstrate the efficacy of environmental DNA (eDNA) as a detection tool in freshwater environments. Specifically, we delimit the invasion fronts of two species of Asian carps in Chicago, Illinois, USA area canals and waterways. Quantitative comparisons with traditional fisheries surveillance tools illustrate the greater sensitivity of eDNA and reveal that the risk of invasion to the Laurentian Great Lakes is imminent.

Where there’s smoke there’s fire…

…right?

LOOP NORTH NEWS

CHICAGO RIVER

Chicago River businesses to Corps of Engineers…

Show us the carp!

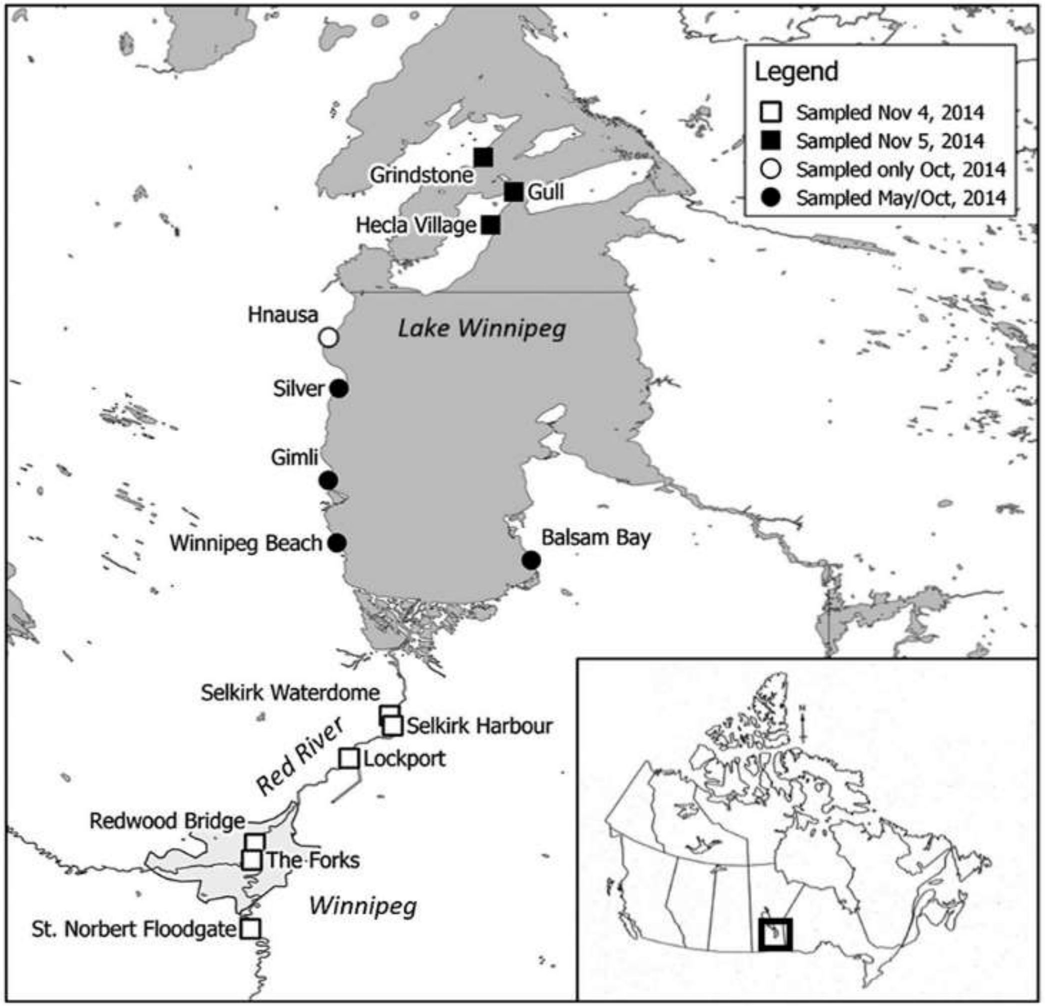
By Steven Dahlman

- Specter of lock closure already having economic impact on river
- Commercial users of Chicago River urge feds to find another way to control Asian carp

The Central Challenge of Environmental DNA

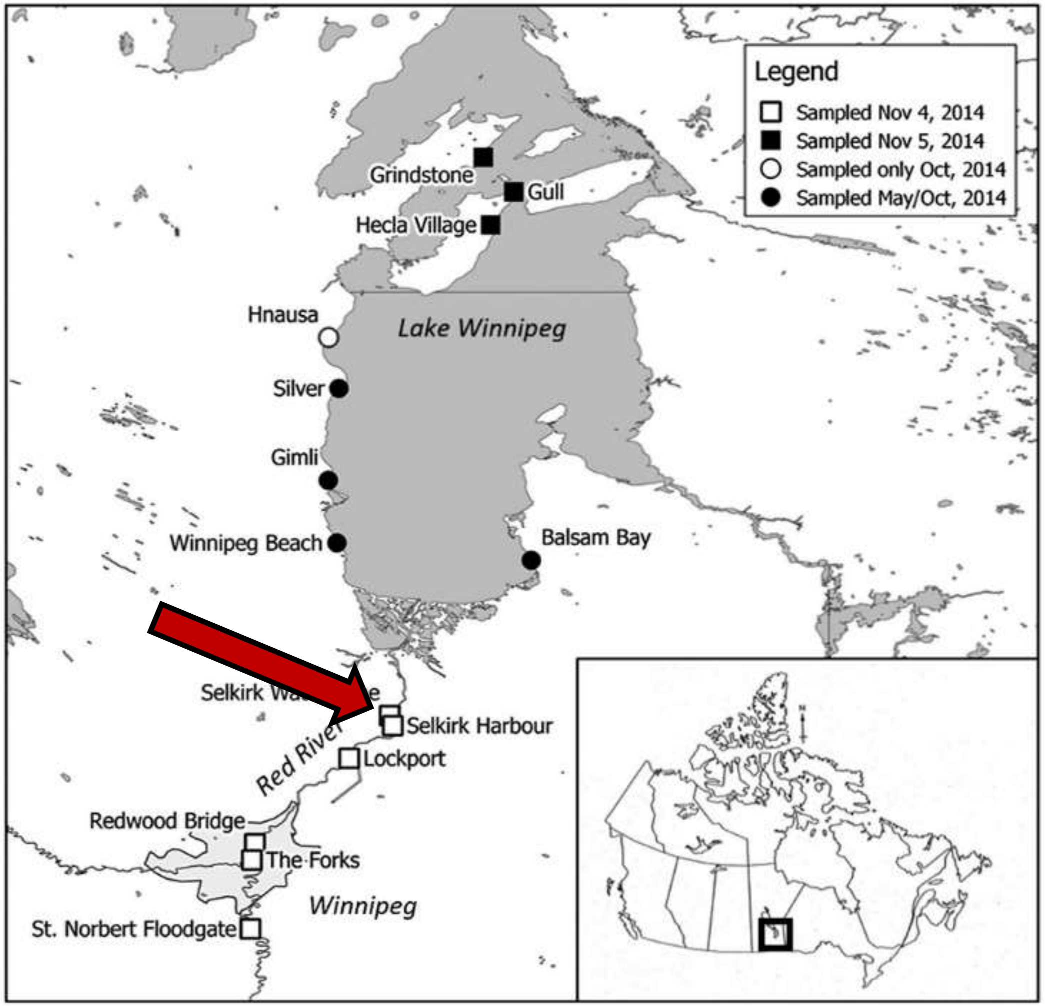
Is it possible to infer an underlying population distribution from a pattern of DNA detections?

eDNA can provide us with valuable new information



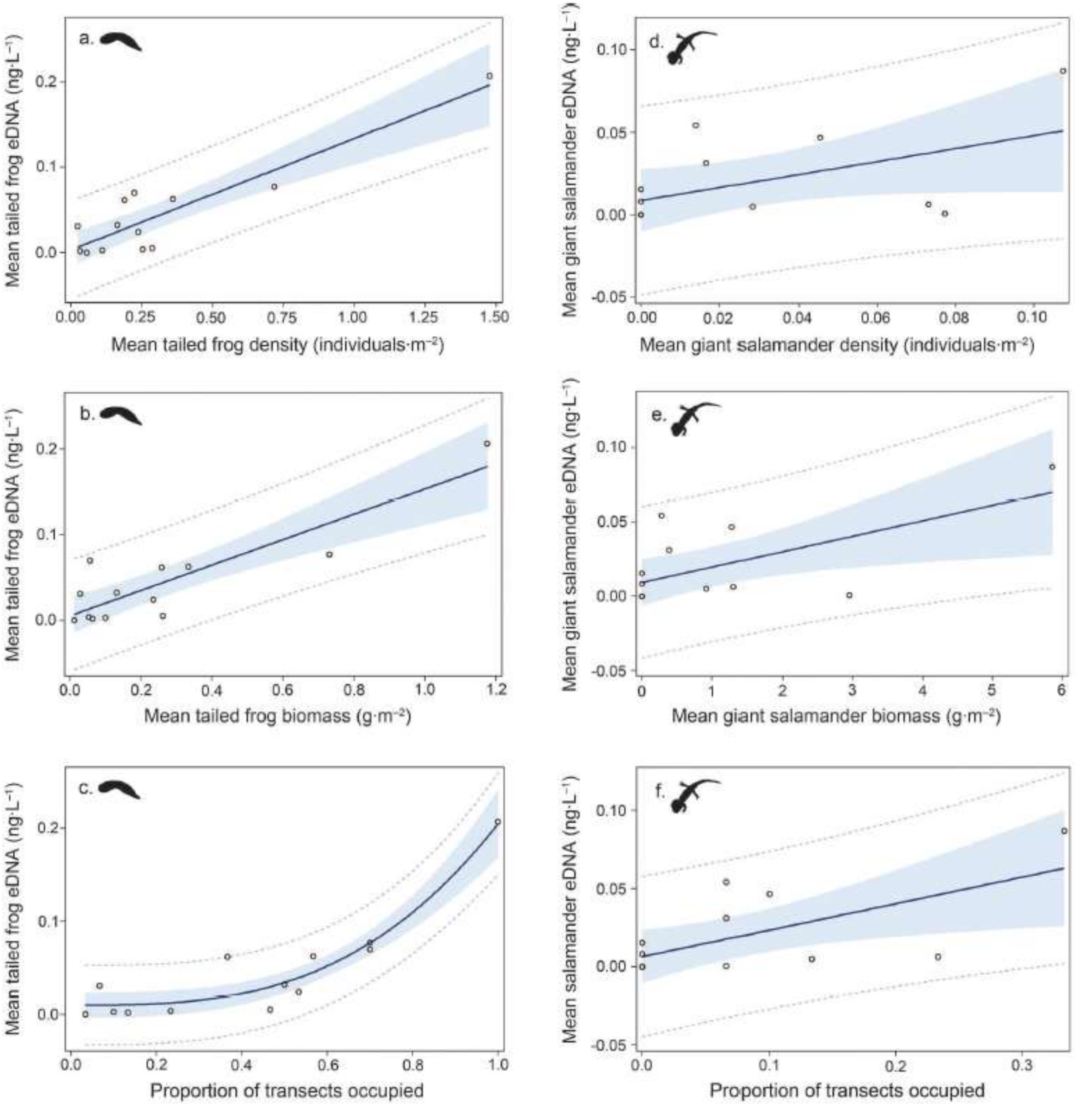
Gingera et al. 2017. *Management of Biological Invasions*

eDNA can provide us with valuable new information

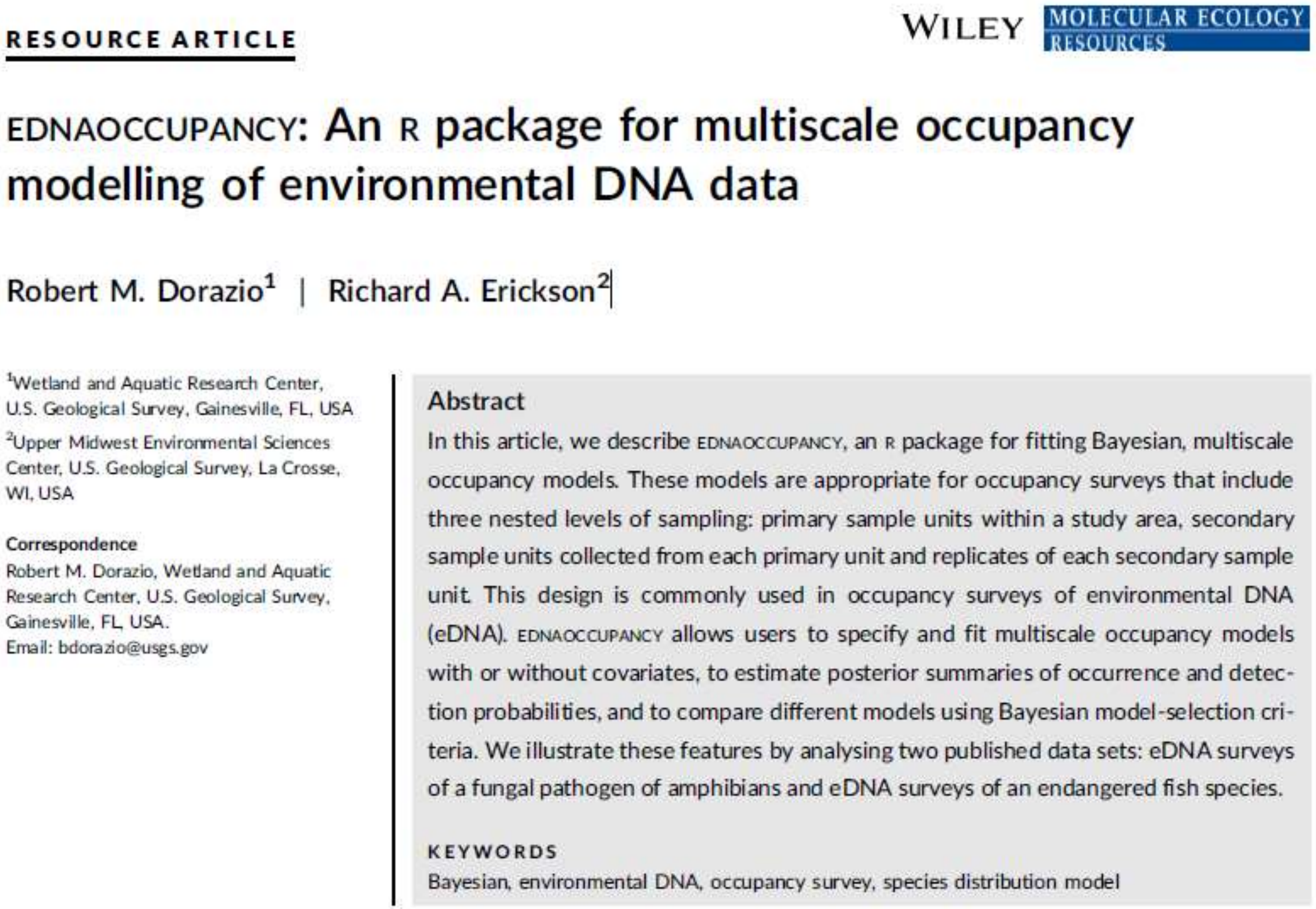


Gingera et al. 2017. *Management of Biological Invasions*

eDNA detections can be correlated with underlying population density



Pilliod et al. 2013. *Canadian Journal of Fisheries and Aquatic Sciences*



RESOURCE ARTICLE

WILEY MOLECULAR ECOLOGY RESOURCES

EDNAOCCUPANCY: An R package for multiscale occupancy modelling of environmental DNA data

Robert M. Dorazio[1] | Richard A. Erickson[2]

[1]Wetland and Aquatic Research Center, U.S. Geological Survey, Gainesville, FL, USA

[2]Upper Midwest Environmental Sciences Center, U.S. Geological Survey, La Crosse, WI, USA

Correspondence
Robert M. Dorazio, Wetland and Aquatic Research Center, U.S. Geological Survey, Gainesville, FL, USA.
Email: bdorazio@usgs.gov

Abstract

In this article, we describe EDNAOCCUPANCY, an R package for fitting Bayesian, multiscale occupancy models. These models are appropriate for occupancy surveys that include three nested levels of sampling: primary sample units within a study area, secondary sample units collected from each primary unit and replicates of each secondary sample unit. This design is commonly used in occupancy surveys of environmental DNA (eDNA). EDNAOCCUPANCY allows users to specify and fit multiscale occupancy models with or without covariates, to estimate posterior summaries of occurrence and detection probabilities, and to compare different models using Bayesian model-selection criteria. We illustrate these features by analysing two published data sets: eDNA surveys of a fungal pathogen of amphibians and eDNA surveys of an endangered fish species.

KEYWORDS
Bayesian, environmental DNA, occupancy survey, species distribution model

The Problem of Detection

More sensitive

Faster

Less expensive

More easily deployable

The Problem of Detection

- More sensitive ✓
- Faster
- Less expensive
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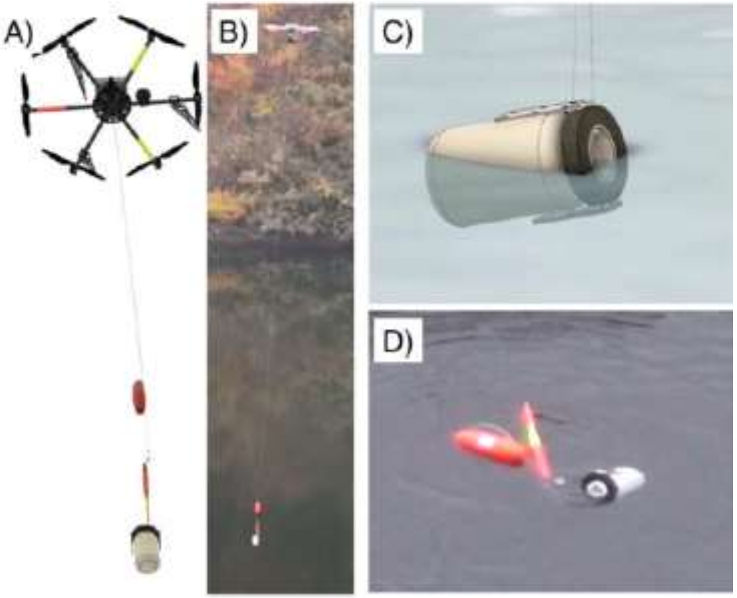
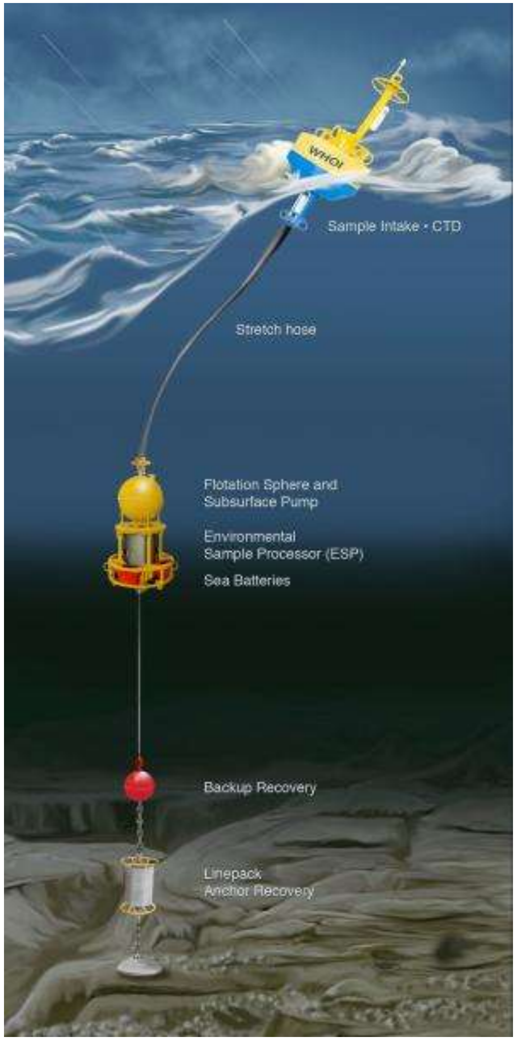
Science? Or science fiction?





We couldn't afford one of those cool PCR robots,
so we just got an undergrad and a cardboard box.

BUT WHAT ABOUT FALSE POSITIVES?

THE CORONAVIRUS CRISIS

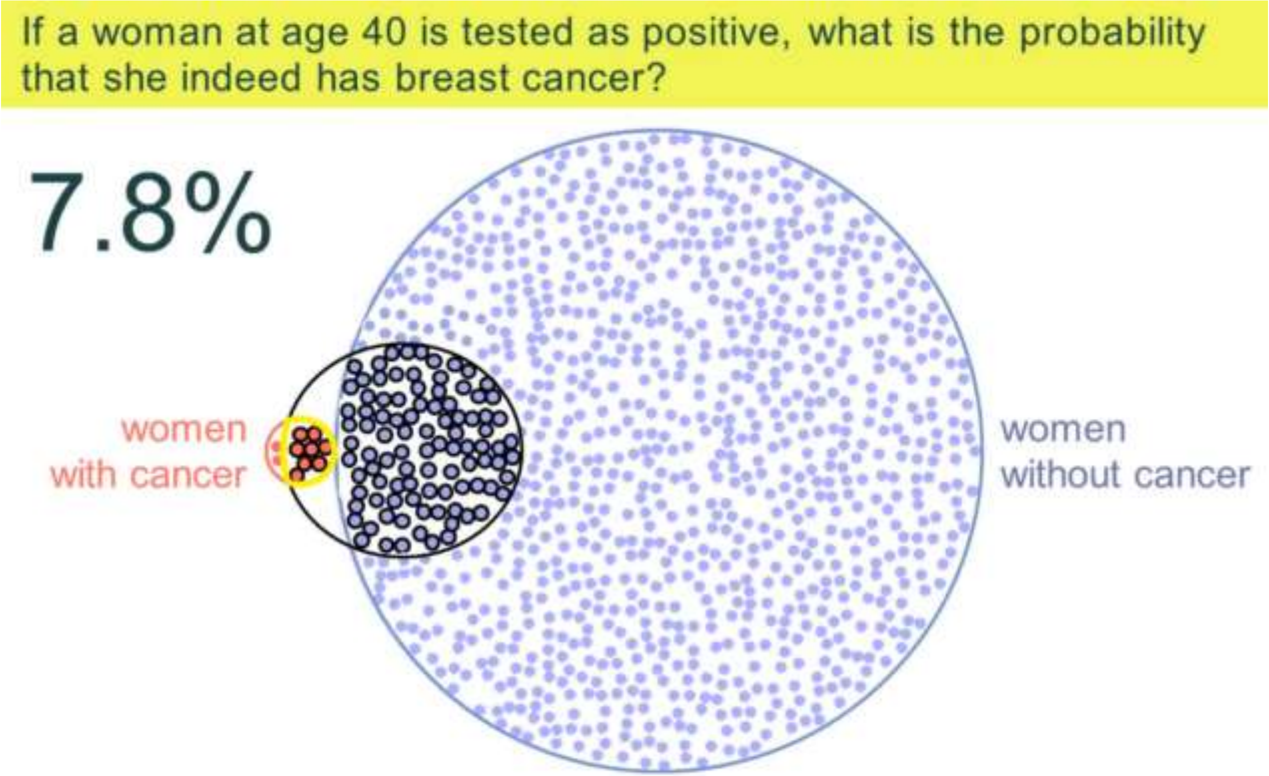
What Zebra Mussels Can Tell Us About Errors In Coronavirus Tests

June 15, 2020 · 5:00 AM ET

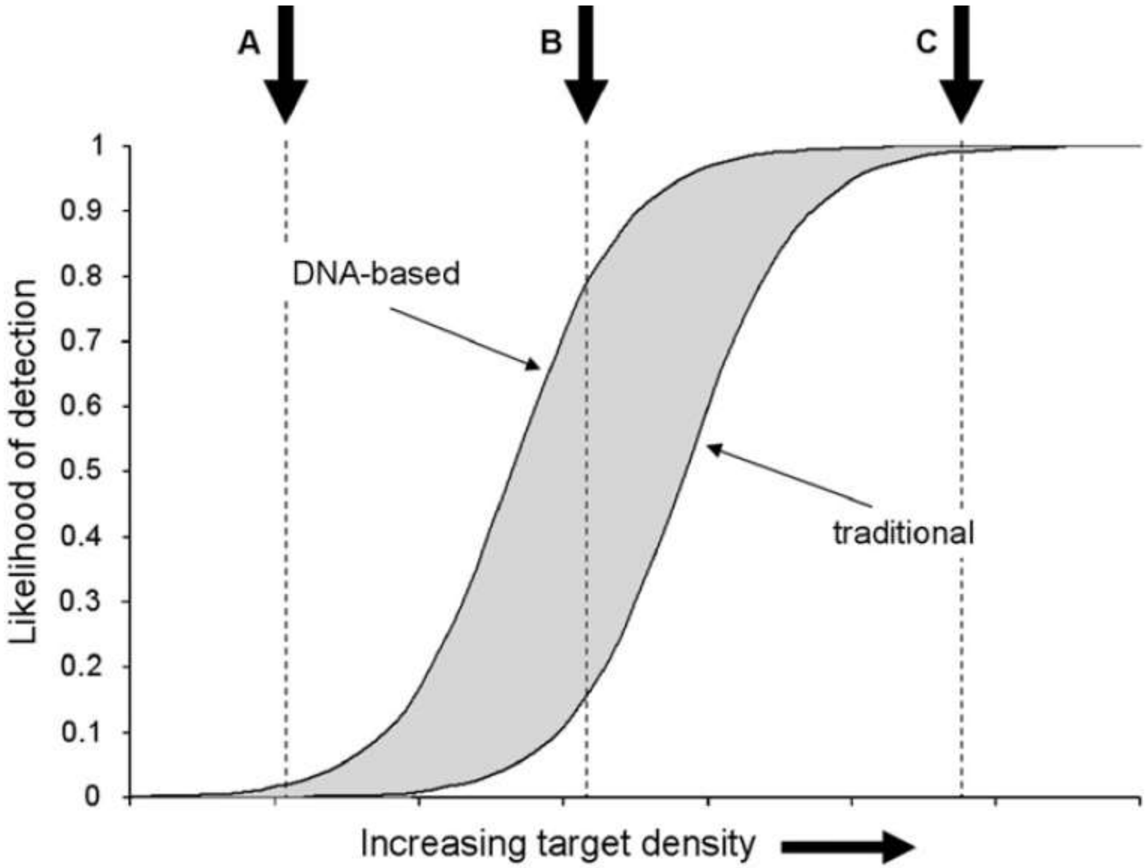
RICHARD HARRIS

3-Minute Listen

The Base Rate Fallacy



If a woman at age 40 is tested as positive, what is the probability that she indeed has breast cancer?


A
B
C
1
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
Likelihood of detection
DNA-based
traditional
Increasing target density

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A technological breakthrough allowing description of entire communities

HIGH THROUGHPUT SEQUENCING

DNA barcode

noun

A short DNA sequence that can be uniquely associated with a particular species

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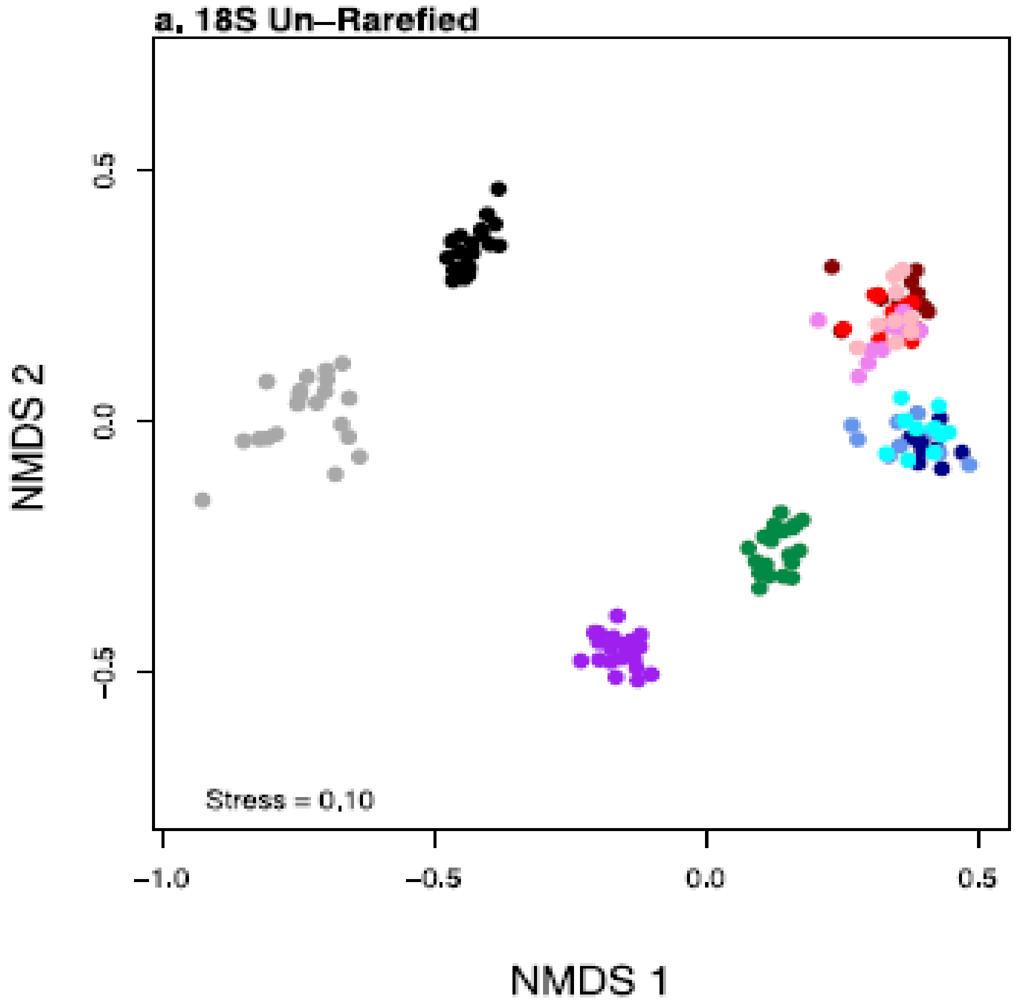
DNA metabarcode

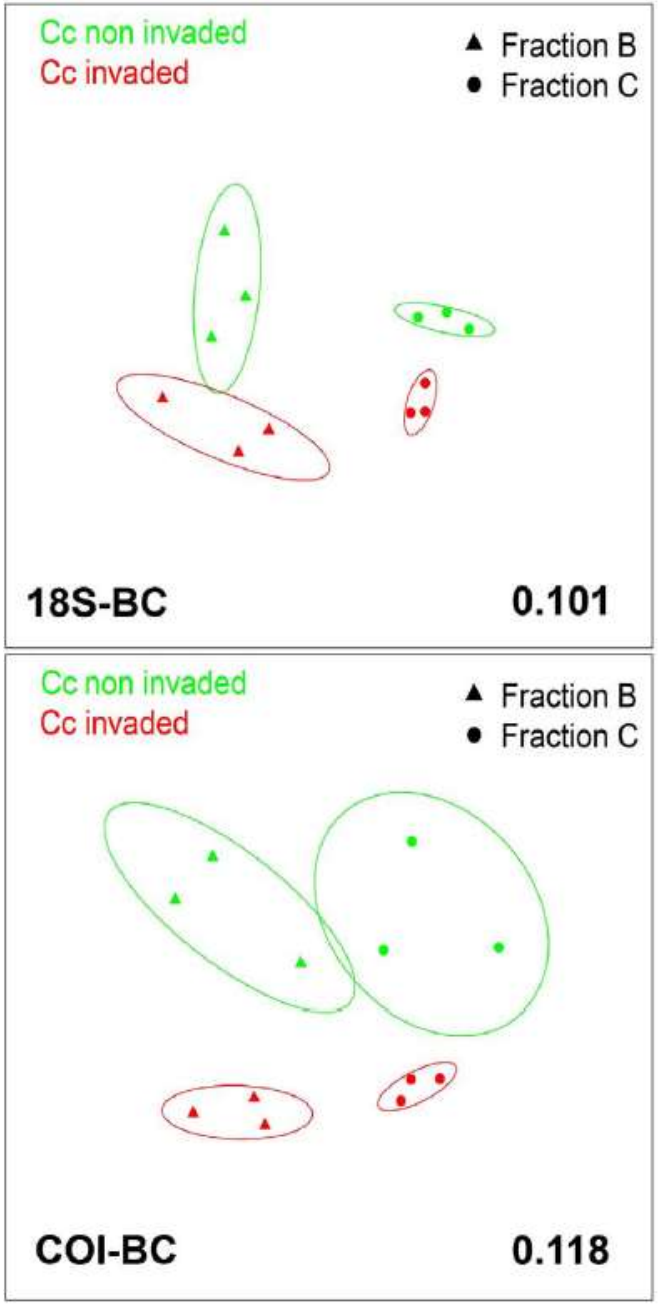
noun

A collection of short DNA sequences that can be uniquely associated with a particular environmental sample



Metabarcodes can identify samples based on source location

Grey et al. 2018. *Scientific Reports*



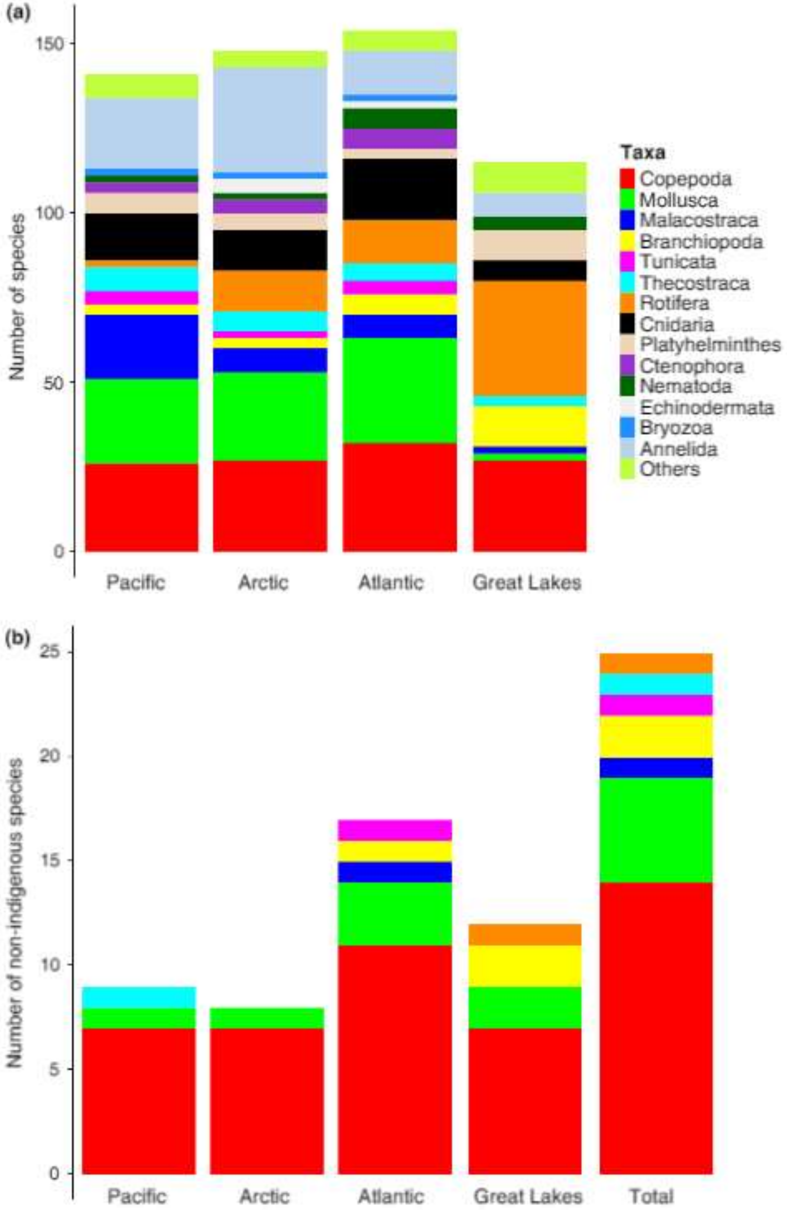
Wagensteen et al. 2018. *Marine Pollution Bulletin*

Metabarcodes can recognize changes in community structure associated with invasions

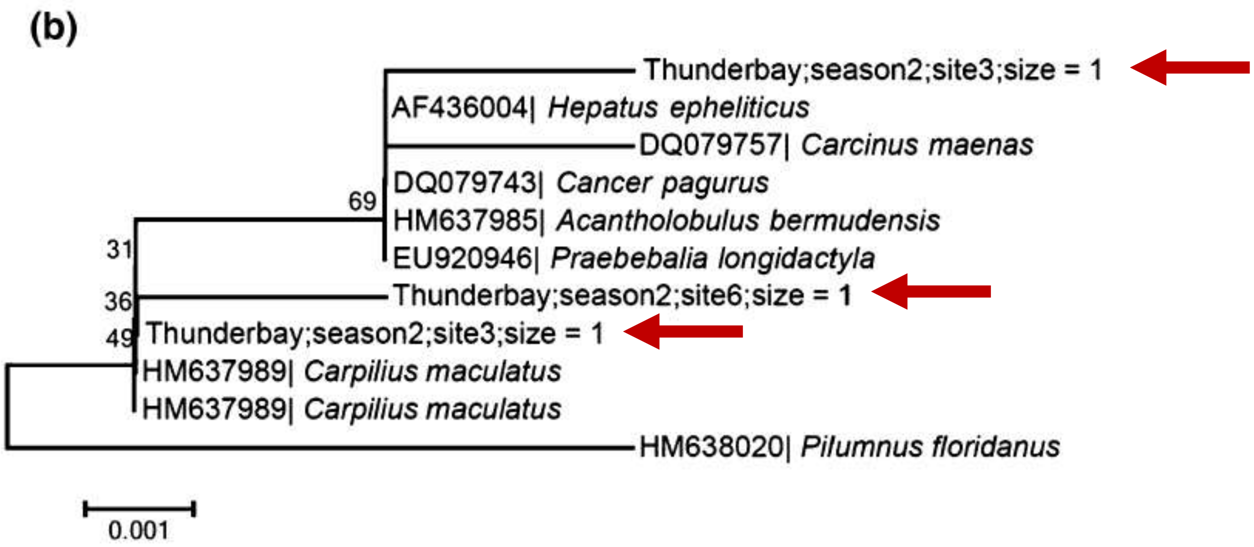
The Central Challenges of DNA metabarcoding

1. Can we develop standardized methods to generate metabarcodes that informatively and reproducibly reflect the biodiversity in a sample?

Metabarcodes identify more than 20 non-native aquatic species from 147 samples taken from 16 Canadian ports



Brown et al. 2016. *Diversity & Distributions*



Assignment of species-level identities can be challenging.

Brown et al. 2016. *Diversity & Distributions*

The Central Challenges of DNA metabarcoding

1. Can we find standardized methods to generate metabarcodes that informatively and reproducibly reflect the biodiversity in a sample?

2. Can we develop methods that consistently enable confident taxonomic assignments at informative resolution?

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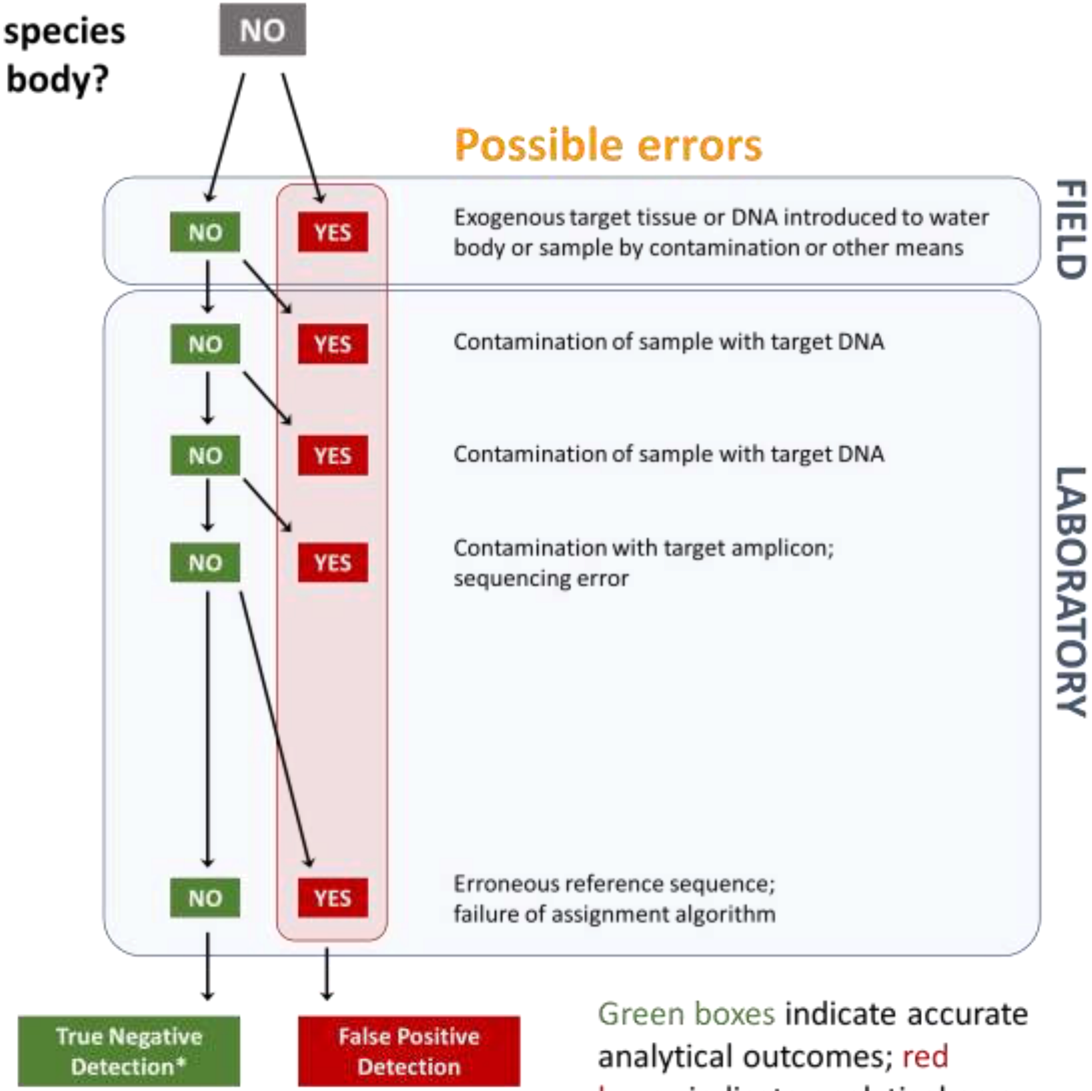
HOW CAN WE TRUST INCIDENTAL DETECTIONS OF SPECIES OF CONCERN?

Is the target species in the water body?



NO

Possible errors

FIELD

NO | YES — Exogenous target tissue or DNA introduced to water body or sample by contamination or other means

LABORATORY

NO | YES — Contamination of sample with target DNA

NO | YES — Contamination of sample with target DNA

NO | YES — Contamination with target amplicon; sequencing error

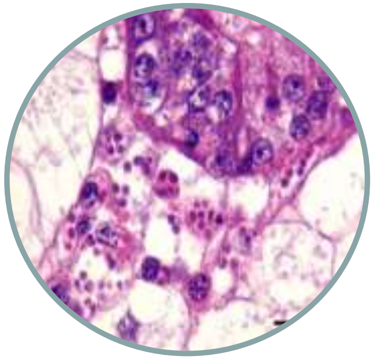
NO | YES — Erroneous reference sequence; failure of assignment algorithm

True Negative Detection*

False Positive Detection

Green boxes indicate accurate analytical outcomes; red boxes indicate analytical error

*assumes that sampling intensity is sufficient to provide high statistical likelihood of capturing target when present



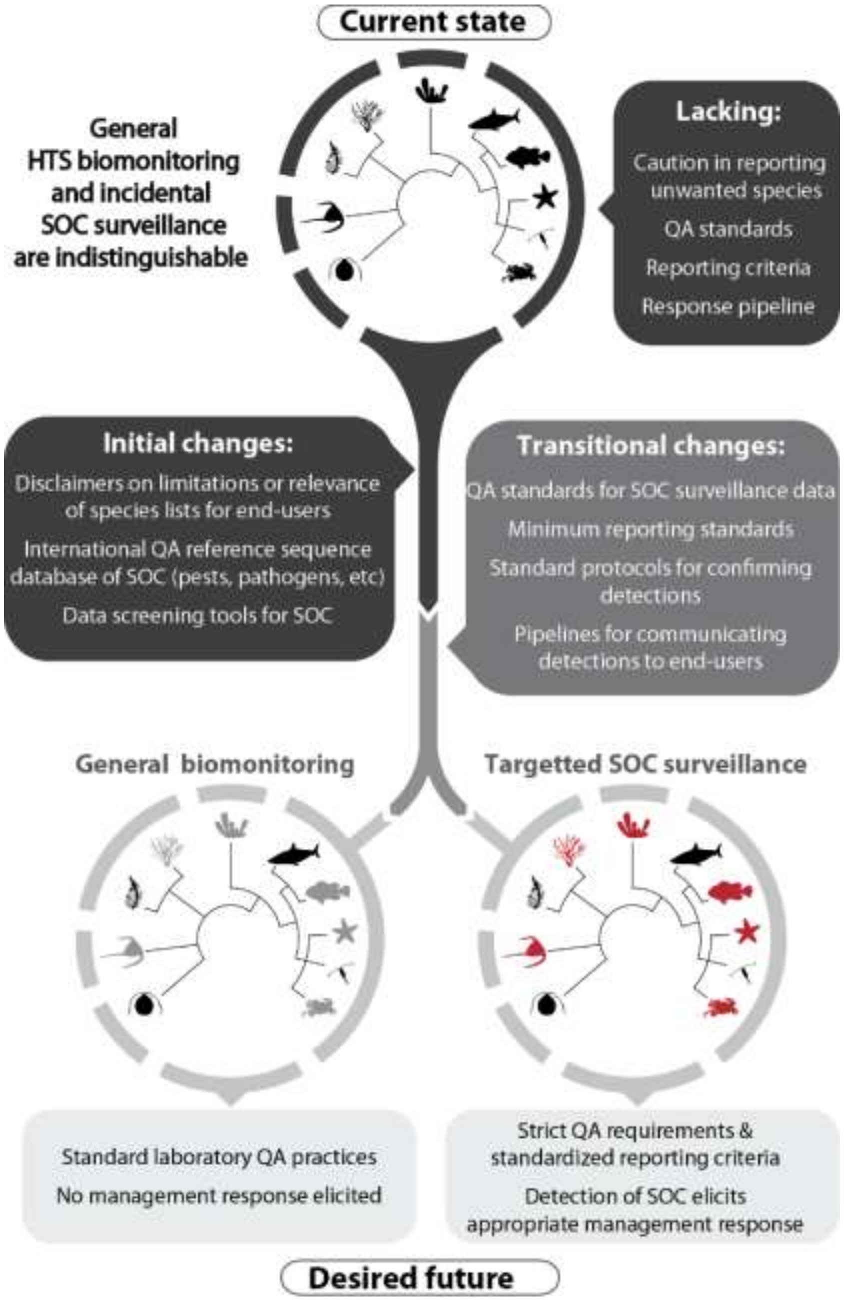
Ministry for Primary Industries
Manatū Ahu Matua

CONTROLLED AREA NOTICE

NOTICE UNDER THE BIOSECURITY ACT 1993

SECTION 131 - CONTROLLED AREA, MOVEMENT CONTROLS AND PROCEDURES IN RESPECT OF BONAMIA OSTREAE (*B. ostreae*)

How can we meet the needs of end-users without over-burdening scientists?



Current state

General HTS biomonitoring and incidental SOC surveillance are indistinguishable

Lacking:

Caution in reporting unwanted species

QA standards

Reporting criteria

Response pipeline

Initial changes:

Disclaimers on limitations or relevance of species lists for end-users

International QA reference sequence database of SOC (pests, pathogens, etc)

Data screening tools for SOC

Transitional changes:

QA standards for SOC surveillance data

Minimum reporting standards

Standard protocols for confirming detections

Pipelines for communicating detections to end-users

General biomonitoring

Standard laboratory QA practices

No management response elicited

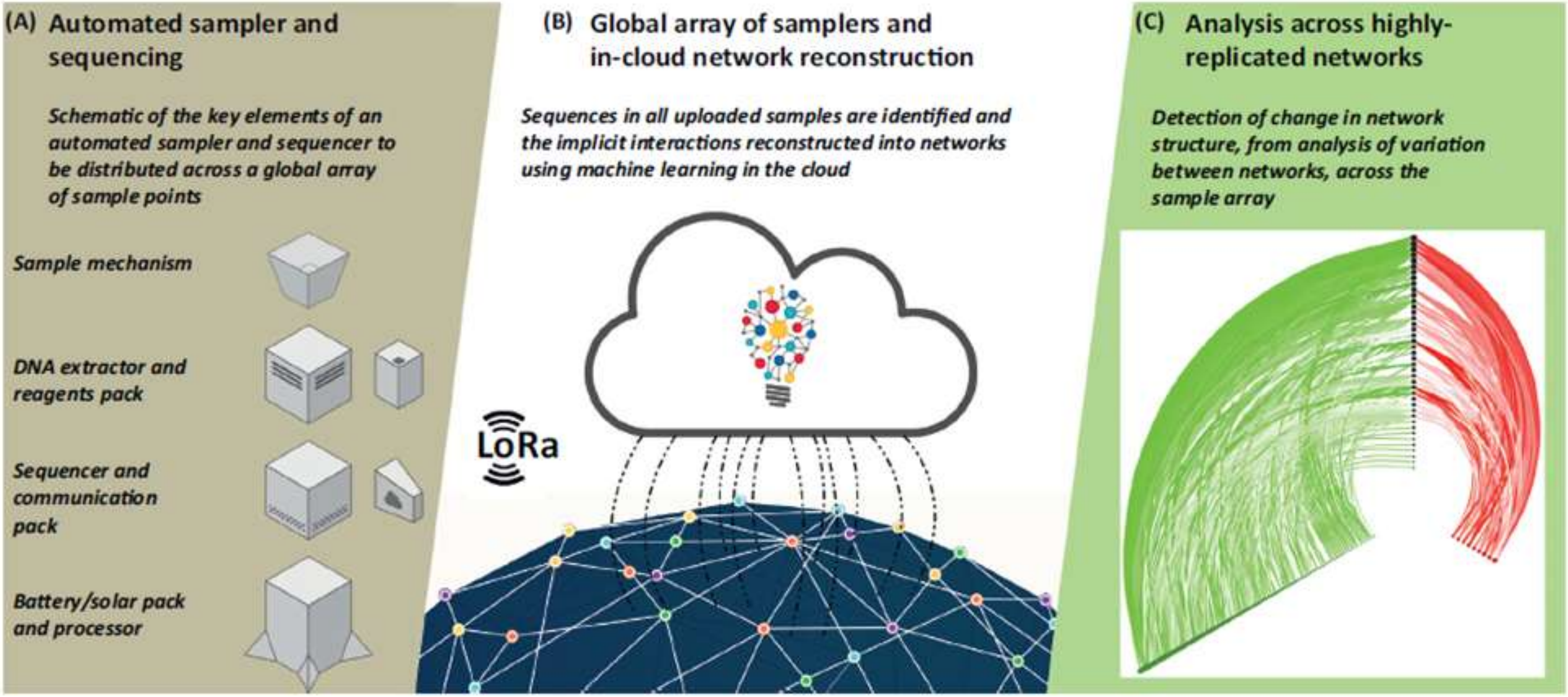
Targetted SOC surveillance

Strict QA requirements & standardized reporting criteria

Detection of SOC elicits appropriate management response

Desired future

Science? Or science fiction?



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Trends in Ecology & Evolution

Bohan et al. 2017. *Trends in Ecology and Evolution*

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THANK YOU!

Please feel free to direct
any questions to

Darling.John@epa.gov