Advances in eDNA monitoring of marine mammals: Current capabilities and future directions

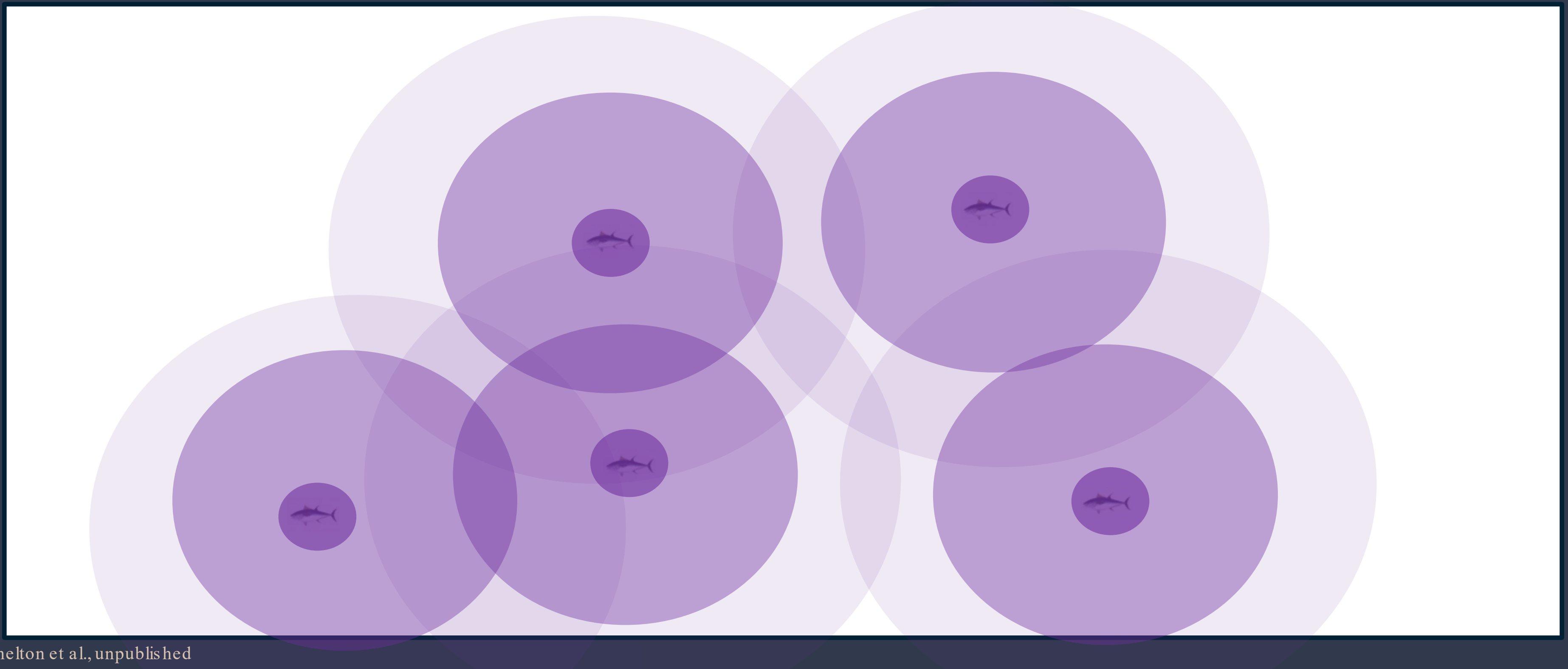
Ryan P. Kelly
University of Washington

September 10, 2025

eDNA = genetic traces recovered from the water

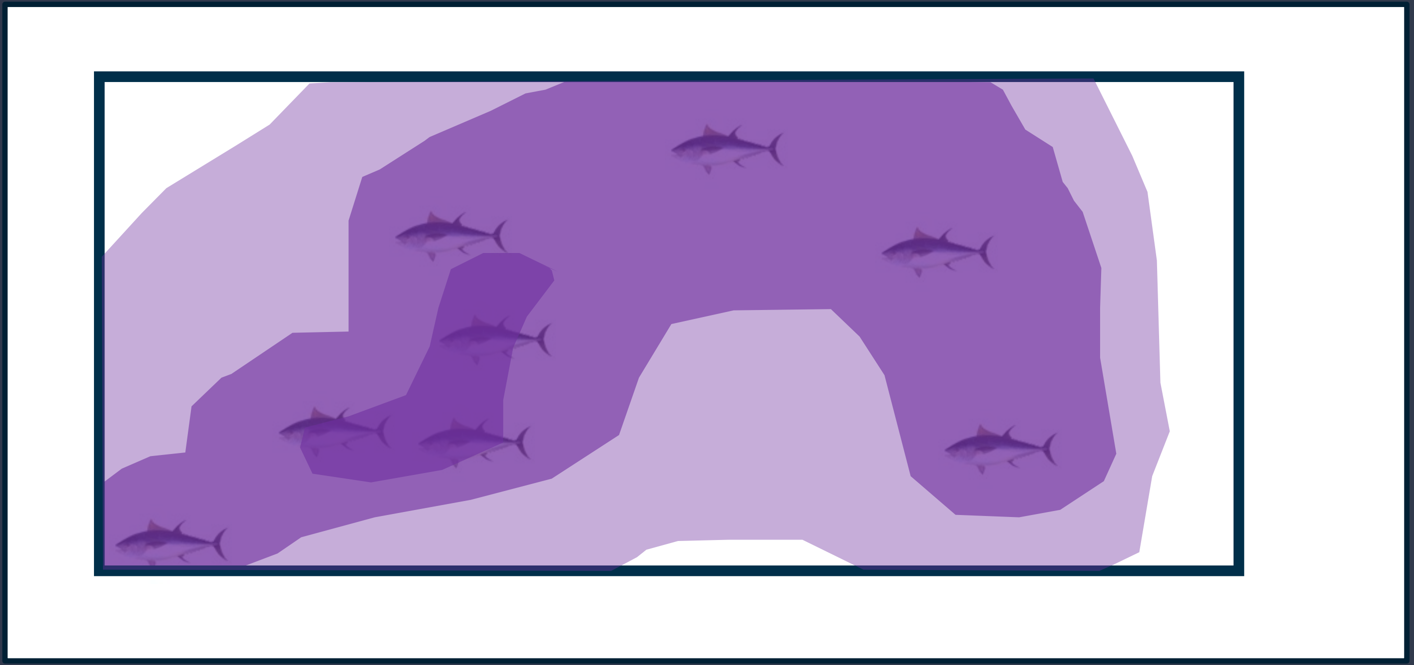
But what does it mean? What are we sampling?

More of a species = more of its DNA (in the world)



Shelton et al., unpublished

Organisms are discrete; eDNA is more continuous



Shelton et al., unpublished

Forms of Information from eDNA (+ eRNA)

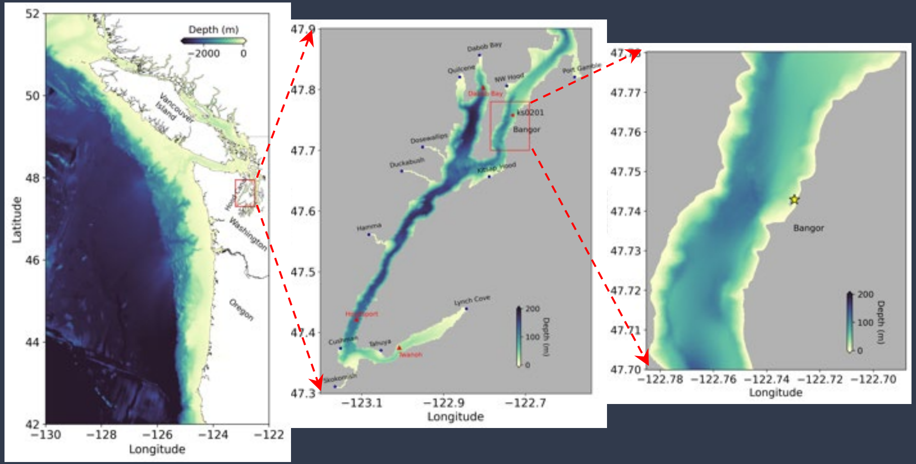
- Detection
- Concentration
  - eDNA (various fragments)
  - eRNA (various fragments)
- Sequence Information
  - Haplotypes
  - Functional genetics + expression
  - Methylation

Challenge: Linking this information to parameters of interest in the real world

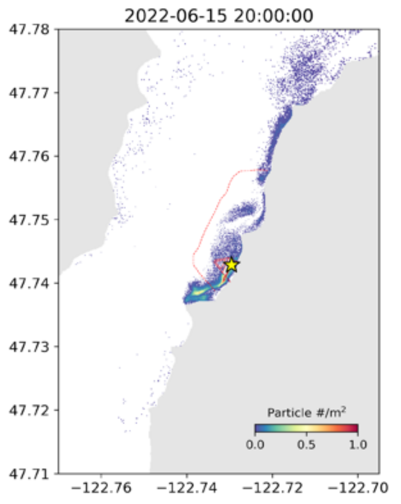
Cetacean eDNA in Space and Time

Captive Tursiops as model

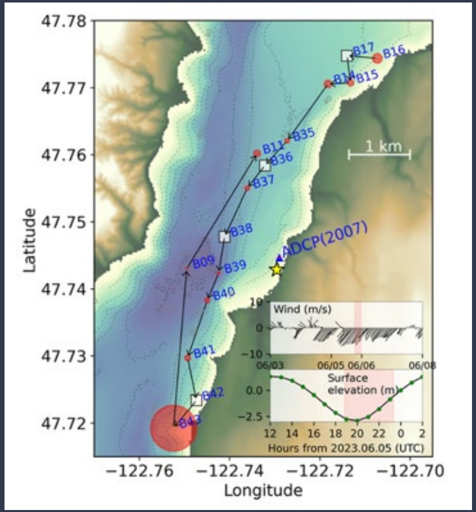
High-res oceanographic model



Particle tracks predict eDNA dispersal

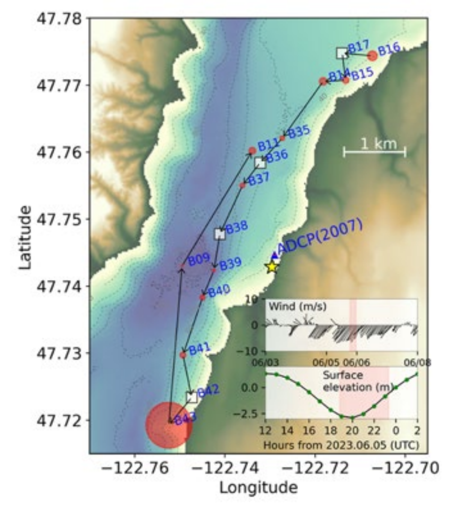


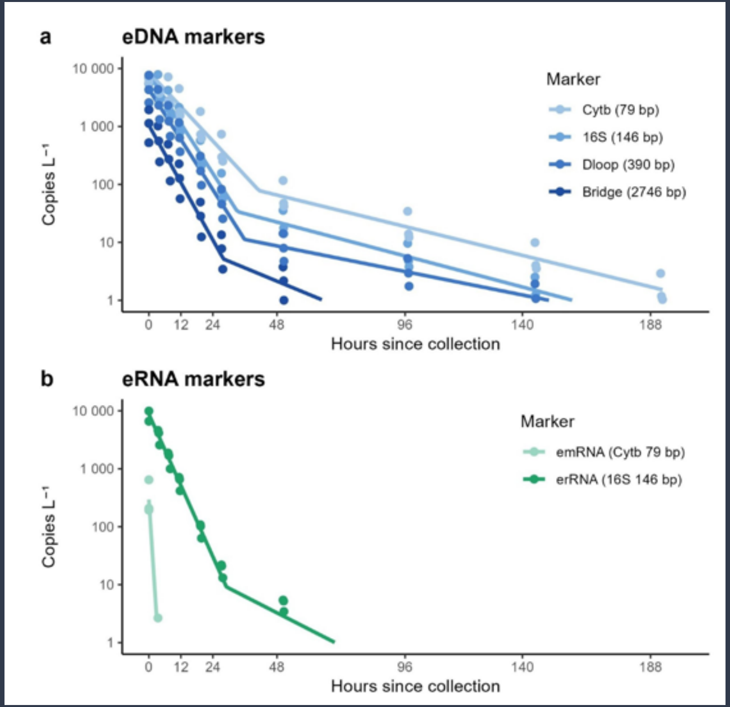
Expected vs real-world observations



Xiong et al. 2025

Cetacean eDNA in Space and Time





Brendão et al. 2025

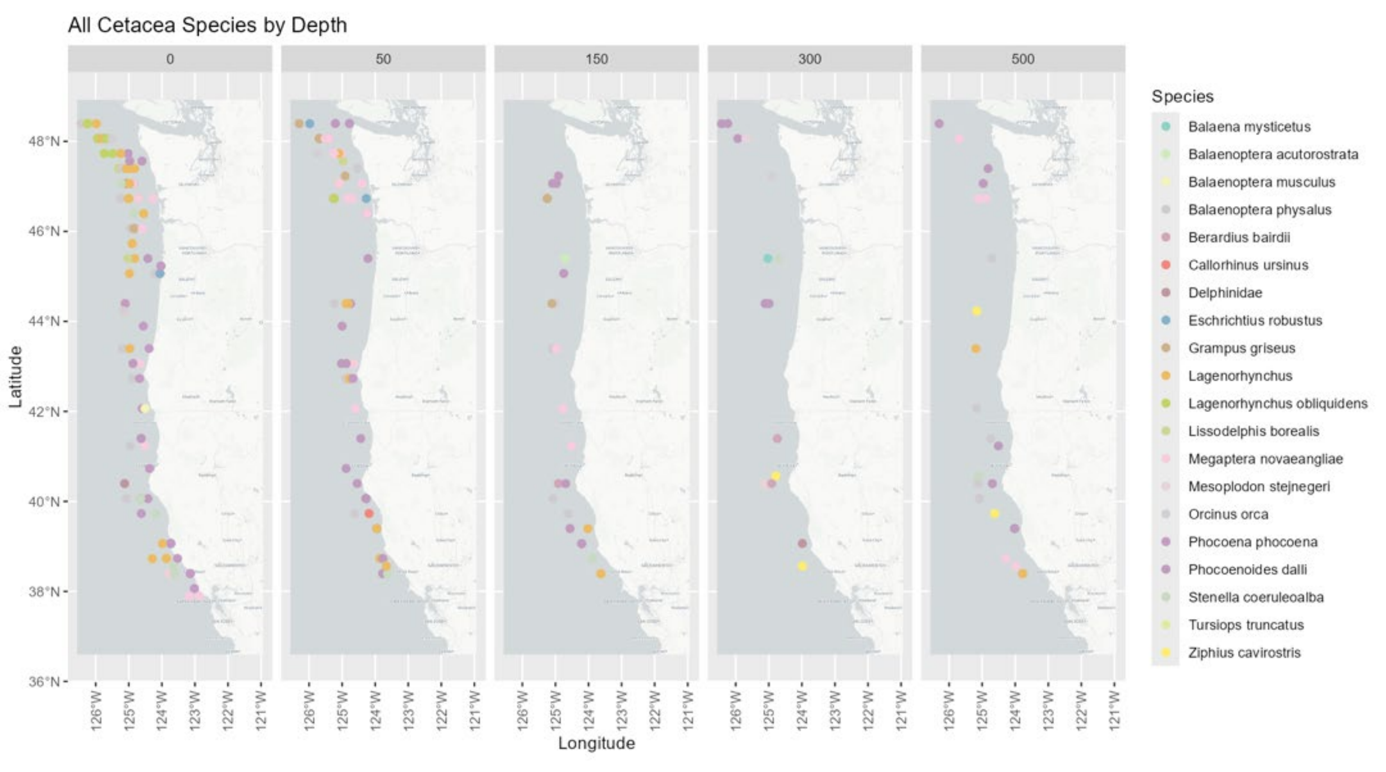
At scales of 1-10km:

- we can trace eDNA dispersal via oceanography
- eRNA degrades very quickly; eDNA pretty quickly

Cetacean eDNA at Large Spatial Scales

West coast samples via NOAA

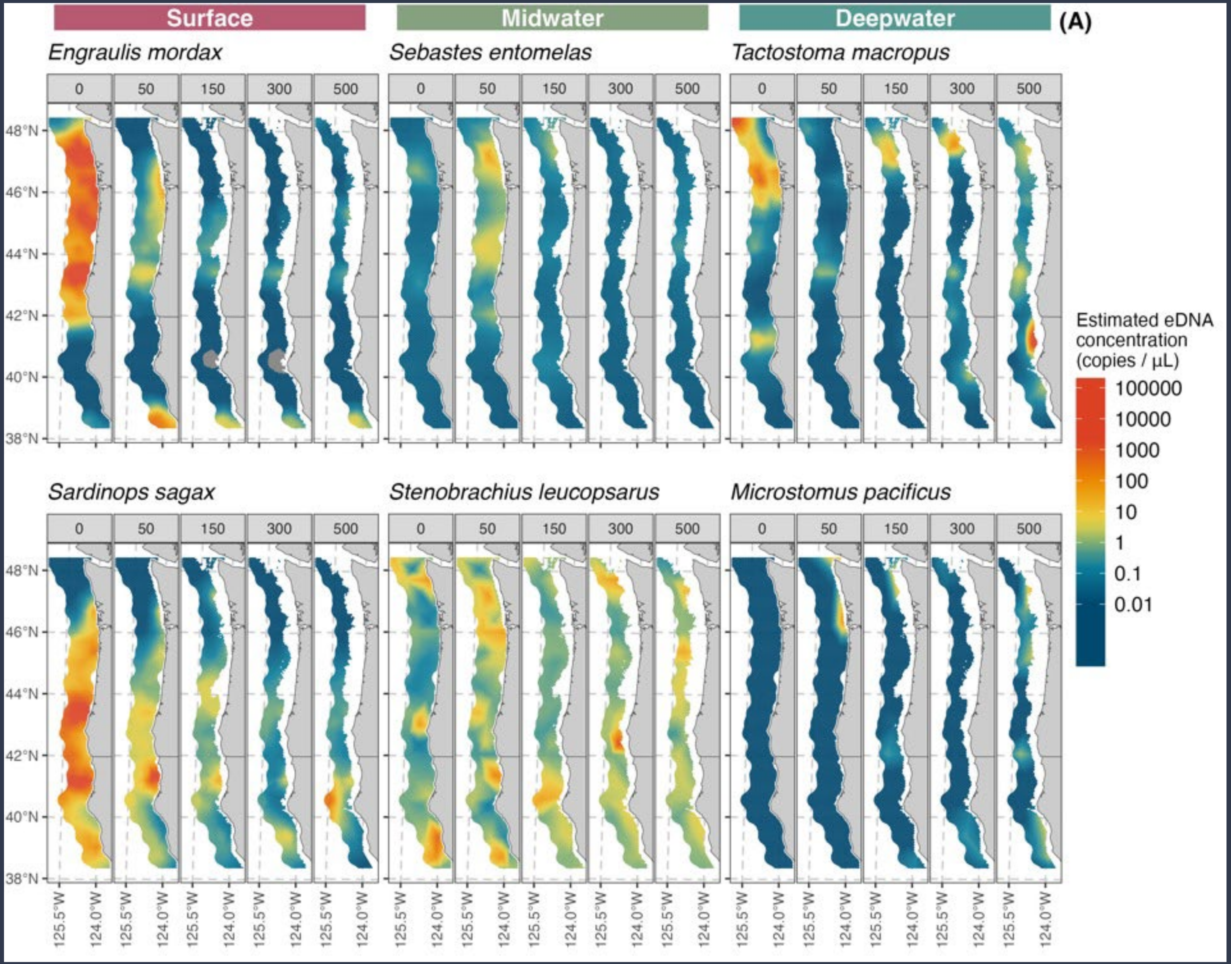
50% of all samples have cetacean sequences



Next Up

Quantifying and Smoothing

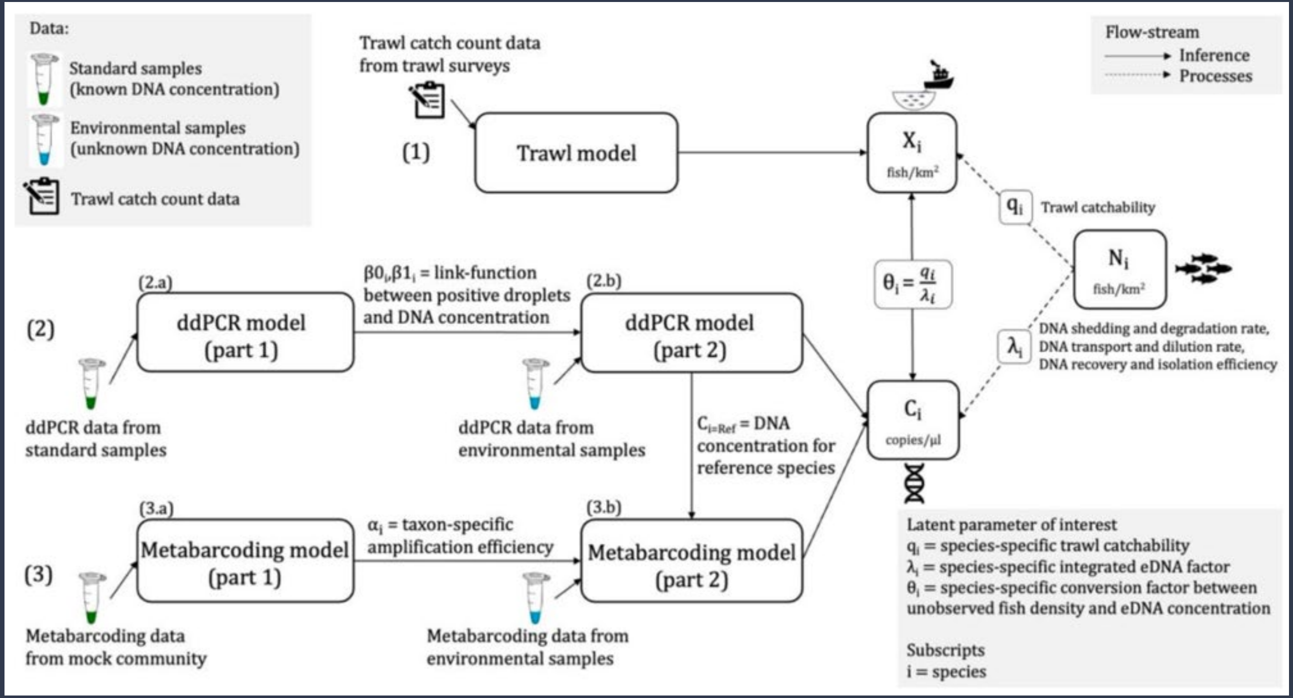
Applying fisheries work to cetaceans

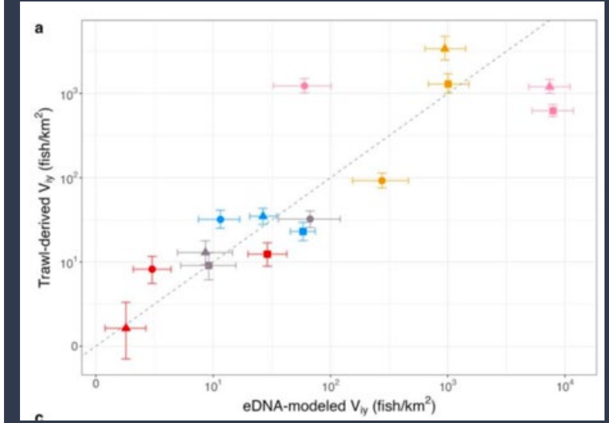


Guri et al. (in review)

Next Up

Jointly estimating cetacean abundance from visual, acoustic, and eDNA observations





Reciprocal out-of-sample cross-validation

Guri et al. 2024 ICES J Mar Sci – Commercial Fisheries in Norwegian Fjords

Thanks!

Ole Shelton
Eily Allan
Megan Shaffer
Gled Guri
Kate Bertko
Pedro Brendão
Jilian Xiong
Shana Hirsch
Aden Ip
Owen Liu
Kim Parsons
Krista Nichols

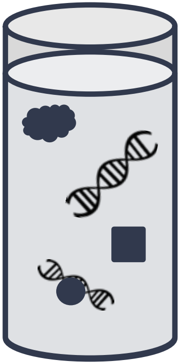
Olivia Scott
Stephanie Matthews
Len Thomas
Brice Semmens
Simone Baumann-Pickering
Michaela Alksne
Nastassia Patin

The David and Lucile Packard Foundation
Oceankind
Office of Naval Research
NOAA Fisheries

Extra Slides

What is eDNA?

A soup of information

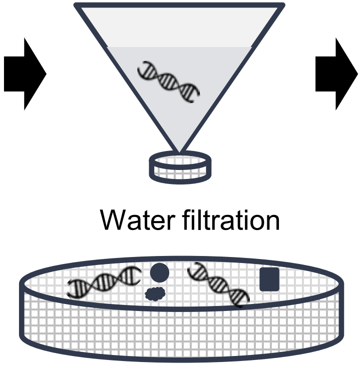


Skin and scales

Tissue

Metabolic waste

Free DNA / RNA / Proteins



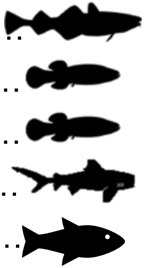
Water filtration

DNA extraction

PCR

Metabarcoding:
Hundreds/thousands of species, less quantitative

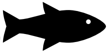
GAATCGC...
GTCGATA...
GTCGATA...
CTCGATA...
AGCACTC...



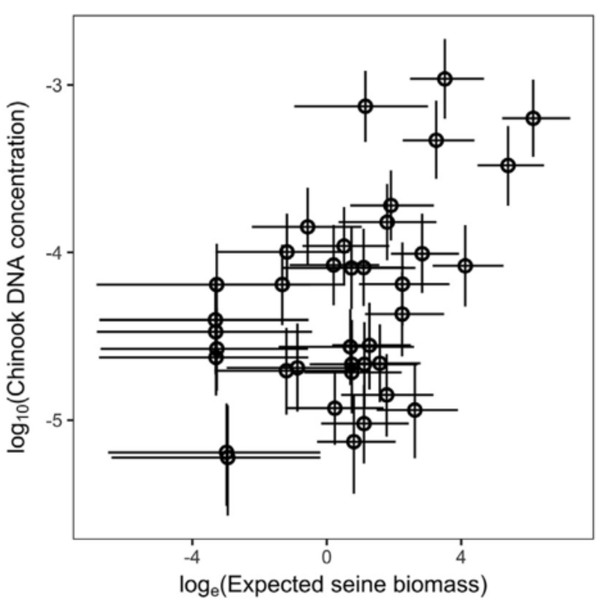
Scalable
Automatable
Sensitive
Non-invasive

Quantitative PCR:
single-target, quantitative

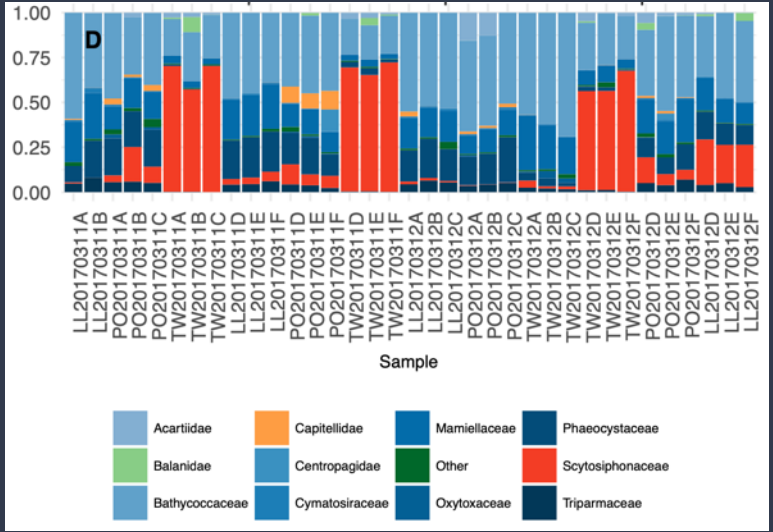
AGCACTC...



Single-Species (qPCR / ddPCR) vs. Multi-Species (Metabarcoding)



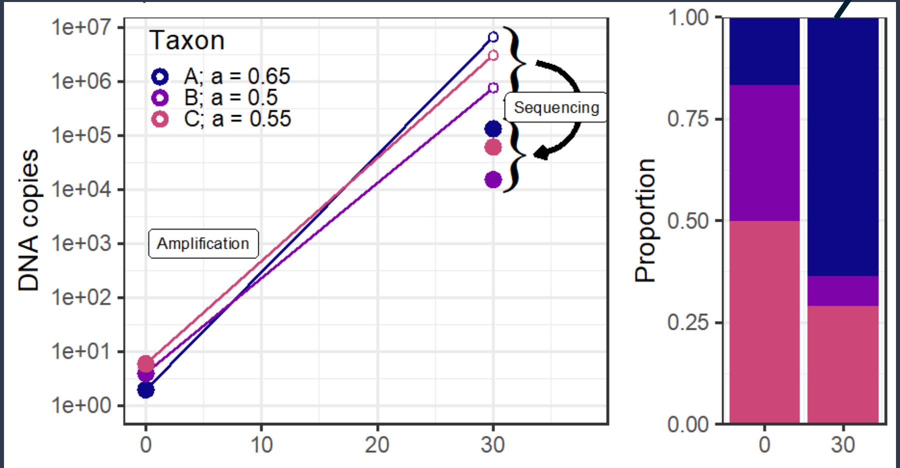
Sheelton et al. 2019 Biol. Conserv.



Kelly et al. 2019 PeerJ

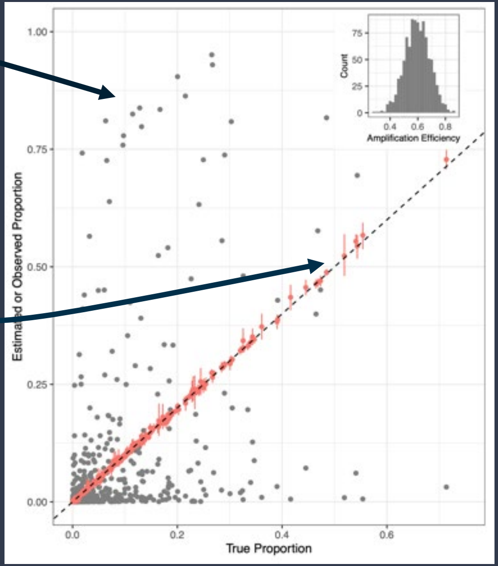
Important Note on Metabarcoding

Amplification Bias: Different species may/do amplify at different rates



Uncalibrated

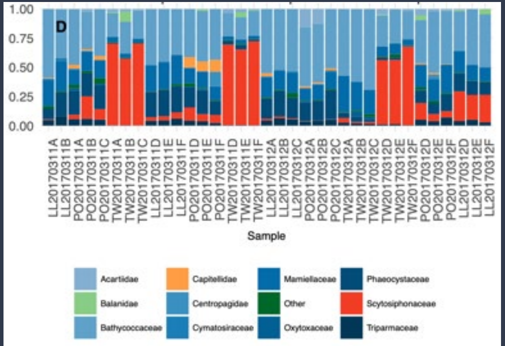
Calibrated

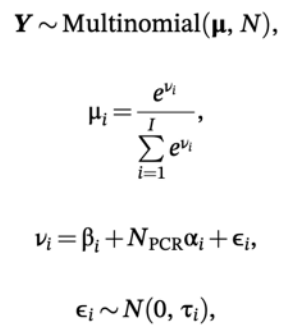


Shelton et al. 2022 Ecology

Other Important Note on Metabarcoding

The resulting dataset is <u>compositional</u> and contains little/no info about absolute concentration





$$\boldsymbol{Y} \sim \text{Multinomial}(\boldsymbol{\mu}, N),$$

$$\mu_i = \frac{e^{\nu_i}}{\sum_{i=1}^{I} e^{\nu_i}},$$

$$\nu_i = \beta_i + N_{\text{PCR}}\alpha_i + \epsilon_i,$$

$$\epsilon_i \sim N(0, \tau_i),$$

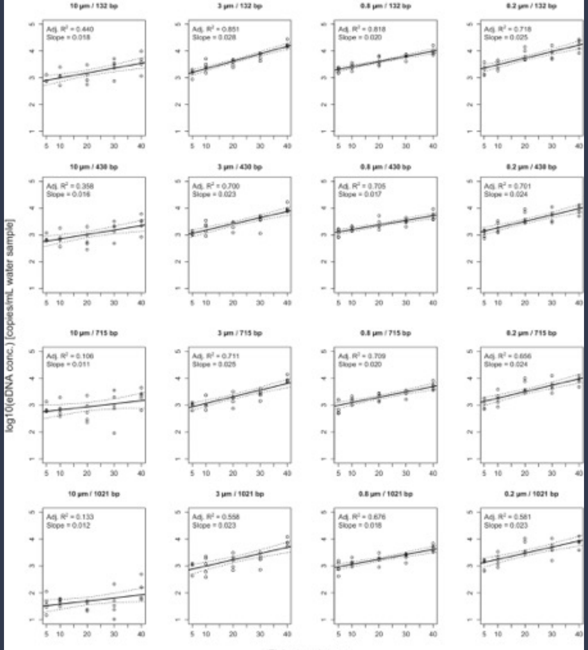
- We model the PCR process for each species in a composition
- Getting to absolute abundance requires additional information
  - e.g., visual counts, trawl, trap, whatever

Shelton et al. 2022 Ecology

Single Species – qPCR / ddPCR

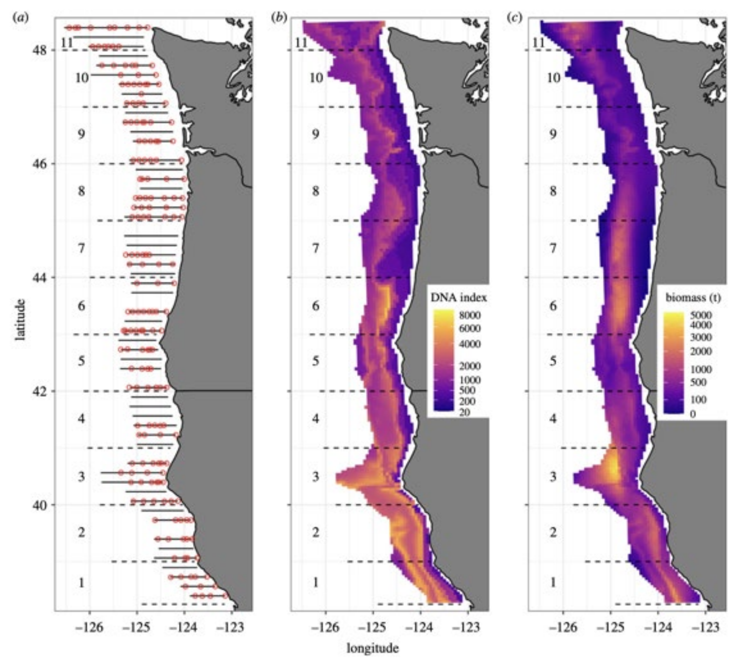
Quantitative estimates of eDNA concentration

Tiny Scale



Jo and Yamanaka (2022) – Zebrafish aquarium study across pore sizes + fragment sizes.

Large Scale

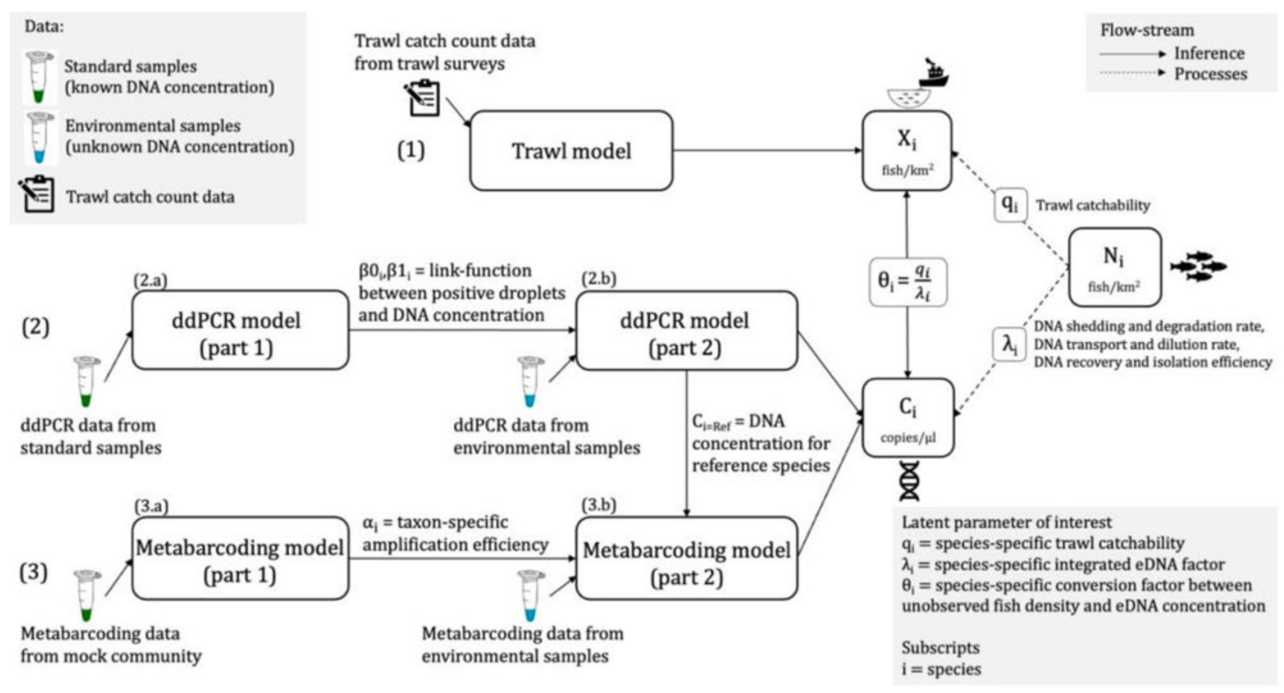


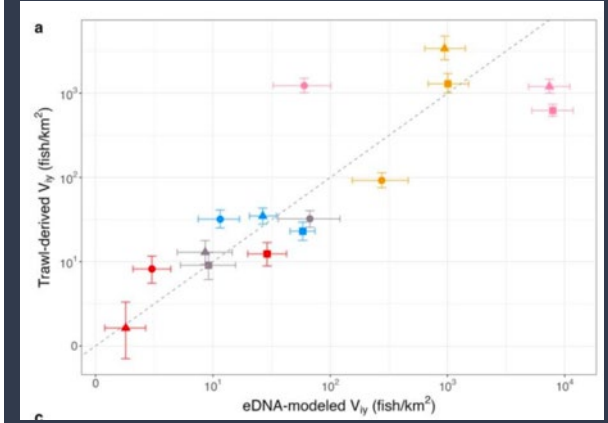
Shelton et al. (2022): smoothed qPCR signal reflects Hake (Merluccius productus) eDNA distribution

Multispecies (Metabarcoding)

Metabarcoding (proportions) + dPCR (ref species quantity) + trawls

Quantitative estimates of species abundance





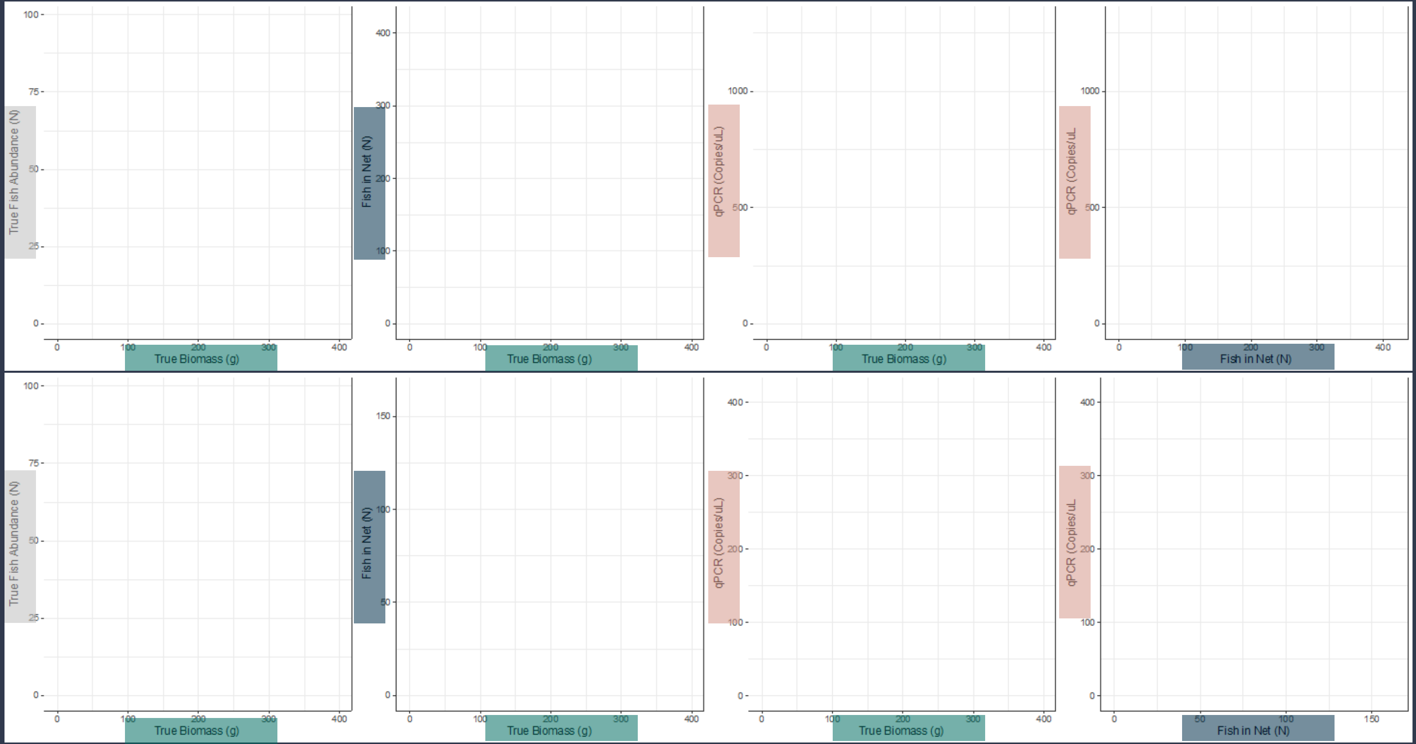
Reciprocal out-of-sample cross-validation

Guri et al. 2024 ICES J Mar Sci – Commercial Fisheries in Norwegian Fjords

Compounding Noise

Variable mass-per-fish

1:1 eDNA copies per unit mass



Moderate Observation Variability

Low Observation Variability

The spatial/temporal scale of process + observation variability determine what correlations might exist