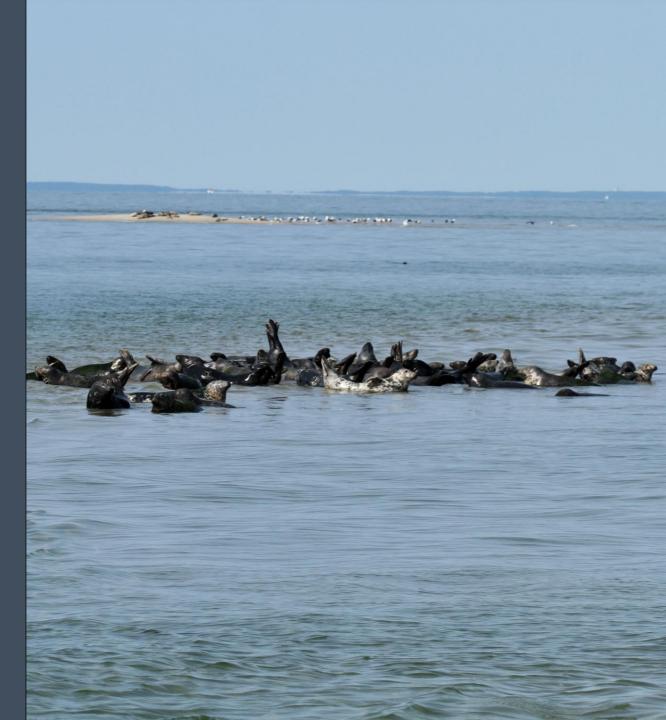
# Application of two novel qPCR assays for quantifying pinniped environmental DNA (eDNA) in coastal environments

Julia Clem

PhD Candidate
University of Maine

3<sup>rd</sup> Marine Mammal eDNA Workshop SMM 2024



# Acknowledgements

#### **Advisors and Co-Authors**

- Kristina Cammen, University of Maine
- Michael Kinnison, University of Maine
- Lisa Sette, Center for Coastal Studies
- Christine Hudak, Center for Coastal Studies
- Justin Stevens, Maine Sea Grant
- Sydney Jackson, University of Maine
- Geneva York, University of Maine Environmental
   CORE Facility

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- Joshua A. Nickerson Conservation Fellowship
- Maine Outdoor Heritage Fund





















### Primer Development

#### in silico Design and Testing

- Identify gene region candidates
- Minimize potential for cross-amplification of non-target species

#### **Specificity Testing**

- Tissue extract from target and non-target species
- eDNA extract from rehabilitation pools

#### Assay Optimization

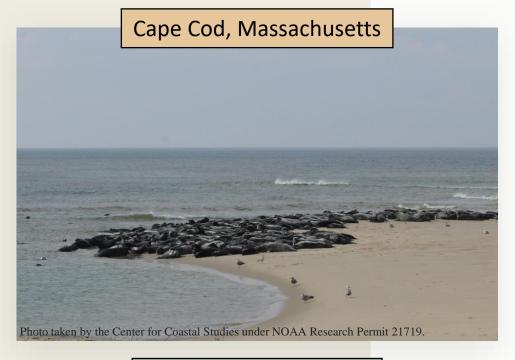
- Primer/probe concentrations
- Annealing temperature
- Amplification efficiency

#### **Gray Seal Assay**

106 bp ND4 gene

#### Harbor Seal Assay

173 bp cytb gene





# Primer Deployment

Large gray seal aggregations (18-325 individuals)

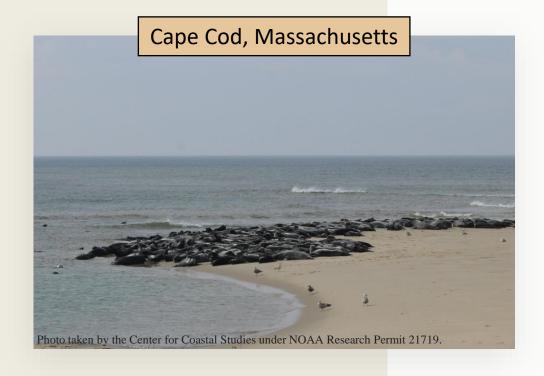
Targeted sampling around haul-outs (along shoreline and 50m offshore)

Tested for gray seal

Smaller seal aggregations (1-30 individuals)

Samples collected along a transect up the lower estuary

Tested for gray and harbor seals

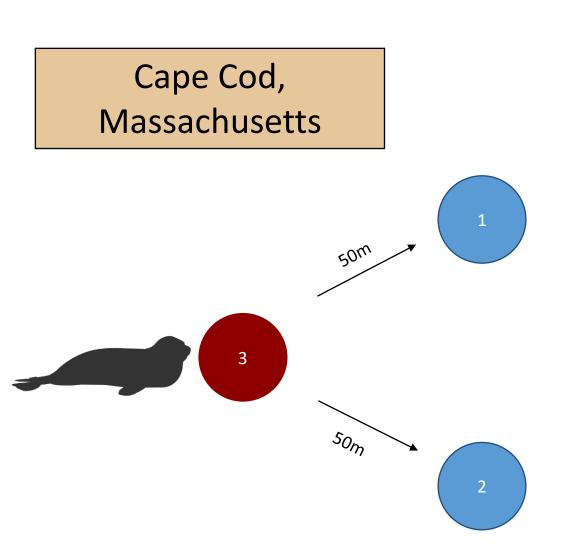


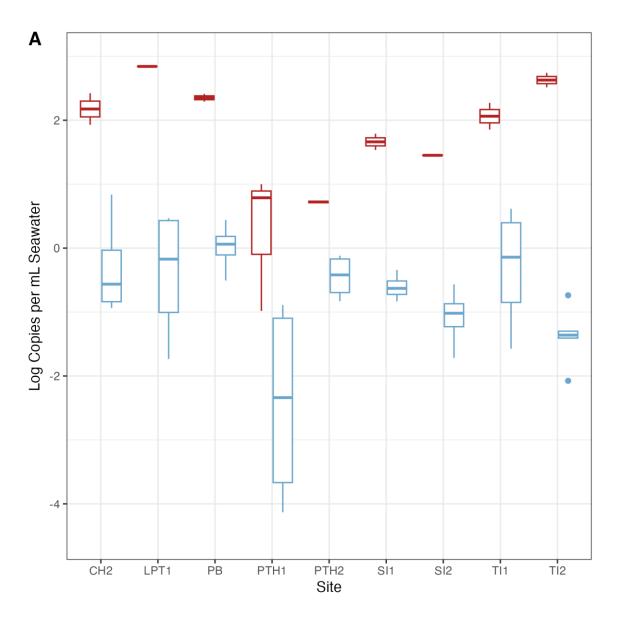
#### Detection Success Across Systems

92% samples collected 0 - 50 meters from shore detected gray seal eDNA at haulouts with 18-325 seals present

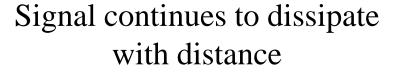
In 2 expanded surveys, gray seal eDNA was detected up to 150 meters from shore

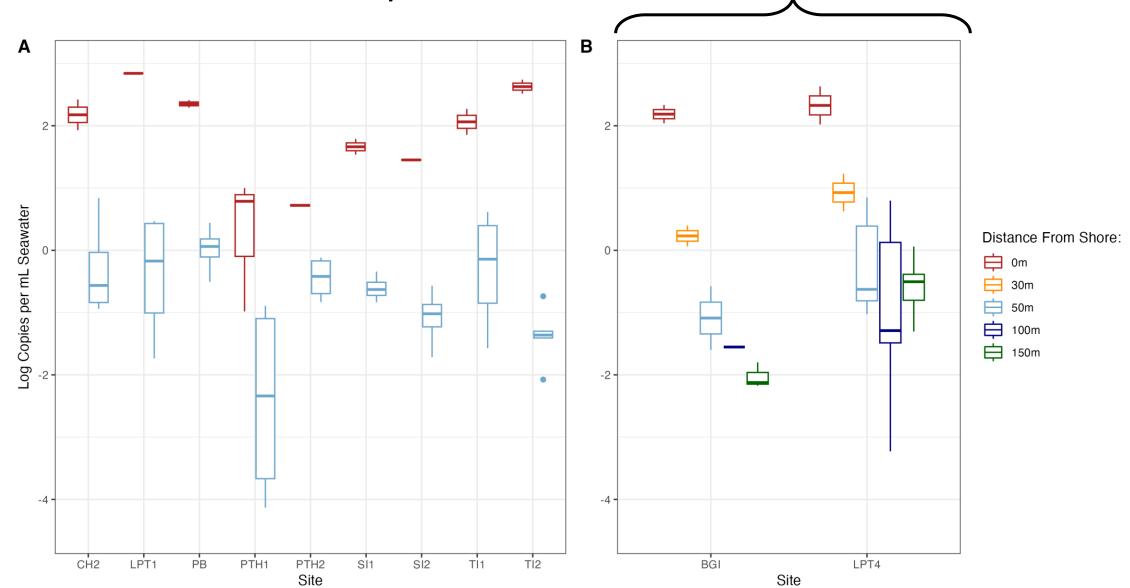
# Quantification in Space



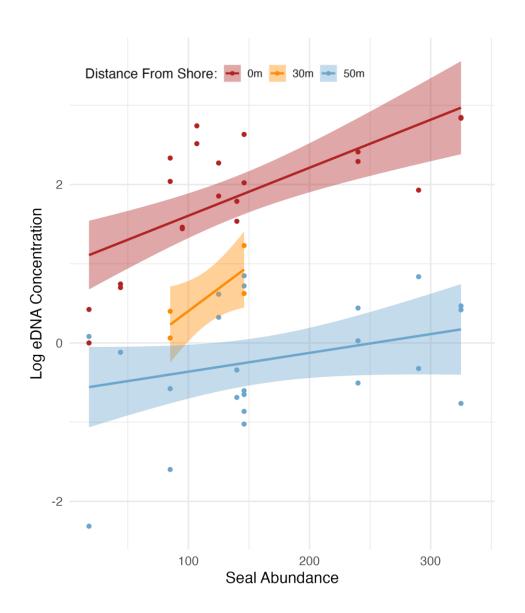


# Quantification in Space





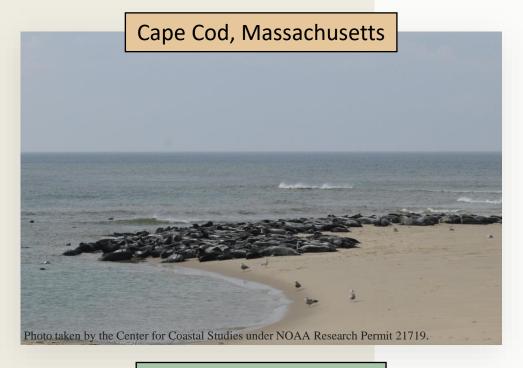
#### eDNA verses Abundance

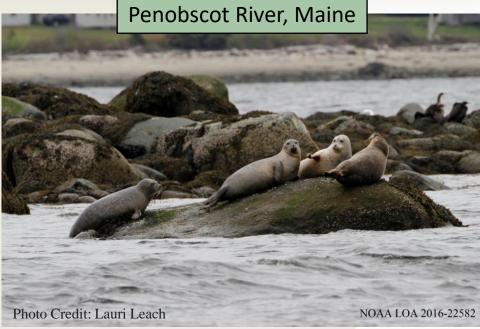


Wide range of haul-out sizes offered the opportunity to test the influence of abundance on eDNA concentration

Together, distance from shore and seal abundance explained 73.88% of observed deviance in eDNA concentration

Distance had a stronger effect on eDNA concentration than seal abundance





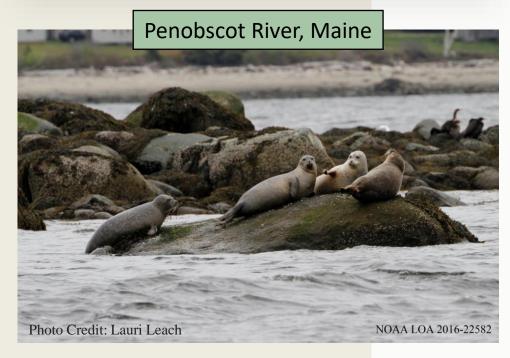
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System characteristics and sampling scheme support a high rate of detection

# Photo taken by the Center for Coastal Studies under NOAA Research Permit 21719.



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Targeted analysis of samples collected during surveys with the highest number of seals observed (<30 individuals)

12% samples detected gray seal, 17% detected harbor seal

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Detection more sporadic, high rate of false positives

# qPCR as a supporting data stream

#### Cape Cod, Massachusetts

- Accompanied by eDNA haplotyping
- qPCR data established a baseline understanding of eDNA signal in space around haul-out sites
  - Guide haplotyping efforts and help interpret detections

# qPCR as a supporting data stream

Cape Cod, Massachu

Accompanied by eDNA

Learn more about our eDNA haplotyping efforts on Monday!



haplotyp A Program Track 1 **Ecology and Evolution - eDNA Application** Mon, November 11 BelleVue Ballroom 2 ① 11:30 AM - 12:30 PM Video) Presentations Session understa Evaluating the Use of Environmental DNA for Pinniped Detection and Population 12:18 PM **Genetics at Haul-Out Sites** 12:30 PM space are Julia Sunnarborg<sup>1</sup>, Christine Hudak<sup>2</sup>, Lisa Sette<sup>2</sup>, Geneva York<sup>3</sup>, Sydney Jackson<sup>4</sup>, Michael Kinnison<sup>4</sup>, Kristina Cammen<sup>4</sup> <sup>1</sup>University of Maine, Bangor, Maine, <sup>2</sup>Center for Coastal Studies, Provincetown, Massachusetts, <sup>3</sup>University of Maine Environmental DNA CORE Laboratory, Orono, Maine, <sup>4</sup>University of Maine, Orono, Guide Maine

# qPCR as a supporting data stream

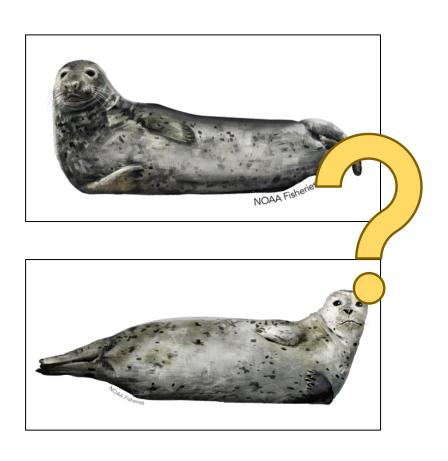
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#### Penobscot River, Maine

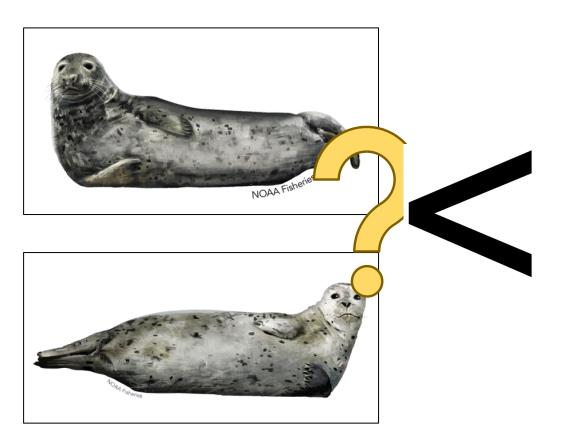
Accompanied by 12S rRNA
 metabarcoding to characterize
 prey community

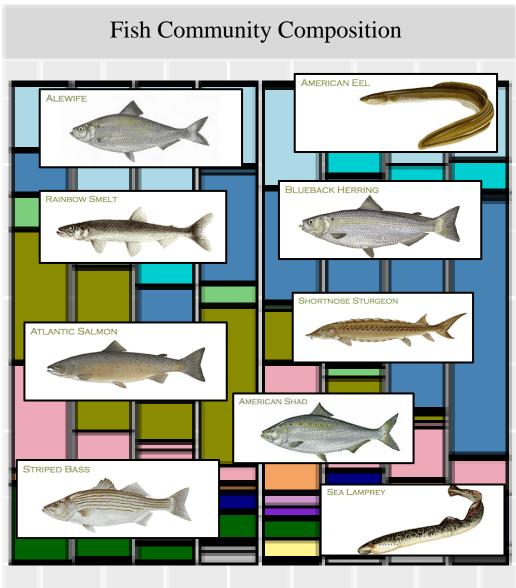
# Metabarcoding – Where are the seals?



No seal reads even when visually observed

# Metabarcoding – Where are the seals?





### Takeaways



qPCR assays created and field tested for gray and harbor seals



Conditions of the system and sampling setup influence detection rates and the potential for false negatives



Quantifying eDNA variation in space helps us understand the underlying processes of transport and signal dissipation for a given system



qPCR tools may provide a way to "pick out" seal detections where they might otherwise be swamped out



