



Can Environmental DNA Reveal Fish Abundance? Modeling Salmonid eDNA Fate at the Reach Scale

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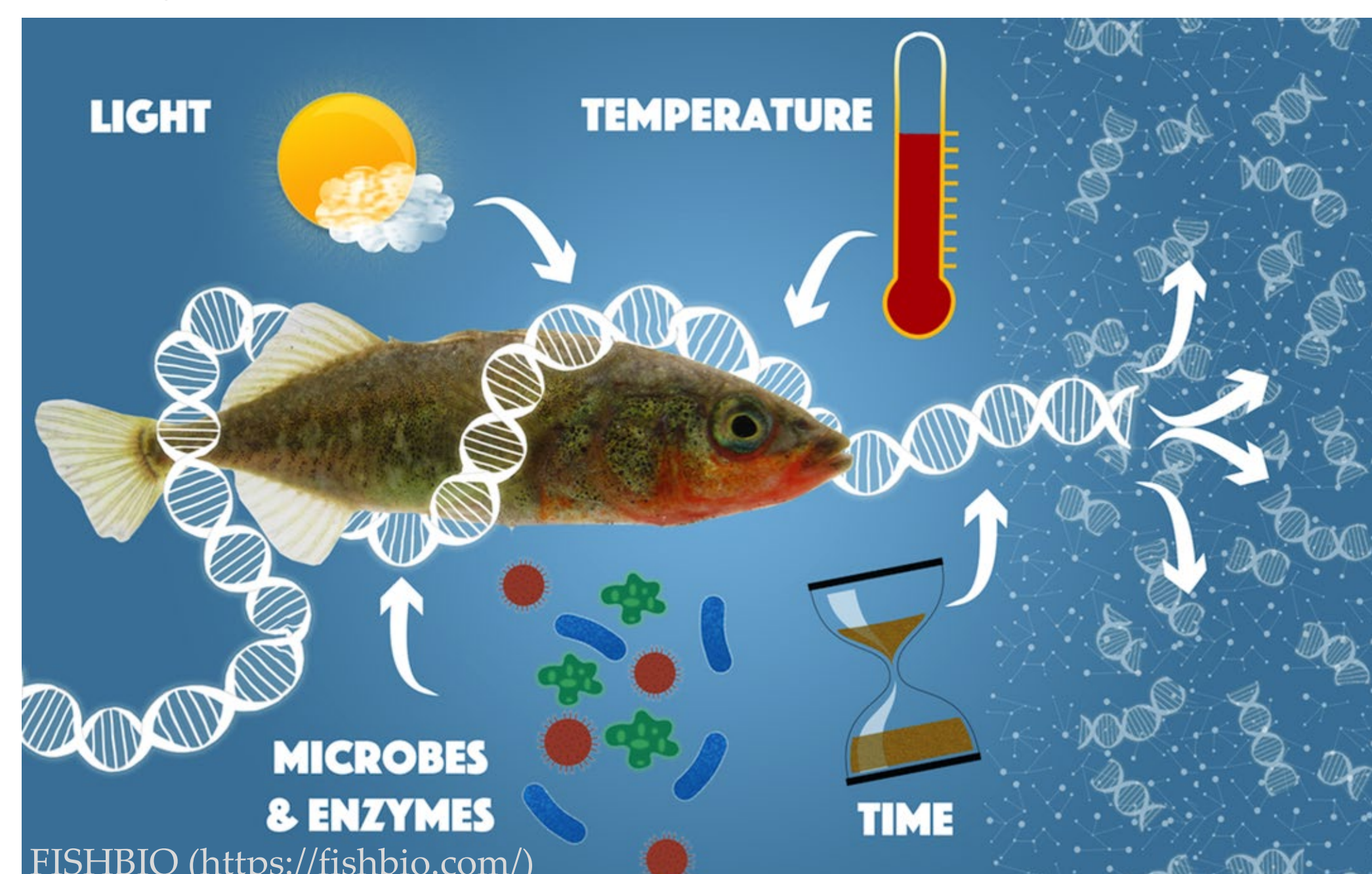


ABSTRACT

Salmon are essential to the health of many river ecosystems in the United States, requiring careful monitoring of their populations. Environmental DNA (eDNA) offers a promising new method for enumerating salmon, but remains limited by poor understanding of salmon eDNA fate (transport, degradation, settling, resuspension). Here, we aim to characterize salmonid eDNA fate at the reach-scale using a random forest modeling approach. We will add Brook Trout (*S. fontinalis*) eDNA to 10 river sites of the central California coast, and sample eDNA at sequential downstream distances for qPCR analysis. We will model the amount of eDNA recovered according to river characteristics, including discharge, width, depth, temperature, pH, conductivity, biological oxygen demand (BOD), substrate cobble size, and biofilm thickness. Our results will describe salmonid eDNA fate at the reach-scale with novel precision, inform the relative impacts of water and substrate characteristics on eDNA fate in a natural system, and offer an approach for characterizing reach-specific eDNA fate profiles. This knowledge will lay the groundwork for eDNA-based enumeration of salmon, while improving knowledge of eDNA detection probabilities across river taxa.

INTRODUCTION

eDNA Fate



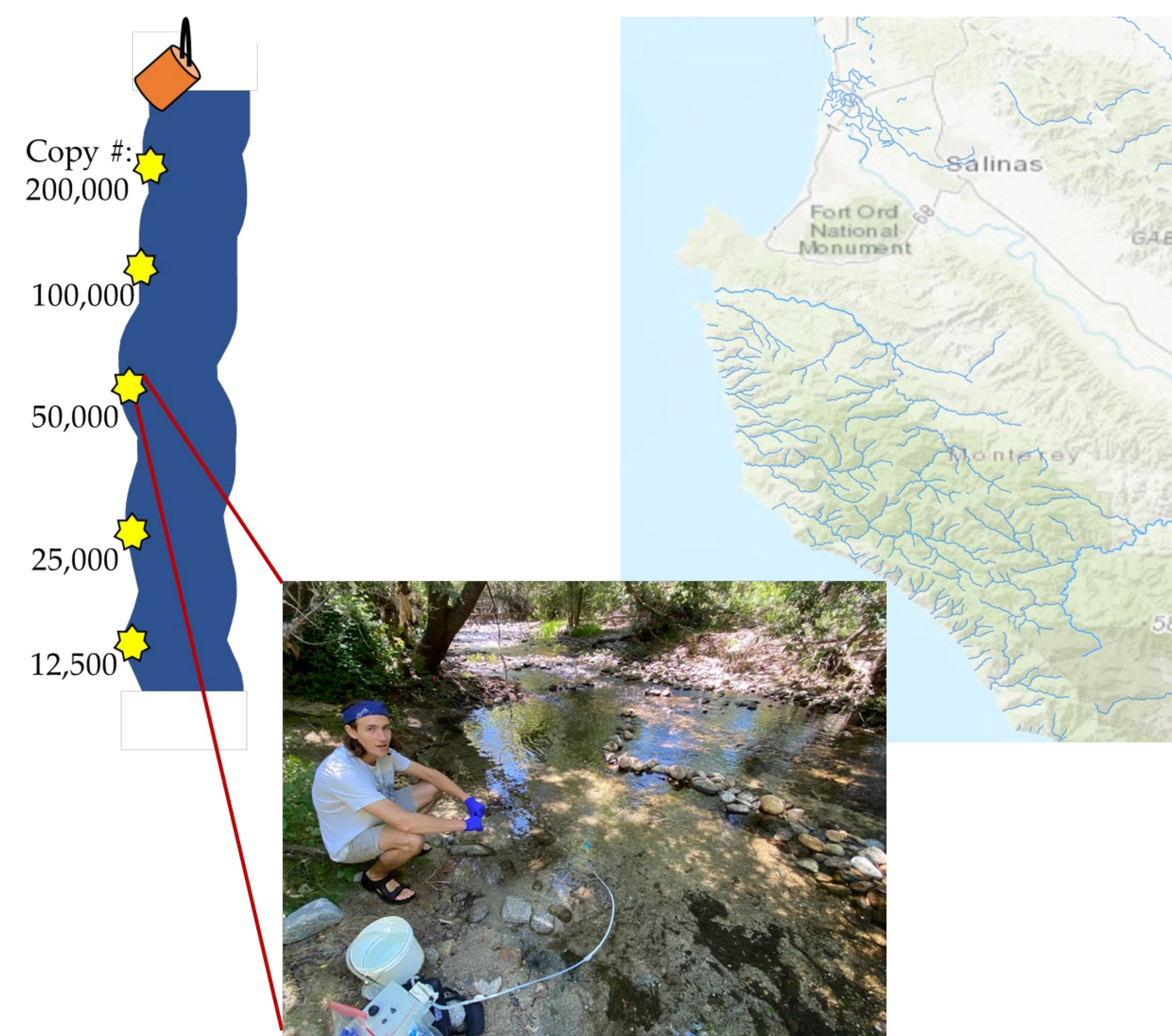
eDNA Fate Profiles

- Different streams will have different eDNA fate profiles (set of characteristics relevant to eDNA fate in the system)



METHODS

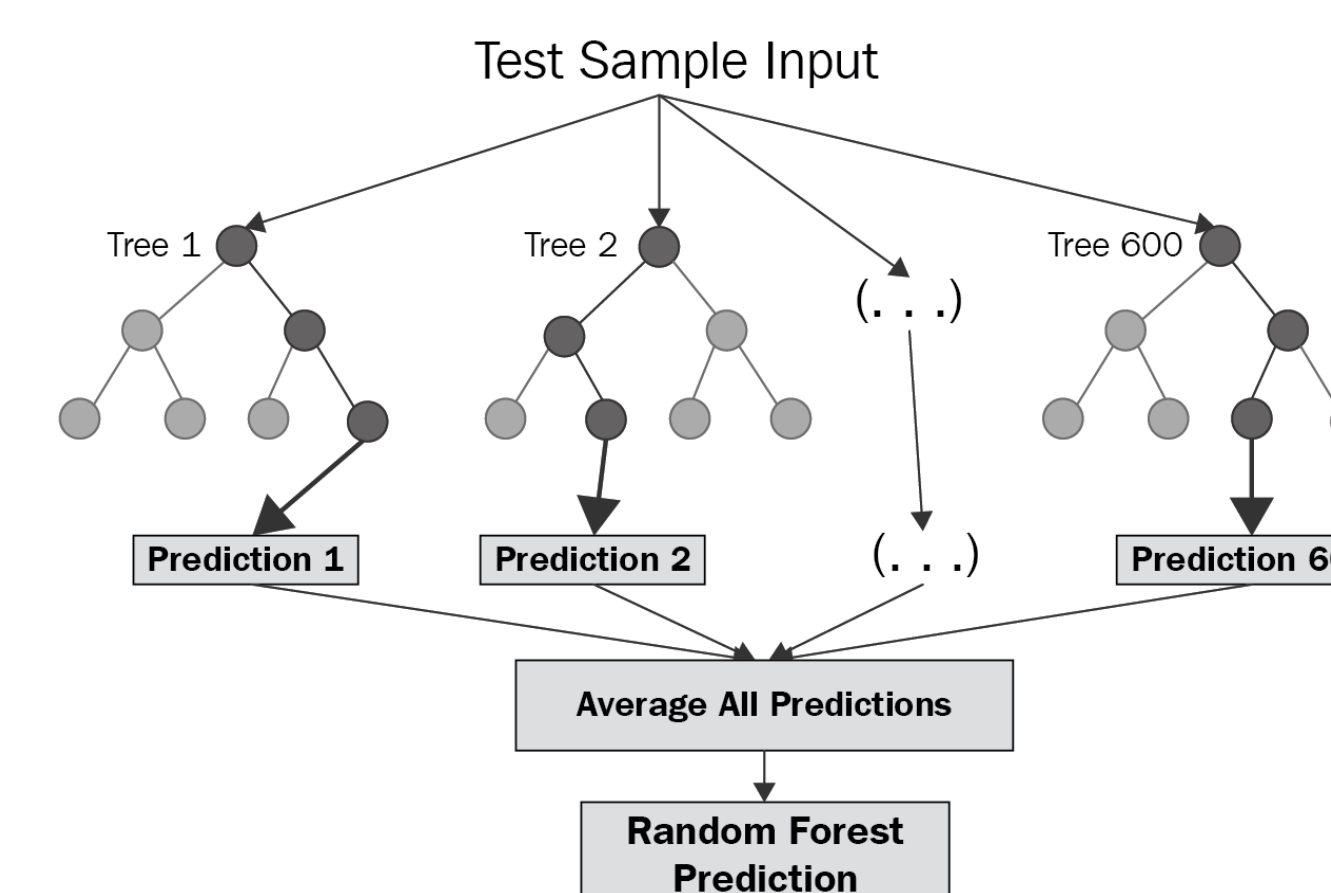
- Add a known amount of salmonid eDNA upstream
- Recover eDNA at sequential distances downstream, quantify using qPCR
- Sample 10 river sites across the central California coast, capturing a range of eDNA fate profiles



- Develop a Random Forest model of salmonid eDNA fate according to reach-specific environmental factors

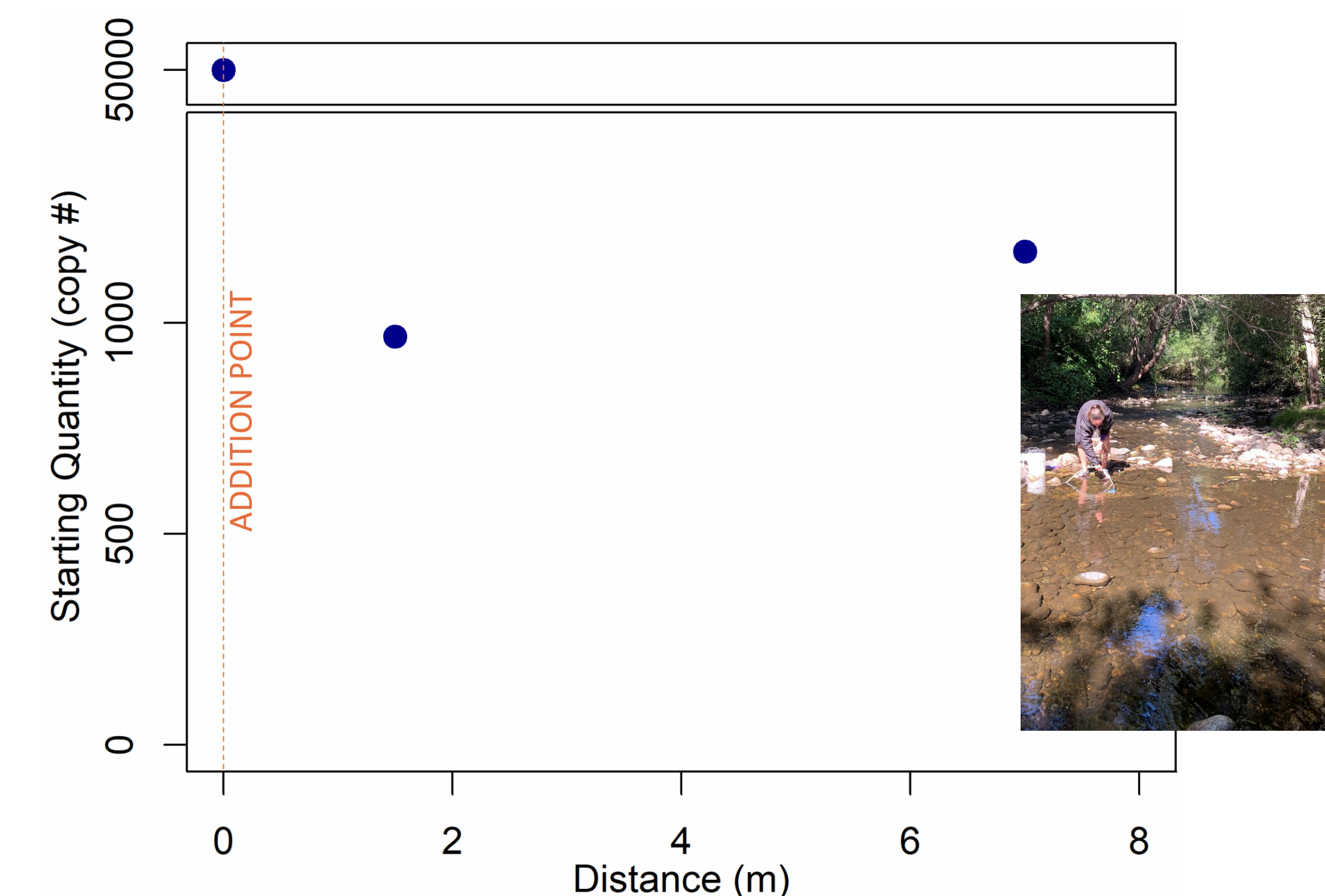
Predictor Variables

Geomorphological Features
(e.g., stream slope, cobble size)
Flow velocity and discharge
Water body width and depth
Water Chemistry
(e.g., temperature, salinity, pH)
Turbidity
DOM
Chlorophyll *a*
Biofilm thickness
Soil type/percentage
Catchment land use



- Random Forest model will describe salmonid eDNA fate at the reach scale and give importance of predictor variables

PRELIMINARY RESULTS



Pilot experiment to validate qPCR assay

- eDNA successfully amplified in downstream samples
- Higher amount recovered at 7 m than at 1.5 m, likely due to more complete mixing
- Suggests first downstream sample should be collected > 5 m downstream to allow for complete mixing (depending on flow and stream segment)
- Also measured no decline in eDNA recovered from a bucket (stored at room temperature) over 40 hours

EXPECTED OUTCOMES

- Lay the groundwork for eDNA-based enumeration by:
 - Describing salmonid eDNA fate at the reach scale with novel precision
 - Revealing the most important environmental factors for determining fate, both within and across various fate profiles
 - Demonstrating the variation in eDNA fate within watersheds, emphasizing the importance of site selection and characterization
- Help optimize eDNA presence/absence sampling to avoid false negatives

ACKNOWLEDGEMENTS

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