Abstract:

Organisms of all kinds shed cells containing diagnostic DNA into the environment, which can be recovered and assigned to a taxon based upon its match to known sequences. Because DNA degrades under most ambient environmental conditions—the half-life of DNA in fresh- and saltwater is approximately 24-48 hours (*1,2*)—this environmental DNA (eDNA) provides a snapshot of the species recently present in the sampled habitat. However, while it is widely accepted that DNA can be collected and identified from a range of environmental samples, connecting field collections of eDNA with abundance surveys remains largely unexplored.

Here, we propose to develop eDNA survey methods to quantify fish communities (with a focus on salmon, herring, and smelt species) in a nearshore estuarine habitat in Puget Sound. To compare the efficacy of eDNA and traditional methods, we will collect water samples in parallel with collections made via three traditional net sampling methods, targeting nearshore fish communities that provide a range of spatial sampling scales (from meters to 100s of meters). We will use both quantitative PCR (qPCR) and massively parallel DNA sequencing technologies to provide eDNA data. We will then apply a newly developed statistical framework to provide field estimates of the relationship between species abundance and eDNA. Our replicated sampling design—using three field methods at three spatial scales—provides an opportunity to understand the appropriate spatial scale for eDNA sampling, and the potential value and pitfalls of eDNA surveys for understanding patterns of fish abundance.