High Quality Stream Evaluation Framework – A Tool to Assist Conservation and Protection Management Under the U.S. Clean Water Act

Introduction

Significant progress has been made to clean up rivers since the passage of the 1972 U.S. Federal Water Pollution and Control Act amendments, more commonly referred to as the Clean Water Act, fifty years ago. However, since that time much of the focus has been on restoring waste-receiving streams with overt pollution problems which has left high quality streams vulnerable and open to degradation (U.S. EPA, 2012). High quality streams support aquatic species not found in streams with higher levels of pollution (Bellucci et al 2011) along with a wide array of critical ecosystem services that benefit the social and economic well-being of humans (EPA 2012).

Biological integrity is the ability of an aquatic ecosystem to support and maintain a balanced, adaptive community of organisms having a species composition, diversity, and functional organization comparable to that of natural habitats within a region. The presence, condition, numbers and types of fish, insects, algae, plants, and other organisms provide direct, accurate information about the health of water bodies. Biological assessments measure these factors and are the primary tool used to evaluate the condition of water bodies. Because biological communities are affected by all of the stressors to which they are exposed over time, bioassessments provide information on disturbances not always revealed by water chemistry or other measurements.

The Connecticut Department of Energy and Environmental Protection (CT DEEP) samples several aquatic biological communities, including benthic macro-invertebrates and fish. Preliminary work conducted in Connecticut suggests the possible reduction of species sensitive to pollution in some high-quality streams sampling sites monitored over the past 30 years (Eltz & Beauchene 2020, Becker 2021, Becker & Bellucci 2021).

This project will seek to develop and effectively communicate modernized landscape level assessment methods that continue to augment the success of the Clean Water Act in the State of Connecticut by incorporating the concept of the biological condition gradient. The Biological Condition Gradient (BCG) is a scientific framework to interpret biological responses to anthropogenic stress (Davies & Jackson, 2006). The BCG framework provides a way to designate refined aquatic life uses along a gradient of stress. This allows for a more precise measure of biological condition rather than a ‘pass’/’fail’ system that has been previously used for biological assessment(ref - CALM). There are 6 levels of biological condition described by the framework (Figure 1). The levels are described in terms of changes in the structure and function of native aquatic communities. The levels range from a natural pristine condition with little anthropogenic stress (Level 1) to a severely stressed and altered condition that exhibits extreme changes in structure and ecosystem function (Level 6).

![\*Figure 1. Biological Condition Gradient Conceptual Model\*](images/BCG.png)

Using existing biological and land cover datasets I will develop methods to identify high quality streams using the BCG. This includes first using biological datasets to identify waters that support sensitive species typically found in areas that are least disturbed by human activity. Next, I will calculate and identify the landscape features in the drainage basins and catchments that contribute to high quality biological samples. Finally, I will develop a model using these landscape characteristics to predict the likelihood of stream catchments where samples have not been collected. I will use these predictions to identify those high-quality streams that are most vulnerable to degradation if human disturbance is increased in those catchments.

This information could be used by aquatic resource managers, decision makers and the public to prioritize preservation efforts, as well as support management to prevent further degradation in these streams and implement anti-degradation measures under the Clean Water Act. An interactive web-mapping application will be developed to convey this data on high quality streams and drainage systems to decision makers. The application would allow for a simplified high-level overview of statewide conditions, while still allowing the user to dig deeper into the site and watershed scale data through leveled zoom and click functions with popup information. The application will display the likelihood of a stream catchment supporting high quality waters. A slider will be used to change the predictions on the map if human disturbance is increased in a particular catchment. This will allow for a 'what if' analysis that identifies those catchments that are most vulnerable to small increases in disturbance.

Methods

*Sampling Methods*

Fish samples were collected by the CT DEEP Inland Fisheries and Ambient Monitoring and Assessment program using comparable methods during a May - October index period (Hagstrom et al. 1995, CT DEEP 2013). Crews sampled 10-20 mean stream widths with the average sample width being approximately 118 meters. Reach widths used in this dataset ranged from 25 to 500 meters. The type of gear that a crew used depended on the stream width. In small streams, crews typically sample with one backpack shocker. In medium-sized streams, they used 2 backpack shockers or 1 tote barge, and in large streams, crews sampled with multi-tote barges. All captured individuals were measured to the nearest centimeter and are identified to the species level.

Benthic macroinvertebrate samples were collected by the CT DEEP Ambient Monitoring and Assessment program from September through November using an 800-u m-mesh kick net. A total of 2 meters squared of riffle habitat (12 kicks composited from multiple riffles of a stream reach) were sampled at each location. Samples were preserved in 70% ethyl alcohol and brought back to the laboratory for subsampling. A 200-organism subsample was taken using a random grid design (Plafkin et al. 1989) from each sampling location. Organisms were identified to the lowest practical taxon, generally species.

*Metrics*