



A Modeling Framework for Quantifying Spatial Recruitment Dynamics Using Abundance Estimation and Sibship Analysis

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Funding Agency: Great Lakes Fishery Commission, QFC Base Funds

Active Dates: 2020 – 2024

Goal: Improve fine-scale understanding of fish recruitment through development and evaluation of an integrated sibship-abundance modeling framework that enables mechanistic, spatially-explicit inference on recruitment, dispersal, and survival

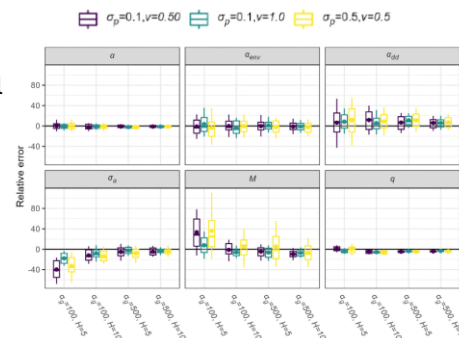


Caption: Depiction of double-helix shape of DNA. Image from PublicDomainPictures through Creative Commons CC0 (public domain)

- Objectives:**
1. Develop a continuous-time, multi-state modeling framework that integrates sibship data with abundance estimation to quantify recruitment dynamics at the sibling-group scale in spatially structured fish populations
 2. Evaluate ability of the framework to estimate key recruitment and demographic processes, including mean sibling group size, environmental and density-dependent effects on recruitment, dispersal among habitat patches, and mortality rates
 3. Conduct stochastic simulations to assess how model performance is affected by sampling intensity, capture probability uncertainty, subsampling within habitat patches, and sibling group size

Management Implications: The developed framework provides a methodology for linking genetic sibship data to spatially-explicit abundance estimates, enabling more mechanistic understanding of how recruitment, dispersal, and survival vary across habitats. By improving the ability to quantify environmental and density-dependent drivers of recruitment under realistic sampling conditions, the developed framework can support more informed decisions about harvest regulations, habitat restoration, and spatial management actions.

- Methods:**
- Developed modeling framework that integrated sibship reconstruction with abundance estimation to model sibling-group recruitment, dispersal among habitat patches, and mortality in a metapopulation context
 - Formulated recruitment as a sibling-group-level process, incorporating environmental covariates, density-dependent compensation, and stochastic process error to explain spatial variation in sibling group size
 - Simulated fish metapopulation dynamics and sampling processes, including dispersal, mortality, imperfect detection, subsampling within habitat patches, and uncertainty in capture probability, to generate realistic synthetic datasets.
 - Evaluated estimation accuracy and precision across simulation scenarios to assess how sampling intensity and sibling group size affect inference on recruitment and demographic parameters.



Caption: Relative error in parameter estimates across different combinations of sampled habitat patches, sibling group size, capture-probability variability, and % of sampled habitat

- Key Findings:**
- Mean sibling group size, environmental effects on recruitment, and dispersal rates were estimated accurately across a wide range of sampling designs
 - Density-dependent recruitment effects and recruitment process error were more difficult to estimate reliably, although accuracy improved with increased sampling effort and larger average sibling group sizes
 - Mortality estimates were sensitive to sampling intensity and sibling group size with reliable estimates obtained under moderate to high sampling effort
 - The developed modeling framework was robust to realistic sampling constraints, demonstrating that informative inferences about spatial recruitment dynamics could be made without exhaustive sampling of all habitat patches

Deliverables: Lewandoski, S.A., and T.O. Brenden. 2025. A modeling framework for quantifying spatial recruitment dynamics using abundance estimation and sibship analysis. Canadian Journal of Fisheries and Aquatic Sciences 82:1-14. [Download here](#)

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