

Evaluation of sampling designs for data-limited populations of Pacific salmon in Canada

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Abstract:

A common challenge in status assessments for fish populations is aligning sampling designs with underlying biological processes to accurately capture conservation risks. For data-limited populations, mismatches in the spatial scale between sampled data and the biological processes are especially problematic. In Canada, biological assessments of Pacific salmon populations are based on lower and upper benchmarks to delineate three status zones that represent increasing probability of extirpation and reduced production. Although benchmarks for data-limited populations have been evaluated for their ability to detect conservation risks in simulation, the performance of current and alternative sampling designs to generate required data for assessments have not been rigorously assessed. Alternative designs include those that employ random components (e.g., random panels) and/or are stratified by the spatial scale at which productivity covaries among populations. The primary objective of this study was to evaluate the ability of current and alternative sampling designs to detect conservation risks for data-limited populations of Pacific salmon in a closed-loop simulation model. Furthermore, we evaluated the role of assumptions about metapopulation dynamics, covariation in recruitment among subpopulations, and uncertainty in spawning abundances, catches and exploitation rates on design performance. This study demonstrates the importance of rigorously testing sampling designs for data-limited populations prior to implementation, and highlights sensitivity of their performance to data uncertainties and underlying population dynamics.

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Keywords: sampling design, pacific salmon, uncertainty, closed-loop simulation, metapopulation dynamics