Hierarchical bayesian models : a framework for addressing issues of nested scales in ntegrated life cycle models for exploited fish populations

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Hierarchical Bayesian Models: A framework for addressing issues of nested scales in integrated life cycle models for exploited fish populations

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Integrated life cycle models are key tools for an ecosystem approach to fish population dynamics and stock assessment. They allow analysing ecological processes underlying the spatio-temporal variability of different life stages, together with the integration of multiple interacting sources of environmental and anthropogenic stressors experienced along the life cycle at different spatial and temporal scales.

The quantitative analysis of fish life cycles still remains challenging as it requires flexible tools to merge different pieces of knowledge and data sources. We demonstrate how Hierarchical Bayesian Models (HBMs) offer a comprehensive framework for such a synthesis. HBMs allow embedding complex demographic models within statistical models for various sources of data. They have the potential to increase biological and ecological realism of fisheries stock assessment models.

We present a body of work on fish species (*e.g.*, common sole, Atlantic salmon) with life cycle shaped by an alternation of dispersion and concentration phases during ontogenic migrations. In particular, we demonstrate how HBMs allow addressing issues of nested scales in the process or observation components of integrated models. They are a red thread for linking together disparate observations (e.g., surveys, catches, realized at various life stages and different scales) in a coherent whole. They also provide tools for separating out signals at different temporal (*e.g.*, year, decades) and spatial (*e.g.*, local, global) scales in demographic traits (*i.e.*, abundance and vital rates at different life stages, vital rates). Hence, they improve the capacity to identify responses to key influential stressors associated with different scales.