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A numerical study of stochastic larval settlement in the California Current system

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Abstract

Key to the predictive understanding of many nearshore marine ecosystems is the transport of larvae by ocean circulation processes. Many species release thousands to billions of larvae to develop in pelagic waters, but only a few lucky ones successfully settle to suitable habitat and recruit to adult life stages. Methodologies for predicting the larval dispersal are still primitive, and simple diffusive analyses are still used for many important applications. In this study, we investigate mechanisms of larval dispersal using idealized simulations of time-evolving coastal circulations in the California Current system with Lagrangian particles as models for planktonic larvae. Connectivity matrices, which describe the source-to-destination relationships for larval dispersal for a given larval development time course, are used to diagnose the time–space dynamics of larval settlement. The resulting connectivity matrices are shown to be a function of several important time scales, such as the planktonic larval duration, the frequency and duration of larval release events and inherent time scales for the coastal circulations. Many important fishery management applications require knowledge of fish stocks on a year-to-year or generation-to-generation basis. For these short time scales (typically less than 1 year), larval dispersal is generally far from a simple diffusive process and the consideration of the stochastic and episodic nature of larval dispersal is required. This work provides new insights into the spatial–temporal dynamics of nearshore fish stocks.

Keywords: Larval dispersal; Dispersal kernel; Coastal oceanography; California Current; Marine resource management

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1. Introduction

The quantitative description of larval dispersal remains a central challenge in contemporary marine ecology. Marine life cycles commonly involve a dispersive planktonic larval stage, during which larvae are transported by coastal circulations while they develop their competency for the adult life stage. Only a few lucky larvae can settle upon a suitable habitat during their competency time window. This planktonic larval stage is often the predominant means of dispersal that connects spatially separated subpopulations within a region. Hence, a predictive knowledge of larval dispersal (larval dispersal distances, source and destination locations and the degree of their connectivity) is of importance for the study of marine population dynamics, management of fishery stock variations, and the design of marine reserves.

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Present knowledge of larval dispersal is still inadequate (e.g., Warner and Cowen, 2002; Largier, 2003; Kinlan and Gaines, 2003; Siegel et al., 2003; Sale et al., 2005). A complete description of larval dispersal should consist of an ensemble of dispersal trajectories for all successful settlers. In the study of population dynamics, this information is often reduced to a connectivity matrix (also called the dispersal kernel) that describes the number of the successful settlers from a given source location to a given destination location. This connectivity matrix is a function of several time scales, such as planktonic larval duration, the frequency and duration of larval release, and the inherent time scale of coastal circulation processes. The connectivity matrix is typically simplified to a simple functional form described by two or more parameters, partly for mathematical convenience and partly owing to a lack of knowledge of the matrix or dispersal kernel.

For many important applications, larval dispersal is modeled using a classic advection–diffusion formalism which assumes uniformity in advection and diffusivity. Accordingly, connectivity among sites is represented as a smooth and homogeneous functions (e.g., Roughgarden et al., 1988; Gaylord and Gaines, 2000; Gaines et al., 2003; Siegel et al., 2003; Largier, 2003). Advection–diffusion models are good starting points; however they have important limitations, particularly for assessing processes on relatively short time scales, that limit their applicability (Siegel et al., 2003). For example, advection–diffusion models cannot account for the pulses of settlements (e.g., Caffey, 1985; Farrell, 1991; Swearer et al., 1999; Siegel et al., 2003). Furthermore, advection–diffusion models make all sites potential sources of larvae for all other sites, which will artificially inflate the rate of exchange among populations that are in reality unconnected.

One way to account for pulses of larvae is by advection onshore by wind-driven circulations (e.g., Parrish et al., 1981; Bakun and Parrish, 1982; Roughgarden et al., 1991; Farrell, 1991). Downwelling favorable winds drive cross-isobath flows which advect larvae in the surface layers to nearshore habitats. While this idea brings physical insight to time series of settlement, it does not account for regional differences in settlement rates for homogeneous domains. Nor can these models explain cases where settlement occurs without downwelling favorable winds.

It is possible to numerically model coastal circulation at high-resolution and to simulate a large number of Lagrangian particles as models of planktonic larvae. Numerical models of larval transport are promising in that they can account for the appropriate time/space scales as well as regional differences in flow field while yielding detailed dispersal trajectories and connectivity matrices. Few studies have attempted to calculate connectivity matrices to date. For example, James et al. (2002) simulated the connectivity of larval transport among 321 coral reefs around the Cairns Section of the Great Barrier Reef. In another study, Cowen et al. (2003) examine the probability of larval dispersal to downstream islands within different regions of the Caribbean.

While the above studies have provided useful information regarding each of the settings they have been designed to simulate, they do not assess the underlying mechanisms of larval dispersal. For example, how applicable are diffusion-based models of larval transport? What are the time scales over which these simplified models hold? How do fluid stirring processes in the coastal ocean regulate the time–space characteristics of larval dispersal? The answers to these questions can only be assessed from looking at detailed description of larval transport. Here, we investigate the underlying mechanisms of larval dispersal and corresponding alongshore connectivity by developing “idealized” simulations of the California Current system, tied to observation data. Although more complicated simulations (e.g., James et al., 2002; Cowen et al., 2003) will be useful in more detailed studies, e.g., designing marine reserve for particular locations and particular seasons, considerable insights into the nature of larval transport can be gained using only idealized simulations.

The simulation results presented here suggest that larval dispersal, when viewed on the time scale of a single season or year, is a heterogeneous and intermittent process driven by coastal ocean stirring. This fact has many important consequences for the population dynamics of marine organisms and the management of these organisms. Our focus is on the role of the coastal circulation processes on planktonic larval dispersal. Hence, the modeling of potentially important biological factors, such as larval behavior, larval production and larval mortality, is beyond the scope of the present study. Although many of these factors can be readily accounted for using the framework presented for the abiotic case.

2. Numerical modeling of larval transport

2.1. Physical problem description

We develop “idealized” flow fields of California Current environments tied to observational data. Here, “idealized” means that the flow fields are statistically stationary and homogeneous in the alongshore direction.