

Modelling and visualisation of connectivity on the Great Barrier Reef

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Abstract. Connectivity between reefs has been identified as a major determinant of resilience in coral reef systems. Conversely, connectivity to onshore and offshore human activities can pose major threats to reef systems. While realized patterns of biological connectivity are difficult to infer, a complementary approach is to predict likely dispersal from an understanding of oceanographic currents and the swimming behaviours of organisms. We have developed an online tool CONNIE (www.csiro.au/connie2/) that allows users to estimate connectivity rapidly between reefs and exposure of reefs to coastal inputs. It uses ocean currents generated by a high-resolution three-dimensional hydrodynamic model covering the entire Great Barrier Reef (GBR) region. The underlying particle tracking techniques allow a wide range of biological behaviours to be specified, including vertical migration, horizontal swimming, surface slick formation, and ontogenetic changes. We demonstrate the approach by testing the hypothesis that the connectivity patterns on the GBR change significantly from north to south. Potential implications for southward movement of species under climate change are then briefly discussed.

Key words: Connectivity, Larval dispersion, Larval behaviour, Coral reef, Great Barrier Reef.

Introduction

The connectivity of coral reef populations is often a major factor in determining their resilience and ability to recover from major disturbances such as tropical cyclones, bleaching events or crown-of-thorns predation, any of which may increase in frequency or severity with changes in climate. For broadcast spawning corals and many reef fish, exchange between reefs is largely limited to their pelagic larval phase, when ocean currents can have a major influence (e.g. Leis 2002, James et al. 2002, Treml et al. 2008, Condie and Andrewartha 2008, McCook et al. 2009). While these processes may increase the resilience of coral reef systems, the connectivity patterns themselves may be modified by climate change.

While understanding and predicting reef connectivity is clearly central to designing effective conservation strategies (McCook et al. 2009, Mumby et al. 2011), key capabilities such as biophysical modelling, analysis and visualisation have only been available for a relatively small number of regions and often then only to a limited number of specialists. Increasing their accessibility to the point where such tools can be routinely incorporated into genetic studies, larval tagging programs and other ecological studies should lead to more comprehensive insights into the processes contributing to regional

connectivity patterns and their implications for conservation management.

Visual representations of reef connectivity, such as connectivity matrices (e.g. James et al. 2002, Condie 2008) and graph theory (Treml et al. 2008) have proven to be very effective aids in identifying underlying structures in reef connectivity patterns. Approaches have also recently been developed to provide more dynamic modelling and analyses that can be tailored to new applications and made available online (Condie et al. 2005, Condie and Andrewartha 2008, Condie et al. 2011). Here we describe the further development and application of these approaches to the Great Barrier Reef (GBR). A significant advance in this context has been incorporation of a flexible range of larval behaviours. We demonstrate the approach by testing the hypothesis that the connectivity patterns on the GBR change significantly from north to south. The implications for southward movement of species under climate change are briefly discussed.

Material and Methods

The online tool CONNIE (www.csiro.au/connie2/) combines archived currents from oceanographic models, particle-tracking techniques, and simple behavioural models to estimate connectivity statistics. These statistics are mapped using an online graphical-

user-interface (GUI) and can be downloaded as a CSV file.

Estimates of ocean currents in the GBR region were based on outputs from a three-dimensional baroclinic hydrodynamic model known as SHOC (Herzfeld 2009). This model uses a curvilinear grid with horizontal spatial resolution mostly varying between 2.5 and 4 km. The model domain includes the continental shelf, slope and deep-ocean from Moreton Bay in southeast Queensland to the mainland of Papua New Guinea, and extends eastwards into the Coral Sea beyond the Queensland and Marion plateaus. Boundary conditions were provided by a global, data-assimilating, eddy-resolving model known as the Ocean Forecasting Ocean Model or OFAM (Oke et al. 2008, Schiller et al. 2008) and the global tidal model of Cartwright and Ray (1990).

Within the GUI, particles can be seeded anywhere on a regular latitude-longitude grid at a constant rate (currently 25 particles per grid cell per day) over a user-specified release period. They are subsequently tracked individually using a 4th-order Runge-Kutta ODE solver that linearly interpolates in time and horizontal space to find the horizontal velocity at the required depth and time. An additional horizontal velocity component (constant or random) can be added to represent unresolved fluctuations or biological swimming behaviours. Vertical migration can also be represented as instantaneous jumps between vertical levels (including attachment to the seafloor).

The online GUI currently provides analysis for three regions – the GBR, Australasia and Southeast Asia, and the Mediterranean Sea. It allows the user to specify (i) the source (or destination) region on the map (e.g. a reef); (ii) a particle release period (e.g. the spawning period); (iii) the particle dispersal time (e.g. larval pelagic duration); (iv) any particle behaviour including swimming depth(s) (e.g. vertical diel migration); (v) the statistic to plot (e.g. distribution at the end of the dispersal time); and (vi) graphic colour bar characteristics for display purposes (Fig. 1).

Options for larval behaviour include (i) horizontal swimming at any constant velocity or with random walk; (ii) diel vertical migration between any specified depths; or (iii) floating on the surface with any required windage effect. Any of these options can be applied sequentially in order to simulate ontogenetic changes in larvae or juveniles (Fig. 2).

As a simple demonstration of the analyses that can be undertaken using CONNIE, we examined the potential for southward migration through sequential spawning and dispersal events. For the purposes of this example, it was assumed that spawning occurred over a seven-day period in early November (main coral spawning on the GBR) and that larvae remained

in the water column for a maximum of 14 days, while maintaining a depth of around 5 m (i.e. the conditions specified on the GUI screenshot in Fig. 1). While the pelagic duration of reef species varies widely (Bay et al. 2006, Jones et al. 2009), 14 days is within the range typically reported for many broadcast spawning corals (e.g. *Acropora*) and reef fish (e.g. *Amphiprion*).

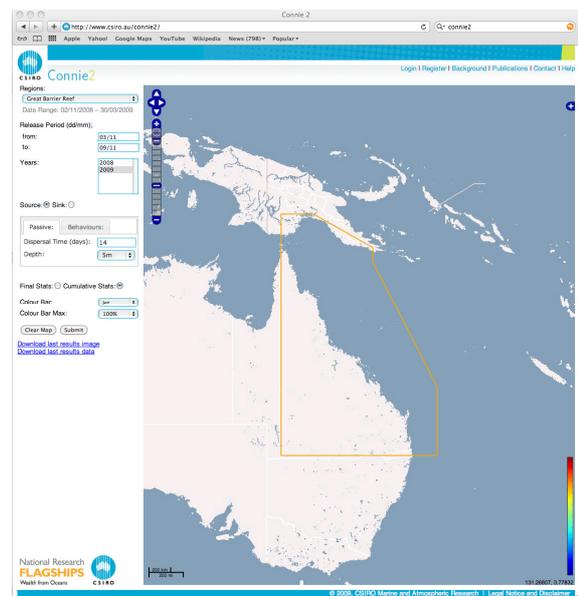


Figure 1: The graphical-user-interface “CONNIE” used to calculate connectivity statistics.

Starting with spawning at a site near Kai-Damun Reef in the far northern GBR (represented by a 0.025 x 0.025 degree cell), sequential spawning events were initiated at the southern most cell of each dispersion cloud. Where the cloud included multiple cells along the southern extremity, the highest probability cell was selected as the next spawning site. This system of linked spawning events effectively formed a Markov chain.

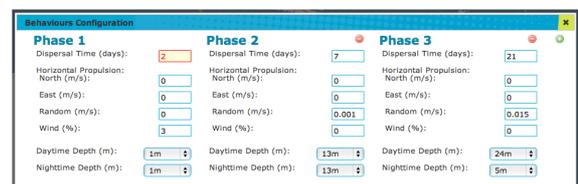


Figure 2: Window for specifying larval behaviours in CONNIE. In this example, the first phase corresponds to a surface slick; the second to weak random swimming at mid-depth; and the third with stronger random swimming combined with diel vertical migration.

Results

Modelled larval dispersal patterns on the GBR varied significantly with latitude. During the November period, subtidal dispersal north of 14°S was

dominated by northward currents driven by the southeasterly trade winds and the Hiri Current further offshore. Southward transport was extremely slow within this region (Fig. 3a), relying almost entirely on tidal mixing (Fig. 4). The geography around Princess Charlotte Bay also helped to trap larvae and impede their southward progression.

South of Cape Melville, winds became northeasterly and the East Australia Current began to dominate the offshore environment. As a consequence, the southward transport of larvae accelerated rapidly with migrations of up to 100 km typical within the 14-day pelagic larval duration (Figs. 3b, 4). This pattern is broadly consistent with earlier fine-scale modelling of the area between 14°S and 18°S using on a depth integrated model (James et al. 2002).

Dispersal patterns became more complex around the Swain Reefs due to the presence of a large cyclonic eddy on the broader continental shelf (Fig. 3c). As the shelf narrowed to the south, the influence of the East Australia Current increased and larvae were rapidly transported towards the subtropical reefs of northern New South Wales (Figure 4).

Discussion

The analysis of dispersal patterns on the GBR during November 2008 has served to demonstrate the capabilities of CONNIE. However, it is clearly only a small first step in exploring the system's broader connectivity characteristics, which are certain to change both seasonally and inter-annually. Another area of ongoing analysis using CONNIE is the connectivity between estuaries and reefs, which is important for both recruitment to coastal nursery habitats and exposure of the reef to a range of terrestrially derived contaminants.

While limited in scope, the preliminary analysis presented in Figs. 3 and 4 is interesting in that it supports our initial hypothesis that connectivity patterns on the GBR change significantly from north to south. Cape Melville represents a significant transition point, where transport switches from predominantly northward (under the influence of southeasterly trade-winds and the Hiri Current) to predominantly southward (under northeasterly winds and the East Australia Current).

In applying the model results to issues such as population migration and maintenance, it is important to recognize that limitations in the hydrodynamic model resolution and number of particles may influence potential connectivity, with many more factors determining realized connectivity (e.g. larval mortality and distribution of settlement habitats). However, the strong contrast in conditions north and south of Cape Melville reflects known oceanographic patterns and is likely to be a robust feature.

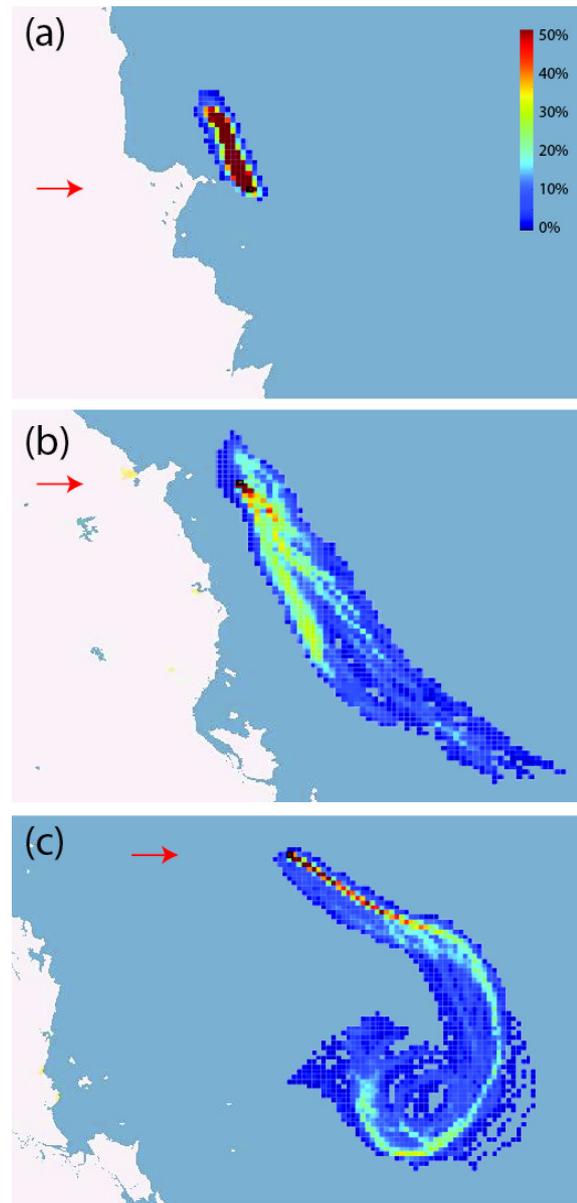


Figure 3: Modeled dispersal patterns from spawning cells at the latitudes indicated by red arrows: (a) 12°S; (b) 17°S adjacent to Cairns; and (c) 22°S. In each case spawning was from 3-9 November 2008 and the pelagic larval duration was 14 days, during which time all larvae were assumed to remain at a depth of 5m. The colour-bar indicates the percentage of spawned larvae that pass through each cell. Each image spans at total of 2° in latitude.

If the currents used for the analysis were representative of every November, then any coral or fish spawning restricted to that time of year would take almost a century to spread from the tip of Cape York to Cape Melville, and then only another decade to reach subtropical reefs far to the south (Fig. 4). However, high interannual variability in the connectivity of other reef populations has been

measured (Hogan et al. 2012) and on the GBR it is more plausible that most southward transport on the northern side of Cape Melville is associated with years of anomalous winds and currents (relative to 2008).

Even taking the limited timeframe of the analysis into account, it seems likely that Cape Melville represents a significant break in connectivity patterns at this time of the year when coral spawning is near its peak. If this is the case, then we can speculate that replenishment of disturbed reefs in the northern GBR will tend to be from the south, which may perpetuate any previous vulnerability to temperature stress and potentially accelerate predicted increases in bleaching (Guinotte et al. 2003).

We have only considered one of many potential applications of CONNIE in this report. One aspect of connectivity that has generally not been explored in detail within biophysical models is the influence of larval behaviour. This is presumably due to the associated uncertainties and the high computational costs traditionally associated with running large numbers of larval behavioural scenarios. However, there is significant evidence that behaviour can be an important factor in determining connectivity patterns (e.g. Leis 2002, Hogan and Mora 2005). CONNIE now provides a very efficient platform from which to conduct sensitivity analyses and test hypotheses relating to larval behaviour (Fig. 2).

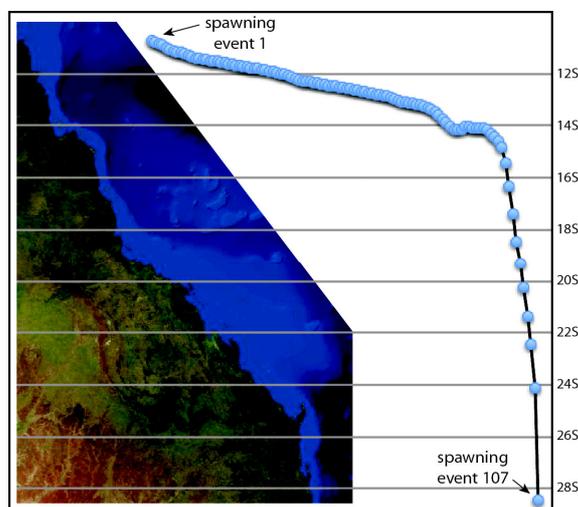


Figure 4: Spawning event number versus furthest southward dispersion latitude, where each spawning event starts at the furthest southward dispersion point of the previous event. In every case the timing and larval properties are as in Fig. 3.

Priorities for ongoing development of CONNIE for the GBR include extending the time-series to the present and implementing the system as a near-real-time tool (potentially using higher spatial resolution

than the current version). Efforts are also underway to couple CONNIE to ecosystem models such as ELFSim (Little et al. 2007) and Atlantis (Fulton 2011), as well as to the reserve design tool MARXAN (Beger et al. 2010).

Acknowledgement

Our thanks to Mike Herzfeld for providing access to output from the high-resolution hydrodynamic model of the Great Barrier Reef.

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