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Testing the robustness of a linked-ecosystem trophic model of the Great Barrier Reef, World Heritage Area

Dr Neil A Gribble

Queensland DEEDI, PI&F Northern Fisheries Centre, PO Box 5396Cairns
Email: neil.gribble@dpi.qld.gov.au

Abstract

This presentation summarises the results of an international collaboration between the University of British Columbia, Aquatic Ecosystems Research Laboratory, and the Department of Primary Industries and Fisheries, Queensland. The project represented a unique opportunity to test the robustness (c.f. validation) of a large scale ecological model of one of Australia's iconic natural wonders; the linked-ecosystems of the Great Barrier Reef. (GBR)

The original ECOPATH EwE©, GBR ecosystem models were based on survey data of 1000 taxa from a 10,000 sq nautical mile cross-shelf transect of the far northern Great Barrier Reef. Although large, this area is only a small proportion of the GBR in its entirety. In 2007 however, we completed comprehensive surveys of the entire reef as part of the CSIRO, AIMS, QM, DPI&F, ReefCRC; "***Mapping seabed biodiversity of the Great Barrier Reef*"**. These surveys provided a larger dataset to test the models against; i.e., to validate them. Not only is validation of large-scale ecological models rare anywhere in the world, but the validated GBR models would potentially provide one of the few tested ecosystem based management (EBM) tools available.

Two methods of testing the models were trialled:
1. Various scenarios of fishing effort profiles, time-scales, and tuning the model for species vulnerabilities were trialled to attempt to understand the dynamics of the model. Following this painstaking process, visual comparisons were run for the temporal simulations of biomass profiles against the ensuing 10 year time-series of logbook CPUE for species groups taken in the Trawl, Reef-line, and inshore Gill Net fisheries (as the estimate of "observed" changes in relative biomass of those species groups).
2. Spatial expansion of the GBR Linked-ecosystem model to a more realistic GIS basemap of the whole GBR. Habitat type from the smaller GBR Linked-ecosystem cross-shelf simulations were assigned to depth contours that were available in the larger GBR GIS Map. Visual comparisons were then possible between the models predicted spatial distributions of species groups over the whole GBR, against those observed from survey data obtained by the "***Mapping seabed biodiversity of the Great Barrier Reef*"** project.

Within a tightly controlled set of constraints the current model does provide useful predictions of the cumulative impacts of the Trawl, Reef-line, and inshore Gill Net fisheries on the "virtual" GBR cross-shelf. The expansion of the model to the full GBR will require a re-specification of the basic model; however, useful predictions can be made of the impacts of fishing if these are treated as hypotheses that need independent testing. The latter is probably a general caveat that should be applied to the output from any model.

Key Words*: ECOPATH, ecosystem models, validation*

1. **INTRODUCTION**

The current paper is the latest instalment in the development of GBR Ecosystem models (Gribble 2005a & b, 2007) and briefly summarises the results of an international collaboration to test the robustness (c.f., validation) of a large-scale ecological model of Australia's iconic natural wonder; the linked-ecosystems of the Great Barrier Reef. (GBR).

The original "GBRprawn" and the later enhanced "GBR Linked-Ecosystem" models (Gribble 2005a & b, 2007) were based on extensive cross-shelf surveys of the far northern Great Barrier Reef (Poiner et al 1998). As with most large-scale ecological models, all data available at that time was used in the building of these models. An independent data-set to test the model only became available in 2006-07, after the completion of the CSIRO, AIMS, QM, DPI&F, ReefCRC; *Mapping seabed biodiversity of the Great Barrier Reef* (Pitcher *et al.,* 2007). This project documented the species composition, biomass, and spatial distribution of 8,000 taxa from the entire GRB World Heritage area. The resultant comprehensive dataset provided the opportunity to validate the "GBR Linked Ecosystem" model, by reality-checking the models' behaviour through time and via comparisons of the predicted spatial distributions against the observed distributions derived from the larger, independent survey dataset. This is theoretically the optimum process for validating an ecological model; where one dataset is used for building the model and a second independent set is used for testing it. Given the size and complexity of the ecosystems usually being studied in large-scale models, in this case the Great Barrier Reef, such a process is difficult to achieve if not logistically impossible.

The "reality-checking" reported here is essentially heuristic, not a statistical goodness-of-fit validation between predicted and observed values, so is treated as testing the "robustness" of the model rather than as a classical validation process.

2. METHODS

The linked-ecosystem model is a "cross-shelf" representation of the GBR habitats and trophic associations (see fig 1) using the ECOPATH EWE 5.1 software platform (Gribble 2005a). The base model is an equilibrium trophic hierarchy, with biomass flows balanced such that there are not more predators than prey to feed them, nor conversely are there "wasted" prey with insufficient predators to exploit the resource There are 32 cross-shelf trophic guilds, spread across inshore, lagoon, reef and outer reef habitats. Three major fisheries are simulated; inshore set-net, prawn-trawl, and reef-line, see fig 1. For a detailed description of the model and biological parameter estimates for each trophic guild see Gribble (2005a).

Commercial fisheries catch and effort data, 1988 to 2005, were obtained from the QFISH compulsory logbook database. A representative sub-sample of these logbook records have been validated by Queensland fisheries observers (Jason Stapley, PI&F Fisheries Observer Supervisor, North; pers comm. 2009). Recreational catch and effort could only be roughly estimated from the three approximately biannual surveys carried out by the Primary Industries and Fishing in Queensland over the same period (see also Gribble 2007).

The spatial comparisons for the full-scale GBR simulations used the distributions of species and species-groups reported in Pitcher *et al.,* 2007.

As noted in previous articles "estimates of biomass, consumption, production, and diet matrices represent the underlying assumptions of the model and a different set of assumptions may also produce a balanced model." With all models the aim is to capture the major biomass dynamics and flows of the much more complex, "real" system.

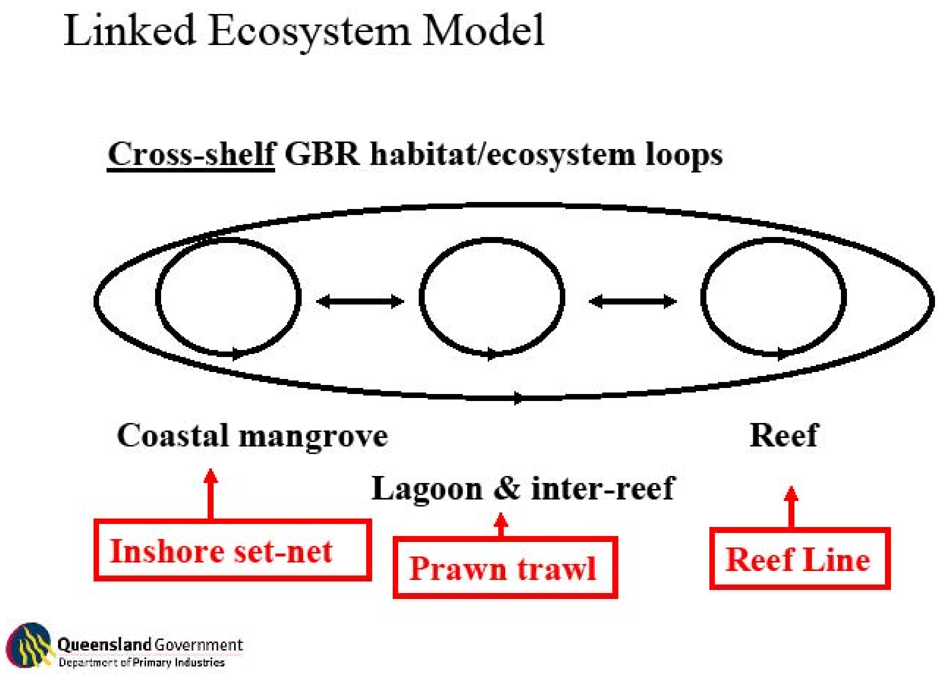

Figure 1. Diagrammatical representation of the GBR Linked-ecosystem model showing the basic trophic pathways within and between the three cross-shelf habitats, and the impacting fisheries (source Gribble 2005b).

3. SIMULATIONS

3.1. Temporal Patterns

Given that ten years had passed since the basic model had been built, the effects of fishing in the intervening time needed to be included to bring the simulations up-to-date. The time-series of logbook derived catch-per-unit-effort (CPUE) for the major fished “trophic guilds” and fishing effort in each of the three fisheries (inshore set-gillnet, prawn Otter-trawl, reef line-fishery,) was entered into the ECOPATH ECOSIM temporal simulation module (see Christensen et al., 2000).

That is, both the temporal pattern in relative biomass (estimated by CPUE) and the spatial pattern in species distribution could be compared between the model and independent data sources (i.e., commercial logbook CPUE and research survey data).

The ECOSIM subroutine requires the vulnerability to predation of each trophic guild to be tuned to give a stable model, balancing biomass trajectories across the 32 trophic guilds that roughly followed the relative biomass indicated by the CPUE. This was an iterative process with the aim to produce a balanced stable model, then the comparison of observed to predicted could be carried out (Christensen pers com, 2008). An example of the resultant fit of the predicted biomass to the observed CPUE timeseries for the major fished species in given in Fig 2., and summarised in the concluding comments.

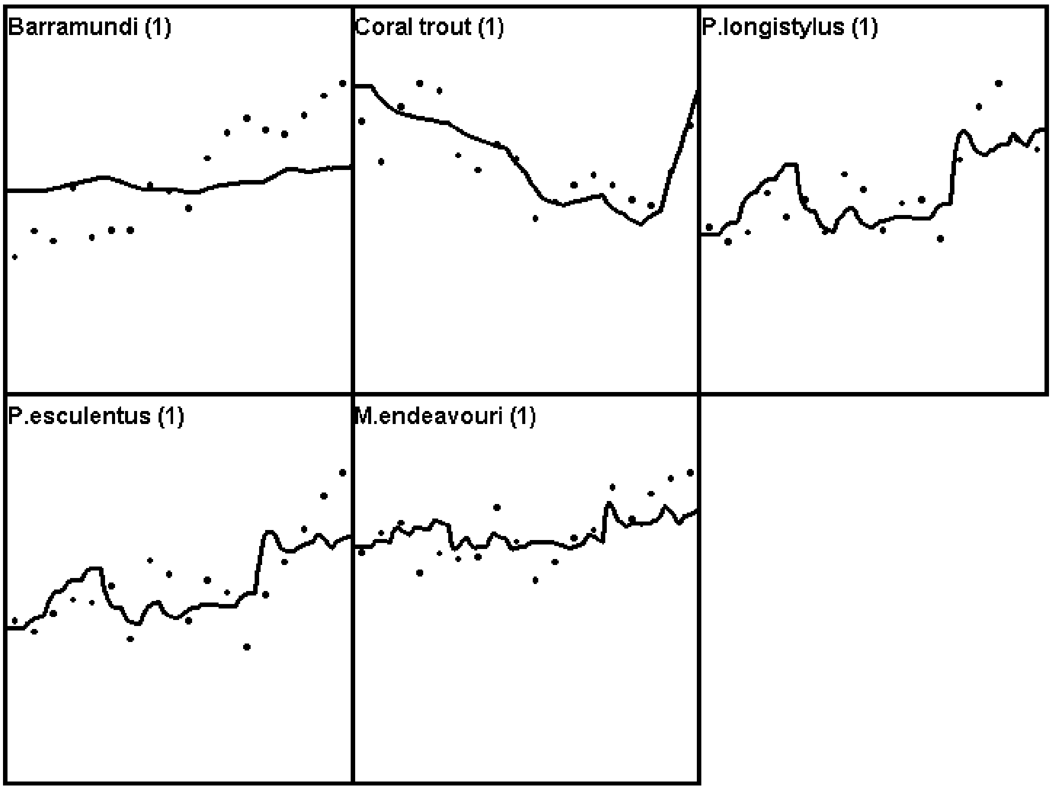

Figure 2. GBR Linked-ecosystem ECOSIM simulation of the biomass profile of selected trophic guilds, shown as the solid lines, with the logbook CPUE shown as overlaid dots. The time series plotted is for 18 years, 1988-2005 [For species groups predominantly fished by the commercial fisheries, except for recreationally important Barramundi].

3.2. Spatial patterns.

To test the robustness of model, the ECOSIM simulation was “extrapolated” onto a full-scale GIS map of the GBR world Heritage Area, using the ECOPATH ECOSPACE spatial simulation module. A virtual map of the Queensland north-east coast and the GBR world heritage area was produced, fig 3.

Habitat type from the smaller GBR Linked-ecosystem cross-shelf simulations (Gribble 2007) were assigned to appropriate depth contours that were available in the larger GBR GIS Map. Visual comparisons were then possible between the models predicted spatial distributions of species groups over the whole GBR, against those observed from survey data. Statistical comparisons will be reported in a later publication.

Note: in the following figures, the ECOSPACE model-predicted distribution is on the right of the figure with the observed distribution inset on the upper left The colour scale/legend for the observed data is set next to the insert, and a photo of the relevant species is inset at the lower right of the predicted distribution.

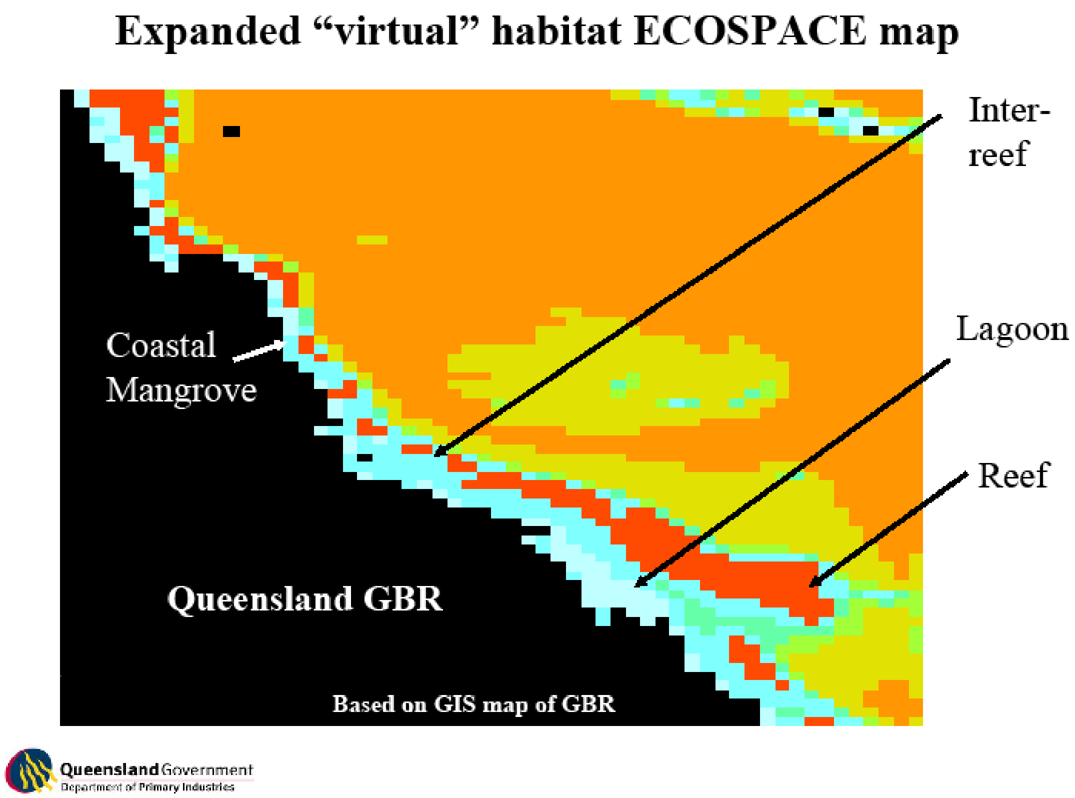

Figure 3. ECOSPACE virtual map of the the area of the 1,800 km long Great Barrier, Reef World Heritage Area.

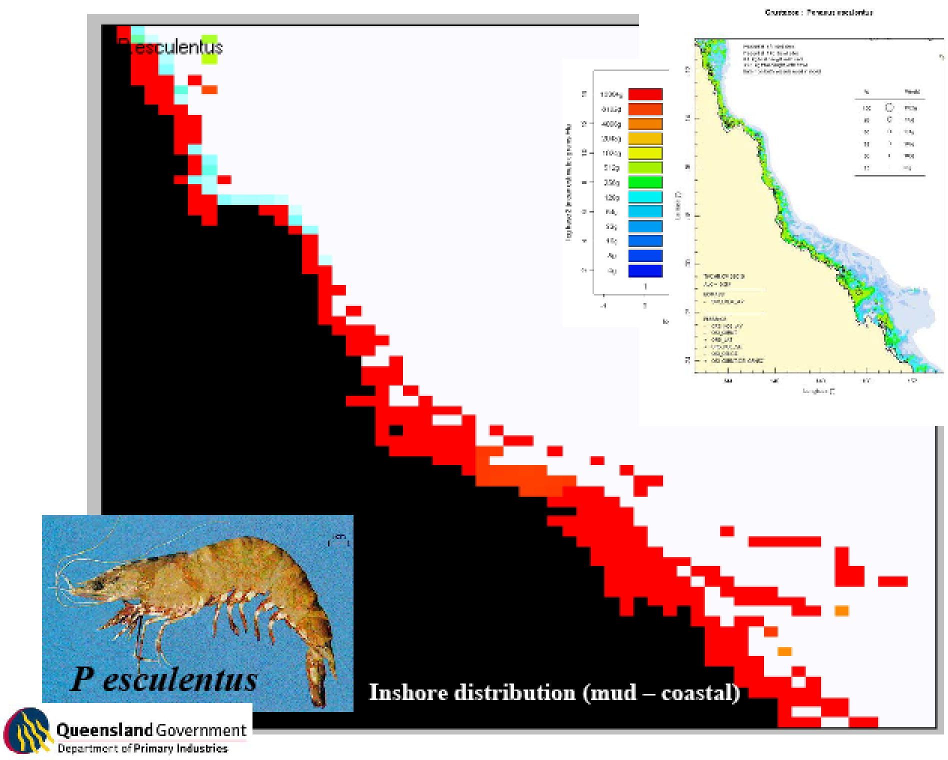

Figure 4. Full scale simulation of the distribution of the brown tiger prawn. The survey data (insert) shows an almost identical inshore shallow-water distribution of this species.

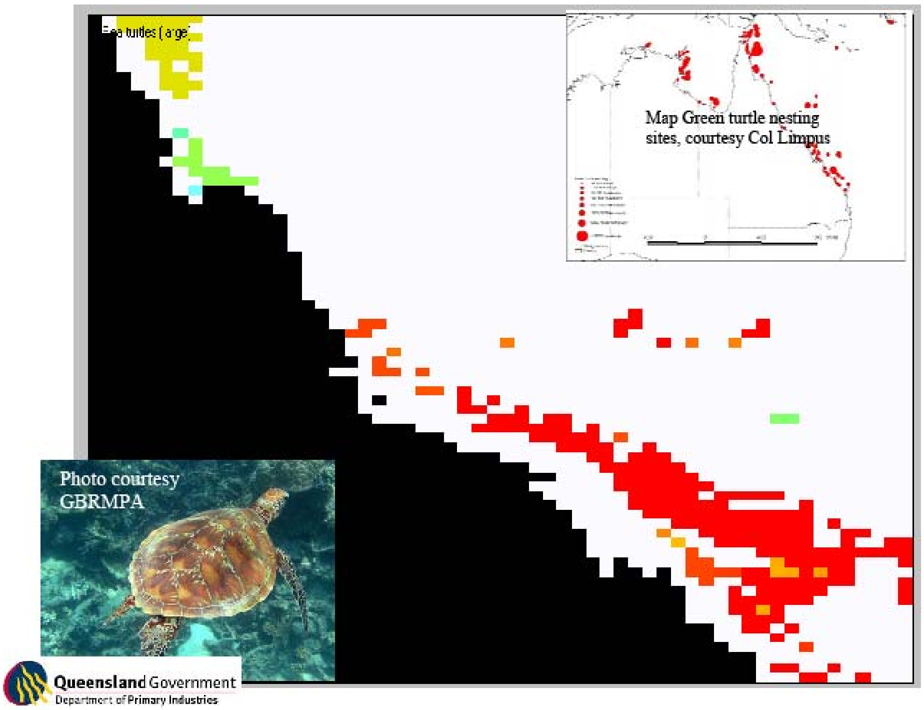

Figure 5. Full scale map simulation of the distribution of the "Sea-Turtles". The nesting site data (insert) provided by the sea turtle project of Dr Col Limpus QPWS, shows a similar, mainly southern inshore distribution for this species.

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The patterns in longitudinal cross-shelf distribution, and in most cases the latitudinal distribution, of trophic guilds predicted by the full scale simulations of the GBR Linked-ecosystem model, were consistent with the survey data observed by the Pitcher *et al* (2007). Single species comparisons can give an uncanny similarity between the predicted and observed distributions (see fig 4 and 5).

4, DISCUSSION AND CONCLUDING COMMENTS

A number of challenges were thrown-up during the fitting/validation process:

1. Despite the excellent visual fit between predicted and observed spatial distributions, the correct way to model separate distinct areas of the coast at this stage of ECOPATH development would be to build separate distinct ECOPATH models with the relevant species biomass spread over that smaller area(s). Spreading the surveyed biomass over the whole area of the model tends to over generalise the result. This challenge relates to the inherent problem of detail versus generality within large ecosystem models.
2. Paradoxically CPUE profiles from logbook data were almost identical when recalculated for the larger-scale "GIS" model. The problem was that the Queensland logbook database records "Days on which fish were recorded caught" as "Days fished", therefore fishing effort tends to follow the catch (or vice-vesa) and consequently CPUE appears constant across spatial scales.
3. In some cases the CPUE is actually a poor indicator of relative biomass (see fig 2). The poorest fit in my simulations was in trophic guilds with the highest proportion of "unrecorded" recreational catch/effort (e.g,. Barramundi). This highlights a real problem of making comparisons with "observed" CUPE that is missing significant "extractions" and therefore is almost certainly not a good indicator of the underlying biomass.
4. Given points 2 and 3 above it was not surprising that further fitting of the vulnerabilities tended to send the model chaotic, either in the ECOSIM or ECOSPACE simulations. Less severe changes in the vulnerabilities gave a stable model but predicted biomass(s) that were only roughly close to the relative biomass profiles inferred solely from CPUE data (see fig 2).

Therefore at the current stage of model development, temporal and spatial simulation of the ecosystem impacts of fishing on the GBR need to be treated as "useful working hypotheses", that require independent testing; i.e., robust but with caveats.

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