

FISHBASE, SEALIFEBASE AND DATABASE-DRIVEN ECOSYSTEM MODELING¹

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Building trophic network models in ecosystems consists of the following steps: (1) determine the species or species groups occurring in it and the niches they occupy; (2) establish the predator-prey matrix; (3) determine how much of each prey is consumed by each predator; (4) establish how much of these groups stay in the ecosystem in terms of mass and surface area; and (5) quantify how fast each component renews itself. These data requirements make trophic network modeling tools, e.g., Ecopath with Ecosim (EwE), currently used in ecosystem-based resource management, rather 'data hungry' (Christensen *et al.*, 2009). Moreover, these parameters are not easy to measure, are often not included in sampling designs and usually entail tedious and time consuming literature searches. A Biodiversity Information System (BIS) which includes data on life-history parameters and which can 'speak' to modeling software such as Ecopath with Ecosim is one solution to this problem.

FishBase and SeaLifeBase are two such Biodiversity Information Systems, which, by nature of the data they contain, can become mainstay companions to EwE.

FishBase (www.fishbase.org) is an online information system on key life-history parameters of the world's fish species, conceived in the late 1980s by Daniel Pauly and developed by a team of marine biologists led by Rainer Froese in the 1990s (see Froese & Pauly, 2000). It has since grown into a popular online resource, averaging 33 million hits per month with a network of more than 1700 collaborators (individuals and institutions). FishBase's structure has more than 250 tables holding more than 4 million records of information for more than 31 000 fish species of the world, 5 000 of which are commercial fish species. These tables are related in this manner: (a) FishBase assigns a species to a taxonomic group, i.e., Family, Order, Class, etc.; (b) once clearly established nomenclaturally and taxonomically, a fish species is then assigned to geographical areas where it is known to occur, i.e., country, FAO zones, established ecosystems (e.g., large marine ecosystems, rivers, lakes, etc.); (c) biological (growth parameters, maximum sizes, spawning and reproduction, etc.), ecological (habitat, food items, diet composition, trophic levels, predators, etc.) and fisheries information are then attached to a species. These 'related' data allow FishBase to make lists of species, viz.: (i) in a given taxonomic group; (ii) found in a country or given geographic zone; (iii) in a given habitat (e.g., pelagic, demersal, etc.); (iv) in a given trophic level; and (v) combinations of (i) to (iv) sorted by maximum size. These lists respond to the data needs of EwE as enumerated in 1-3 above as provided by the 'Ecopath data', 'Species Ecology Matrix', 'Trophic pyramids' tools in the 'Information by Country/Island' and 'Information by Ecosystem' searches of the FishBase online version. However, these were provided for fish groups alone.

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In response to the need to cover organisms other than fishes also occurring in marine ecosystem, the *Sea Around Us* Project, with additional funding from the Oak Foundation (Geneva, Switzerland), initiated work on SeaLifeBase (www.sealifebase.org) to produce a similar service for all of the world's marine animals. This joint project with the WorldFish Center is an activity endorsed and monitored by the FishBase Consortium since 2006, thus benefitting from FishBase's 21 years of experience. SeaLifeBase was developed from an empty FishBase database shell adapted to the different forms of metazoans, but with as few changes as possible, making the adaptation of SeaLifeBase data to the common web interface shared with FishBase more efficient with less programming and development (i.e., skipping at least 5 years of work on database structure and web interface construction) and thus, maintaining a consistent form of data access for fish and metazoan species. Unlike FishBase, which was started without a taxonomic standard (though the current standards followed are that of the Catalog of Fishes (Eschmeyer, 1998) and hierarchy proposed by Nelson, 2006), SeaLifeBase's taxonomic structure was adapted from that of the Catalogue of Life (www.catalogueoflife.org) which is itself enhanced by expert-reviewed taxonomic data of the World Register of Marine Species (www.marinespecies.org); again saving development and encoding time for the SeaLifeBase team. These two global catalogues are the source of 56 % of the nearly 98 000 scientific names of metazoan species in SeaLifeBase (excluding data on algae from another BIS, AlgaeBase (see www.algaebase.org), which takes the species count currently available in SeaLifeBase to more than 105 000), including comprehensive information for commercially important non-fish metazoans.

FishBase and SeaLifeBase together, may respond to user demands in varying degrees (see Bailly, 2003). However, they both respond to the data needs of ecosystem-based models (see 1-3 above) for marine ecosystems and will allow for biological comparisons across species groups (e.g., Palomares & Pauly, 2009; Gascuel *et al.*, 2008), notably using the EwE approach (see, e.g., Pauly *et al.*, 2009).

Developments with EwE include extraction routines to turn FishBase and SeaLifeBase data into direct inputs for preliminary models of large marine ecosystems (see Christensen *et al.*, 2009). The use of FishBase and SeaLifeBase in ecosystem models are here demonstrated with models of the large marine

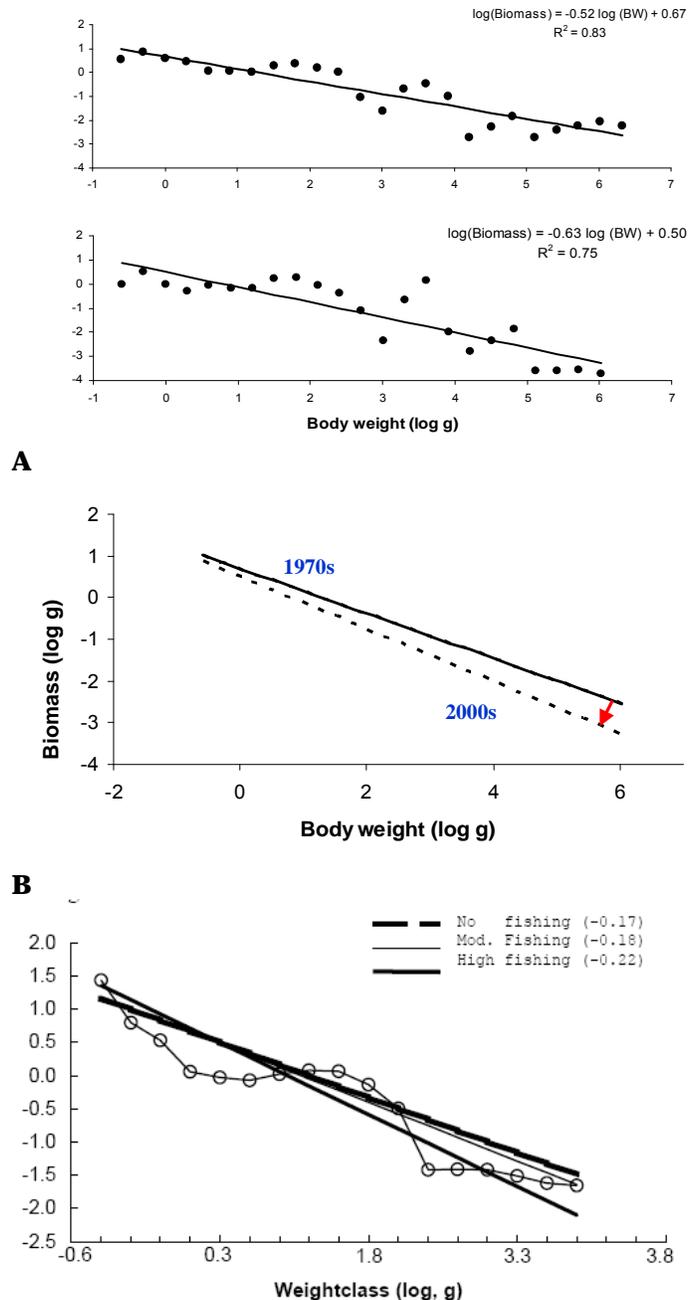


Figure 1. Results of Ecopath with Ecosim version 5 particle size distribution (PSD) routine for 35 fish and metazoan functional groups of the large marine ecosystem of the north South China Sea. Panel A: 1970s, top and 2000s, bottom; Panel B: comparison of the slopes of results in Panel A; Panel C: results of the Gulf of Thailand from Christensen (1998) emulated by results illustrated in Panels A and B.

ecosystem of the north South China Sea in the 1970s and 2000s (Cheung, W.W.F., University of East Anglia, pers. comm.) through the particle size distribution routine of EwE (v. 5). Growth parameters of the 35 fish and metazoan functional groups were extracted from FishBase and SeaLifeBase to obtain a log-log plot of biomass vs body weights (see Pauly & Christensen, 2002). The results (1970s model: $\log(\text{biomass}) = -0.52 \log(\text{body weight}) + 0.67$, $r^2=0.83$; 2000s model: $\log(\text{biomass}) = -0.63 \log(\text{body weight}) + 0.50$, $r^2=0.75$; Figure 1a) show that the 2000s model has a steeper slope (Figure 1b), reflecting an increase in fishing pressure on the larger-sized groups and thus confirm and extend earlier results for the Gulf of Thailand (Christensen, 1998; see Figure 1c).

This exercise shows that FishBase and SeaLifeBase not only contribute to the global coverage of marine biodiversity, but makes feasible the modelling of, e.g., large marine ecosystems in which this biodiversity thrives.

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