BIODIVERSITY INDICATORS

USING 'AQUAMAPS' FOR REPRESENTING SPECIES DISTRIBUTIONS IN REGIONAL SEAS[1]

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ABSTRACT

AquaMaps (www.aquamaps.org) are the products of an on-line approach for generating distribution range maps of marine organisms, which currently covers over 10,000 marine species of fish, marine mammals and invertebrates, the intention being to eventually generate standardized range maps for all species in the oceans. These range maps can be used to generate check-lists or inventories of species occurrence in data-poor areas, e.g., in Regional Seas.

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Introduction

The traditional method of drawing distribution range maps, applicable to species for which many occurrence records (positive and negative) exist, is for an expert on the species in question to plot the occurrence records as dots on a map, and to interpolate (or not) between them, based on knowledge of the species habitat requirements and other (partly intuitive) ecological knowledge.

Unfortunately, there are too few occurrence records, too many species and too few experts for more than a small fraction of marine biodiversity to be mapped this way. Also, intensive biological sampling has taken place in only a few parts of the ocean, e.g., the Northeast Pacific and the North Atlantic, and the small areas covered relative to the distribution range of most marine species makes extrapolation of ocean-scale marine biodiversity difficult.

One alternative to the traditional method of mapping distribution ranges is to use the environmental characteristic — especially temperature and depth — associated with the occurrence records (originating from museum collections and other sources), to define the environmental 'envelope' of a species, then to project a probable distribution through maps of temperature, depth, etc.

AquaMaps is a type of environmental envelope model, i.e., a modified version of the relative environmental suitability model (RES) developed by Kaschner *et al.* (2006b) to predict global distributions of marine mammals, but later modified and expanded to cover all marine species (Kaschner *et al.*, 2008). The model was specifically developed to deal with the sampling biases affecting most large-scale data sets currently available for species distribution modeling in the marine realm by supplementing occurrence records with alternative sources of information about habitat usage.

Material and Methods

Using all available information, the model determines the environmental tolerance of a given species with respect to a pre-defined set of parameters including depth, salinity, temperature, primary production and sea ice concentration. It then predicts the maximum range extents for a given species including the relative probability of species occurrence (PSO) within that range by relating these environmental tolerances (or envelopes) to the physical and oceanographic attributes of each cell in a global grid with 0.5 latitude/longitude cell dimensions (Kaschner *et al.*, 2008, Ready *et al.*, 2010).

Two types of input data are used to generate AquaMaps species predictions. Available point occurrence records for the respective species, used to calculate all environmental envelopes (except for depth preferences) are harvested from online data repositories such as the Ocean Biogeographic Information System (OBIS), and the Global Biodiversity Information Facility (GBIF). Such point data sets are compiled from a variety of different sources and are generally affected by a number of sampling biases including, but not limited to, non-representative coverage of habitats and species misidentifications. To address these issues, AquaMaps supplements point occurrence data with other types of habitat use information obtained directly from online species databases such as FishBase (www.fishbase.org) and SeaLifeBase (www.sealifebase.org). This includes information about the general occurrence of species in the form of bounding boxes, delineating the known maximum range extents for species as described in the scientific literature or FAO area checklists, which is then used as a primary filter to identify possible misidentifications. Heterogeneous sampling, due to the concentration of sampling efforts in continental shelf areas, often results in a mis-representation of the true depth usage of species. To counteract this bias, AquaMaps relies on depth information taken from the literature, as encoded in online species databases. In addition, an expert review function in the AquaMaps algorithm explicitly allows for the incorporation of expert knowledge about species occurrence to further counteract or compensate known sampling biases.

Once the occurrence records have been harvested and verified, they are complemented with the supplementary data, and then processed via a General Linear Model, which access environmental data on a global grid of ½ cells of ½° latitude/longitude cells, until a model is found which generates a statistically robust global distribution map of probabilities of occurrence. The resulting maps then sometimes need to be trimmed (unless a bounding box was used at the onset), as the procedure cannot distinguish by itself, say tropical shallow habitat in the Indo-Pacific from the same habitat type in the Atlantic.

For the purposes of this report, the biodiversity information available in all completed AquaMaps, expressed on ½° latitude by ½° longitude cells was summarized by Regional Seas. Particularly, the minimum, maximum and mean probability of occurrence was summarized for each of the 86 subsets of species in Table 1.

Table 1. Breakdown of the subsets of species used to summarize for each Regional Sea. The # of species used is the number of species that have data available, and # of species is the total number of species in each group.

Taxon	Category	# of species used	# of species	Taxon	Category	# of species used	# of species
Animalia	kingdom	8393	909760	Cypraeidae	family	15	26
Arthropoda	phylum	263	780288	Dasyatidae	family	28	77
Cnidaria	phylum	198	9937	Engraulidae	family	51	141
Porifera	phylum	7	8368	Euclichthyidae	family	1	25
Actinopterygii	class	6544	29184	Fucaceae	family	1	18
Anthozoa	class	185	5953	Fundulidae	family	6	24
Appendicularia	class	1	65	Gadidae	family	23	32
Cephalaspidomorphi	class	6	42	Gasterosteidae	family	5	137
Cephalopoda	class	77	775	Gempylidae	family	18	84
Elasmobranchii	class	460	996	Gonostomatidae	family	27	11
Holocephali	class	20	40	Haemulidae	family	78	5
Mammalia	class	116	7237	Holocentridae	family	48	25
Maxillopoda	class	6	5234	Istiophoridae	family	7	23
Myxini	class	12	72	Lamnidae	family	5	108
Reptilia	class	16	13106	Lophiidae	family	17	387
Acipenseriformes	order	4	32	Lotidae	family	13	25
Anguilliformes	order	281	878	Lutjanidae	family	78	6
Cetacea	order	83	121	Macrouridae	family	146	249
Characiformes	order	0	1851	Merlucciidae	family	15	57
Clupeiformes	order	132	388	Moronidae	family	4	208
Cyprinodontiformes	order	8	1155	Myctophidae	family	173	17
Gadiformes	order	265	604	Nototheniidae	family	32	42
Scleractinia	order	181	1501	Octopodidae	family	7	11
Stomiiformes	order	209	407	Osmeridae	family	8	102
Acanthuridae	family	56	81	Petromyzontidae	family	6	43
Achiridae	family	12	33	Phycidae	family	9	86
Agonidae	family	29	47	Pleuronectidae	family	62	369
Anguillidae	family	10	24	Polynemidae	family	17	18
Antennariidae	family	24	45	Pomacanthidae	family	45	7
Apogonidae	family	156	337	Pomacentridae	family	197	214
Argentinidae	family	12	25	Priacanthidae	family	13	282
Artedidraconidae	family	12	25	Pristidae	family	4	57
Atherinidae	family	25	66	Salmonidae	family	21	138
Balistidae	family	29	42	Sciaenidae	family	101	503
Blenniidae	family	143	385	Scombridae	family	45	129
Carangidae	family	127	150	Sebastidae	family	77	9
Carcharhinidae	family	40	50	Serranidae	family	234	280
Centrolophidae	family	22	31	Sparidae	family	85	65
Chaetodontidae	family	83	128	Sphyrnidae	family	7	1
Cheilodactylidae	family	14	27	Stomiidae	family	133	4
Clupeidae	family	71	213	Synodontidae	family	39	–
Cottidae	family	81	250	Xiphiidae	family	1	–
Cynoglossidae	family	55	137	Balaenidae	family	4	–

Results and Discussion

Presently, over 10,000 AquaMaps, mainly for marine fishes, have been produced using this approach (and used here). Also, their outputs have been successfully validated using independent, effort-corrected survey data and, in the face of the existing sub-optimal input data sets, AquaMaps model performance compares well with that of other presence-only habitat prediction models, such as GARP, Maxent or GAMs (Ready *et al.*, 2010).

Using the tools available on the AquaMaps web site, subsets of AquaMaps species predictions have been used in various analyses investigating patterns of species richness in different geographic regions (Froese, *in press*). Marine species diversity maps can be generated by overlaying AquaMaps predictions of all or subsets of species and counting all species predicted to be present in a given cell based on a pre-defined probability threshold. As an example we show the distribution of anguilliform fishes (European and American eels, conger eels, etc.) in Figure 1.

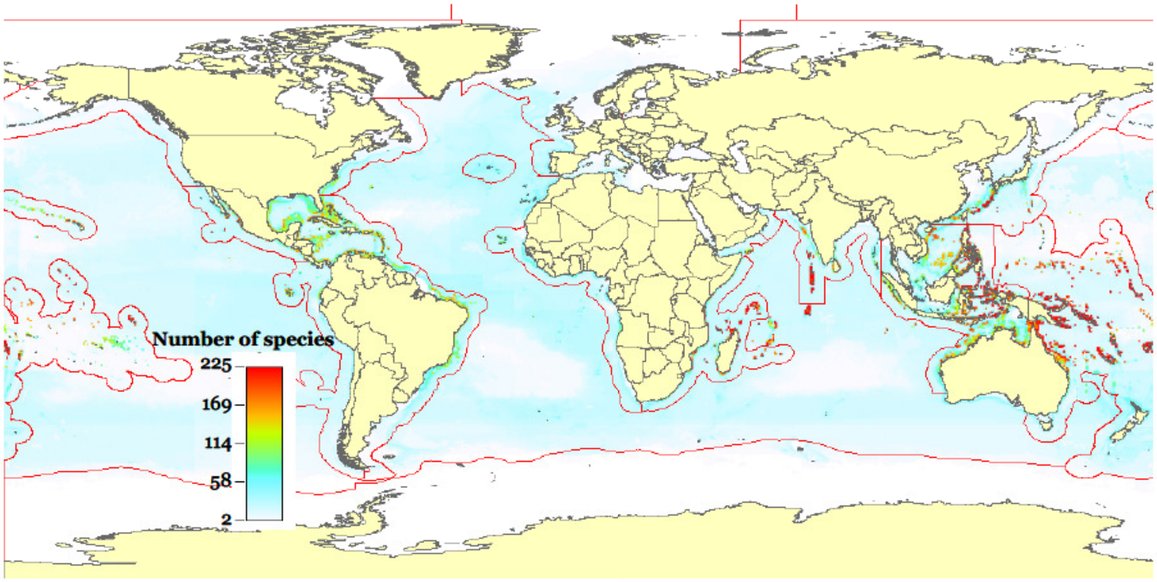

Figure 1. Global distribution of the order Anguilliformes (eel-like fishes; approximately 800 species in 19 families). The legend indicates the predicted number of species occurring in each half-degree cell.

Specific case studies include investigations of the association of marine mammal biodiversity hotspots and global seamount habitat (Kaschner, 2007), the impact of climate change on global marine mammal biodiversity (Kaschner *et al*., submitted) and European fish fauna (Kaschner *et al*., *in press*) or to provide an overview of Mediterranean Sea biodiversity patterns (Coll *et al*., 2010).

Large-scale species distribution models currently probably represent the best, if not only choice to produce species richness maps or comprehensive inventories in many of the often data-poor off-shore regions of the world's oceans. However, the concentration of sampling effort in more accessible habitats, such as the continental shelf regions of the northern hemisphere, also represents a great challenge for the application of any species distribution modeling technique, and the results of all models therefore need to be viewed with caution. In addition, species distribution models predict broad range extents, which often do not consider seasonal movements of animals or subspecies level population structure, and may thus potentially overlook critical habitat needed during certain life stages or for maintaining subspecies level diversity.

For a given species, we are often interested in attributes such as abundance, genetic uniqueness, endemism, and endangered status. However, most models and diversity indices derived from such predictions do not consider relative or absolute abundances of individual species and are indifferent to species substitutions. Hence, mapping of biodiversity hotspots may not reliably pick up on areas important to species of special concern, such as endangered and/or extremely rare species.

Despite these caveats, which affect most currently existing models, AquaMaps-based biodiversity predictions may provide a starting point for species inventories in different Regional Seas (Table 1).

The tools and features available on the AquaMaps website allow for the selection of different subsets of species based on a range of different conservation and management criteria. Currently, taxa such as ray-finned fishes and elasmobranchs as well as marine mammals are either complete or comprehensively covered by AquaMaps, and coverage is currently being expanded to invertebrates, algae and hexacoral taxa. The incorporated expert review process represents a Wiki approach that can greatly facilitate the review of existing data and resulting predictions through expert panels such as IUCN species working groups.

However, to identify most reliably areas of high biological diversity, a range of different modeling techniques should ideally be applied to determine which regions are consistently – across all model outputs – predicted to represent hotspots. Model selection and spatial and temporal scales of the analysis should be based on data availability and the ecology and life history of the taxa in question and outputs should be validated with independent, effort-corrected survey data to the extent possible. Forward projections of changes in species distributions and related areas of high biodiversity under different climate change scenarios can help to identify those significant areas most likely to ensure long-term protection of high biological diversity.

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References

Coll, M., Piroddi, C., Steenbeek, J., Kaschner, K., Ben, F., Lasram, R., Aguzzi, J., Ballesteros, E., Bianchi, C.N., Corbera, Dailianis, R. Danovaro, J.T., Estrada, M., Froglia, C., Galil, B.S., Gasol, J.M., Gertwagen, R., Gil, J., Guilhaumon, F., Kesner-Reyes, K., Kitsos, M.-S., Koukouras, A., Lampadariou, N., Laxamana, E., López-Fé de la Cuadra, C.M., Lotze, H.K., Martin, D., Mouillot, D., Oro, D., Raicevich, S., Rius-Barile, J., Saiz-Salinas, J.I., San Vicente, C., Somot, S., Templado, J., Turon, X., Vafidis, D., Villanueva, R., Voultsiadou, E., 2010. The Biodiversity of the Mediterranean Sea: estimates, patterns, and threats. *PLoS ONE* 5(8), e11842. doi:10.1371/journal.pone.0011842.

Froese, R. 2011. The Science in FishBase. P. 47-53 *In:* Christensen, V., Maclean, J. (eds.), *Ecosystem Approaches to Fisheries: A Global Perspective*. Cambridge University Press.

Kaschner, K., Watson, R., Trites, A.W., Pauly, D., 2006. Mapping worldwide distributions of marine mammals using a Relative Environmental Suitability (RES) model. *Marine Ecology Progress Series* 316, 285-310.

Kaschner, K., 2007. Air-breathing visitors to seamounts. Section A: Marine mammals. In: Pitcher, T., Morato, T., Hart, P.J.B., Clark, M.R., Haggan, N., Santos, R.S. (eds.), *Seamounts: Ecology, Fisheries & Conservation*, pp. 230-238. Blackwell Fish and Aquatic Resources Series. 12, Oxford, U.K.

Kaschner, K., Ready, J.S., Agbayani, E., Rius, J., Kesner-Reyes, K., Eastwood, P.D., South, A.B., Kullander, S.O., Rees, T., Close, C.H., Watson, R., Pauly, D., Froese, R., 2008. *AquaMaps: Predicted Range Maps for Aquatic Species*. World wide web electronic publication, www.aquamaps.org, Version 10/2008.

Kaschner, K., Kesner-Reyes, K., Barile-Rius, J., Rees, T., Ready, J., Garilao, C., Kullander, S., Froese, R. Impacts of climate change on biodiversity patterns of fish and other marine species in European waters. *BfN-Skripten* (*in press*).

Kaschner, K., Titensor, D, Ready, J, Gerodette, T., Worm, B. Current and future patterns of global marine mammal biodiversity. [Unpublished data].

Ready, J., Kaschner, K., South, A.B., Eastwood, P.D., Rees, T., Rius, J., Agbayani, E., Kullander, S., Froese, R., 2010. Predicting the distributions of marine organisms at the global scale. *Ecological Modelling* 221(3), 467-478.