

The newly redesigned user interface organizes metadata records by presenting relevant records through a ranking and filtering system controlled by the user. The new NBII Clearinghouse system is based on a Service Oriented Architecture and supports enhanced search features, including an ability to search geographically or by specific data provider, then bookmark or email record results. Users can view search results in a combined view from all providers, or use filters to dynamically sort search results. A Really Simple Syndication (RSS) feed can be set up to inform a user about new records in the Clearinghouse reflecting a particular query. RSS feeds are currently being broadcast to several NBII partners including the Global Forestry Initiative, World Data Center for Biodiversity and Ecology and the primary NBII web-site (www.nbii.gov).

Support is acknowledged from: NASA, USGS, DOE

18.8. IRMNG – The Interim Register of Marine and Nonmarine Genera

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IRMNG, the Interim Register of Marine and Nonmarine Genera (www.obis.org.au/irmng/), is an initiative of OBIS Australia implemented at CSIRO (Commonwealth Scientific and Industrial Research Organisation) Marine and Atmospheric Research, Australia (CMAR), which aims to provide a machine-addressable system that will discriminate marine from non-marine, and extant from fossil taxa in species lists, either on the basis of their genus alone, or (if required) by the full species binomen. To enable this, a database of as many genus names as possible (with associated species names as readily available) has been compiled at CMAR, with all names embedded in a “provisional” or working taxonomic hierarchy, with the facility to mark up (“flag”) families, genera, or individual species with their relevant characteristics – either marine, non-marine, or both (where “marine” also includes brackish water species), and either extant, fossil, or both.

This project presents interesting challenges in two areas: first, assembly of a sufficiently comprehensive reference database (which could be viewed as an expanded “Catalogue of Life” with particular emphasis at genus level and above, also including extinct organisms), and second, application of the relevant habitat and extant flags in as efficient a manner as possible. The present (version 1) IRMNG database has been assembled as a merger of information from over 40 printed and electronic sources, and currently includes some 220,000 genus names and more than 1.4 million species (with hybrids and infraspecies currently excluded). With the addition of data not yet loaded, IRMNG version 1.1 is likely to include significantly more names, with the aim of over 90% complete coverage at genus level.

Application of the relevant habitat and extant flags is implemented as a hierarchical approach, in that flags are applied at as high a level as possible in the taxonomic hierarchy, with all child taxa inheriting flags from their parent taxon wherever the latter are flagged unambiguously: marine or non-marine, extant or fossil, *e.g.*, all echinoderms are marine, all dinosaurs are fossil, most insects are non-marine, etc. By this means, the task of applying flags at an individual genus or species level is considerably reduced. In addition, reasonably comprehensive (although in some aspects dated) family-level treatments, for example Parker’s “Synopsis and Classification of Living Organisms” (1982) and Benton’s “The Fossil Record 2” (1993), are followed as far as available. Flagging then needs to proceed to the genus level and below only where a particular family has an ambiguous habitat or extant flag (*i.e.*, both permitted states present).

Mechanisms for the further ongoing development and population of IRMNG, potentially in collaboration with similar or overlapping projects elsewhere, are appropriate topics for discussion.

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several key groups. I also thank numerous other contributors of individual taxonomic data compilations that have been used as input to IRMNG, as listed on the IRMNG website.

18.9. Using AquaMaps for biodiversity assessment, including a prototype MPA (Marine Protected Area) network design tool

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AquaMaps (www.aquamaps.org/) is a biogeographic and biodiversity information tool for marine species developed by R. Froese, K. Kaschner and others. It uses a niche modelling approach to generate predicted distributions for marine species based on presently available distribution data and/or described ecological tolerances. In essence, provided that a minimum “acceptable” level of information is available, the tool will generate a modelled (unreviewed) predicted distribution for any species, as calculated probability of occurrence in all 0.5 x 0.5 degree cells in the ocean. This model can then be further refined if necessary by appropriate experts with relevant detailed knowledge of the particular species concerned and its distribution. Most species information systems display either individual data points or approximate, hand-drawn maps to depict known areas of species’ presence. The aim of AquaMaps is to produce an improved, transparent and reproducible version based on the available point data and other information. The system attempts to “intelligently” fill in gaps between disparate data points where suitable environmental conditions are deemed to exist. AquaMaps produces modelled quantitative (probability) distribution maps that are independent of sampling effort or the geographic patchiness of available point data.

Once predicted (modelled) distributions are available for a sufficiently large number of taxa, and their quality is considered acceptable, it then becomes possible to use AquaMaps data in an integrated fashion for biodiversity assessment purposes. An example would be to determine the predicted diversity of all, or any desired subset of taxa at any scale from global down to the limit of resolution of the system (0.5 degree squares, measuring approximately 55 x 55 km at their maximum size, adjacent to the equator). As one of a range of currently available options, a prototype MPA (Marine Protected Area) network design tool has been developed that permits a user to specify a subset of species according to their particular characteristics for conservation purposes. These currently include endemism; IUCN listing; resilience (capacity to withstand exploitation); and overfishing status, in a region of choice (currently large marine ecosystem, country’s exclusive economic zone, or any pre-defined FAO area). The system will then plot a map in real time, colour-coded as to the number of the selected species occurring in every 0.5 degree cell; clicking on any cell will generate the respective list of species with probability of occurrence, plus additional information on the locality. Areas of highest computed biodiversity may be considered as possible MPA sites.

In practice, the tool is limited by the availability of suitable base data (currently some 8,000 species maps have been generated covering fishes, marine mammals and selected invertebrates) and the status of the maps themselves (auto-generated, *i.e.*, unreviewed, vs. expert reviewed). The potential of the system is apparent from its utility, content and associated tools that have been developed or envisaged.

Support is acknowledged from: Pew Foundation; European Commission/IncoFish. AquaMaps has been developed by K. Kaschner, J. Ready, E. Agbayani, P. Eastwood, T. Rees, K. Reyes, J. Rius and R. Froese. The AquaMaps MPA Planning Tool was designed by Rainer Froese and Will Le Quesne and implemented by Eli Agbayani in the context of the European Commission INCOFISH Project