

Phyloinformatics in the age of Wikipedia

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One of the great challenges of phyloinformatics is linking together information on phylogenies, taxa, genomes, specimens, and publications. One approach to linking disparate data is to use shared identifiers. For example, if a bibliographic database and a nomenclature database both use the same identifier for a publication (such as a DOI), then we can easily link the two pieces of information together using that identifier. An obstacle to this approach is the lack of identifiers, or failure to reuse existing identifiers (Page, 2008). For example, sequences in GenBank may lack bibliographic identifiers, even if the paper in which the sequences were published has an identifier (Miller et al., 2009). This low "link density" is a major obstacle to linked data approaches to integrating biodiversity data. Link density can be increased either by reusing existing identifiers, or by creating maps between existing identifiers.

This talk describes a mapping between the NCBI taxonomy database and Wikipedia. These two databases were chosen because the NCBI taxonomy contains all the taxa for which sequences are publicly available, and for many taxa Wikipedia is the first site returned in a Google search on that taxon's scientific name (Page, 2010). The bulk of the mapping was created automatically by matching strings in the two databases, either directly, or via synonyms (NCBI) or redirect pages (Wikipedia). To support manual editing and correction the mapping was loaded into a wiki available at <http://iphylo.org/linkout>. Implemented using semantic wiki (<http://semantic-mediawiki.org/>), the wiki provides RDF export of the mapping. NCBI taxonomy ids are linked to the equivalent URI in the Uniprot database (<http://www.uniprot.org>), and Wikipedia pages are mapped to the equivalent URI in Dbpedia (<http://dbpedia.org>). Both Uniprot and Dbpedia provide data in RDF, which when combined with the mapping from <http://iphylo.org/Linkout> enable a wide range of queries. For example, we could query Wikipedia for images of taxa in GenBank, or query GenBank for sequences from taxa in the International Union for Conservation of Nature Red List of Threatened Species (<http://www.iucnredlist.org/>).

To date a total of 52,956 NCBI taxa have been mapped to the corresponding taxa in Wikipedia. The mapping for any individual NCBI taxon can be found by appending the taxonomy id to the URL "<http://iphylo.org/linkout/Ncbi>", for example <http://iphylo.org/linkout/Ncbi:87131>. The mapping has also been uploaded to NCBI's Linkout, so that the link to Wikipedia is shown on the NCBI page for the taxon (Fig. 1).

The image shows two overlapping web pages. The top page is the NCBI Taxonomy Browser entry for *Himantura chaophraya* (Taxonomy ID: 87131). It includes fields for Genbank common name (freshwater whipray), Inherited blast name (sharks and rays), Rank (species), Genetic code (Translation table 1 (Standard)), Mitochondrial genetic code (Translation table 2 (Vertebrate Mitochondrial)), and Other names (authority: Himantura chaophraya Monkolprasit & Roberts, 1990). It also lists cellular organisms and various taxonomic links. The bottom page is the Wikipedia article for the Giant freshwater stingray, which includes a description of the species, its distribution in Southeast Asia, and its conservation status (Vulnerable (IUCN 3.1)). An arrow points from the 'External Information Resources (NCBI LinkOut)' section of the NCBI page to the Wikipedia article.

Fig. 1. The NCBI page for *Himantura chaophraya* (taxonomy id 87131) linked to the Wikipedia page for the Giant freshwater stingray.

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