

# Fish Ontology framework for taxonomy-based fish recognition

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Life science ontologies play an important role in semantic web. Given the diversity in fish species and associated wealth of information, it is imperative to develop an ontology capable of linking and integrating this information in an automated fashion. As such, we introduce the Fish Ontology (FO), an automated classification architecture of existing fish taxa which provides taxonomic information on unknown fish based on metadata restrictions. It is designed to support knowledge discovery, provide semantic annotation of fish and fisheries resources, data integration, and information retrieval. Automated classification for unknown specimens is a unique feature that currently does not appear to exist in other known ontologies. Examples of automated classification for major groups of fish are demonstrated, showing the inferred information by introducing several restrictions at the species or specimen level. The current version of FO has 1830 classes, includes widely used fisheries terminology, and models major aspects of fish taxonomy, grouping, and character. With more than 30,000 known fish species globally, the FO will be an indispensable tool for fish scientists and other interested users.

# 1 Fish Ontology Framework For Taxonomy-Based Fish 2 Recognition

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## 11 ABSTRACT

12 Life science ontologies play an important role in semantic web. Given the diversity in fish species and  
13 associated wealth of information, it is imperative to develop an ontology capable of linking and integrating  
14 this information in an automated fashion. As such, we introduce the Fish Ontology (FO), an automated  
15 classification architecture of existing fish taxa which provides taxonomic information on unknown fish  
16 based on metadata restrictions. It is designed to support knowledge discovery, provide semantic  
17 annotation of fish and fisheries resources, data integration, and information retrieval. Automated  
18 classification for unknown specimens is a unique feature that currently does not appear to exist in other  
19 known ontologies. Examples of automated classification for major groups of fish are demonstrated,  
20 showing the inferred information by introducing several restrictions at the species or specimen level. The  
21 current version of FO has 1830 classes, includes widely used fisheries terminology, and models major  
22 aspects of fish taxonomy, grouping, and character. With more than 30,000 known fish species globally,  
23 the FO will be an indispensable tool for fish scientists and other interested users.

24

## 25 INTRODUCTION

26 Increasing amount of data produced on a single species has made it harder for fish researchers to manage  
27 and provide fish data in a single database. Moreover, the high demand for related data (metadata) for a  
28 single species is driving researchers to find a better alternative for the current database structure  
29 (discussed further below). The semantic web technology, with the capability to give well-defined meaning  
30 to information and to enable better cooperation between human and computer, provides a promising  
31 platform for biodiversity researchers who are interested to link and share their data in common public  
32 repository.

33 Presently, most of the fish databases are constructed using relational database models, focusing on  
34 species related information. Data in these repositories are usually structured based on the researcher's  
35 interests and personal needs, which in turn restrict the application of a uniform naming standard. Hence  
36 a preferred way to provide species data is in the form of an ontology, a structured vocabulary that

37 describes entities of a domain of interest and their relationships (Shadbolt, Hall & Berners-Lee, 2006). A  
38 relational database focuses on the data whereas, an ontology provide meaning to the data with the help  
39 of metadata. Using metadata, an ontology can be linked and mapped to other related ontologies and this  
40 information can be used to automatically infer and recognize the most suitable result for a given search.

41 There are several important and popular projects in the fish and fisheries domain developed as  
42 conventional back-end databases such as the Catalog of Fishes ("Catalog of Fishes Classification"),  
43 FishBase (Froese & Pauly, 2000), IGFA Fish Database ("Fish Species Database"), The New Zealand  
44 Freshwater Fish Database ("NZ Freshwater Fish Database"), The Fish Database of Taiwan (Shao, 2001),  
45 Fish Stocking Database("Fish Stocking Database"), FishTraits (Emmanuel & Angermeier, 2013), and Fish  
46 Barcode of Life ("FISH-BOL"). While these databases provide extensive and up to date information on fish,  
47 they are not based on ontology and hence do not support semantic web deployment unless converted  
48 into appropriate formats (Ankolekar et al., 2007). Furthermore, most of them are not created based on  
49 semantic web principles (Berners-Lee) and there is little effort dedicated to create an automated fish  
50 species identification using the semantic web approach. An ontology can enhance information providing  
51 capability for a database by the use of metadata to discover and gather new information from other  
52 databases, or by linking them to create a better information network. Thus, the work laid out in this paper  
53 is created as an effort to address these problems.

54 To date, no dedicated ontology with automated classification for fish exists, with the exception of  
55 the Network of Fisheries Ontology (NFO) (Caracciolo et al., 2012) which focuses on fisheries activity and  
56 selected species of commercial interests, and the Marine Top Layer Ontology (MarineTLO) (Tzitzikas et  
57 al., 2016) which focuses on marine animal. Both of these ontologies are not primarily focused on fish, and  
58 they do not possess automated classification capability. Given that the total number of fish species has  
59 been estimated at 32,000 to 40,000 globally (Nelson, 2006; Chapman, 2009; Eschmeyer et al., 2010), an  
60 automated and comprehensive fish classification platform would be an indispensable tool for fisheries  
61 biologists, marine scientists, and even laypersons with interest in fish. Thus, in this paper, we propose a  
62 fish-based ontology that is able to automate group classification, and to link terms used by research on  
63 the fish domain with related terms from other research domain.

64 This paper describes the framework of the Fish Ontology (FO) for precise and comprehensive  
65 semantic annotation of fish resources (e.g. datasets, documents, and models) where it can be used to fill  
66 in the gap of distinct terms which are missing in other ontologies. The FO is an effort to develop and  
67 maintain a controlled, structured vocabulary of terms which describe fish anatomy, morphology, ecology  
68 and various developmental stages. The FO reuses many terms from other ontologies which are related to  
69 and appropriate for the fish and fisheries domain. Additionally some terms such as "Location", "Shape",  
70 and "Threat" are implemented to add more description to fish, with the intention to provide more diverse  
71 search results.

72 Originally the FO was developed as a data warehouse for several database formats. It has since  
73 evolved to host information on captured and observed fish specimen (e.g. data on captured samples,  
74 captive specimens, or from observational experiments). After undergoing several modifications based on  
75 reviews by fish experts, both of these features were merged in the current FO, expanding its functionality  
76 to incorporate fish classification and reasoning capability. The FO framework outlined in this paper  
77 (current version v1.0.2, Aug 2016) is designed to facilitate integration with related ontologies which is in  
78 line with the Big Data Initiative ("IEEE Big Data") that aims for diverse analytic options.

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## 80 **METHODS**

81 We used Protégé to create, edit and manage the Fish Ontology and all its terms and relationships  
82 ("Protégé," 2016). This open access software contains all the tools needed for this research since it  
83 contains sufficient plugins to assist in development and visualization of ontology. Furthermore, Protégé

84 provides several reasoner engines such as Hermit, FaCT++, and Pellet, to provide variation in ontology  
 85 validation and reasoning (Tsarkov & Horrocks, 2006; Sirin et al., 2007; Glimm et al., 2014). There are also  
 86 various visualization tools that are provided by Protégé such as OWLVIZ, Ontograf, and VOWL (Falconer,  
 87 2010; Horridge, 2010; Negru, Lohmann & Haag, 2014). Each tool visualizes the ontology differently.

88 The FO is created using Web Ontology Language (OWL) which allows us to query using triple based  
 89 query languages such as SPARQL (Prud'hommeaux & Seaborne, 2008), SPARQL-DL (Sirin & Parsia, 2007),  
 90 and Description Logic (DL) (Baader et al., 2003). A triple query (composed of subject-predicate-object) can  
 91 perform more complex query compared to a relational database query (composed of columns and rows),  
 92 and is able to retrieve more information due to the semantic web architecture which enables them to pull  
 93 data from URIs or URLs with related metadata (Alexander, 2013).

94 "The Diversity of Fishes: Biology, Evolution, and Ecology" was the main reference used in identifying  
 95 terms and definitions while devising the FO (Helfman et al., 2009). This book is a well-established  
 96 reference that follows standard fish taxonomy nomenclature proposed by Nelson (Nelson, 2006). Most of  
 97 the class labels, synonyms and definitions in the FO correspond to those in the reference book. Some of  
 98 the terms for specimen entries are taken from experimental data such as sampling data provided by Chong  
 99 et al (Chong, Lee & Lau, 2010), while others are taken from public online entries such as Wikipedia  
 100 ("Wikipedia") and DBpedia (Heath & Bizer, 2011). We also incorporated classes from other ontologies  
 101 such as the VTO into our ontology to model the FO classes and enhance its automatic recognition  
 102 capabilities.

103 One of the most important aspects in ontology creation is consistency; hence, we sought to follow a  
 104 standard naming convention while creating the FO. There are no obligatory naming conventions for the  
 105 creation of OWL classes and properties; however, we decided to use the Camel Case (also known as Camel  
 106 Back) notation to ensure that the ontology terms and naming are consistent (Campbell, 2006; Horridge et  
 107 al., 2011). This naming convention has the advantage of creating more meaningful names by using an  
 108 expressive sequence of words while respecting the naming constraint (Horridge et al., 2011). As such, all  
 109 of the classes in the FO use the Upper Camel Case notation, while all of its properties use the Lower Camel  
 110 Case notation. Furthermore some properties are appended with the prefixes of 'has', or 'is', as per the  
 111 convention recommendation (e.g. "hasBodyPart", "isPartOf"). This naming convention helps clarify the  
 112 properties to human and to some tools in Protégé (e.g. The "English Prose Tooltip Generator" which uses  
 113 this naming convention to generate more human readable expressions for class description).

114 As for the terms and structures involving taxonomic rank and hierarchy, we referred to the  
 115 Vertebrate Taxonomy Ontology (VTO) (Midford et al., 2013) and imported several of its major classes  
 116 (with subclasses and all the annotations) in order to demonstrate the functionality of the FO. We also  
 117 considered the biodiversity standard outlined in the Darwin Core (Wieczorek et al., 2012), and other  
 118 related ontologies such as the Zebrafish Information Network (ZFIN) (Sprague, 2003), as the references  
 119 for the FO vocabulary creation. These ontologies are related to fish, popular in their domain, frequently  
 120 used, and regularly updated by the research community. Hence, they are the most relevant choices as the  
 121 main vocabulary provider for fish rank and terms for the FO. As an example, we imported the class  
 122 "Chordata" and all of the subclasses for the genus *Rastrelliger* and *Chiloscyllium* from the VTO, and reused  
 123 the terms "Location" and "Taxon" from the Darwin Core in the FO. Some generic terms like "Species" were  
 124 adopted due to their usage in many popular ontologies. The summary of imported classes is shown in  
 125 Table 1.

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Ontology or Standard	Number of classes
Zebrafish Anatomy and Stage Ontology (ZFA, ZFS)	2
Darwin Core	2
Vertebrate Taxonomy Ontology (VTO)	1345

NCBI organismal classification (NCBITaxon)	13
Total	1362

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**Table 1.** Statistic of imported or integrated class and properties.

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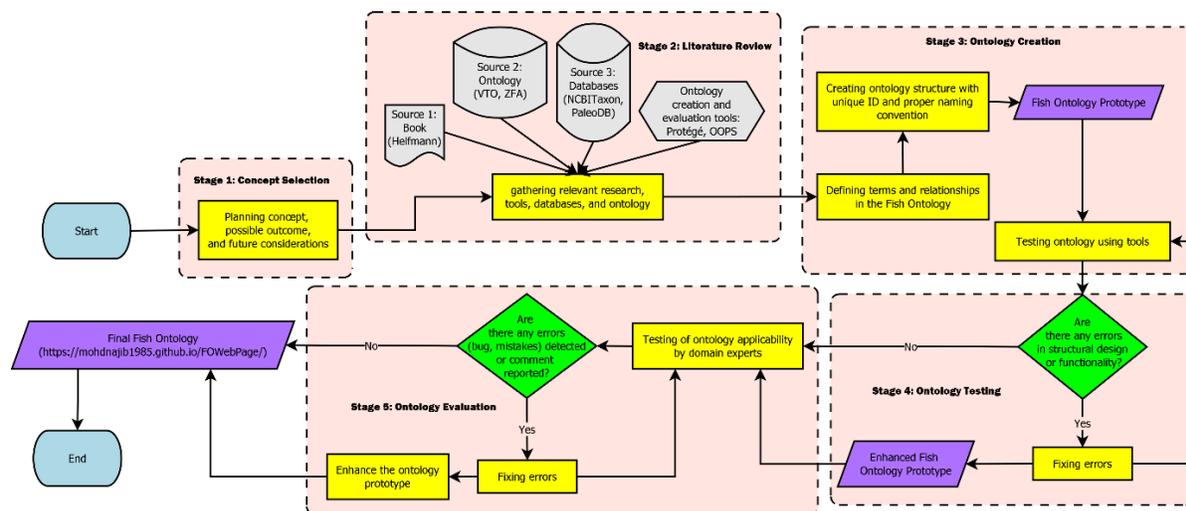
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The FO is created with the aim of integration and standardization; thus it is imperative to ensure that the terms in the ontology have a unique identifier (ID) that has not been used in other ontologies. A unique ID for a term allows cross-referencing between related databases and ontologies, without the confusion of same existing terms with different functions. There are many ways to create a unique ID; however following an example of a globally accepted guideline will ease future integration with the FO. As such, we adopted the guidelines issued by the Open Biological and Biomedical Ontologies (OBO Foundry) ("The OBO Foundry"; Smith et al., 2007) and created each term in the FO using an ID which starts with the prefix 'FO' followed by unique digit numbers (e.g. "FO\_XXXXXXX" where X is a digit).

There are many tools created for ontology validation such as the inference and rule engine. However, it is apparent that human validation is still mandatory in the current state of practice for ontology learning (Zhou, 2007). Furthermore, most ontology learning results have mainly been evaluated by domain experts manually. As such, a logical evaluation was conducted by fish experts to verify the naming of concepts and to validate the hierarchy of the terms, which the FO presented. Criteria such as accuracy, complexity, semantic consistency, terms redundancy, naturalness, precision, completeness, and verifiability were checked using questions such as "what if we do not know the name of the specimen?", "what if we only know its common name?", "what if the specimen is similar to certain kind of known specimen?", or "what if we were to find a completely unknown specimen?".



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**Figure 1.** Workflow for the Fish Ontology creation.

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The workflow for creating the FO in this paper is separated into five stages which are: (1) Concept Selection, (2) Literature Review, (3) Ontology Creation, (4) Ontology Testing, and (5) Ontology Evaluation. Figure 1 shows the workflow of the FO creation. In the concept selection stage, we first decided on the ontology concept, its possible structure, and future considerations needed to create the ontology. During the literature review, relevant research, such as papers, books, and tools were gathered. Databases and ontologies that are relevant for adoption into the FO were also researched at this stage. Next, in the ontology creation stage, terms and relationship to be used in the ontology were defined and a proper

159 structure of the ontology was created. Additionally, at this stage, the naming convention used for the  
 160 terms were selected, and any relevant databases and ontologies were imported to the ontology.  
 161 Subsequently, in the ontology testing stage, the functionality of the FO was tested to detect and fix  
 162 problems with the terms, structure, or relationships. Finally, during the evaluation, the ontology was  
 163 evaluated by the fish and biodiversity researchers for its applicability. At this stage, mistakes, bugs, or  
 164 comments were collected and resolved to improve the ontology.

165 In this work, we show the applicability of the FO on several areas such as determining if a specimen  
 166 is a fish, determining the type of fish based on characteristic(s), morphology, name, or taxonomic rank,  
 167 determining its conservation status (extant or extinct), and determining whether or not it is an ancient  
 168 species. Examples of its applicability are presented in the Results section.

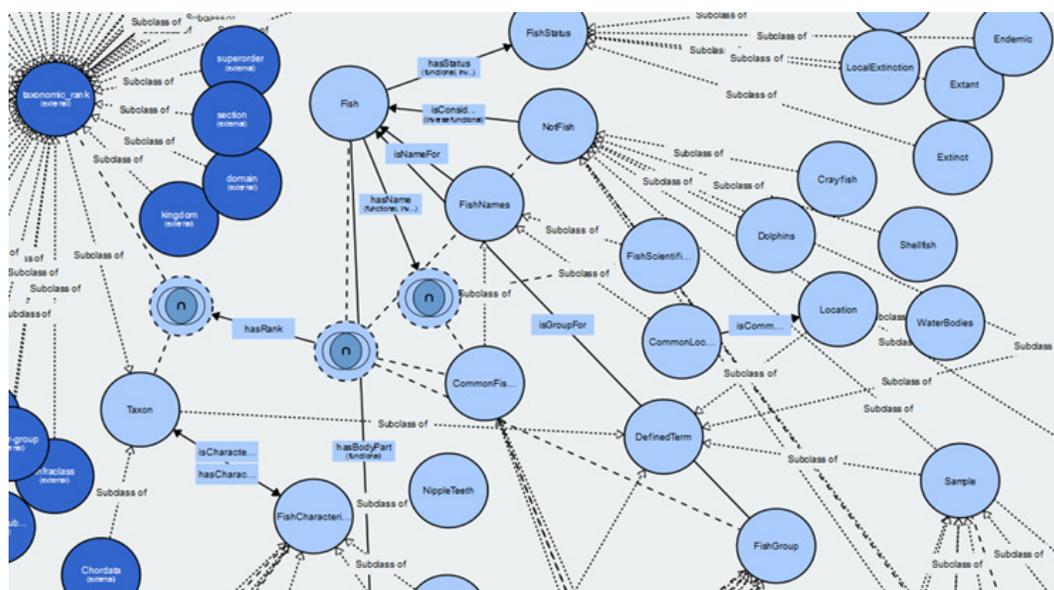
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## 170 RESULTS

### 171 Fish Ontology Framework and Content

172 The Fish Ontology proposed in this paper contains 1830 classes, 27 object properties, 500 species names,  
 173 with 1223 synonyms, 8 fish groups, and 9 fish characteristics. It is the first of its kind to provide automated  
 174 fish classification based on taxonomic rank, group, name and characteristics. Given that the FO is intended  
 175 for broad classification of fish, including common extinct ones, the FO is able to classify jawless fish, early  
 176 jawed fish and living fossil fish. A graphical illustration of several main classes in the FO and its integration  
 177 with other ontologies such as the VTO is demonstrated in Figure 2. The online version of the ontology can  
 178 be accessed at <https://mohdnajib1985.github.io/FOWebPage/>. The OWL file for the FO with all of its  
 179 imported classes is available as a supplementary material (Refer to Additional File FishOntology.owl).

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183 **Figure 2.** The Fish Ontology (FO) architecture. A portion of the FO is shown here on how the classes are  
 184 related to each other and to other ontology classes. The dark blue circles represent terms from other  
 185 ontologies while light blue circles represent terms from the FO.

186 The classes in the FO are created as a base for integration with other ontologies mentioned in Table  
 187 1, and with any related ontologies that might be useful for fish recognition such as the popular Gene  
 188 Ontology (GO). For the "Taxon" class, it is organized in single inheritance, up to the species level whenever  
 189 possible to increase the reasoning capabilities and expand its scope by including relationship(s) and

190 annotation to the terms. This includes imported classes, which are linked to their respective class types.  
 191 Each FO branch is organized hierarchically by the means of "is\_a" (or subclass of) relationship, by  
 192 appropriately placing it under a single root term. Each class has annotations to enrich its meaning and  
 193 purpose. Examples of the relationships are shown in Table 2.  
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Properties	Explanation	Example
is_a	A subclass in OWL	Overharvesting is_a CausesOfThreat
hasRank (FO:0000097)	Describe a term which has a taxonomic rank	Carpet Shark hasRank of Orectolobiformes
isNameFor (FO:0000235)	Describe a name for some other class	FishNames isNameFor Fish
isGroupFor (FO:0000171)	Describe a group of some class	FishGroup isGroupFor Fish
isPartOf (FO:0000280)	Describe a situation where the class is part of something	PreflexionLarva isPartOf Larva

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**Table 2.** Example of relationships in the Fish Ontology.

198 The FO contains 253 classes dedicated to fish studies and 38 classes related to fish sampling  
 199 processes. These classes are well suited for describing sample and specimen related terms. In combination  
 200 with suitable classes, relations, and annotations, the utility of the FO for automated fish species  
 201 recognition through sample and specimen data is likely to be improved. Some of the classes such as  
 202 "FishSampling" and "FishName" are structured in a multiple inheritance structure, with some classes being  
 203 subclasses of the same class; an example is the class "Trap" which is the subclass of "FishingGear" and  
 204 "FishSamplingMethod". As aforementioned, most of the new terms were created based on the reference  
 205 book (Helfman et al., 2009) because to the best of our knowledge, there are no suitable ontologies from  
 206 which we could import these classes, while some of the terms that we found were poorly defined and  
 207 structured. However, we have included cross-references of several classes for potential mapping to  
 208 relevant external resources, including the FishBase, Teleost Taxonomy Ontology (TTO), and National  
 209 Centre of Biotechnology Information Taxonomy Database (NCBITaxon) (Froese & Pauly, 2000; Midford et  
 210 al., 2010; Federhen, 2011). Table 3 shows the statistics of cross referencing of the FO classes to other  
 211 resources.  
 212

Resources	Number of Cross References
NCBITaxon	264
Teleost Taxonomy Ontology (TTO)	317
PaleoDB	1091
Marine Top Layer Ontology (MarineTLO)	14
Gene Ontology (GO)	2
Total	1688

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**Table 3.** Statistics for the Fish Ontology cross references.

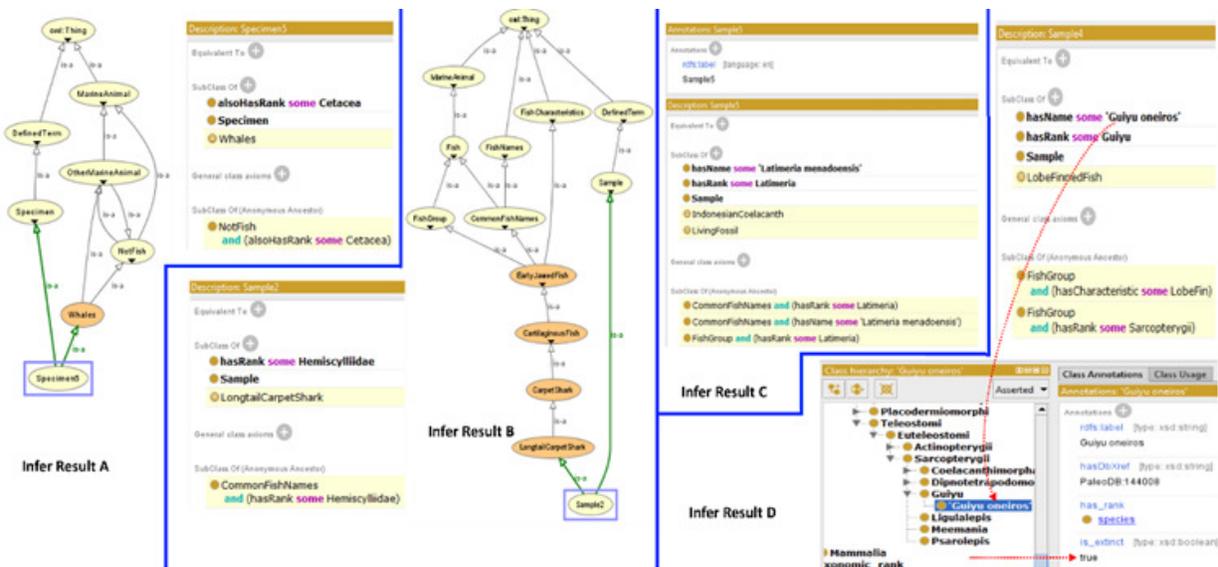
### 215 Inference Capabilities

216 We have created relationships which allow a specimen (and sample) to be inferred and automatically  
 217 analyzed in the areas of fish grouping, taxonomic rank, and common fish names. We focused most of our

218 modelling activities on these aspects. The specimen (and sample) which is not inferred would only be  
 219 shown as subclasses of "Sample" or "Specimen" classes; however after being inferred using the reasoner  
 220 provided by Protégé, each one of them will be properly classified according to their respective parameters.  
 221 Furthermore the inferred results can show which individual shares the same trait(s) as the sample and  
 222 suggest what kind of group it fits into based on its characteristics.

223 The FO also provides a structure to determine whether a specimen or a species is actually a fish or  
 224 otherwise by using the reasoning capability. Figure 3 shows the results of the inferring process which  
 225 demonstrates the classification of specimen as a fish or otherwise, and what group it belongs to in the  
 226 taxonomic hierarchy. Infer Result A shows how a specimen (Specimen5) is recognized by the reasoner as  
 227 a "Whale" and leads the reasoner to recognize it as "OtherMarineAnimal" and "NotFish". Infer Result B  
 228 shows how a sample (Sample2) is recognized as a "LongtailCarpetShark", which leads the reasoner to  
 229 recognize that it is a fish. Infer Result C shows that Sample5 is recognized as a "LivingFossil" while Infer  
 230 Result D shows that Sample4 is actually a species called *Guiyu oneiros* and subsequently recognized as an  
 231 extinct species.

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235 **Figure 3.** Results from the Fish Ontology inferring process.

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237 Sample queries are presented in Figure 4 using SPARQL (Query A) and SPARQL-DL (Query B).  
 238 Improved results were obtained using the SPARQL-DL query, which could query inferred data in the  
 239 ontology compared to a SPARQL query. As shown in Figure 4, new classes were found in Query B results,  
 240 which are obtained from the imported class and integrated terms from other ontologies. The results in  
 241 Figure 5 show how additional data can be retrieved from the FO using the DL query.

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```

Snap SPARQL Query:
PREFIX rdf: <http://www.w3.org/1999/02/22-rdf-syntax-ns#>
PREFIX owl: <http://www.w3.org/2002/07/owl#>
PREFIX rdfs: <http://www.w3.org/2000/01/rdf-schema#>
PREFIX xsd: <http://www.w3.org/2001/XMLSchema#>
PREFIX fo: <http://mybiodiversityontologies.um.edu.my/FO.owl#>
SELECT * WHERE {
fo:Sample1 rdfs:subClassOf ?sub.
}

fo:Sample1                                     ?sub

Query A

Snap SPARQL Query:
PREFIX rdf: <http://www.w3.org/1999/02/22-rdf-syntax-ns#>
PREFIX owl: <http://www.w3.org/2002/07/owl#>
PREFIX rdfs: <http://www.w3.org/2000/01/rdf-schema#>
PREFIX xsd: <http://www.w3.org/2001/XMLSchema#>
PREFIX fo: <http://mybiodiversityontologies.um.edu.my/FO.owl#>
SELECT * WHERE {
fo:Sample1 rdfs:subClassOf ?sub.
}

fo:CartilaginousFish
fo:Sample
owl:Thing
fo:FishNames
fo:DefinedTerm
fo:EarlyJawedFish
fo:Fish
fo:FishGroup
fo:CommonFishNames
fo:Sample1                                     ?sub

Query B

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**Figure 4.** A sample of query to check the inferred results. Results from Query A (using SPARQL) were retrieved before the inferring process, while results from Query B (SPARQL-DL) were retrieved after the inferring process.

The screenshot displays a SPARQL-DL query interface. On the left, the 'Query results' pane shows a tree of inferred classes, with 'Fish' highlighted. A red arrow labeled 'B' points to this class. Above the results, the 'Query (class expression)' pane shows 'LongtailCarpetShark' with a red arrow labeled 'A' pointing to it. On the right, the 'Explanation' pane shows four explanations for the inference, with a red arrow labeled 'C' pointing to the first explanation: 'LongtailCarpetShark EquivalentTo CommonFishNames and (hasRank some Hemiscyllidae)'. At the bottom, the 'Class Annotations' pane shows a taxonomic hierarchy, with a red arrow labeled 'D' pointing to the 'Hemiscyllidae' class.

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**Figure 5.** Types of information obtained from the Description Logic (DL) query. The DL query shows how a long tail carpet shark is inferred in the DL query (A). In B, the shark is inferred as Fish. In C, the DL query shows what kind of fish it is while in D, the shark rank in the fish taxonomic structure is subsequently inferred.

## 256 Evaluation

257 To evaluate the quality of the Fish Ontology, we follow the Gruber method for ontology construction  
 258 (Gruber, 1995). There are five criteria highlighted which are clarity, coherence, extendibility, minimal  
 259 encoding bias, and minimal ontological commitment. To measure the clarity level of the FO, the ontology  
 260 definitions should be objective and independent of the social and computational context. In FO, all the  
 261 definitions are stated in such a way that the number of possible interpretations of a concept would be  
 262 restricted. The clarity test results for the FO are divided into five parts, which are:

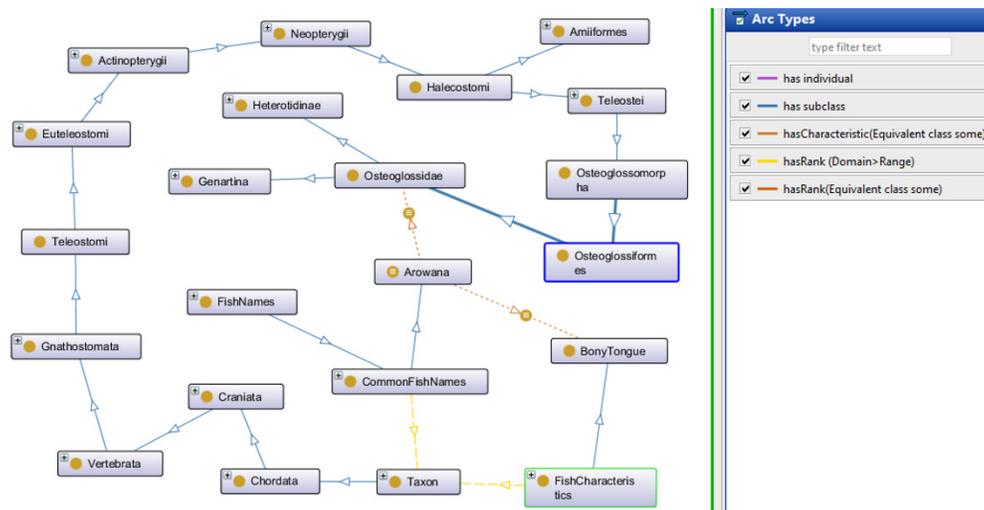
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- 264 1. No Cardinality Restriction on Transitive Properties
- 265 2. No Meta-Class
- 266 3. No Subclasses of RDF Classes
- 267 4. No Super or Sub-Properties of Annotation Properties
- 268 5. Transitive Properties cannot be Functional

269

270 Results for clarity test 1 and clarity test 5 are shown in Figure 6 below. Since fish data are large in  
 271 volume, there is a need to add more data to the FO over time. As such, there is no cardinality restriction  
 272 assigned to any transitive properties in the FO. Figure 6 also shows that the transitive properties in the  
 273 FO are not functional because it relates to more than one instance via the property. As for clarity test 2,  
 274 clarity test 3 and clarity test 4, Figure 7 and Figure 8 show that there are no meta-classes, no properties  
 275 with a class as a range, and no sub-classes of RDF classes in the FO. All the five clarity tests are  
 276 automatically performed in the latest Protégé version.

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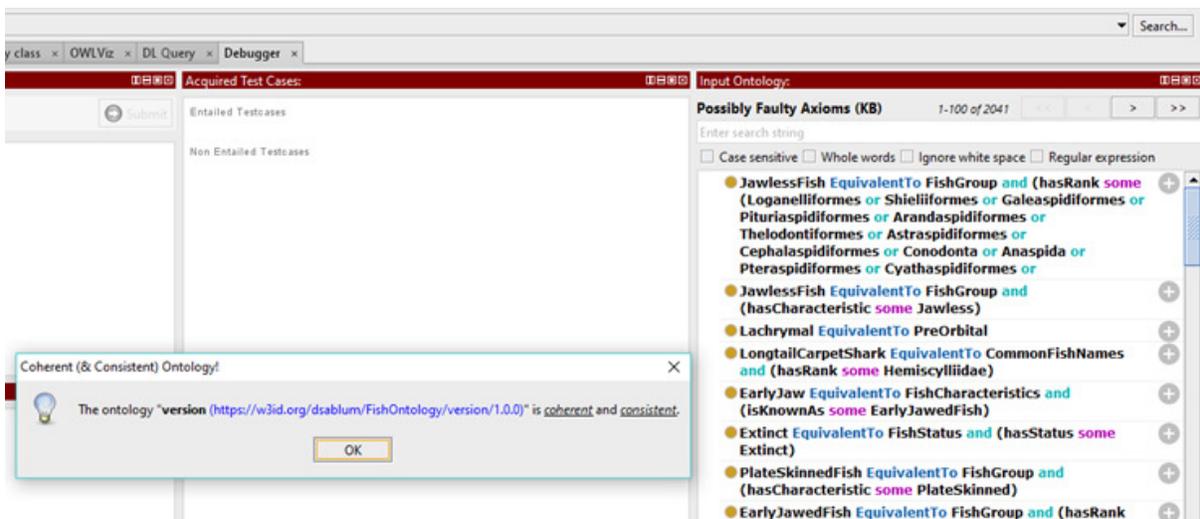
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**Figure 6.** Results for clarity test 1 and clarity test 5.

282 To ensure the coherence quality of the FO, the definitions of concepts given in the ontology as well  
 283 as the inferences drawn from the ontology must be consistent with its definitions and axioms. Based on  
 284 our evaluation, most of the inferred terms from the FO appeared to be consistent with its definition and  
 285 axioms. As an example, in Figure 3 when the FO inferred that specimen5 is a whale, it also inferred that  
 286 it is not a fish, and it also showed the correct taxon rank. The formal part of the FO is checked by  
 287 following these 5 consistency criteria listed below and ensuring that all return true:

- 288 1. Domain of a Property should not be empty  
 289 2. Domain of a Property should not contain redundant Classes  
 290 3. Range of a Property should not contain redundant Classes  
 291 4. Inverse of Symmetric Property must be Symmetric Property  
 292 5. Inverse Property must have matching Range and Domain  
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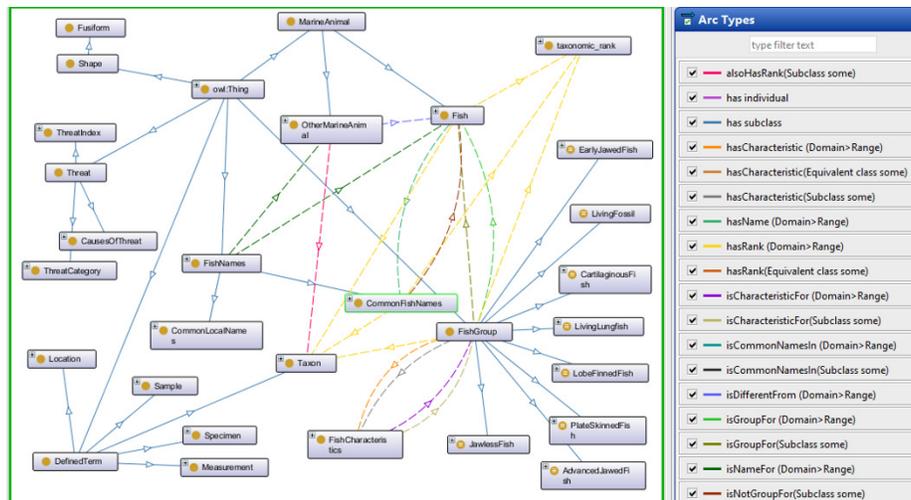


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296 **Figure 7.** Results of the coherence test using Protégé Ontology Debugger tool.  
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298 The usage of Protégé forces the user to always be wary about an empty domain, redundant classes,  
 299 and properties. As such, coherence tests 1 to 3 are achieved and can be further viewed via the ontology  
 300 itself. For coherence test 4, we provide an example of the property "isSimilarTo". The class  
 301 "CosmoidScales" is related to the class "PlacoidScales" via the "isSimilarTo" property. Then we can infer  
 302 that "PlacoidScales" must also be related to "CosmoidScales" via the "isSimilarTo" property. Figure 7  
 303 shows the results of coherence test using the Ontology Debugger Tool from Protégé. The coherence test  
 304 from this tool checks for possible faulty axioms. The ontology passed the coherence test provided by this  
 305 tool. Figure 8 shows the results for test 5 displaying that the properties "hasCharacteristic" and  
 306 "isCharacteristicFor" have matching range and domain.

307 An ontology should be extensible which means allowing addition of new concepts, according to the  
 308 current development in the field (Barbosa & da Silva, 2001). In this paper, the FO is made extensible via  
 309 the design consisting of concepts, classification hierarchy represented as classes, from general to specific.  
 310 Applying reasoning to the FO helps to define new concepts (generated from an ontology) from defined  
 311 generic concepts (books and other databases). As such, the FO place any related concepts derived from  
 312 other generic concepts in its class hierarchy to represent information that defines a specimen. Classes and  
 313 annotations that may be useful for future integration such as genetic are added, since such content will  
 314 further enhance FO's extensibility. Table 1 and Table 3 show all the classes that are linked or cross-  
 315 referenced by the FO to demonstrate the extensibility of the FO. Since the first FO design, we have  
 316 considered integrating terms from other ontologies into the FO. By placing any related concepts derived  
 317 from other generic concepts in its class hierarchy, the FO represents information that defines a fish  
 318 specimen, linking it with terms from other ontologies.  
 319



**Figure 8.** Results for clarity tests (2, 3, and 4) and coherence test (5).

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324 It is a preferred practice to make an ontology which would require minimal ontological commitment  
325 so that it is sufficient to support the intended knowledge sharing (Man, 2013). Ontology modelers  
326 sometimes have a vague idea of the role each concept will play such as their semantic interconnections,  
327 within the ontology. If necessary, they can annotate new development ideas during subsequent ontology  
328 updates (Nicola D., Missikoff & Navigli, 2005). As such, an ontology should make as few claims as possible  
329 about the domain while still supporting the intended knowledge sharing. By reusing existing concepts  
330 from books, databases and other ontologies on fish, the FO has low ontological commitment, making it  
331 more extendible and reusable (Freitas, Stuckenschmidt & Noy, 2005). Also, since most of the new  
332 concepts introduced in the FO are from books and published journal articles, they are likely to be more  
333 understandable and preferred among the user community (Helfman et al., 2009; Last et al., 2010; Chong,  
334 Lee & Lau, 2010).

335 Encoding bias occurs when a representation choice is made for the convenience of notation or  
336 implementation. By minimizing encoding bias, knowledge-sharing agents may be implemented in  
337 different representation systems and styles of representation. An ontology that is independent of the  
338 issues of implementing language is considered to have minimal encoding bias. Also, the conceptualization  
339 of the ontology should be specified at the knowledge level and must be independent of symbol-level  
340 encoding. As shown in Table 1, Table 2, and Table 3, encoding bias in the FO is reduced by the choices of  
341 using OWL as the representation language, and of adopting terms from books, database, and related  
342 ontology. As demonstrated in Figure 7, the Protégé Ontology Debugger tools have fully examined all  
343 possible encoding biases in the ontology and have cleared the FO as coherent and consistent.

344 To strengthen the results of the FO evaluation, we use an online ontology evaluation tool named  
345 Ontology Pitfall Scanner! (OOPS!) (Poveda-Villalón, Gómez-Pérez & Suárez-Figueroa, 2014). OOPS! uses a  
346 checklist to ensure that best practices of ontology creation are followed and that the bad practices are  
347 avoided. The inventor created a catalog of bad practices and automated the detection of as many of them  
348 as possible (41 currently). The evaluation of the FO using the OOPS! tools is shown in Figure 9. There are  
349 1794 cases listed in the minor pitfall categories, 19 cases in 4 important pitfall categories, and 11 cases in  
350 4 critical pitfall categories. Compared to the ontology debugger tools in the Protégé, there are many error  
351 flags that can be found in the FO by using OOPS!. However, most of them are minor, and the important  
352 and critical pitfalls problems are mostly caused by the same features in the FO, and is further elaborated  
353 in paragraphs 6 and 7 in the discussion section.

## Evaluation results

It is obvious that not all the pitfalls are equally important; their impact in the ontology will depend on multiple factors. For this reason, each pitfall has an importance level attached indicating how important it is. We have identified three levels:

- **Critical** 🚫 : It is crucial to correct the pitfall. Otherwise, it could affect the ontology consistency, reasoning, applicability, etc.
- **Important** ⚠️ : Though not critical for ontology function, it is important to correct this type of pitfall.
- **Minor** 🟡 : It is not really a problem, but by correcting it we will make the ontology nicer.

[Expand All] | [Collapse All]

Results for P02: Creating synonyms as classes.	10 cases   Minor 🟡
Results for P04: Creating unconnected ontology elements.	5 cases   Minor 🟡
Results for P05: Defining wrong inverse relationships.	1 case   Critical 🚫
Results for P08: Missing annotations.	1747 cases   Minor 🟡
Results for P11: Missing domain or range in properties.	13 cases   Important ⚠️
Results for P13: Inverse relationships not explicitly declared.	21 cases   Minor 🟡
Results for P19: Defining multiple domains or ranges in properties.	6 cases   Critical 🚫
Results for P24: Using recursive definitions.	2 cases   Important ⚠️
Results for P30: Equivalent classes not explicitly declared.	2 cases   Important ⚠️
Results for P32: Several classes with the same label.	12 cases   Minor 🟡
Results for P36: URI contains file extension.	ontology*   Minor 🟡
Results for P40: Namespace hijacking.	1 case   Critical 🚫
Results for P41: No license declared.	ontology*   Important ⚠️

According to the highest importance level of pitfall found in your ontology the conformance badge suggested is "Critical pitfalls" (see below). You can use the following HTML code to insert the badge within your ontology documentation:



```
<p>
<a href="http://oops.linkeddata.es"></a>
```

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**Figure 9.** Results of the Fish Ontology evaluation using the Ontology Pitfall Scanner tool (Poveda-Villalón, Gómez-Pérez & Suárez-Figueroa, 2014).

## DISCUSSION

360 In this paper, we developed a Fish Ontology framework which is a general-purpose ontology that allows  
 361 integration of fish related ontologies containing standard terms and relationships. The design of the FO is  
 362 flexible enough to accommodate any ontology containing data or knowledge about fish. Even in cases  
 363 where integration can be difficult, the FO can be tweaked in order to incorporate new biodiversity related  
 364 ontology. One example is linking the FO to the MarineTLO which is an upper level ontology for marine  
 365 species (Tzitzikas et al., 2016). The MarineTLO does not have a class named "Fish" that can map to data  
 366 from the FO; however since the MarineTLO provides classes of taxonomic rank such as "Species" and  
 367 "Genus", and related classes such as "MarineAnimal" and "Specimen", the FO provides classes and  
 368 annotations to link to these classes. The same steps can be done with the ZFIN, which contains "zebrafish  
 369 anatomical entity" and "Stages" as main classes. The FO provides complementing classes to match the  
 370 classes provided by the ZFIN such as "FishAnatomicalEntity" and "OtherStagesTerminology".

371 The FO is able to prepare captured and observed fish specimen data, mapped and structured in a  
 372 way that the meaning is expressed in a machine understandable format. Since data representation in the  
 373 form of an ontology allows the information to be linked by using semantic web applications, we envision  
 374 several practical cases of real life applications using this ontology. As shown in the results, the FO can infer  
 375 conservation and evolutionary statuses of a fish as well as show related characteristics, e.g. early jawed  
 376 fish, which are useful information for interested museum visitors. The FO's ability to infer location and  
 377 habitat of the fish can be useful for students or researchers. They can use the FO to identify species using  
 378 local names, since all fish names in the FO are linked to other database repositories. Linkage of the FO to

379 other ontologies via reusing of terms allows the search for relevant information such as genetic data of a  
380 specific fish species. In this way, the FO is able to produce new knowledge which is useful to biologists.

381 The current version of the FO can utilize specimen grouping and characteristics to determine  
382 whether a specimen is a fish or otherwise, provide taxonomic information and heredity of a characteristic  
383 rank, and determine conservation status, evolutionary status (ancient or modern) and type (jawless fish  
384 is an ancient species). The power of the FO lies in its ability to automate group classification, and ability  
385 to link the terms used by fish domain researchers, and other researchers outside the domain. This version  
386 uses simple character classification where the user provides the necessary character for the specimen. As  
387 an example, the user can specify that "Sample 1 has the characteristic of Plate Skinned", and manually  
388 add the characteristic of "Plate Skinned" into the FO. We believe the ideal FO version should also contain  
389 anatomical and phenotype data from several classes in the ontology such as "AnatomicalCharacters",  
390 "MeristicCharacters", "MolecularCharacters", and "Morphometric Characters" and these features will be  
391 included in the near future. These classes can be useful for pattern recognition, and species taxon  
392 recognition studies.

393 In general, we extract information such as synonym, name, fish grouping, group rank, fisheries, and  
394 other fish-related terms from Helfman et al. to form the general structure of the FO. We adopt the usage  
395 of the VTO for taxonomic hierarchy, taxonomic related information, and terms related to taxonomic rank.  
396 In most cases, the taxonomic structure of the VTO is followed as it is a regularly updated ontology.  
397 However, there are exceptions to this, such as the class "Mammalia" which is placed as a subclass of  
398 "Sarcopterygii" in the VTO. Although this classification is consistent with the cladistics standpoint that  
399 mammals are derived from fish, explicit classification of mammals under Sarcopterygii in the FO would  
400 result in the erroneous recognition of a fish-like mammal, e.g. whale, as both a fish and a mammal. We  
401 have therefore placed Mammalia under the higher taxonomic rank of Chordata and made annotation  
402 within the FO to highlight this choice.

403 The NCBITaxon, an automatic translation of the NCBI taxonomy database into OBO or OWL format  
404 (Federhen, 2011), is also used by the FO as a secondary source for terms regarding taxonomic rank. Both  
405 the VTO and NCBITaxon differ in hierarchical organization and definitions. One of the most distinctive  
406 feature of the VTO compared to the NCBITaxon is its broad taxonomic coverage of vertebrates. The  
407 NCBITaxon excludes many extant and nearly all extinct taxa while largely includes only species associated  
408 with archived genetic data, complemented by data from the PaleoDB and the TTO to provide an  
409 authoritative hierarchy and a richer set of names for specific taxonomic groups (Midford et al., 2013).  
410 Therefore the VTO is more relevant to the FO's purpose for a comprehensive fish taxonomy information  
411 (Foote; Dahdul et al., 2010), since the VTO is built based on several taxonomic resources including the  
412 NCBITaxon the Paleobiology Database (PaleoDB), and the Teleost Taxonomy Ontology (TTO). Having said  
413 that, any taxonomic ranks covered by the NCBITaxon but are not covered by the VTO, such as the species  
414 *Protanguilla palau* and the subfamily Oxudercinae are incorporated in the FO to improve coverage of fish  
415 data. More examples on the differences between the main reference book, the VTO, and the NCBITaxon,  
416 as well as what the FO uses are shown in Table 4.

417 New knowledge emerges everyday so there may be a need to add new concepts and relationships to  
418 the existing ontology. Proposing new vocabulary in biodiversity is not uncommon, since ontologies in this  
419 domain are presently insufficient and many are under development. Available standard vocabulary is not  
420 comprehensive enough to cover all the terms needed to make an ontology in the fish domain. In most  
421 cases, new terms must be proposed based on the rationale utilized in the ontology. One such example is  
422 that of Hymenoptera Anatomy Ontology, where new terms had to be proposed to expand the ontology  
423 (Seltmann et al., 2012, 2013). It should be possible to extend an ontology without altering the existing  
424 definitions. As such, the need for easy ontology extension is prioritized while creating the FO. The new  
425 terms are checked for its suitability to be adopted as a standard vocabulary for fish scientists. The use of  
426 adopted terms and concepts from our main references is further clarified with domain experts (Amy Y.

427 Then, Chong V. Ching) in order to represent and map the appropriate contents to reflect the diverse  
 428 aspects of fish (Helfman et al., 2009).

429

Term Example	Helfman et al. (2009)	VTO (Midford et al., 2013)	NCBITaxon (Federhen, 2011)	Fish Ontology (FO)
Furcacaudiformes (order)	Classified as Subclass of Thelodonti (superclass).	Classified as subclass of Agnatha (class).	Not classified.	Follows and reuses the VTO terms.
JawlessFish	Contains species and information for jawless fish species.	No classes and annotations found, but related species are classified.	No classes and annotations found, but related species are classified.	Follows Helfman et al. (2009) for labeling.
LobeFinnedFish	Classify as Sarcopterygii (page 4).	No classes and annotations found, but related species are classified.	Classified as Coelacanthiformes	Follows Helfman et al. (2009) for classification and labeling.
Gobiidae (family)	Listed and classified as family.	Listed and classified as family.	Listed and classified as family.	Follows and reuses the VTO terms.
Oxudercinae (subfamily)	Not listed.	Not listed.	Classified as a subclass of Gobiidae (family).	Follows and reuses the VTO classification up to the lowest existing taxonomic terms covered (Family Gobiidae). Adopts NCBITaxon terms for Subfamily Oxudercinae onwards.

430

431

**Table 4.** Term adoption example in the Fish Ontology.

432

433 Regarding ontology evaluation, there are reasons a number of errors were flagged by the Ontology  
 434 Pitfall Scanner (OOPS!) but none can be detected by using the tools from Protégé. The most apparent  
 435 reason is because the scope of evaluation for both methods are different. In Protégé, only the classes and  
 436 its relationship structures created in the ontology are being evaluated, while in OOPS!, the classes,  
 437 relationships, mapping and future integration problems are being evaluated, giving different results. A  
 438 number of errors detected by OOPS! can be attributed to the important FO feature of reusing terms from  
 439 other ontologies in order to reduce redundancy in global usage. As mentioned earlier, terms and  
 440 structures taken from other ontologies have their own unique ID and metadata to indicate associated  
 441 function. However, since most of these terms are directly used in the FO, the OOPS! tool flagged these  
 442 occurrences as critical errors such as "P24: Using recursive definitions", "P32: Several classes with same  
 443 labels", and "P40: Namespace hijacking".

444 Other pitfalls such as P02, P04, P08, P11, P13, P30, P36, and P41 (refer to Figure 7) are considered  
 445 acceptable since there are constantly new items to be added to the ontology along with the necessary  
 446 annotations, relations and property constraints. As an example, errors flagged under pitfall "P19: Defining

447 multiple domains or ranges in properties”, is due to the modeling of FO for increased inference capacity  
 448 (Poveda-Villalón, Gómez-Pérez & Suárez-Figueroa, 2014). In a typical ontology, inferring capabilities is  
 449 used to discover new relationships. In our work, we used inferring capabilities for automated fish species  
 450 recognition. As such, we had to avoid using 1 to 1 relationships for the domain and range, instead we  
 451 expanded the domain and range of each property for a more reliable automated species discovery.  
 452 Although OOPS! flagged these property expansions as pitfall errors, we deem these as minor for the  
 453 purpose of the FO development.  
 454

	FishBase	MarineTLO	NFO	FO
Domain Coverage	Fish and Fisheries	Marine Life	Fisheries	Fish
Ontology Based	No	Yes	Yes	Yes
Underlying Sources	33500 Species, 319000 Common names, 58100 Pictures, 53800 References information from the FishBase Consortium and 2270 Collaborators	FLOD (Fisheries Linked Open Data), ECOSCOPE (A Knowledge Base About Marine Ecosystems), WORMS (World Register of Marine Species), DBpedia, and FishBase	ISSCAAP (International Standard Statistical Classification of Aquatic Animals and Plants), AGROVOC (a portmanteau of agriculture and vocabulary) thesaurus, ASFA (Aquatic Sciences and Fisheries Abstracts) thesaurus, and FIGIS (Fisheries Global Information System) data	TTO, NCBITaxon, and VTO (with linked information from FishBase and PaleoDB)
Fish Information Provided	Common Name, Scientific Name (both species and genus, and species id), Information by Family, by country/island, by ecosystem, or by specific topic	Species, Scientific Names, Common Names, Predators, Authorships, Ecosystems, Countries, Water Areas, Vessels, Gears, EEZ, Bibliography, Statistical Indicators	Imported data sources in the owl file cover the topic of water areas, species taxonomic classification, ISSCAAP commercial classification, Aquatic resources, Land areas, Fisheries commodities, Vessel types and size, Gear types, AGROVOC data and ASFA data.	Species, Taxon Information, Fish Name, classes related to fish studies and fisheries.
Difference in fish searching concept	When searching for a fish species in FishBase, details such as names (common, scientific, other language), taxon classifications, environment, climate, range, distribution, size, weight, age, short description, biology, life cycle, mating behavior, main references, IUCN red list status, threat to human, and human uses will be provided (if available). Furthermore, other information such as the species countries, FAO areas, occurrences, ecology, genetics, internet sources, special reports, tools, and xml data sources are available as additional information sources.	Searching a fish species through the MarineTLO owl file is not possible. However its competency query v4 suggested that it covers a wide range of search topics such as species and its scientific name, its WORMS classification, prey and predator information, references, images, general terms, identifiers, competitors, biotic type of predator, assignment data, its biological environment, common name with complementary information, and water areas with their FAO codes.	Searching a fish species through the NFO owl file is also not possible. However it's imported data sources suggested the you can get information on fish species' ISSCAAP classification, ASFIS list (covers names and extensive details of species taxonomic rank), Aquatic Sciences and Fisheries Abstracts (ASFA) bibliographic database (links to FAO Fish Finder Fact Sheets which cover synonyms, FAO names, scientific names with original description, diagnostic features, Geographical distribution, habitat and biology, size, interest to fisheries, local names, source of information and Bibliography)	When FO search for a fish, it provide its taxon information, scientific name, common name, synonym, and links to TTO, FishBase and PaleoDB (if available). When unknown species is inferred in the FO, it can find whether a specimen or a sample is a fish or not fish, providing its taxon rank, full name, its characteristic, grouping, and its extinction status. Future concepts will allows it to provide data on fish morphology, genetic content and other fish species related information such as country maturity and other related information (like FishBase). FO infers the type of fish based on parameters provided.

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**Table 5.** Differences between Fish Ontology with other related ontology and database.

458 The FO covers the terms for fish domain which are not well described by other ontologies, such as  
459 terms used for fish studies ("maturity", "age") or sampling experiment ("weight", "length"), particularly  
460 those related to automatic classifications, annotations, and relationships. There are however some terms  
461 in the FO created using parameters rarely used outside of this domain, such as "FishDatabases" which are  
462 for any known databases for fish, or "GasBladder" which is a specific organ for "Actinopterygii". The  
463 differences between the FO and other fish related ontologies and databases is its ability to provide  
464 automated classification of unknown specimen.

465 There has been efforts to create ontologies for recognition purposes such as Hymenoptera (Balhoff  
466 et al., 2013), however in the fish domain, ontologies were created to focus more on classification rather  
467 than recognition, such as the MarineTLO, NFO, TTO and the ZFA. In this paper, the FO was created to focus  
468 on automated fish recognition. The comparison of FO with other related ontologies in the fish domain is  
469 presented in Table 5. For the purpose of this paper, we considered ontologies which are most related to  
470 Fish Ontology while not taking into consideration systems that use these ontologies as their underlying  
471 framework. FishBase was included as it is the most referred portal in this domain (600000 Visits/Month).  
472 Development of the FO for classification of several highly diverse groups, such as bony fishes, advanced  
473 jawed fish, sharks, skates, and rays, is an ongoing effort.

474 We envision the FO to expand by incorporating additional components such as fish models, fisheries  
475 parameters, gene annotations and other relevant information as aforementioned. These parameters will  
476 further enhance fish recognition capabilities to recognize fish based on physical features or gene  
477 annotations. We will focus on parameters that influence the grouping process such as shape and  
478 characteristic recognition, and anatomical metric distinctions. Other than including more terms and  
479 defined relationships, we are considering to increase granularity by linking to other relevant and  
480 established ontologies, such as the Gene Ontology (GO), the Zebrafish Information Network (ZFIN), the  
481 Vertebrate Skeletal Ontology (VSAO), and the Protein Ontology (PO) (Ashburner et al., 2000; Sprague,  
482 2003; Dahdul et al., 2010; Natale et al., 2011). In the near future we aim to integrate the FO with other  
483 ongoing efforts in our research group such as the Otolith Ontology, Monogenean Ontology, and the  
484 Monogenean Haptoral Bar Ontology (MHBI) (Abu et al., 2013). There is also consideration to link related  
485 ontologies to existing fish databases using the FO as a mediator ("Fish Stocking Database", "FISH-BOL",  
486 "Fish Species Database", "NZ Freshwater Fish Database"; Froese & Pauly; Shao, 2001). Furthermore we  
487 also hope to evolve the FO so that in the future, our other ongoing works on different type of fish related  
488 recognition tools or technique can be applied to enhance its inferencing capabilities (Abu et al., 2013a;  
489 Leow et al., 2015; See et al., 2016; Salimi et al., 2016; Wong et al., 2016; Kalafi et al., 2016).

490 The annotation of fish and fisheries resources in the FO and other related ontologies is a response  
491 to the emerging need for data sharing and integration especially for fish data resources (Ashburner et al.,  
492 2000; Gangemi et al., 2004; Bizer et al., 2009; Dahdul et al., 2010, 2012, Midford et al., 2010, 2013;  
493 Federhen, 2011; Natale et al., 2011; Schriml et al., 2012; Tzitzikas et al., 2013; Van Slyke et al., 2014;  
494 Pesquita et al., 2014) and will be highly relevant for the future of fish and fisheries related research.

495

## 496 CONCLUSION

497

498 An ontology for the fish and fisheries domain with automated fish recognition is introduced and discussed  
499 in this paper. The Fish Ontology (FO) is a new ontology with the feature of taxonomic-based recognition  
500 of fish by importing existing ontologies related to fish such as the VTO, ZFA, and TTO. The ontology infers  
501 information based on criteria such as names, rank, or characteristics, thus allowing recognition from  
502 specimen characteristics. The base terms are taken or imported from related ontologies or naming  
503 standards which enhanced the FO's fish recognition and cross-referencing capabilities. The potential  
504 usage of the ontology is huge especially as a comprehensive information provider for interested users

505 such as fishermen, museums, restaurants, or for research purposes. More importantly, the FO could be  
506 used as a framework to build semantic web systems for data integration to be applied in biodiversity  
507 research in the fish and fishery domain.

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## 511 REFERENCES

512

513 Abu A., Lim S., Sidhu A., Dhillon S. 2013a. Biodiversity image retrieval framework for monogeneans.  
514 *Systematics and Biodiversity* 11:19–33.

515 Abu A., Susan L., Sidhu A., Dhillon S. 2013b. Semantic representation of monogenean haptor Bar image  
516 annotation. *BMC bioinformatics* 14:48.

517 Alexander K. 2013. The Difference Between a Triplestore and a Relational Database. Available at  
518 [http://www.krisalexander.com/uncategorized/2013/07/16/the-difference-between-a-triplestore-](http://www.krisalexander.com/uncategorized/2013/07/16/the-difference-between-a-triplestore-and-a-relational-database/)  
519 [and-a-relational-database/](http://www.krisalexander.com/uncategorized/2013/07/16/the-difference-between-a-triplestore-and-a-relational-database/) (accessed July 27, 2017).

520 Ankolekar A., Krotzsch M., Tran T., Vrandečić D. 2007. The two cultures: Mashing up Web 2.0 and the  
521 Semantic Web. In: *Proceedings of the 16th international conference on World Wide Web*. ACM  
522 Press, 825–834.

523 Ashburner M., Ball CA., Blake JA., Botstein D., Butler H., Cherry JM., Davis AP., Dolinski K., Dwight SS.,  
524 Eppig JT., Harris MA., Hill DP., Issel-Tarver L., Kasarskis A., Lewis S., Matese JC., Richardson JE.,  
525 Ringwald M., Rubin GM., Sherlock G. 2000. Gene Ontology: Tool for The Unification of Biology.  
526 *Nature Genetics* 25:25–29.

527 Baader F., Calvanese D., McGuinness DL., Patel-Schneider P., Nardi D. 2003. *The description logic*  
528 *handbook: theory, implementation, and applications*. Cambridge, England: Cambridge university  
529 press.

530 Balhoff JP., Mikó I., Yoder MJ., Mullins PL., Deans AR. 2013. A Semantic Model for Species Description  
531 Applied to the Ensign Wasps (Hymenoptera: Evaniidae) of New Caledonia. *Systematic Biology*  
532 62:639–659.

533 Barbosa GP., da Silva FQB. 2001. An Electronic Marketplace Architecture Based on Technology of  
534 Intelligent Agents and Knowledge. In: *E-Commerce Agents, Marketplace Solutions, Security Issues,*  
535 *and Supply and Demand*. Springer-Verlag, 39–60.

536 Berners-Lee T. Linked Data - Design Issues. Available at  
537 <http://www.w3.org/DesignIssues/LinkedData.html> (accessed September 10, 2016).

538 Bizer C., Lehmann J., Kobilarov G., Auer S., Becker C., Cyganiak R., Hellmann S. 2009. DBpedia - A  
539 crystallization point for the Web of Data. *Web Semantics: Science, Services and Agents on the*  
540 *World Wide Web* 7:154–165.

541 Campbell GA. 2006. *Ontology for Call Control*. Department of Computing Science and Mathematics,  
542 University of Stirling.

543 Caracciolo C., Heguiabehere J., Gangemi A., Baldassarre C., Johannes K., Taconet M. 2012. Knowledge  
544 management at FAO: A case study on network of ontologies in fisheries. *Ontology Engineering in a*  
545 *Networked World*:383–405.

- 546 Catalog of Fishes Classification. Available at [http://www.calacademy.org/scientists/catalog-of-fishes-](http://www.calacademy.org/scientists/catalog-of-fishes-classification/)  
547 [classification/](http://www.calacademy.org/scientists/catalog-of-fishes-classification/) (accessed July 27, 2017).
- 548 Chapman AD. 2009. *Numbers of Living Species in Australia and the World*.
- 549 Chong VC., Lee PKY., Lau CM. 2010. Diversity, extinction risk and conservation of Malaysian fishes.  
550 *Journal of fish biology* 76:2009–2066.
- 551 Dahdul WM., Balhoff JP., Blackburn DC., Diehl AD., Haendel MA., Hall BK., Lapp H., Lundberg JG.,  
552 Mungall CJ., Ringwald M., Segerdell E., Van Slyke CE., Vickaryous MK., Westerfield M., Mabee PM.  
553 2012. A unified anatomy ontology of the vertebrate skeletal system. *PLoS one* 7:e51070.
- 554 Dahdul WM., Lundberg JG., Midford PE., Balhoff JP., Lapp H., Vision TJ., Haendel MA., Westerfield M.,  
555 Mabee PM. 2010. The teleost anatomy ontology: anatomical representation for the genomics age.  
556 *Systematic biology* 59:369–383.
- 557 Emmanuel FA., Angermeier PL. 2013. FishTraits. Available at <http://www.fishtraits.info/> (accessed May  
558 22, 2016).
- 559 Eschmeyer WN., Fricke R., Fong JD., Polack DA. 2010. Marine fish diversity: history of knowledge and  
560 discovery (Pisces). *Zootaxa* 2525:19–50.
- 561 Falconer S. 2010. OntoGraf - Protege Wiki. Available at <http://protegewiki.stanford.edu/wiki/OntoGraf>  
562 (accessed May 25, 2016).
- 563 Federhen S. 2011. The NCBI Taxonomy Database. *Nucleic Acids Research* 40:136–143.
- 564 FISH-BOL. Available at <http://www.fishbol.org/> (accessed May 22, 2016).
- 565 Fish Species Database. Available at <https://www.igfa.org/fish/fish-database.aspx> (accessed May 22,  
566 2016).
- 567 Fish Stocking Database. Available at <http://www.glfc.org/fishstocking/> (accessed May 22, 2016).
- 568 Foote M. The Paleobiology Database. Available at <http://fossilworks.org/?page=paleodb>
- 569 Freitas F., Stuckenschmidt H., Noy NF. 2005. Guest editor's introduction: Ontology issues and  
570 applications. *Journal of the Brazilian Computer Society* 11:5–16.
- 571 Froese R., Pauly D. FishBase. Available at <http://www.fishbase.org/> (accessed May 22, 2016).
- 572 Froese R., Pauly D. 2000. *FishBase 2000: Concepts, Designs and Data Source*. WorldFish.
- 573 Gangemi A., Fisseha F., Keizer J., Lehmann J., Liang A., Pettman I., Sini M., Taconet M. 2004. A core  
574 ontology of fishery and its use in the fishery ontology service project. *EKA04 Workshop on Core*  
575 *Ontologies in Ontology Engineering*.
- 576 Glimm B., Horrocks I., Motik B., Stoilos G., Wang Z. 2014. HermiT: An OWL 2 Reasoner. *Journal of*  
577 *Automated Reasoning* 53:245–269.
- 578 Gruber TR. 1995. Toward principles for the design of ontologies used for knowledge sharing.  
579 *International Journal of Human-Computer Studies* 43:907–928.
- 580 Heath T., Bizer C. 2011. Linked Data: Evolving the Web Into a Global Data Space. *Synthesis lectures on*  
581 *the semantic web: theory and technology* 1:136.
- 582 Helfman GS., Collette BB., Facey DE., Bowen BW. 2009. *The diversity of fishes: biology, evolution, and*  
583 *ecology*. John Wiley & Sons.

- 584 Horridge M. 2010. Owlviz. Available at <http://protegewiki.stanford.edu/wiki/OWLviz> (accessed May 25,  
585 2016).
- 586 Horridge M., Knublauch H., Rector A., Stevens R., Wroe C., Jupp S., Moulton G., Drummond N., Brandt S.  
587 2011. A Practical Guide To Building OWL Ontologies Using Protégé 4 and CO-ODE Tools Edition 1.3.  
588 *The University Of Manchester*:107.
- 589 IEEE Big Data. Available at <http://www.bigdata.ieee.org> (accessed May 28, 2016).
- 590 Kalafi EY., Tan WB., Town C., Dhillon SK. 2016. Automated identification of Monogeneans using digital  
591 image processing and K-nearest neighbour approaches. *BMC Bioinformatics* 17:755–778.
- 592 Last PR., White WT., Caira JN., Dharmadi., Fahmi., Jensen K., Lim a PK., Manjaji-Matsumoto BM., Naylor  
593 GJP., Pogonoski JJ., Stevens JD., Yearsley GK. 2010. *Sharks and Rays of Borneo*. Collingwood: CSIRO  
594 Publishing.
- 595 Leow LK., Chew L-L., Chong VC., Dhillon SK. 2015. Automated identification of copepods using digital  
596 image processing and artificial neural network. *BMC Bioinformatics* 16:S4.
- 597 Man D. 2013. Ontologies in Computer Science. *Didactica Mathematica* 31:43–46.
- 598 Midford P., Balhoff J., Dahdul W., Kothari C., Lapp H., Lundberg J., Mabee P., Vision T., Westerfield M.  
599 2010. The Teleost Taxonomy Ontology. *Nature Precedings*.
- 600 Midford P., Dececchi T., Balhoff J., Dahdul W., Ibrahim N., Lapp H., Lundberg J., Mabee P., Sereno P.,  
601 Westerfield M., Vision T., Blackburn D. 2013. The vertebrate taxonomy ontology: a framework for  
602 reasoning across model organism and species phenotypes. *Journal of biomedical semantics* 4:34.
- 603 Natale DA., Arighi CN., Barker WC., Blake JA., Bult CJ., Caudy M., Drabkin HJ., D'Eustachio P., Evsikov A  
604 V., Huang H., Nchoutmboube J., Roberts N V., Smith B., Zhang J., Wu CH. 2011. The Protein  
605 Ontology: a structured representation of protein forms and complexes. *Nucleic acids research*  
606 39:D539–D545.
- 607 Negru S., Lohmann S., Haag F. 2014. Visual Notation for OWL Ontologies. Available at  
608 <http://vowl.visualdataweb.org/v2/>
- 609 Nelson JS. 2006. *Fishes of the World*. John Wiley & Sons.
- 610 Nicola D. A., Missikoff M., Navigli R. 2005. A Proposal for a Unified Process for Ontology Building: UPON.  
611 In: *Proceedings of the 16th International Conference on Database and Expert Systems Applications*.  
612 Berlin, Heidelberg: Springer, 655–664.
- 613 NZ Freshwater Fish Database. Available at [https://www.niwa.co.nz/our-services/online-  
614 services/freshwater-fish-database](https://www.niwa.co.nz/our-services/online-services/freshwater-fish-database) (accessed May 22, 2016).
- 615 Pesquita C., Ferreira JD., Couto FM., Silva MJ. 2014. The epidemiology ontology: an ontology for the  
616 semantic annotation of epidemiological resources. *Journal of biomedical semantics* 5:4.
- 617 Poveda-Villalón M., Gómez-Pérez A., Suárez-Figueroa MC. 2014. OOPS! (Ontology Pitfall Scanner!):  
618 supporting ontology evaluation on-line. *International Journal on Semantic Web & Information  
619 Systems* 10:7–34.
- 620 Protégé 2016. Available at <http://protege.stanford.edu/> (accessed May 23, 2016).
- 621 Prud'hommeaux E., Seaborne A. 2008. SPARQL Query Language for RDF. Available at  
622 <http://www.w3.org/TR/rdf-sparql-query/> (accessed May 23, 2016).
- 623 Salimi N., Loh KH., Kaur Dhillon S., Chong VC. 2016. Fully-automated identification of fish species based

- 624 on otolith contour: using short-time Fourier transform and discriminant analysis (STFT-DA). *PeerJ*  
625 4:e1664.
- 626 Schriml LM., Arze C., Nadendla S., Chang YWW., Mazaitis M., Felix V., Feng G., Kibbe WA. 2012. Disease  
627 ontology: A backbone for disease semantic integration. *Nucleic Acids Research* 40:940–946.
- 628 See M., Marsham S., Chang CW., Chong VC., Sasekumar A., Dhillon SK., Loh KH. 2016. The use of otolith  
629 morphometrics in determining the size and species identification of eight mullets (Mugiliformes:  
630 Mugilidae) from Malaysia. *Sains Malaysiana* 45:735–743.
- 631 Seltmann K., Pénczes Z., Yoder M., Bertone M., Deans A. 2013. Utilizing Descriptive Statements from the  
632 Biodiversity Heritage Library to Expand the Hymenoptera Anatomy Ontology. *PLoS ONE* 8:e55674.
- 633 Seltmann K., Yoder M., Miko I., Forshage M., Bertone M., Agosti D., Austin A., Balhoff J., Borowiec M.,  
634 Brady S., Broad G., Brothers D., Burks R., Buffington M., Campbell H., Dew K., Ernst A., Fernandez-  
635 Triana J., Gates M., Gibson G., Jennings J., Johnson N., Karlsson D., Kawada R., Krogmann L., Kula R.,  
636 Mullins P., Ohl M., Rasmussen C., Ronquist F., Schulmeister S., Sharkey M., Talamas E., Tucker E.,  
637 Vilhelmsen L., Ward PS., Wharton R., Deans A. 2012. A hymenopterists' guide to the Hymenoptera  
638 Anatomy Ontology: utility, clarification, and future directions. *Journal of Hymenoptera Research*  
639 27:67–88.
- 640 Shadbolt N., Hall W., Berners-Lee T. 2006. The semantic web revisited. *IEEE Intelligent Systems* 21:96–  
641 101.
- 642 Shao K-T. 2001. Fish Database of Taiwan. Available at <http://fishdb.sinica.edu.tw/eng/home.php>  
643 (accessed May 22, 2016).
- 644 Sirin E., Parsia B. 2007. SPARQL-DL: SPARQL query for OWL-DL. *CEUR Workshop Proceedings* 258.
- 645 Sirin E., Parsia B., Grau BC., Kalyanpur A., Katz Y. 2007. Pellet: A practical OWL-DL reasoner. *Web*  
646 *Semantics: Science, Services and Agents on the World Wide Web* 5:51–53.
- 647 Van Slyke C., Bradford Y., Westerfield M., Haendel M. 2014. The zebrafish anatomy and stage  
648 ontologies: representing the anatomy and development of *Danio rerio*. *Journal of biomedical*  
649 *semantics* 5:12.
- 650 Smith B., Ashburner M., Rosse C., Bard J., Bug W., Ceusters W., Goldberg LJ., Eilbeck K., Ireland A.,  
651 Mungall CJ., Leontis N., Rocca-Serra P., Ruttenberg A., Sansone S-A., Scheuermann RH., Shah N.,  
652 Whetzel PL., Lewis S. 2007. The OBO Foundry: coordinated evolution of ontologies to support  
653 biomedical data integration. *Nature biotechnology* 25:1251–1255.
- 654 Sprague J. 2003. The Zebrafish Information Network (ZFIN): the zebrafish model organism database.  
655 *Nucleic Acids Research* 31:241–243.
- 656 The OBO Foundry. Available at <http://obofoundry.org/> (accessed May 24, 2016).
- 657 Tsarkov D., Horrocks I. 2006. FaCT++ Description Logic Reasoner: System Description. *Proceedings of the*  
658 *Third International Joint Conference (IJCAR):292–297*.
- 659 Tzitzikas Y., Allocca C., Bekiari C., Marketakis Y., Fafalios P., Doerr M., Minadakis N., Patkos T., Candela L.  
660 2013. Integrating Heterogeneous and Distributed Information about Marine Species through a Top  
661 Level Ontology. In: *Research Conference on Metadata and Semantic Research*. 289–301.
- 662 Tzitzikas Y., Allocca C., Bekiari C., Marketakis Y., Fafalios P., Doerr M., Minadakis N., Patkos T., Candela L.  
663 2016. Unifying heterogeneous and distributed information about marine species through the top  
664 level ontology MarineTLO. *Program* 50:16–40.

- 665 Wieczorek J., Bloom D., Guralnick R., Blum S., Döring M., Giovanni R., Robertson T., Vieglais D. 2012.  
666 Darwin Core: An Evolving Community-Developed Biodiversity Data Standard. *PLoS ONE* 7:e29715.
- 667 Wikipedia. Available at <http://www.wikipedia.org>
- 668 Wong JY., Chu C., Chong VC., Dhillon SK., Loh KH. 2016. Automated otolith image classification with  
669 multiple views: an evaluation on Sciaenidae. *Journal of Fish Biology* 89:1324–1344.
- 670 Zhou L. 2007. Ontology learning: state of the art and open issues. *Information Technology and*  
671 *Management* 8:241–252.
- 672