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Data Extraction from Ontologies Used in Biological Sciences

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Abstract: ***In addition to outlining the basic steps involved in retrieving information, this article goes over some of the most well-known traditional methods, including keyword-based and ontology-based approaches. This chapter provides a high-level summary of image retrieval systems. This chapter provides a brief overview of many types of picture retrieval, including those that rely on keywords, content, or ontologies. An ontology-based biological information system evaluation methodology is also detailed. This study topic describes the Neo4j graph database and provides examples of graph databases and various kinds of graph databases. An ontology-based biological information system is extensively detailed in this work. In the ontology creation model, we talk about taxonomies and the idea of ontologies. In this article, we will go over the current state of the art in biology graph database construction, with the goal of inspiring you to use neo4j and introducing you to its strengths. The suggested system's implementation is covered in this paper. This chapter also includes the Java implementation. We talk about a methodology for evaluating biological information systems that are built on ontologies. This chapter provides a description of UML diagrams. Analyses and descriptions of the query results and experimental outcomes are included in this study.***

Index Terms: Keyword-Based Information Retrieval, Ontology-Based Information Retrieval, Biological Information System, Graph Database.

I. INTRODUCTION

There is a pressing need for very rapid processing times from data storage, and information retrieval is now a crucial system for all. The various data representation approaches and storage formats have been the subject of much academic discussion. What we call "information extraction" (IE) is the process of extracting relevant data from documents written in natural language. With the rise of the internet, IE has taken on a more commercially significant role. In IE, unseen texts are fed into the system and, in return, fixed format, unambiguous data is produced. Because it is well-suited for semantic information retrieval from certain domains, ontology has become the most preferred store format.

Knowledge in computational form may be shared and reused; this is what ontology is all about. The word "ontology" may mean several things depending on the context, book, and field of study. A taxonomy of the world's concepts, "The study of existence," or "A theory of what there is in the world" are all ways to describe ontology in the fields of philosophy and linguistics. In the theoretical perspective of the IT and AI communities, "A formal explicit statement of a common conception" or "An abstract and the connections between them" [38]. The integration of a vast array of biological data is considered to be impossible without biologically oriented ontologies. Research and educational tools both make use of ontology-based information services. Using the neo4j graph database server, this thesis constructs biological taxonomies as ontologies. This thesis is driven by a desire to bolster the importance of data extraction for bioinformatics educators and students. At now, the majority of online search engines depend only on statistical methods, and all biological material is published in the form of texts and books. They can't decipher human intent, but they can offer the most relevant results based on statistical measurements of similarity, so that users may have their questions answered. Google, Yahoo!, NCBI, Bioportal, Animal.com, and the like really set a standard that is very hard to surpass. The underlying statistical approaches are more resilient and can scale to the size of the Web,

thanks to their mature nature, making them superior than semantic technologies. The issue, therefore, is that researchers, educators, and students have a hard time finding the biological data and pictures they need without resorting to link sites. They spend a considerable amount of time seeking as a result. Effortlessly locating pertinent and associated data or photos is the goal of this investigation. Additionally, this study delves into the function of ontology and its application to bioinformatics. Data storage in graphs, ontology-based biological data generation, and processing of various information retrieval queries are the three main areas of investigation highlighted in this thesis. The advantage of using ontologies to describe biological knowledge has been quickly recognized by the community, leading to a fast growth in its usage. By adding ontological concepts to biological data, some characteristics of the data may be described more precisely. When building and updating biological ontologies, it is necessary to manually add, remove, and edit concepts and their definitions inside the ontology. Additionally, biological data must be annotated to the ontology's concepts. The motivations of this research are focused with three
factors. The first is essential for the life sciences, since they are seeking alternatives to the standard information retrieval and image retrieval frameworks' keyword-based techniques. The second one is extensive work in text mining which is being done to identify animal-animal interactions and their breeding habits, feeding habits, habitats,

Places, movement, covering one's body, etc. Finally, ontologies based relationships are constructed in neo4j graph database and have been discussed in biological dataset.

II. RELATED WORKS

Information retrieval is the process of finding, inside a database, the specific piece of information that a user is looking for. Metadata and full-text (or other content-based) indexing are two possible foundations for search engines. One way to alleviate the sensation of "information overload" is by making use of automated information retrieval tools. When it comes to making books, journals, and other publications available to the public, many public and academic libraries rely on IR systems. The most well-known uses of IR are web search engines. Inputting a query into the system initiates the information retrieval process. Example queries include search strings used in online search engines, which are explicit declarations of information demands. No particular item in a collection can be "found" by an information retrieval query. On the contrary, it's possible for many items to match the query, each with its own level of relevance. A database entry represents an object, which is a real-life thing. Data from the database is cross-referenced with user inquiries. Data objects may be anything from text documents to pictures to audio files to mind maps to movies, depending on the use case. It is common practice to use document surrogates or metadata in place of actual documents when storing them in an IR system.

In order to rank the items in the database, the majority of IR systems calculate a numerical score that represents how well each object fits the query. The highest ranked things are subsequently shown to the user. The user has the option to repeat the procedure in order to make their inquiry more specific.
Vu Long Hieu Vu et al. [48] have given explanation that database management systems offer a comprehensive solution to data storage, while they require deep knowledge of the schema, as well as the data manipulation language, in order to perform effective retrieval. Since these requirements pose a problem to lie or occasional users, several methods incorporate keyword search (KS) into relational databases. Nevertheless, the majority of the current methods only address the querying of one DBMS. On the other hand, the proliferation of distributed databases in several conventional and emerging applications necessitates the support for keyword-based data sharing and querying over multiple DMBSs. In order to avoid the high cost of searching in numerous, potentially irrelevant, databases in such systems, G-KS is proposed as a novel method for selecting the top-K candidates based on their potential to contain results for a given query. G-KS summarizes each database by a keyword relationship graph, where nodes represent terms and edges describe relationships between them. Keyword relationship graphs are utilized for computing the similarity between each database and a KS query, so that, during query processing, only the most promising databases are searched. An

extensive experimental evaluation demonstrates G-KS that achieve better results than the current state-of-the-art technique on all aspects, including precision, recall, efficiency, space overhead and flexibility of accommodating different semantics. David W. Embley et al. [12] have presented a new approach to extracting information

from unstructured documents based on an application ontology that describes a domain of interest. Starting with such ontology, the system has been formulated rules to extract constants and context keywords from unstructured documents. For each unstructured document of interest, which is extracted its constants and keywords and apply a recognizer to organize extracted constants as attribute values of tuples in a generated database schema. Generally, researchers have fixed all the processes and change only the ontological description for a different application domain. In experiments their system have been conducted on two different types of unstructured documents taken from the Web, their approach attained recall ratios in the 80% and 90% range and precision ratios near 98%. And the researchers have proposed a framework for an ontology-based system that extracts and structures information found in data-rich unstructured documents. Except for ontology creation, the processes in their framework are automatic and do not require human intervention. A prototype system has also been built based on this framework and has been applied two application areas—car advertisements and a computer jobs listing. As raw data for these applications, researchers have used documents placed on the Web by the Salt Lake Tribune and the Los Angeles Times. So, near 99% recall and precision on tuning data and roughly 90% recall and 98% precision on test data are conducted and obtained as result. They have observed that most of the errors in recall and precision were due to incomplete lexicons and incomplete ontologies. Without changing the framework, better lexicons and richer ontologies will overcome both of these short comings. Improvements in heuristics, front-end processing, and back-end processing are also possible.

Martin Labsky [24] has presented that the information
extraction from websites using extracting ontologies and described that the advent of the Semantic Web initiatives around 2000, modeling parts of reality with domain ontologies became increasingly popular and a number of ontology authoring tools appeared. IE techniques became the natural choice to populate these ontologies with instances from text (semi-)automatically. The CREAM approach defines a methodology and tooling support for visually annotating web pages and for storing annotations as instances of ontology classes. The original approach was manual but it was soon coupled with a trainable IE system Amilcare that utilized the LP2 named entity extraction algorithm and a GATE annotator for preprocessing. The combined system was named Semi-automatic CREAM (SCREAM).

Siegfried Handschuh, Steffen Staab, and Fabio Ciravegna
[16] have defined that CREAM is a comprehensive framework for creating annotations, relational metadata in particular, the foundation of the future Semantic Web. The new version of S-CREAM (semi-automatic creation of metadata) have been presented here supports metadata creation with the help of information extraction in addition to all the other nice features of CREAM, like comprises inference services, crawler, document management system,

Ontology guidance/fact browser, document editors/viewers, and a meta ontology. Fabio Ciravegna [9] has presented (LP)2, an algorithm for learning to extract implicit events from documents of different types, has described the algorithm and explained experiments where the algorithm reaches excellent results. How the different features of the algorithm are contributed to such results. In particularly, the researcher has focused on the contribution of linguistic information. (LP) 2 has become the basis for two adaptive IE systems. Borislav Popov et al. [32] have described that the semantic annotation platforme (KIM) which provides a novel Knowledge and Information Management infrastructure and services for automatic semantic annotation, indexing, and retrieval of documents. It provides mature infrastructure for scalable and customizable information extraction (IE) as well as annotation and document management, based on GATE. In order to provide basic level of performance and allow easy bootstrapping of applications, KIM is equipped with upper-level ontology and a knowledge base providing extensive coverage of entities of general importance. The ontologies and knowledge bases involved are handled using cutting edge Semantic Web technology and standards, including RDF(S) repositories, ontology middleware and reasoning. From technical point of view, the platform allows KIM-based applications to use it for automatic semantic annotation, content retrieval based on semantic restrictions, and querying and modifying the underlying ontologies and knowledge bases. While the previous approaches used ontologies mainly for enumerating the extractable concepts, defining their inheritance hierarchy and for storing their extracted instances, another approach emerged that attempted to augment the ontology itself with extraction knowledge

III. RESEARCH METHODOLOGY

For the proposed system, firstly bio data are created as ontological commitments. For example, in this system Class Animalia that may be created based on ontology for teaching aid. Firstly, bio data was created in spreadsheet as CSV format file which supports that simply represents relationships. The CSV format can be obtained from any row data, databases or Excel export. Each line must contain at least two elements. Each row of the file is a node or an edge. Working with spreadsheets are comfortable can be manipulated data in this environment. That is why; this is often a very suitable way of conceptual data based on ontology.

A. Creation of Ontology Based Bio Data

First, create a node table which has a unique identifier (first column: node), a name (second column), and a type/label (third column) and as needed (e.g. Scientific Name, feeding habit, breeding habit, habit, location, locomotion, body cover). The qualities or features are listed in columns three through seven. A graph database management system, such as Neo4j, can make sense of these data imports and provides further context on the connections between them. There is a two-way flow of information between the data and the nodes. All relationships and nodes are included in the two CSV files named nodes.csv and rels.csv. Biological ontology is really built using data from the Animalia domain in biology. All animals, both extant and past, are classified as members of the taxonomic kingdom Animalia, which includes multicellular, eukaryotic creatures. There are six main groups within Animalia, and they are as follows: chondrichthyes, osthychthyes, amphibia, reptiles, avians, and mammals. Chondrichthyes or cartilaginous fishes are jawed fish with paired fins, paired nares, scales, a heart with its chambers in series, and skeletons made of cartilage rather than bone. Osthychthyes or bony fish are a taxonomic group of fish that have bone, as opposed to cartilaginous, skeletons. A unit Amphibia or amphibian is a cold-blooded vertebrate animal that is born in water and breathes with gills. When a larva transforms into an adult, its lungs acquire the capacity to breathe air, allowing it to inhabit land. Those creatures with backbones, cold blood, and a tendency to be slimy or scaly are known as reptiles. Reptiles include species such as crocodiles, frogs, salamanders, and snakes. A class mammalia or mammal is an endothermic amniotes distinguished from reptiles and birds by the possession of hair, three middle ear bones, and mammary glands. The four relationship types are created in this biological
domain such as has, is_a, is_a_ClassName, lives_in. The Animalia Class is the super class (root node in graph database) of this systems.

B. Biological Ontology Graph Database

One major perk of DBMSs is the ease and accuracy with which data may be shared with authorized users or the general public. The database design must take into account the fundamental ideas of a database management system (DBMS), such as the ACID (Atomicity, Consistency, Isolation and Durability) principles, in order to accomplish these aims. Applying the atomicity notion allows the user to regulate the validity of data changes that occur while updating the database.
A graph consists of a set of nodes that are linked together by edges. Similar to Object-Oriented Database Management (OODM), data entities in a graph-based data model are defined as nodes with node properties. To show the binary connection between nodes, we may use the edges between them. The beginning and ending nodes of an edge are always preserved as pointers in the typed edge. Entities containing less descriptive data that have complicated connections may be stored using this data model. To overcome these database models' shortcomings, we came up with a data model that combines object-oriented data modeling (OODM) with graph data modeling in the programmatic data layer (conceptual data layer). This model stores physical biological

entities as objects and their relationships as binary relationships in the graph model, which helps us deal with complex data. To construct classes for this thesis, we modified the Biological ontology's description of a class. These classes were meticulously crafted with object-oriented programming principles in mind.

1. It is necessary to encapsulate and abstract data so that processes and users cannot access a class's attributes or data structure. Only the class interface, operator, provides access to the data stored in the classes. To manage the object's internal data consistency, this design idea is used.
2. One strong object-oriented method is inheritance, which allows code to be reused. The foundation of class definition, including attributes and methods, is inherited by subclasses from their progenitor class, the superclass.

Biological core classes such as Chondrichthyes, Osthychthyes, Amphibia, Reptilia, Aves and Mammalia and relationship types and their relations, properties types and their properties are defined as physical entity class mimicking node in the graph data model. Within the graph data model, the connections between classes are shown as distinct relation class resembling edges.

Section C: Search Engine Implementation

The Search Class, which includes the Group Search() function, is used to develop the search engine. Every animal's graph node has its own Mynodes Class. You may search for any animal in detail by entering both its common and scientific names. When doing a group search, it is possible to return sophisticated queries using factors like feeding behavior, breeding habit, and more. Figure4.5, the Class Diagram of Search, Admin Search, and Database Operations, depicts the whole hierarchy of classes.

User input class name such as Chondrichthyes, the search engine finds the nodes which relationships with Common name Chondrichthyes and relationship type is “is_a_ClassName”. Aslo finds concurrently the nodes which relationships with Scientific name Chondrichthyes and relationship type is “is_a_ClassName”. The nodes with same class “Chrondrichthyes” node are extracted by search engine. The user input with desired common name, “Eagle-Ray” is retrieved from these nodes and displays the detailed information of class name, body cover type, breeding habit type, feeding habit type, locomotion type and scientific name. The user input with desired scientific name, “Myliobatis” is retrieved from these nodes and displays the detailed information of class name, body cover type, breeding habit type, feeding habit type, locomotion type and scientific name. The output description for detailed search is same for searching common name and scientific name.

Group search provides five options types and also mix any option types. Group Search method has two arguments which are one ArrayList and one ArrayList. User input option types ArrayList are passed to GroupSearch and user input option values ArrayList and ArrayList type collection. And then return that list. Public ArrayList GroupSearch(ArrayList rlst,
ArrayList nodelist)

IV. EXPERIMENTAL RESULTS AND EVALUATION

Implementation of ontology-based biological information system is presented in this chapter. The first implementation with Neo4j Community Server installation, configuration, and biology based ontology graph nodes are created in this database server. Biological ontology model is conceptually implemented in biological domain and class orientation of superclass and subclasses hierarchy structure is discussed. Java implementation of Mynode class, query engine class and search and admin search for any simple query and more complex query are also presented. Secondly, in the java implementation, detail search, group search and admin user for database operations are provided. The third implementation of graph engine component with neoclipse configuration and illustrated graph nodes are discussed in detail. Biological ontology plays an important role in representing the unstructured/semi-structured data of this thesis. Java based application is developed to collect different resumes through web search and to convert into common structured format. The most common using standard format can be obtained by the use of ontology. Graph Database Query Syntax and Results are presented.

A. Analysis of Bio Data

In this system, there are 149 elements in animalia to find out how many of them had both Carnivore and Viviparous. The number of elements in Carnivore and Viviparous can be found by calculating and drawing Venn diagram (Figure 5.3). The query results of bio data are given below.

n (C) = number of elements in Carnivore is
94 n (V) = number of elements in
Viviparous is 67

n (C ∩ V) = number of elements in Carnivore and Viviparous is 30.

n (C ∩V) = n (C) + n (V) - n (C U V) = 94 + 67 — 131 =30.

Be sure that the symbols in your equation have been d The results are generally consistent with the results of the analyses. The figures are fully consistent with the query results.

B. Evaluation

Ontology is a fairly complex structure and it is often more practical to focus on the evaluation of different levels of the ontology separately rather than trying to directly evaluate the ontology as a whole. In this thesis, biological ontology is evaluated of Hierarchy or taxonomy level. An ontology typically includes a hierarchical is-a relation between concepts. Although various other relations between concepts may be also defined, the "is-a" relationship is particularly important and may be the focus of specific evaluation efforts. The biological ontology contains other such as is_a_ClassName, has, lives_in. The ontology to be evaluated may also be mapped to an upper ontology that defines constructs that are not in the KR language. For example, an upper ontology may define class, relation, property, attribute, facet, quality, or trope.

Task-based evaluations offer a useful framework for measuring practical aspects of ontology deployment, such as the human ability to formulate queries using the query language provided by the ontology, the accuracy of responses provided by the system's inferential component,

The degree of explanation capability offered by the system, the coverage of the ontology in terms of the degree of reuse across domains, The scalability of the knowledge base, and the ease of use of the query component [29].

Biological ontology identifies and defines a concise set of eight ontology quality criteria and presents as follows:

- Accuracy
- Adaptability
- Clarity
- Completeness
- Computational efficiency
- Conciseness
- Consistency
- Organizational fitness

C. Class Evaluation

Biological ontology has seven classes and 292 subclasses. Animalia is a super class (root node) and it has six subclasses. 292 subclasses are inherited from the corresponding super classes as shown in Table 1. Mammalia class has 108 subclasses which is the largest subclasses in this biological ontology.

Table 1 Biological Ontology Class Name and Number of Sub Classes

No	Class Name	Number of Sub Classes
1	Animalia	6
2	Chondrichthyes	20
3	Osthychthyes	42
4	Amphibia	22
5	Reptilia	64
6	Aves	30
7	Mammalia	108
Total		**292**

D. Relationship Evaluation

Biological ontology has four relationship types such as is_a_ClassName, is_a, has, lives_in, etc. Relationship types and number of relationships are described in Table 2.

Table 2. Relationship Types and Relationships

No	Relationship Type	Relationships
1	is_a_ClassName	286
2	is_a	286
3	Has	242
4	lives_in	143
Total		**957**

E. Precision and Recall

In pattern recognition and information retrieval with binary classification, precision (also called positive predictive value) is the fraction of retrieved instances that are relevant, while recall (also known as sensitivity) is fraction of relevant instances that are retrieved.

Precision = True class A / (True class A + False class A) Recall = True class A / (True class A + False class B)

Where,

True class A (TA) - correctly classified into class A
False class A (FA) - incorrectly classified into class A True class B (TB) - correctly classified into class B False class B (FB) - incorrectly classified into class B

The result data analysis on feeding habit and breeding habit of this biological ontology are described in Table 3 and graph shows in Figure 1. According to the biological data, it can be seen that two complex search group queries for feeding habit (Carnivore) and breeding habit (Viviparous) is 30 and feeding habit (Carnivore) and breeding habit (Oviparous) is 63.

Table 3 Analysis of Feeding Habit and Breeding Habit

Feeding Habit	Breeding Habit	Bio Data	TA	FA	FB	Precision	Recall
Carnivore	Viviparous	30	30	0	0	100%	100%
Carnivore	Oviparous	63	63	0	0	100%	100%

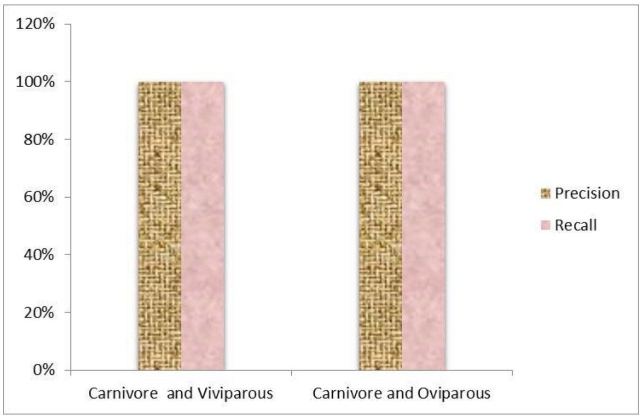

Figure 1 Comparing Result of the Two Complex Search Group Query

The result data analysis on feeding habit, breeding habit and habitat of this biological ontology are described in Table 4 and graph shows in Figure 2. According to the bio data, it can be seen that three complex search group queries for feeding habit (Carnivore), breeding habit (Viviparous), habitat (Marine Water) has 12, feeding habit (Carnivore), breeding habit (Viviparous), habitat (Terrestrial) has 13, feeding habitat (Carnivore), breeding habit (Viviparous), habitat (Arboreal) has 1 and feeding habit (Carnivore), breeding habit (Viviparous), habitat (Tundra) has 4 according to our biological data.

Table 4. Analysis of Feeding Habit, Breeding Habit and Habitat

Feeding Habit	Breeding Habit	Habitat	Bio Data	TA	FA	FB	Precision	Recall
Carnivore	Viviparous	Marine Water	12	10	1	2	91%	83%
Carnivore	Viviparous	Terrestrial	13	12	0	1	100%	92%
Carnivore	Viviparous	Arboreal	1	1	0	0	100%	100%
Carnivore	Viviparous	Tundra	4	4	0	0	100%	100%

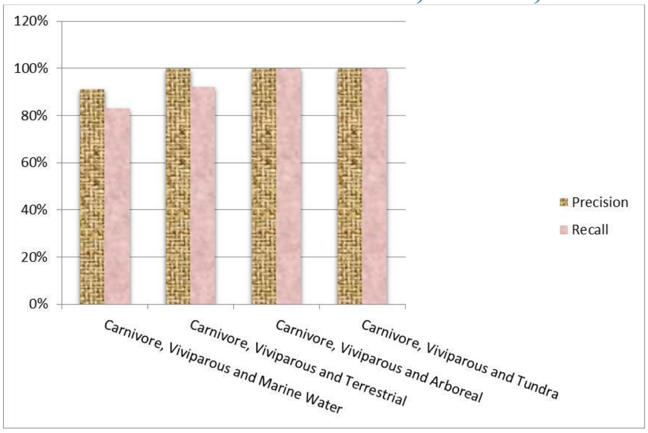

Figure 2 Comparing Result of the Three Complex Search Group Query

V. CONCLUSION

In this research, we provide an ontology-based BI system that offers semantically relevant and efficient data retrieval capabilities. Graph display with cypher query and colored graph nodes; group search; and single search with full descriptions are all possible query processing options. As an alternative to the standard information retrieval and image retrieval frameworks that rely on keyword-based techniques, the neo4j graph database may be used in the life sciences to build associations based on ontologies. Additionally, the cypher query language allows for the retrieval of quick access queries. Relationships between living things may also be retrieved. This study lends credence to an ontology-based information retrieval system that users can rely on to provide the specific research materials they need. The biological domain is used to build these semantic relationship-based query systems. Biodata information in the targeted search region may also be retrieved using semantic ontology searches. An ontology search may provide results for animals together with their common and scientific names, as well as information on their eating and breeding habits, habitat, mode of movement, and body cover. Then, the suggested technique may be used to match different kinds of bio data, such as when using a query for two or three complicated searches.

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