Development of a Semantic Web-Based Ontology for Tropical Diseases in Telemedicine Systems

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Abstract—***Acquiring a comprehensive understanding of Tropical diseases such as COVID-19, Ebola, and Malaria can prove challenging as diagnosis often occurs in isolation. The plethora of symptoms and indicators associated with these diseases makes it hard for healthcare professionals to retain all pertinent information. This often results in an erroneous diagnosis, which poses a significant threat to the patient's well-being. To overcome this, it is necessary to conduct investigations on these diseases by studying different ways to treat diseases such as COVID-19, Ebola, and Malaria and creating a special kind of organization of information, called an ontology, useful in Telemedicine and E-health, and ensuring the ontology is current and has all the necessary information, which improves the accuracy and precision of the information it contains. This project utilizes the Noy and McGuiness methodology, which involves obtaining accurate information from reliable sources about Malaria, Ebola, and COVID-19, including symptoms, prevention, and treatment options. An ontology model was developed for these diseases, and a website has also been created to provide an accessible, user-friendly way to access the knowledge gained about them***.

Keywords—***COVID-19, Ebola, E-health, Malaria, Ontology, Telemedicine, Tropical diseases***

I. Introduction

Ontologies are becoming a key element in the development of the semantic web. They aim to generalize domain knowledge and provide a shared understanding of a specific domain [1]. They can also include representations of the conceptualizations shared in that domain. Applications that use ontologies do not rely on them, which makes it easier to maintain knowledge and software, and supports semantic interoperability between different applications.

Ontologies are often viewed as a way to conceptualize a particular area of interest and can be used to describe, analyze, and reason about the domain. For any conceptualization of a domain to be effective, it must be expressed using a well-defined language, and there must be sound reasoning techniques that can be applied to it.

Ontologies play a crucial role in managing and representing knowledge in Computer science. They provide a formal way to model and express concepts and connections within a specific domain, such as an industry or field of study [2]. This allows data to be understood and organized more effectively, and enables better communication between different systems and software.

In Telemedicine and E-health, ontologies are important for representing and understanding medical and health-related data [3]. They give a common language and framework for describing medical concepts and interactions such as diseases, symptoms, treatments, and patient information. This improves data sharing and communication among healthcare organizations, systems, and providers, leading to greater accuracy [3].

To develop an ontology for tropical diseases, it is necessary to first create a taxonomy of these diseases. The middle-out approach was used to analyze these diseases to develop a taxonomy. This approach starts by identifying the most important concept, and then proceeds to generalize (super-concepts) and specialize from there [4]. The process includes determining the ontology's goal, identifying domain concepts for diseases, finding related narrative relations, organizing the concepts hierarchically, organizing the narrative relations hierarchically, and finally formally and axiomatically describing the concepts using other concepts and narrative relations. It is possible to further improve each phase through iterations if needed.

To provide a long-term solution to diseases such as Malaria, COVID-19 and Ebola in tropical regions, it is essential to have a continuous and reliable flow of information about the conditions, especially in areas where access to data is limited. Therefore, a semantic ontology model using Protégé-OWL needs to be created to address these infections in tropical regions.

Isolated cases of disease diagnosis can pose challenges when it comes to understanding and treating diseases like COVID-19, Ebola, and Malaria. To gain a more comprehensive understanding of these diseases, it is important to study multiple case studies and treatment regimens. By studying multiple cases, researchers can identify patterns and commonalities that may not be apparent from a single case, such as risk factors, transmission patterns, and treatment effectiveness. This can lead to better-informed public health decisions and improved strategies for controlling the spread of disease.

This paper developed an ontology for COVID-19 and tropical diseases such as Malaria and Ebola, which can help ensure that the ontology is based on the most current and comprehensive understanding of the diseases and improve its accuracy and precision.

II LITERATURE REVIEW

The term "ontology" was first used by T.R. Gruber in 1993 to refer to an "explicit specification of a conception." An ontology is a "formal characterization of a shared conceptualization," according to Borst's 1997 definition. This definition also states that the conceptualization should represent a consensus among multiple participants rather than an individual viewpoint. A formal machine-readable format is used to express the conceptualization. In order for a program to be able to compare abstract data between two knowledge bases on the web, it must be able to find common meanings. This is where ontologies come into play. Ontologies are a collection of data at a common location and are technically defined as a set of concepts that express significant generalizations, similar to object classes and the relationships between them to represent a body of knowledge. To reuse and integrate content on the web, ontologies provide a formal semantics, they also provide a vocabulary with clear definitions for terms that can act as a formal basis for communication between software agents.

Over time, ontologies have developed and now hold enormous promise for representing knowledge in terms of knowledge operations and participatory features. The creation of standard platforms for knowledge exchange and practice has been made possible by flaws in healthcare information and communication technology. Due to the unavailability and inconsistency of generalized understandings of domain information, physicians face significant barriers when operating in extreme circumstances. Because of the enormous volume of information on the Internet (and intranets) and the informal nature of that information, some behavior must be adopted to make use of web search engines more easily. This material needs to be processed in a preface with order, relevancy, and organization. The application of ontologies in particular fields is a step in this direction. Ontologies are being used more frequently to organize the web, and the term "ontology" is growing in acceptance. The Semantic Web, which is regarded as an intelligent and significant network, is the focus of many scientists' research **[5]**.

Concept of Semantic Web

The Semantic Web is an expansion of the World Wide Web (W3C) standards. Making Internet data machine-readable is the aim of the Semantic Web.

Semantic Web

The World Wide Web Consortium (W3C) oversees the Semantic Web, a collaborative effort that promotes standardized data formats for the World Wide Web. By promoting the inclusion of semantic content in web pages, the Semantic Web aims to transform the current web of unstructured documents into a "web of data." It advances the Resource Description Framework (RDF) created by the W3C **[6]**. Data can be exchanged and reused across application, company and community borders thanks to the Semantic Web, claims the W3C. Tim Berners-Lee, the man credited with creating the World Wide Web in 2001 and president of the World Wide Web Consortium ("W3C"), which oversees the development of future Semantic Web standards, is credited with coining the term. The Semantic Web, according to him, is "a web of data that can be analyzed by machines directly and indirectly." The semantic web, according to Tim Burns Lee, is an expansion of the current web in which information is given a clear meaning **[7]**.

Resource Description Framework (RDF)

RDF is a web resource and data interchange description standard that was developed and standardized by the World Wide Web Consortium (W3C) **[8]**.. Initially, RDF was defined using the Extensible Markup Language (XML), but now there are other commonly used syntaxes, such as Terse RDF Triple Language (Turtle), JavaScript Object Notation for Linked Data (JSON-LD), and N-Triples. Information is represented as triples: subject-predicate-object statements in RDF. These statements describe relationships between resources and can be thought of as simple sentences **[8]**. The subject is the resource being described, the predicate is the relationship being asserted, and the object is the value of that relationship.

Ontology

The foundation of the semantic web is becoming increasingly reliant on ontologies. Ontologies aim to provide a generally accepted understanding of a subject and to capture domain knowledge in a generic way. The Web Ontology Language (OWL) forms the basis of the Semantic Web and is the most expressive standard language for modeling ontologies [10]. Ontologies play a crucial role in information presentation by providing a vocabulary with clear term definitions that can serve as a formal foundation for communication between software agents. The integration of ontologies and software agents can significantly enhance the efficiency and effectiveness of information retrieval and presentation, thereby simplifying the process of accessing and comprehending vast amounts of data. Software agents can be designed to retrieve and analyze data according to the ontology, thereby ensuring that the information is structured and presented in a user-friendly manner. In addition, ontologies can be employed to augment the functionality of software agents by establishing a structure for reasoning and decision-making.

OWL LANGUAGE

The Web Ontology Language (OWL) is a W3C-recommended language that provides additional vocabulary and powerful relationships for a particular domain and is widely used to build domain ontologies. It is necessary to move beyond the basic semantics of Extensible Markup Language (XML) Schema and RDF Schema to perform effective automated logic operations on web data. Further, a suggestive logic language that expands the vocabulary of RDF is also required. Ontologies are developed using the W3C-recommended Web Ontology Language (OWL) as shown in Figure 1.

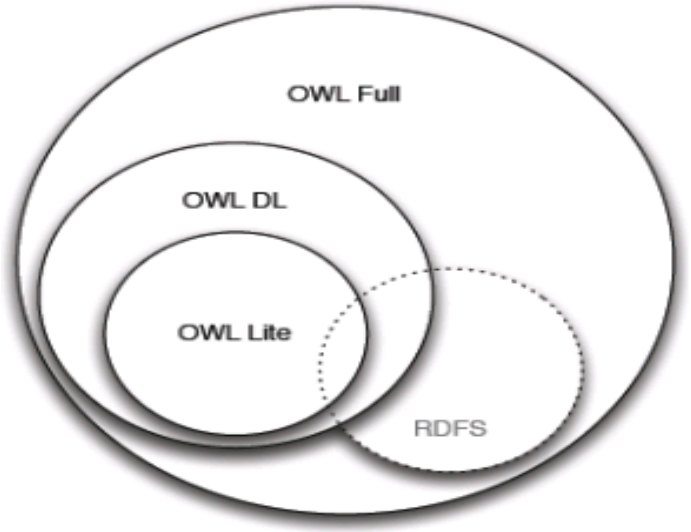

Fig 1: Syntax Classes of OWL (Web Ontology Language) language **[9]**.

ONTOLOGY DEVELOPMENT METHODOLOGY

Methodologies include a list of guiding principles for how the identified ontology design process activities should be properly carried out **[15]**. In addition to methods for developing ontology, ontology representation languages and editors (ontology management tools) also form part of the process of ontology development **[11]**

METHONTOLOGY METHODOLOGY

The tool was developed at Madrid's Artificial Intelligence Lab for building ontologies from scratch or utilizing existing ones from servers. It was based on webODE and ontoEdit, and was initially used for creating chemical ontologies. The process includes specifying the desired end result, gathering knowledge from various sources, linking domain terms and concepts, integrating general classes or properties, using an ontology representation language, evaluating the ontology, and documenting the process **[11]**.

NOY AND MCGUINESS METHODOLOGY

Noy and McGuiness also an iterative method, is based on some fundamental rules. The approach described seven phases for creating ontology. They are as follows:

1. Determine the domain and scope of the ontology.
2. Consider reusing existing ontologies.
3. Enumerate important terms in the ontology.
4. Define the classes and the class hierarchy.
5. Define the properties of the classes.
6. Define the value of the slots.
7. Create instances. The authors consistently used wine ontology to depict the methodology.

USCHOLD AND KING METHODOLOGY

The Uschold and King methodology for ontology is a widely used approach for creating ontologies. This methodology emphasizes the importance of using a formal representation language, and of defining a clear logical structure for the ontology, which makes the ontology more usable for automated reasoning and other tasks.

The four steps outlined in the Uschold and King method for ontology creation are: Defining the goals of the ontology, constructing the ontology, evaluating the ontology and documenting the ontology. The authors also propose three methods for identifying the main concepts in an ontology: a top-down approach in which the most abstract concepts are identified first and then specialized into more specific concepts; a bottom-up approach in which the most specific concepts are identified first and then generalized into more abstract concepts; and a middle-out approach in which the most important concepts are identified first and then generalized and specialized into other concepts.

TROPICAL DISEASES

In recent times, tropical regions have seen a surge in infectious diseases compared to other areas of the world. This can be attributed to various environmental and biological factors that preserve host biodiversity, as well as social factors that ease the management of these diseases. These types of diseases are known as tropical diseases and the study of them has become an important branch of medicine known as tropical medicine. Some tropical diseases, such as malaria, Chagas disease, and sleeping sickness, are caused by protozoan parasites, while others, such as schistosomiasis and onchocerciasis, are caused by worm infections.

A NEED FOR SEMANTIC WEB ONTOLOGY

The concept of ontology, foundational to the Semantic Web, has evolved significantly since Gruber's 1993 definition as an "explicit specification of a conceptualization". Recent literature emphasizes dynamic, consensus-driven ontologies that adapt to concept drift in domains like biomedicine and climate science. This shift reflects the growing recognition that ontologies must be living artifacts, continuously updated through community curation pipelines and automated reasoning. For instance, [16] demonstrate how adaptive ontologies ingesting real-time electronic health record streams improve axiom validity in extreme settings. Simultaneously, the Solid Protocol and Decentralized Identifiers are advancing Berners-Lee's vision of a decentralized, machine-analyzable web, where ontologies serve as the semantic glue enabling cross-application data integration. The knowledge representation stack – XML, RDF, RDFS, OWL – is now treated as a layered reasoning architecture rather than isolated formats. JSON-LD 1.1 has

emerged as the de facto serialization for Web APIs, while OWL 2 profiles (QL, RL, DL) are used to balance expressivity and scalability. [17] show that modern reasoners can classify ontologies with over 1 million axioms within minutes, but OWL-Full remains impractical for production due to undecidability. This technical evolution underscores the document's distinction between OWL sublanguages: OWL-Lite for lightweight vocabularies, OWL-DL for clinical/medical ontologies requiring consistency checking, and OWL-Full for prototyping. The choice of profile now depends on domain-specific trade-offs between reasoning complexity and inference completeness. Ontology development methodologies have converged toward agile, reuse-first, FAIR-aligned processes. The NeOn Methodology v2 extends Noy and McGuiness' iterative approach with explicit support for ontology network design and pattern reuse from repositories like BioPortal. Meanwhile, Large Language Models are being integrated into ontology workflows [18] demonstrate LLMs extracting terms from text corpora to semi-automate METHONTOLOGY's knowledge acquisition phase. However, human expert validation remains critical: [19] report that while LLMs can generate OWL axioms, logical consistency still requires human oversight. This hybrid approach reflects the field's recognition that ontology engineering is increasingly a collaboration between human domain experts and AI assistants. In healthcare and tropical disease research, ontologies are central to infectious disease surveillance and outbreak prediction. The Infectious Disease Ontology and Neglected Tropical Disease Ontology were extended in 2023–2024 to incorporate genomic, vector, and climate variables. [20] use knowledge graph embeddings over these ontologies to link parasite life-cycles to climate models, predicting outbreak risk with higher spatial resolution. [21] further show that ontology-driven software agents can reason over these models using SWRL rules in Protégé to triage cases in low-resource settings. These applications address the document's concern about web data volume and informality by providing structured, quarriable knowledge that supports decision-making.

III. METHODOLOGY

Methodology Development

In this project, the domains to be considered are **COVID-19**, **Ebola** and **Malaria**. Why ontology? Ontology makes machines understands semantic of languages that humans use by producing the abstract modeled representation of already defined finite sets of terms and concepts involved in intelligent information integration and knowledge management. The following procedures shall be followed in the execution of this work:

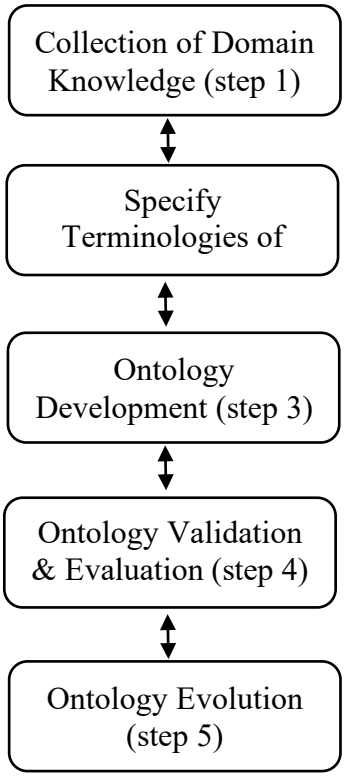

Fig. 2: Ontology Development Methodology **[13]**.

Steps 1 to 3 that is, collection of domain information, specification of ontology's terminologies satisfy the pre-development recommendation. Ontology development and ontology validation or evaluation activities satisfy the development stage. And the ontology evolution satisfies the post-development recommendation

Information and Data Collection of Domain

There is need to capture necessary information pertaining to a disease and its structure, in other to do this related works would be reviewed and anything such as document, websites, articles where more information about the selected disease will be reviewed as well to as to retrieve the expected information.

Construction of Domain Ontology

The OBO Foundry has developed a series of principles for ontology construction which propose principles for modularity, orthogonality and reusability. Although there are several well established and defined methodologies to develop an ontology. **(Jindong, et al., 2021)** Noy and McGuinness methodology [19] used Protégé 5.5 and the necessary process includes the following:

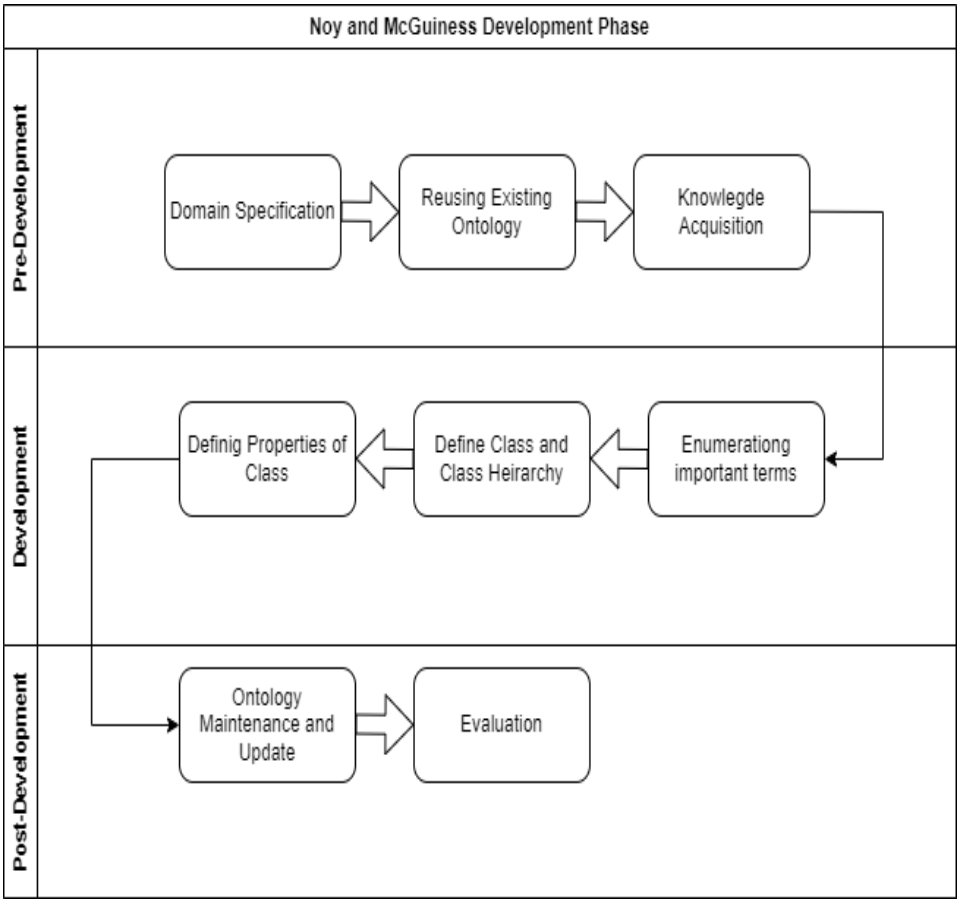

Fig. 3: Noy and McGuiness Ontology Development Phase **[14]**.

a) Determining the domain and scope of the ontology

This is the first stage of any ontology model development, identifying the domain of the ontology model to be developed is very necessary. In this study, the domains are COVID-19, Malaria and Ebola.

b) Considering reusing existing ontologies

For our particular domain and purpose, it is nearly always worthwhile to take into account what others have done and see if we can improve and enhance current sources.

This method includes looking up related studies; if any are discovered, the researcher can expand on the current model. By doing so, the job will move more quickly and the target outcome will be reached on schedule. To accomplish this, several works were examined to shed additional light on my work, and various details pertaining to the chosen ailment were also understudied.

c) Enumerating important terms in the ontology

This process involves identifying the key entities in the domain, such as the symptoms, treatment, preventions and causes.

d) Defining the classes and the class hierarchy

The classes of the diseases are the key entity and its relation and the relation between classes is done in this stage.

The class and class hierarchy would be defined using a top-down development method that begins with the description of the most generic concepts in the domain and progresses to the specialization of the concepts.

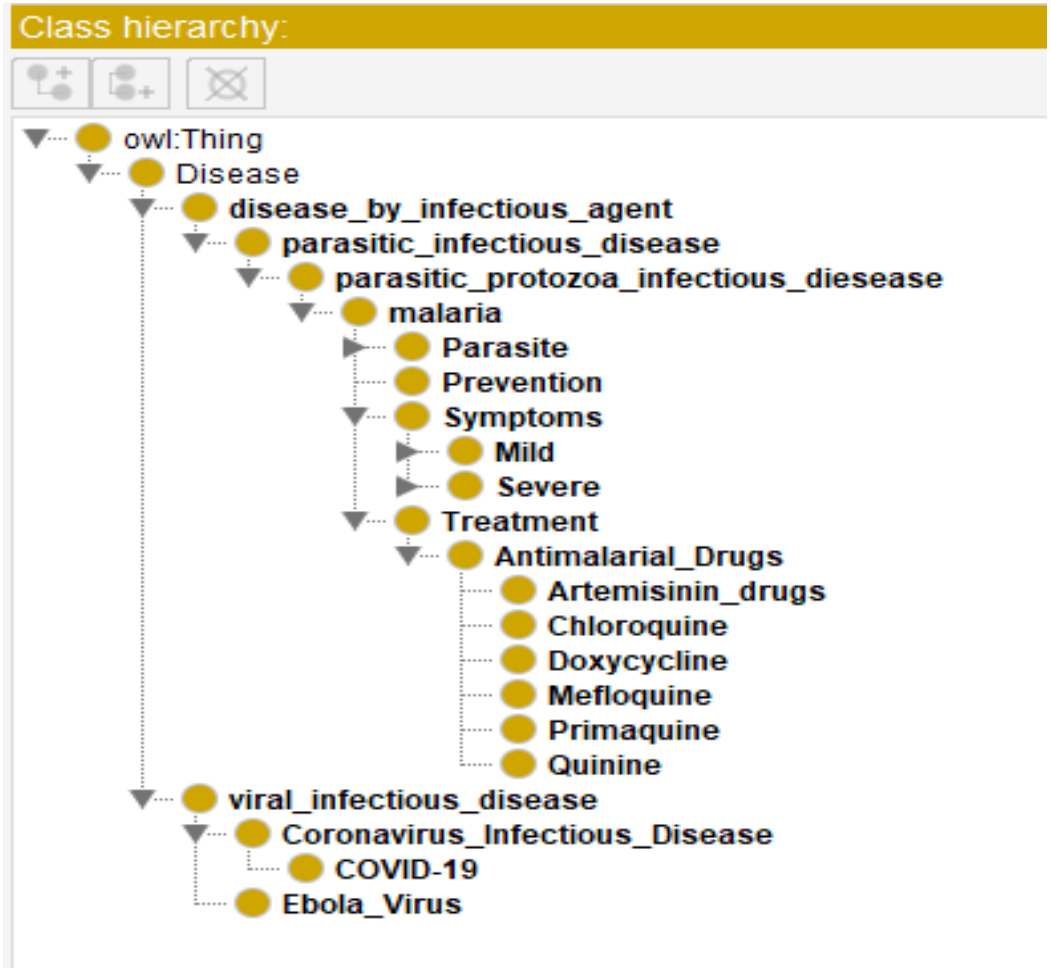

Fig. 4. Protégé-OWL interface showing the classes and subclasses for Disease

e) Defining the properties of classes

Defining the properties of a class involves designing the relationship between classes. Object, Data and Instances are the main properties assigned to classes; this will help describe the various attributes about a class.

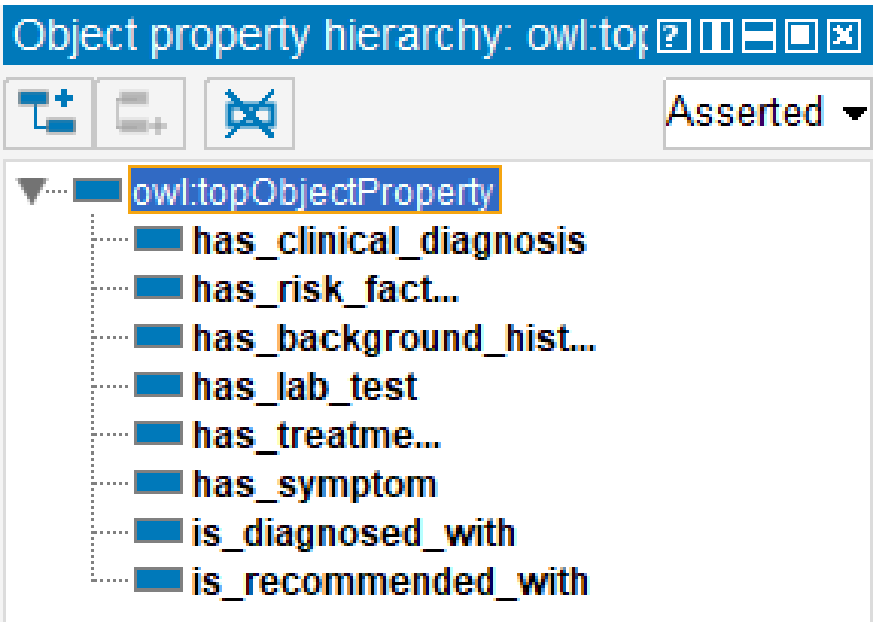

Fig. 5: Object Properties

f) Define facet of the classes

Here, the datatype that can be captured is been defined such as the allowed values, the number value cardinality. There are different types of data that can be captured in ontology, like strings, literals, decimal, integer, float and double.

g) Creating instances

This is the final phase which can be carried out by selecting the class, creating the instances of that class and filling the attribute values.

SYSTEM DESIGN

The system was designed so that the information search results is made available on the website in a comprehensive style. Through the usage of a backend server that enables integration, the design also ensures availability across several platforms. The client website acts as the user's query interface. The user submits a request through this interface to the backend service, which then queries the ontology repository to find the desired result and returns a suitable response to the client. Hypertext Markup Language (HTML), Cascading Style Sheets (CSS), and JavaScript are the suggested building blocks for the system.

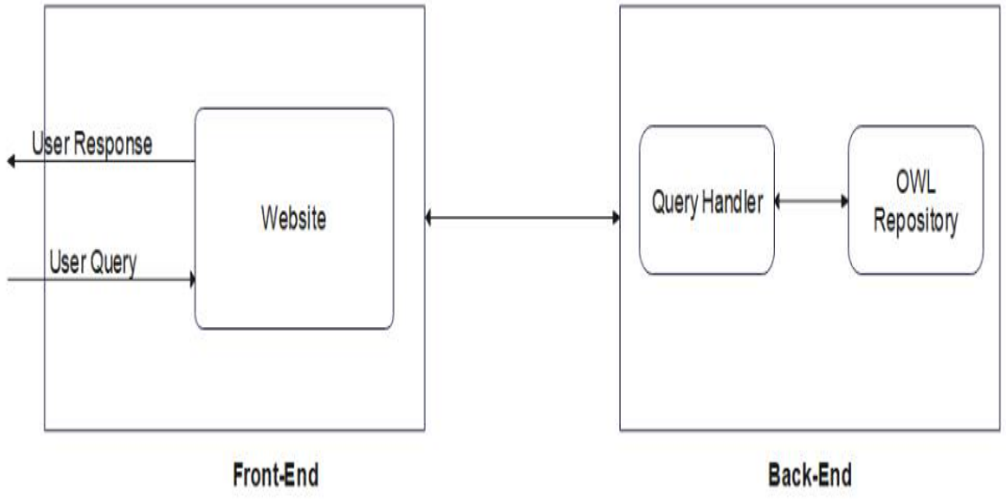

Fig. 6: Proposed System Design

IV. RESULTS AND DISCUSSION

DEFINING CLASSES HIERARCHY

This subsequent step involved acquiring resources from credible sources such as the World Health Organization (WHO), Centers for Disease Control and Prevention (CDC), National Institutes of Health (NIH), Public Health Agency of Canada (PHAC), and other reputable organizations. These resources were in the form of published materials, datasets, and other relevant materials that contain valuable information on malaria, Ebola, and COVID-19. The information gathered from these sources aided in identifying relevant concepts, relationships, and properties to incorporate into the disease ontology. With the aid of the acquired resources, we established the classes and relationships between them. For instance, the "Malaria" class was defined as a subclass of "Parasitic Protozoa Infectious Disease" class, based on the gathered resources. Additionally, it is essential to define the relationships between the classes, such as the causative agent of malaria being the Plasmodium parasite. This process is similarly carried out for other diseases like Ebola and COVID-19, where classes and relationships are established according to the resources available.

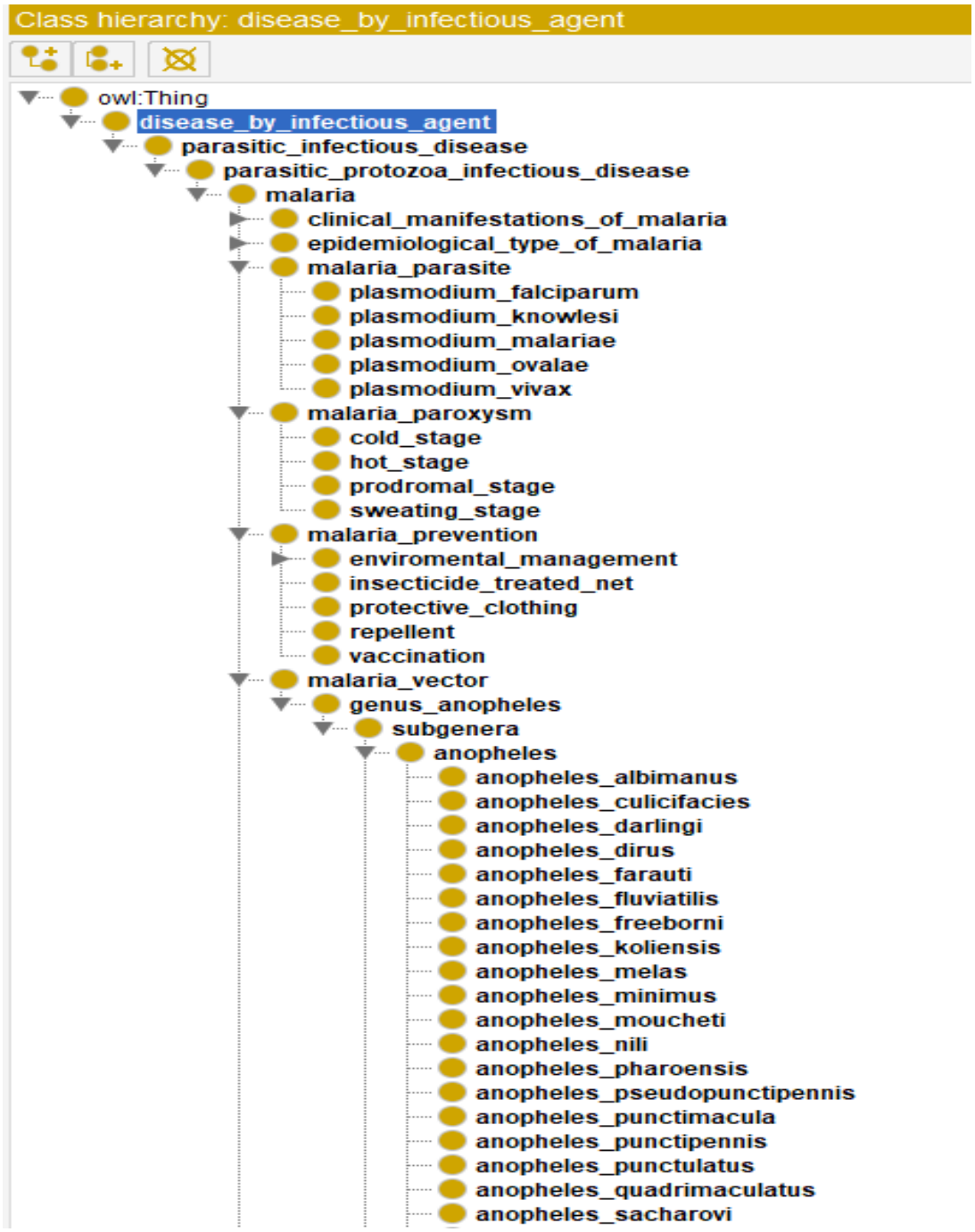

Fig. 7: Screenshot of the class hierarchy for Malaria disease

PROPERTIES AND ATTRIBUTES

Following the definition of classes and relationships, we added object properties and attributes that comprehensively describe the classes. In ontology, properties are characterized as binary links that link a given domain to a corresponding range. This specific relationship is regarded as a subclass of "topObjectProperty", which acts as the point of origin within the Protégé-OWL Object Property. "AgentIn", "bearerOf", "happensDuring", "hasPart", "hasVector", and "participatesIn" are only a few examples of the object properties that involved the specification of a domain and range of the malaria Ontology.

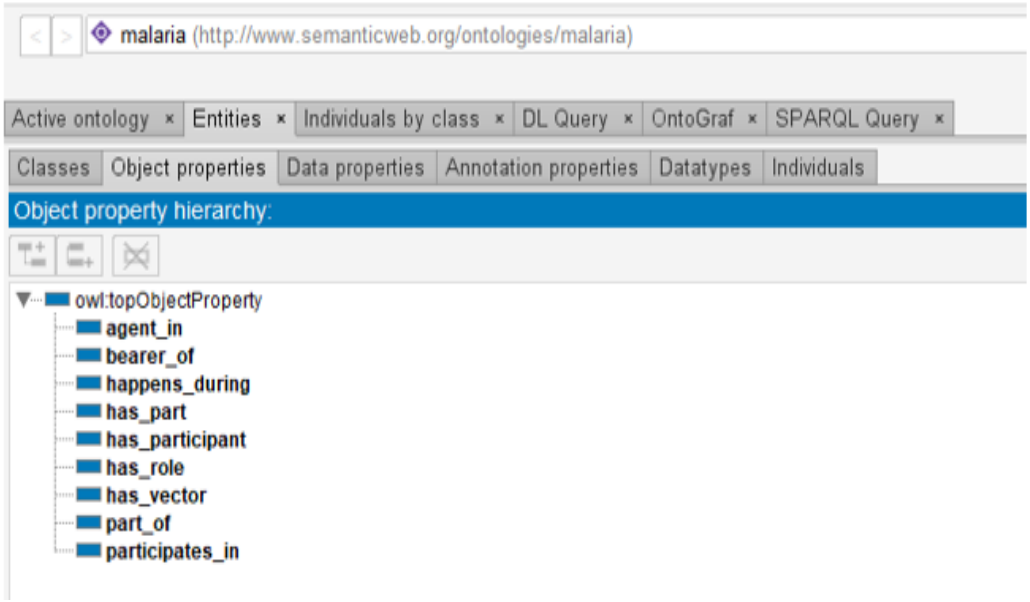

Fig. 8: Screenshot of the object properties for Malaria disease

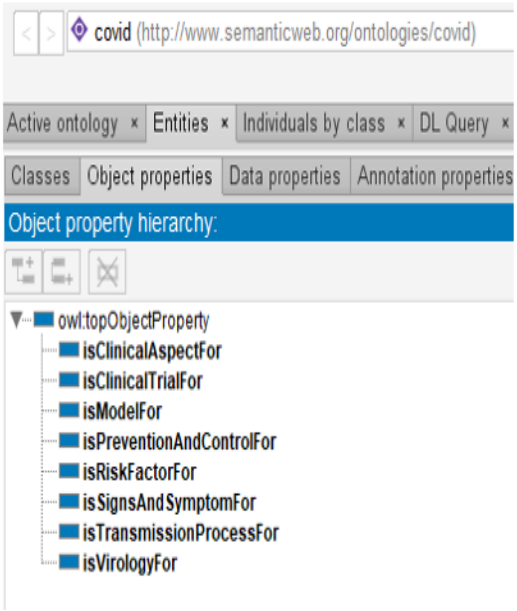

Fig. 9: Screenshot of the object properties for COVID-19 disease

DEPLOYMENT OF ARCHITECTURE IMPLEMENTATION USING SHOWVOC

The first step in deploying the ShowVoc application is to clone the code from the open-source Bitbucket REPL. After cloning the code, the ShowVoc REPL Bitbucket code was edited to have our own representation. A custom distribution package was then created out of the public REPL, which was Dockerized. It was ensured that the Docker points towards the custom distribution. Once the Docker file was created, the next step was to purchase an AWS EC2 server. After purchasing the server, the Docker file was uploaded to the EC2 instance and the Docker image was also built on the EC2 instance. The Docker image was then used to start a container. To expose the necessary port to make the application accessible to the public, we open another port, which is port 1968. To make the application accessible, we needed to get a domain name. A domain name was purchased and connected to the server. This allows the public to access the application using the domain name. Finally, we uploaded the ontologies files developed using Protégé Owl software to ensure that the application is fully functional.

In summary, deploying an application may appear challenging initially, but by adhering to the aforementioned procedure, it is feasible to achieve. This procedure encompasses a series of steps, including cloning the code, generating a personalized distribution package, dockerizing it, acquiring a server, uploading the Docker file, constructing the Docker image, revealing the essential port, acquiring a domain name, and uploading the ontologies files. By strictly adhering to these steps, it is possible to deploy your application and ensure it is available to the public.

IMPLEMENTATION INTERFACE

The "dataset" button leads the user to a list of available ontology files, which may be useful for browsing and searching for specific ontologies. This list could be organized

by various criteria, such as subject area, creator, or date of creation. By clicking on a particular ontology file, the user could access more detailed information about its contents, such as classes, properties, and relationships. The "contribute" button allows users to submit their own ontology files to the platform. This could be done by filling out a form with information about the ontology file, such as its title, author, and subject area, as well as uploading the file itself. Once the file is submitted, it could be reviewed by an administrator or community member to ensure that it meets certain quality criteria, such as adherence to ontology design principles or compatibility with existing ontologies. Overall, this web interface could be a valuable resource for researchers, developers, and other users who work with ontologies and need a convenient and centralized way to discover, share, and contribute to them

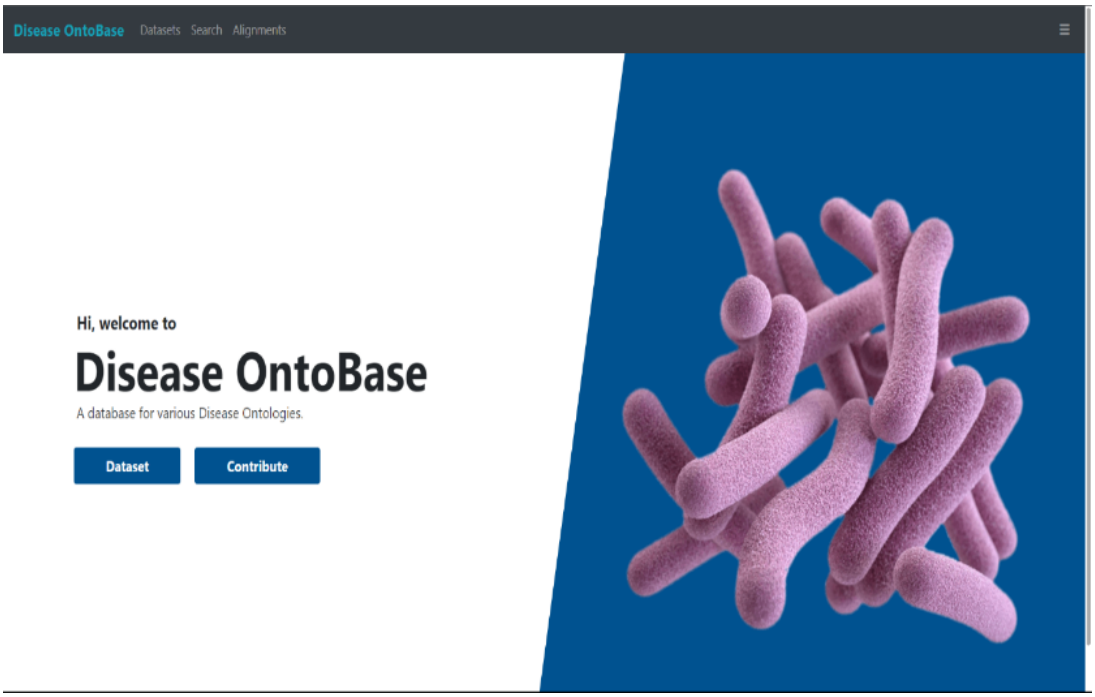

Fig. 10: Screenshot of the Application Interface

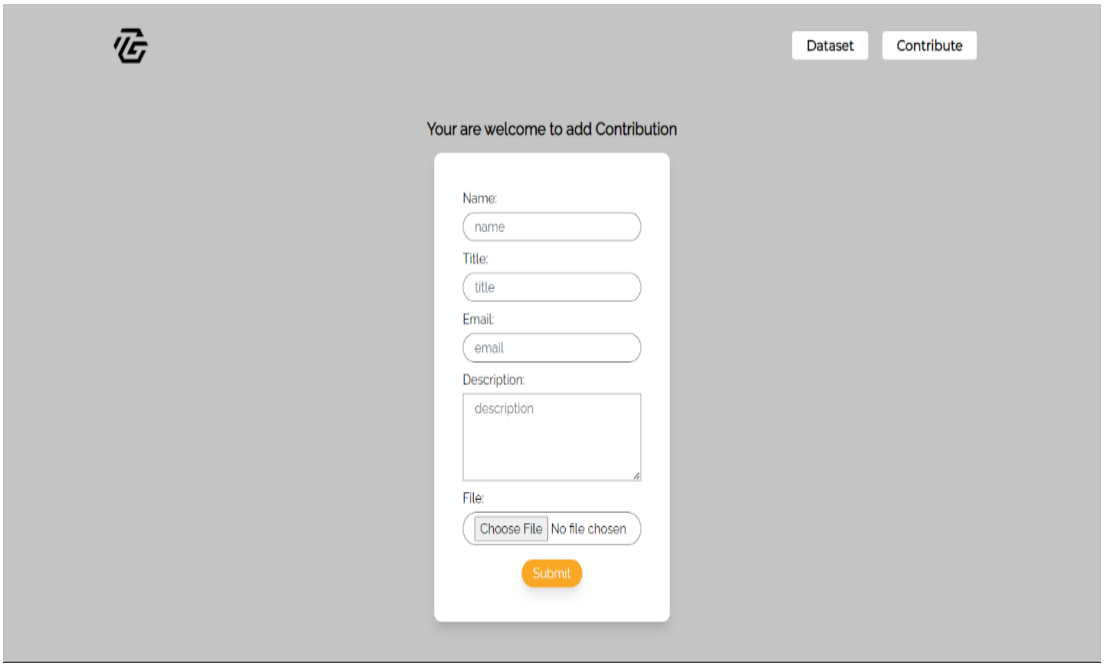

Fig. 11: Screenshot of the Contribution Interface

DATASETS

The Datasets page of ShowVoc provides a comprehensive catalog of all publicly available datasets stored on the platform. On the left-hand side of the page, users can filter the datasets based on their types (KOS, ontologies, or lexicons) and choose to either display or hide closed datasets. It's important to note that closed datasets, if any exist, are not viewable on the user interface.

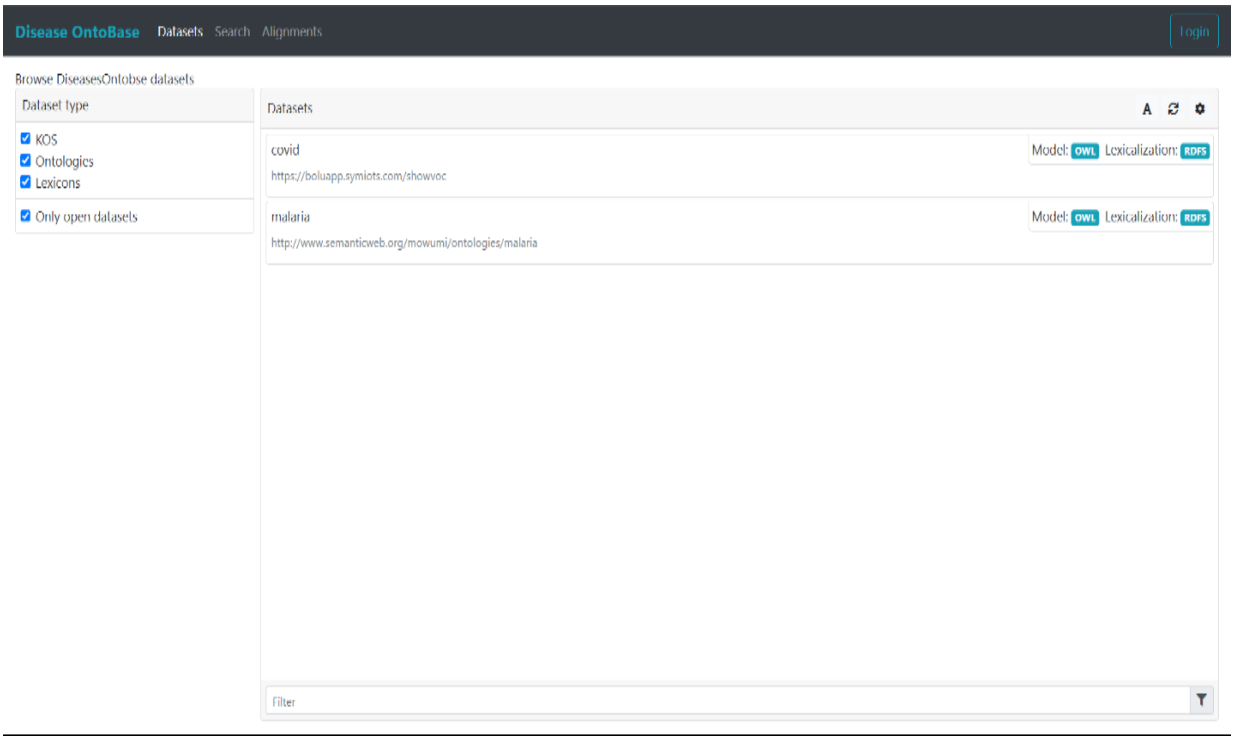

Fig. 11: Screenshot of the Datasets Interface

In the dataset list, each dataset's name is displayed along with the base URI, and an optional description, if available. Users can click on the dataset name to access the Data page, provided the dataset is open. The top right corner of the dataset's information card indicates the lexicalization and data models utilized by the dataset.

ONTOLOGY VIEW

ShowVoc incorporates a user-friendly view that simplifies the exploration of RDFS or OWL ontologies. The Class panel is segmented into two vertical sections. The top section exhibits the class tree, whereas the lower section exhibits any instances that pertain to the selected class, if available.

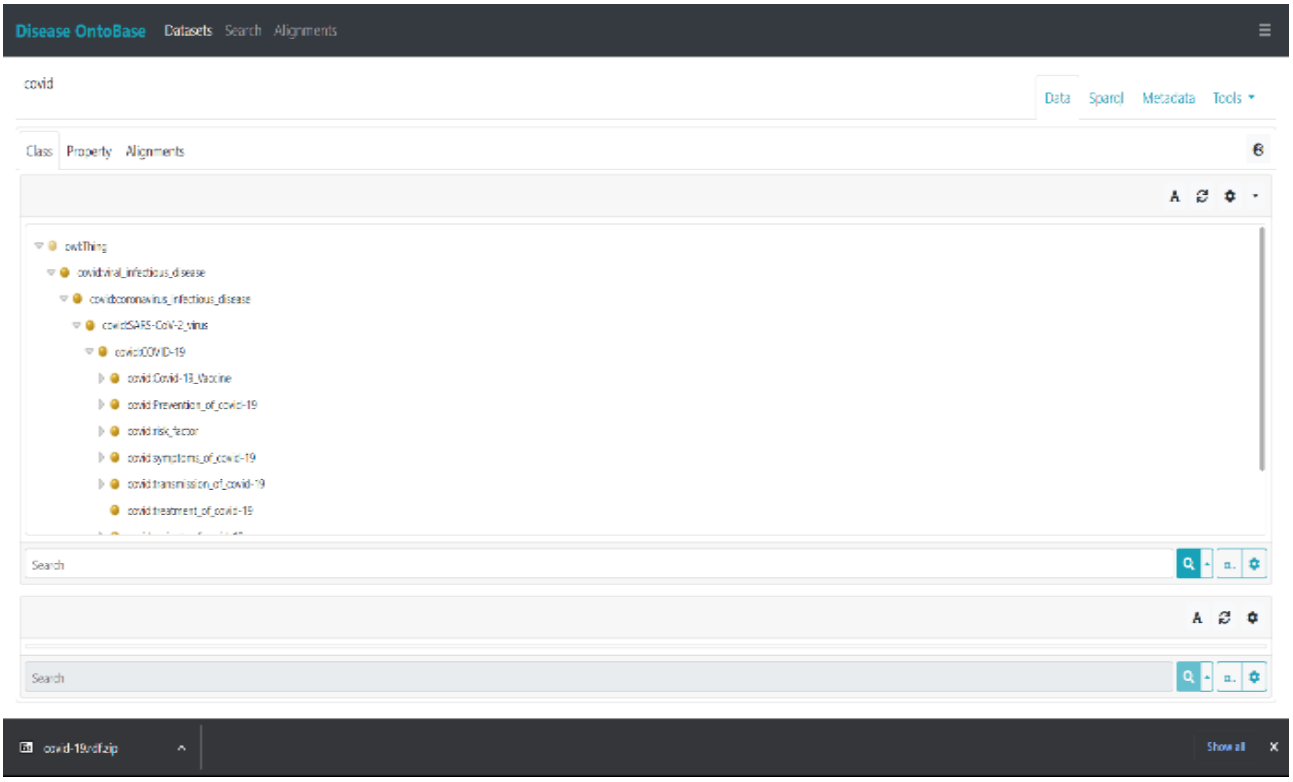

Fig. 12: Screenshot of class hierarchy Ontology View

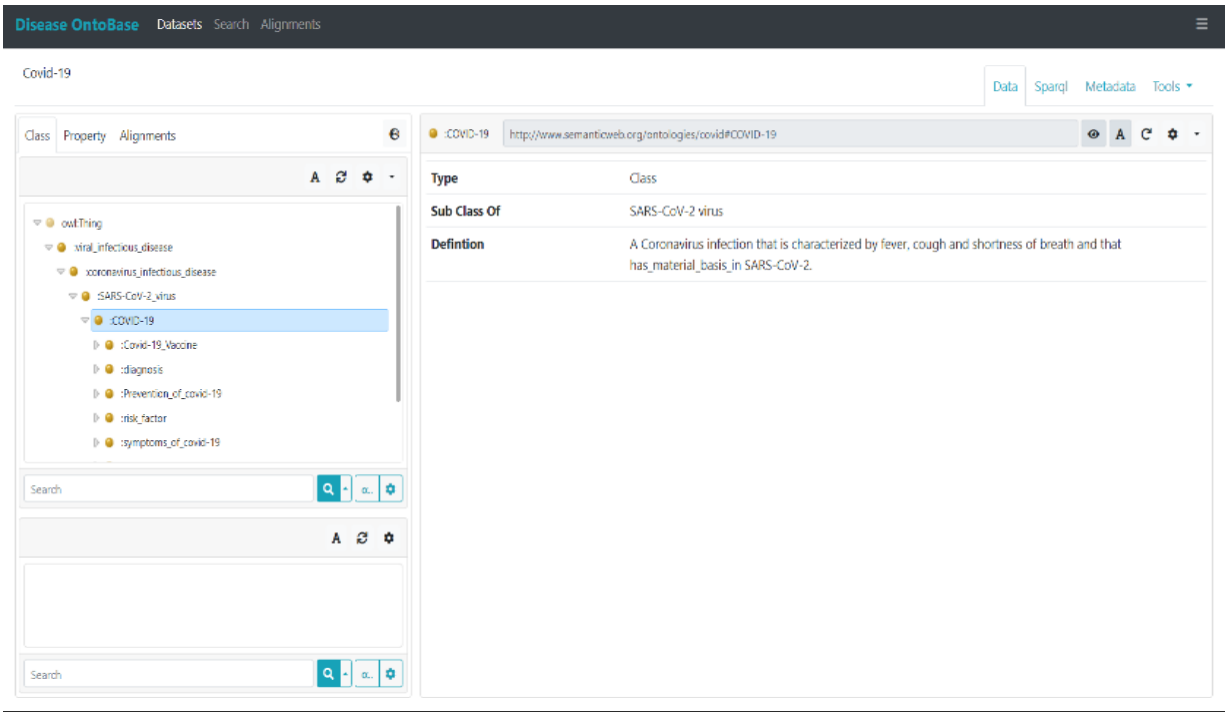

Fig. 13: Screenshot of class hierarchy data View

GRAPH VIEW

ShowVoc provides an alternative approach for data analysis through the Graph View. This function facilitates interactive data visualization via a force-directed graph that employs the d3.js library. Users can personalize their visualization and examine nodes by selecting elements on the graph. Within the Graph View, nodes signify resources, while edges represent properties. Ultimately, each connection between nodes and edges conveys a subject-predicate-object statement.



Fig. 14: Screenshot of model-oriented Graph View

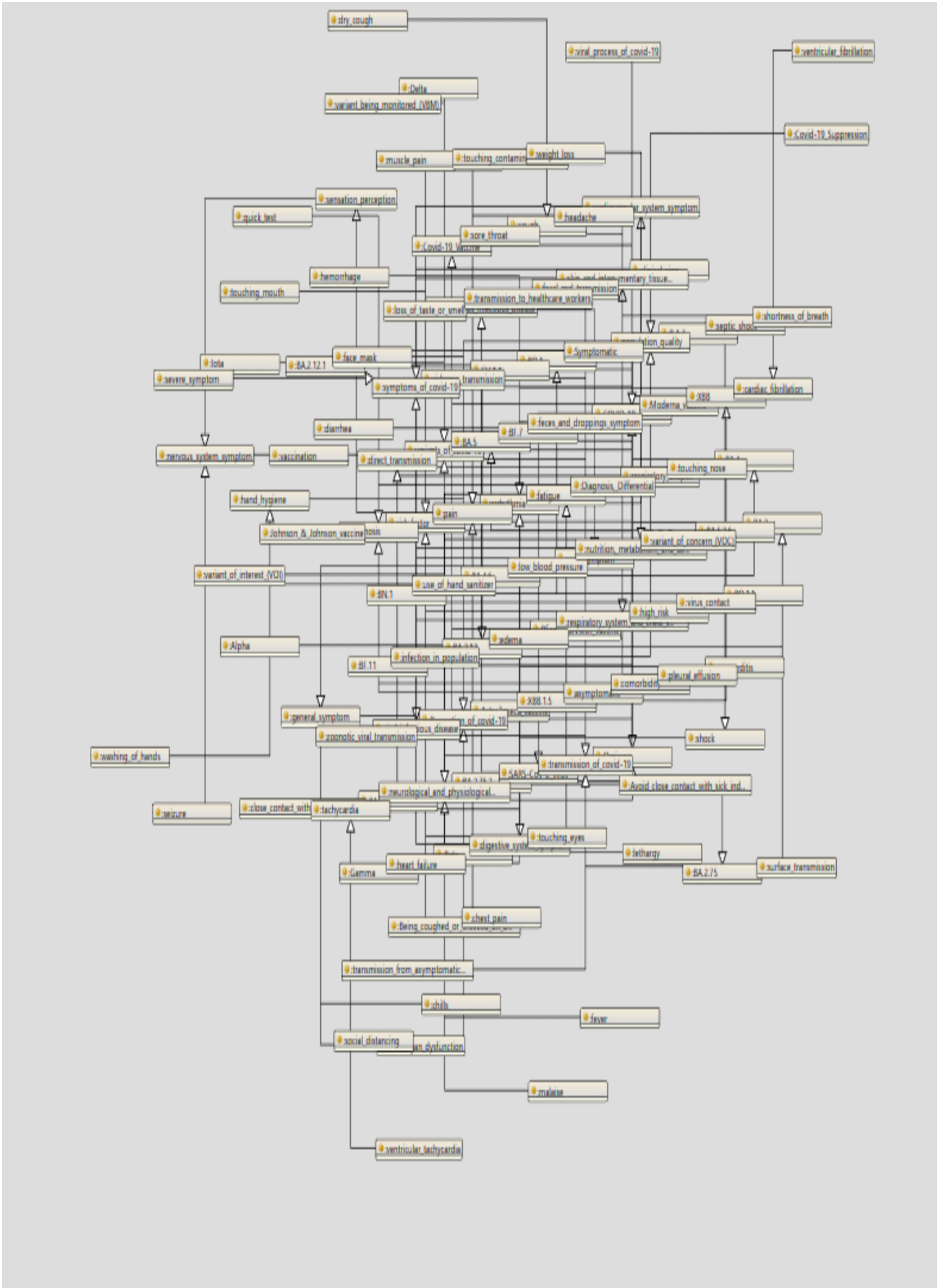

Fig. 15: Screenshot of class-oriented Graph View

METADATA

The Metadata page of ShowVoc displays all metadata linked to a dataset project, which may have been added manually or automatically. This page comprises several tables that outline distinct metadata of the datasets. The Facets panel, situated below the tables, allows authorized users to view and modify the dataset facets, such as Category and Organization. Additionally, customized facets can be presented if properly configured using the Dataset manager. Users can also download specific distributions related to the current dataset in a zipped format.

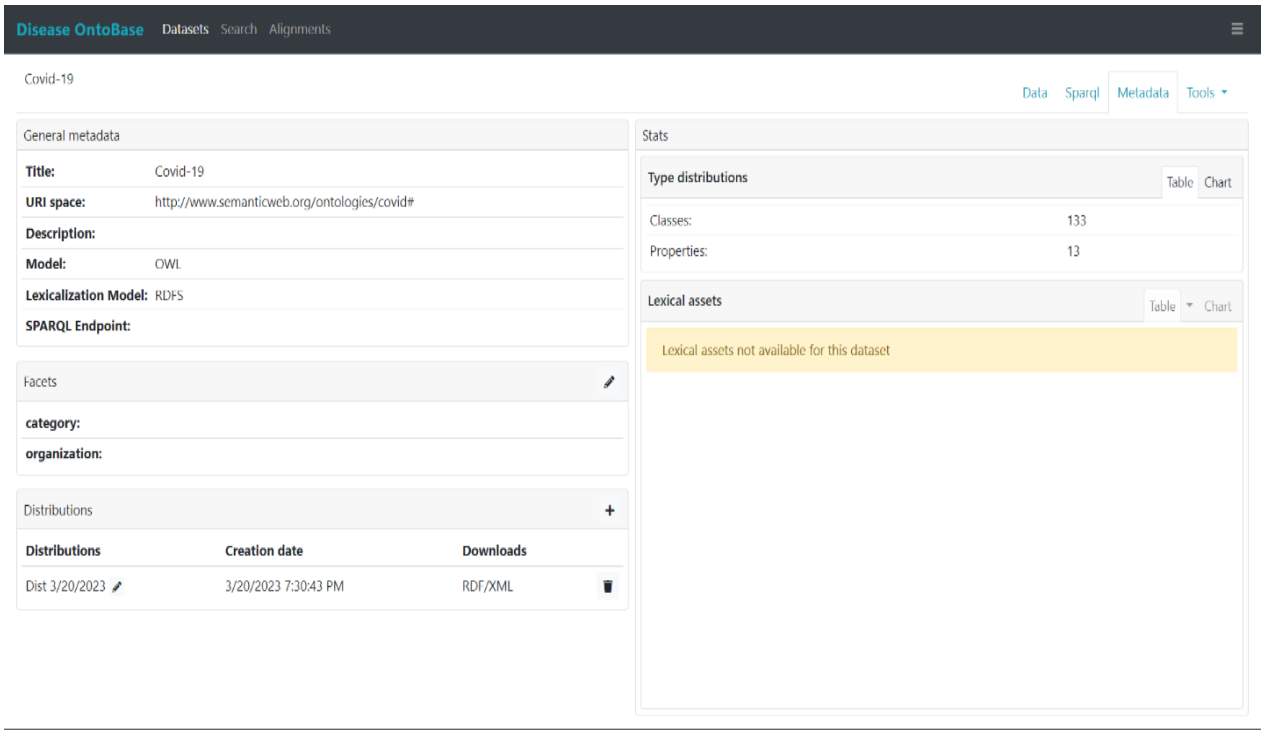

Fig. 16: Screenshot of metadata distribution table view

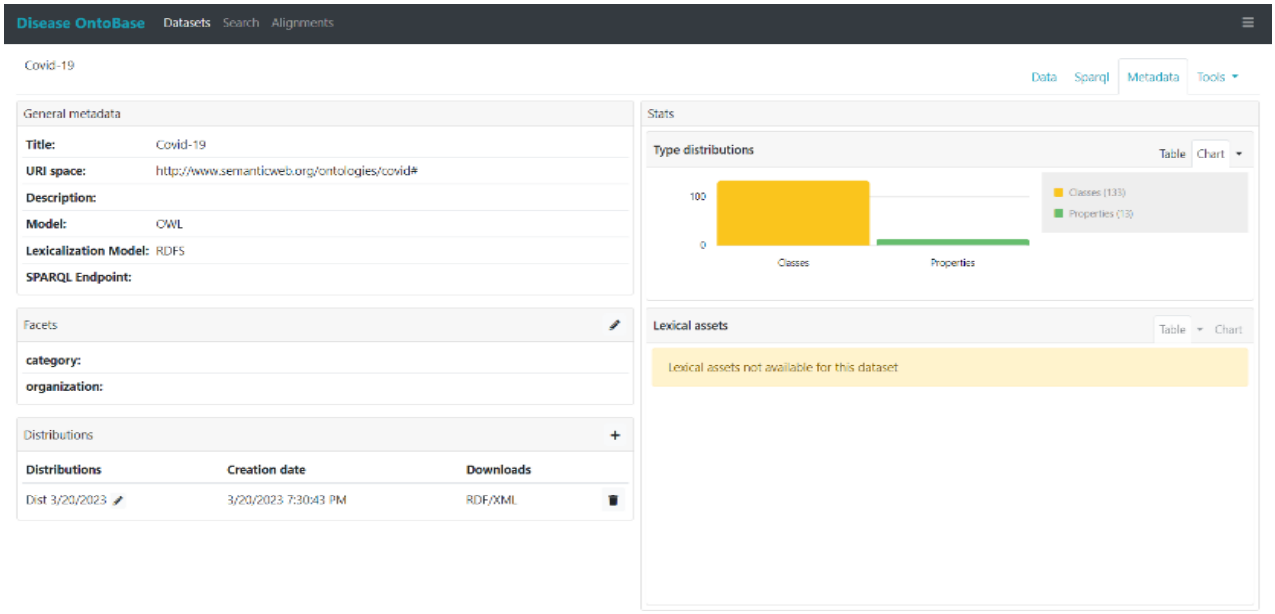

FiG. 17: Screenshot of metadata distribution chart view

V. CONCLUSION

The ontology developed in this research paper is a comprehensive resource that includes information on symptoms, risk factors, and treatment options for each disease. By using this ontology, medical professionals, researchers, and other stakeholders can communicate more effectively and accurately about these diseases, ultimately leading to improved diagnosis, treatment, and prevention. The findings of this research demonstrate the importance of a

standardized vocabulary for telemedicine and e-health. The ontology developed in this paper highlights the similarities and differences in symptoms and risk factors, and can facilitate communication among medical professionals, researchers, and patients in telemedicine settings, enabling more efficient and effective diagnosis, treatment, and prevention of these diseases. Additionally, the ontology can be integrated into e-health systems to help identify patterns and trends in the spread of these diseases, informing prevention and control strategies. By providing a standardized vocabulary for these diseases, the ontology can also facilitate communication among stakeholders, contributing to the development of more effective treatments and prevention strategies. Despite the success of this project, there are some limitations to the ontology developed. For instance, the ontology is not exhaustive, and there may be other important aspects of these diseases that it does not include. Furthermore, the ontology is based on current knowledge of these diseases, and as new research emerges, the ontology will need to be updated to reflect these developments. To address these limitations, future research could focus on expanding the ontology to include other related diseases or on incorporating additional data sources, ensuring that it remains a valuable resource for the telemedicine and e-health fields. Future research in this area could also focus on integrating the ontology into clinical decision support systems. The ontology could be used to develop diagnostic tools, predictive models, or decision-support algorithms to aid in the diagnosis and treatment of these diseases. Additionally, the ontology could also be integrated into telemedicine and e-health platforms, enabling more efficient and effective patient care. Furthermore, ongoing research and updates to the ontology can ensure that it remains a valuable resource for the telemedicine and e-health fields, contributing to better patient outcomes, the ontology could be used to develop surveillance systems that can detect and track disease outbreaks, enabling more effective response and control measures. In conclusion, the development of a web-based ontology of COVID-19, Malaria, and Ebola diseases using Protégé OWL software is a significant contribution to the field of medical informatics. The ontology developed in this project provides a standardized vocabulary for these diseases, facilitating communication among stakeholders and contributing to the development of more effective treatments and prevention strategies. While there are some limitations to the ontology developed, future research can address them and expand its potential applications, ultimately improving patient care and outcomes.

VI. REFERENCES

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