A System for Identifying Entomopathogenic Nematodes

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Abstract

High agricultural production is essential for food security. Hence, it is important to increase crop yields while minimizing losses. Insects cause considerable economic losses. Entomopathogenic Nematodes (EPNs) are alternatives to chemical pesticides for controlling insects. For researchers, determining the type of EPNs is not an easy task. Thus, a tool for identifying EPNs species is needed. In this paper, we introduce a method for developing a system to identify EPNs species according to their morphometric traits. We used Web Ontology Language (OWL) to build the ontology of EPNs species and represent their semantic information. Ontology helps in data representation, exchange, and interoperability. The proposed system was implemented as a mobile application that extracts and retrieves EPNs data from ontology. It displays the details of valid Heterorhabditis and Steinernema species. Also, it enables us to find species that are related to the given infective juveniles (IJs) features. We used techniques of similarity search such as cosine similarity and Euclidean distance to compare different EPNs species and identify similar species based on appearance features. The results indicate that the system can recognize the known EPNs species and it helps to identify similar species.

Key Words: Ontology, knowledge representation, entomopathogenic nematodes (EPNs), computer applications.

1 Introduction

Nematodes are one of the most diverse and numerous organisms that live in aquatic and terrestrial environments [5, 15]. Nematodes are the most plentiful animals on the planet, and over 25,000 species have been identified [8]. They are divided into two types; the first is phytoparasitic nematodes (or phytonematodes) which are severely harming crops and incurring massive economic losses globally [1]. The second type is Entomopathogenic Nematodes (EPNs), which are parasitic nematodes that can destroy harmful insects. They are used as an alternative to chemical pesticides. Both genera

of EPNs, either Heterorhabditis or Steinernema, are regarded as superior biocontrol agents against a variety of insect pests globally. Hence, they contribute to a clean environment [4, 14]. EPNs are incredibly small, with body widths measured in microns. They have developed the ability to live in different habitats and coexist with various creatures in a symbiotic way. Their life cycle includes the egg phase, four larval phases, and the adult phase. The third larval phase called infective juvenile (IJ) is infectious. In actuality, IJ is only a free-living phase; all subsequent developmental phases are only found inside infected hosts. EPNs have a life cycle that spans between 5 and 10 days, according to the temperature, the existence of a bacterial symbiont, and their ability to lower the resistance of their insect host. EPNs are widely dispersed, however, the species differ according to environments and geographic locations [11, 14].

In order to make it possible for nematologists to evaluate and analyze the nematode data, numerous efforts have been made to manage it. For example, an association of scientists in the domains of biology and computer called Wormbase [10] developed an ontology for the Caenorhabditis elegans nematode in order to meet information accessibility requirements. The constructed ontology has a great focus on cells and anatomy and seeks to provide data that can handle sophisticated retrieval system queries. Nemys [12] is another web-based system for databases on nematodes. It avails information about the taxonomies of nematodes such as classification, parent, child, environments, and taxonomic citation.

Researchers also try to use machine learning techniques to automatically identify different nematodes based on microscopic images. For nematodes that parasitize plants, in [17] they developed an image dataset. They present a deep learning model for identifying plant-parasitic nematodes and confirm that machine learning can assist in the identification of pests in Indonesian soil. Further, in [1] (Andre da Silva Abade et al) applied a convolutional neural network(CNN) to identify phytonematodes in soybean crops in Brazil. They proposed a publicly available, open-source dataset called NemaDataset that contains the five major phytonematode species that harm soybean crops. Furthermore, in [18] they investigated the potential of creating a CNN appropriate for categorizing microscope images of three species EPNs (H. bacteriophora, S. carpocapsae, and S. feltiae). For IJs, they reached an average validation accuracy of 88.28%.

The cooperation between nematologists and computer scientists helps in advancing the field of nematodes. Ontology is a way to organize and standardize the used concepts in a specific domain. With the use of ontologies, people and various application systems can communicate about a given topic in a common and shared way [6]. Ontologies provide a generally accepted understanding of a subject and capture domain knowledge generically. An ontology can explain the types of entities that exist in a domain, how they might be related to one another, and what they imply. Ontologies are employed to support communication and understanding among the various parties. By addressing the issue of semantic heterogeneity, ontologies enable semantic interoperability between various online applications and services. With the help of ontologies, the web can become a self-navigating and self-understood environment where search engines return results tailored to the user's needs [7].

Empowering nematologists with a facility to identify the morphometric characteristic of EPNs advances the field of nematology. So we present a tool to identify EPNs species. First, we built an ontology for the species of EPNs Steinernema and Heterorhabditis. This ontology facilitates and accelerates EPNs research by integrating EPNs data. We used the Web Ontology Language (OWL) [2]. OWL is one of the semantic web languages made by The World Wide Web Consortium to represent detailed information about various things, and representing the relation between them. The ontology allows users to easily query these data. Second, we developed

Table 1: Entomopathogenic nematodes species

Heterorhabditis	Steinernema				
H. amazonensi	S. abbasi	S. brazilense	S. huense sp. n	S. ohioense	S. scarabaei
H. atacamensis	S. aciari	S. cameroonense	S. ichnusae	S. oregonense	S. schliemanni
H. bacteriophora	S. affine	S. carpocapsae	S. innovation	S. pakistanense	S. siamkayai
H. baujardi	S. africanum	S. caudatum	S. intermedium	S. papillatum	S. sichuanense
H. beicherriana	S. akhursti	S. caudatum	S. jeffreyense	S. phyllophagae	S. silvaticum
H. brevicaudis	S. anatoliense	S. ceratophorum	S. jollieti	S. poinari	S. surkhetense
H. downesi	S. anomalae	S. changbaiense n. sp.	S. karii	S. populi	S. taiwanensis
H. floridensis	S. apuliae	S. cholashanense	S. khoisanae	S. portoricense	S. tami
H. georgiana	S. arasbaranense	S. citrae	S. khuongi	S. puertoricense	S. texanum
H. hawaiiensis	S. arenarium	S. colombiense	S. kraussei	S. puertoricense	S. thanhi
H. indica	S. ashiuense	S. costaricense	S. kraussei	S. pui	S. thermophilum
H. mexicana	S. asiaticum	S. cubanum	S. kushidai	S. puntauvense	S. tielingense
H. noenieputensis	S. australe	S. cumgarense	S. lamjungense	S. pwaniensis	S. tophus
H. safricana	S. backanense	S. diaprepesi	S. leizhouense	S. ralatorei	S. unicornum
H. taysearae	S. bakwenae	S. eapokense	S. litchii	S. rarum	S. vulcanicum
H. argentinensis	S. balochiense	S. ethiopiense	S. litorale	S. riobrave	S. websteri
H. marelatus	S. bedding	S. everestense	S. loci	S. riojaense	S. weiseri
H. megidis	S. beitlechemi	S. fabii	S. longicaudum	S. ritteri	S. xinbinense
H. zealandica	S. bertusi	S. feltiae	S. minutum	S. robustispiculum	S. xueshanense
	S. bicornutum	S. glaseri	S. monticolum	S. sacchari	S. yirgalemense
	S. biddulphi	S. goweni	S. neocurtillae	S. sandneri	S. scarabaei
	S. bifurcatum	S. guangdongense	S. nepalense	S. sangi	S. schliemanni
	S. boemarei	S. hebeiense	S. nguyeni	S. sasonense	S. siamkayai
	S. borjomiense	S. hermaphroditum	S. nyetense	S. scapterisci	S. sichuanense

a mobile application that reads and queries EPNs ontology and retrieves species details. The app users can get the details of different species and search for specific species based on their morphometric characteristics.

The paper is organized as follows: Section 2 lists the materials and methods. Section 3 presents a validation test for the developed application. Section 4 describes the results and discussion. Finally, Section 5 is the main conclusion.

2 Materials and Methods

2.1 Data Collection

The EPNs data was obtained through conducting a meeting with a domain expert who guided us with a reference book [9]. This book covers the most valid EPNs species till 2016. Hence, we used the most recent research papers to collect EPNs data which are available up to the paper writing date. We collected morphometric data of about 120 species of Steinernema and 19 species of Heterorhabditis. Table 1 shows a list of EPNs species that have been included in the developed EPNs ontology.

2.2 Ontology Building

We used OWL language to build EPNs. Also, we used a web-based version of Protégé [13] to build and edit the ontology. Protégé is available in desktop and web-based versions. We used the web-based version to enable our team to access and edit the ontology. The parent class of the EPNs ontology is Nematode. It has a child which is Entomopathogenic-

nematodes. Steinernema, and Heterorhabditis are represented as subclasses of Entomopathogenic-nematodes.

As shown in Figure 1, S. abbasi and S. affine are subclasses of Steinernema. Subclasses in the ontology represent species. Each class or subclass has properties, these properties (annotation properties) represent morphometric characteristics as shown on the right side of the Figure 1. These properties have values that are used in the class description, for example, a class S. abbasi has L (body length) = 541 μm, W (greatest body width) = 29 μm, EP (distance from anterior end to excretory pore) = 48 μm, NR (distance from anterior end to nerve ring) = 68 μm, ES (esophagus length) = 89 μm.

2.3 Similarity Search

We used a vector space model to represent species in EPNs. We handle each species as a vector and each characteristic as a feature or a dimension of this vector, such as body length, pharynx length, and tail length. So, we can apply distance measures such as Euclidean distance and cosine similarity. First, the Euclidean distance (Ed) between two vectors a={x1, x2, x3, ………., xn} and b={y1,y2,y3,………., yn} is calculated as in Equation (1)

$$\text{Ed}(a, b) = \sqrt[2]{(x_1 - y_1)^2 + (x_2 - y_2)^2 + (x_3 - y_3)^2 + \cdots\cdots + (x_n - y_n)^2}$$
(1)

After calculating the Euclidean distance, we normalize the results using the Min-Max technique in Equation (2) to be in
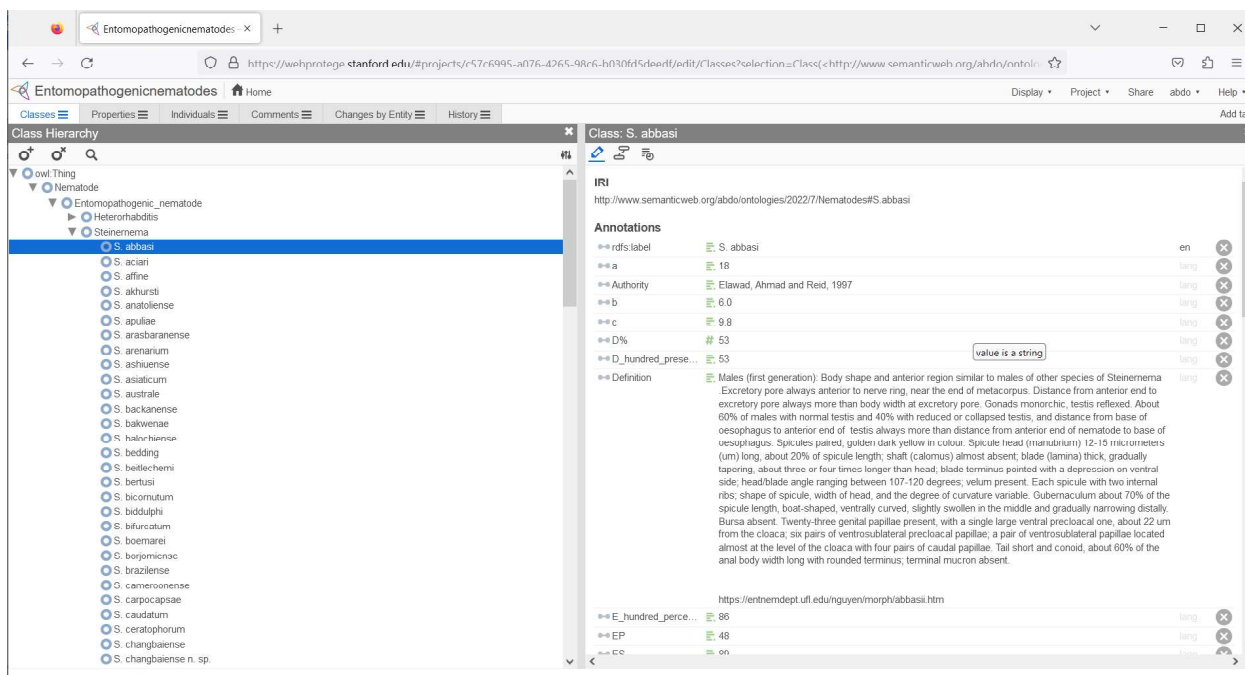

Figure 1: Entomopathogenic nematode ontology

intervals from zero to one [0, 1] typically known as feature scaling [3].

$$Resultscaled = (Result - Resultmin)/(Result_{max} - Result_{min}) \tag{2}$$

In the proposed system, the Min-Max technique is modified by not subtracting the Min-value (Resultmin) from the value (Result).

$$Resultscaled = (Result)/(Result_{max} - Result_{min}) \tag{3}$$

Then we subtracted the result from 1 and multiplied it by 100 to convert the distance to similarity. If we subtracted the minimum result from the result, it would give the first nearest similar species 100 percent, so we removed this step from the Min-Max normalization technique.

Second, the cosine similarity (Cs) between two vectors a and b is calculated as in Equation (4).

$$CS(a, b) = \frac{a.b}{||a||*||b||} \tag{4}$$

The outcome of the cosine similarity falls between (0, 1). Its higher value indicates that the vectors are more similar. Additionally, we multiplied the cosine similarity by 100 to present the results in a way that is easy for system users to understand. The system displays the results in two tables, one using cosine similarity and the other using Euclidean distance.

2.4 Developing a Mobile Application

In this phase, a mobile app was built using ".NET MAUI". It is a development platform introduced by Microsoft. Through .Net MAUI, the developers can develop apps which are compatible with various operating systems, including Android, iOS, Windows, and macOS by writing a single code. First, we downloaded the developed EPNs ontology from the Protégé in RDF/XML format as an OWL file. After that, we wrote a C# programming language code to develop the mobile app. We used XDocument and XPath to parse the OWL file.

We designed a page to display the Heterorhabditis and Steinernema species. It enabled the end user to get details about specific species. Figure 2 displays screenshots of the main page of the developed application and the species details for H. mexicana. Further, we developed a page that allows the end-user to do an advanced search. The end-user finds similar species based on the input characteristics of infective juveniles.
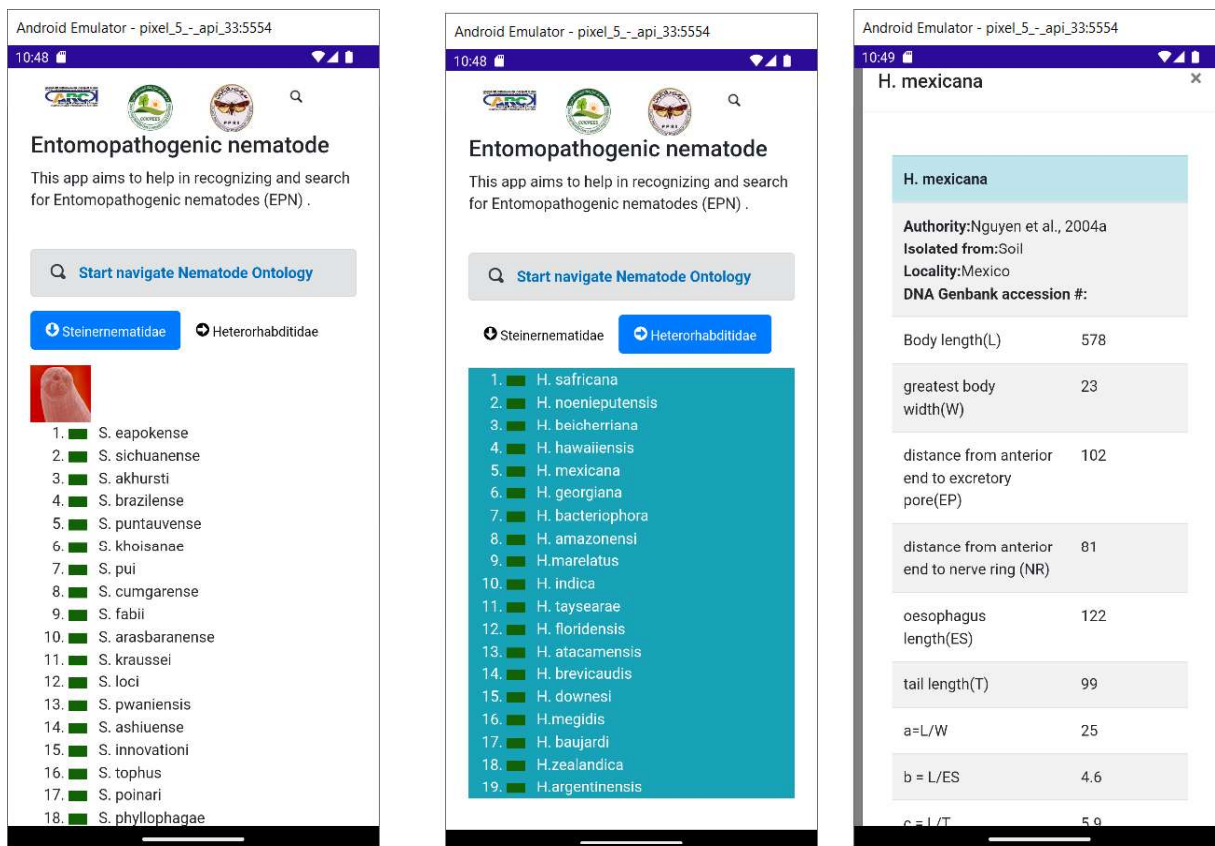

Figure 2: Mani page of the application and the details screen of species

3 Validation Test

To validate the proposed system a group of test cases has been validated by the domain experts and the system gave valid results. Furthermore, a questionnaire was conducted. A group of researchers evaluated the developed applications and answered the following questions.

1. Are you satisfied with the application?
2. Is the information about each type of entomopathogenic nematode adequate?
3. Does the application help in identifying the entomopathogenic nematode and the similarities between them?
4. Add suggestions to improve the application.

Number of researchers who responded to the questionnaire is 15. Figure 3 was their response. All researchers are satisfied with the application and recommend new enhancements.

The researchers suggested the following ideas to enhance the proposed application

- Is it possible to add identification by the standard specifications for males and females?
- The application should not be limited to nematodes, their types, and classification, but should include their relationship to other fields to interest all researchers who are not specialized in nematodes, such as the effect of natural and chemical compounds on them and the degree of toxicity and their impact.
- It is recommended to enter similar strains that were isolated from other places with the genetic number on the GenBank.
- Is it possible to add a picture of each type?
- Can we apply it to the iPhone as well?
- The application is part of an integrated pest control program recommended. Is it possible to add some research on nematode?
- The data should be up to date.

4 Results and Discussion

To evaluate the proposed system, we conducted many experiments. We used morphometric characters of infective juveniles data of some known species. We started with three species of the genus Heterorhabditis (H. megidis, H. bacteriophora, and H. indica). Then we did many experiments for species of the genus Steinernema. The proposed system will find all species that are similar to the given infective juvenile characteristics, and it will display the results in descending order based on the more common similarities.
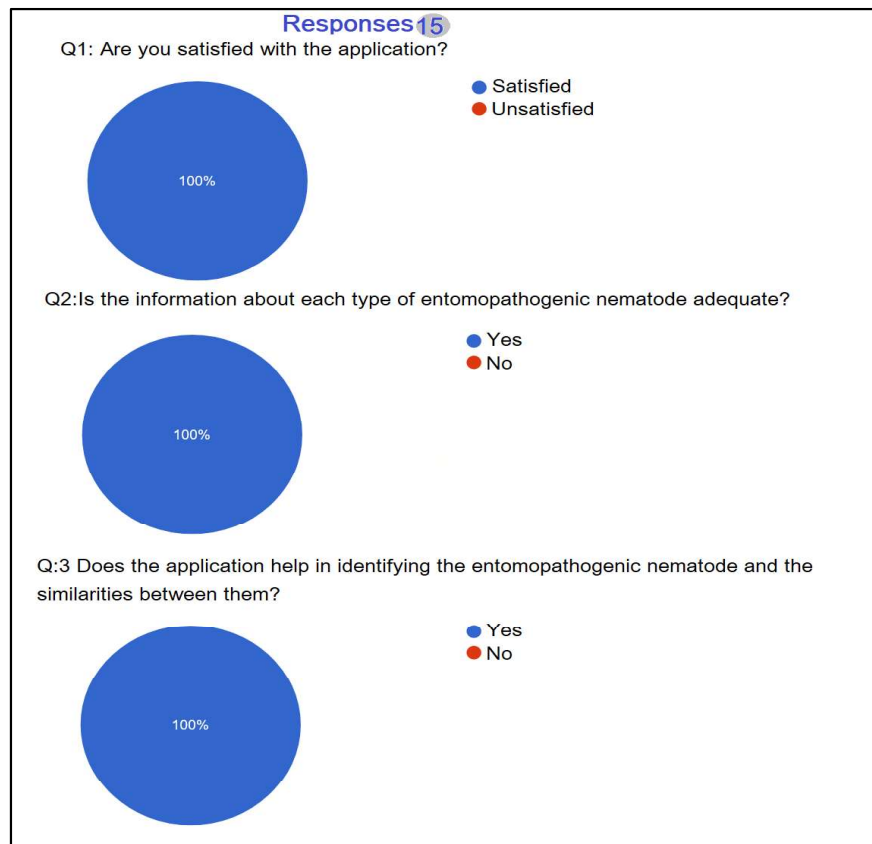

Figure 3: Responses to the evaluation questionnaire

4.1 Heterorhabditis Results

The system was used to compare the infective juvenile properties of (H. megidis, H. bacteriophora, and H. indica) with those of other species. Table 2 shows the top five results of the system using cosine similarity. The system results indicate that the system can identify the given species with 100% of known species. All the remaining five nearest species are of type Heterorhabditis, for example (H. amazonensi) is 99.88% similar to (H. megidis).

On the other hand, Table 3 shows the top five results of the system using Euclidean distance, the top five similar species of (H. bacteriophora and H. indica) are of Heterorhabditis, while in the case of (H. megidis), the system can identify H. megidis is similar to itself with 100 percentage, but the nearest five species are of type Steinernema, Since the body length of (H. megidis) is the tallest one of Heterorhabditis, this property is close to body lengths of these results species of Steinernema (S. ashiuense, S. sangi, S. everestense, S. robustispiculum, and S. unicornum), but the similar ratio is low between (H. megidis) and those results, for example (S. unicornum) is 77.56% similar to (H. megidis) because (H. megidis) belongs to Heterorhabditis, the system results agree with the assumption that (H. megidis) is a distinct species [16].

4.1.1 Identifying *H. atacamensis* Similar Species. We selected (H.atacamensis) to be tested on the system since (Hunt, D. J. and Nguyen, K. B) mention that "H. atacamensis is most similar to H. marelatus, H. downesi, H. amazonensis, H. bacteriophora, H. georgiana and H. safricana," [7]. The system's outcome is based on data results from H. atacamensis as is shown in Figure 4.

The system results state that (H. atacamensis) is 100% similar to itself. Further, the results of the top ten systems when using Euclidean distance are similar to those in the reference book [7] (H. downesi, H. marelatus, H. amazonensis, H. bacteriophora, and H. safricana). On the other hand, the results of the system when using cosine similarity agree with [7] (H. downesi, H. bacteriophora, and H. safricana). According to the findings, Euclidean distance appears to be more effective than cosine similarity in identifying the most closely related species of (H. atacamensis). The lack of recognition of (H. georgiana) using Euclidean distance and cosine similarity may be due to incomplete data on (H. georgiana).

Table 2: The results of running the system on some species of heterorhabditis using cosine similarity

Species	Similar species	Cosine similarity * 100
H. megidis	H. megidis	100%
	H. amazonensi	99.88009 %
	H. marelatus	99.8461 %
	H. mexicana	99.82926 %
	H. beicherriana	99.77374 %
	H. floridensis	99.74422 %
H. bacteriophora	H. bacteriophora	100%
	H. argentinensis	99.99906 %
	H. safricana	99.89509 %
	H. beicherriana	99.89402 %
	H. zealandica	99.8653 %
	H. baujardi	99.85868 %
H. indica	H. indica	100%
	H. baujardi	99.94233 %
	H. mexicana	99.92343 %
	H. beicherriana	99.91491 %
	H. safricana	99.91303 %
	H. amazonensi	99.85803 %

Table 3: The results of running the system on some species of heterorhabditis using euclidean distance

Species	Similar species	Euclidean distance
H. megidis	H. megidis	100%
	S. ashiuense	80.01814 %
	S. sangi	78.93036 %
	S. everestense	78.87545 %
	S. robustispiculum	78.53144 %
	S. unicornum	77.56857 %
H. bacteriophora	H. bacteriophora	100%
	H. argentinensis	99.61745 %
	H. safricana	94.79906 %
	H. mexicana	94.04926 %
	H. beicherriana	93.65662 %
	H. floridensis	91.99536 %
H. indica	H. indica	100%
	H. baujardi	96.65402 %
	H. noenieputensis	95.74544 %
	H. mexicana	93.57463 %
	H. floridensis	91.44147 %
	H. amazonensi	91.41016 %

4.2 Steinernema Results

Tables 4 and 5 display the results of the system by comparing the infective juvenile characteristics of (S. eapokense, S. apuliae, and S. glaseri) with other species using cosine similarity and Euclidean distance, respectively. The system results indicate that the system can identify the given species with 100% of known species. Further, results show the top five similar species for each species.

The system's results show that some results agree with both cosine similarity and Euclidian distance. For instance, common species that are similar to (S. eapokense) are (S. minutum, S. surkhetense, and S. backanense). We observe that Vietnam is the location of (S. eapokense), and the locations of the top species that are comparably shown in Table 6 are located in Asia.

4.2.1 Identifying *S. bicornutum* Similar Species. We selected (S. bicornutum) as a species of Steinernema to evaluate and test the system results. Figure 5 shows screenshots of the search screen and the result of the system on data of (S. bicornutum). It shows how to use the proposed system to locate the closest species that are comparable to one of Steinernema.

The results of the system allow nematologists to compare any species to those that already exist, and to identify those that are similar to one another in terms of physical characteristics. The cosine similarity and Euclidean distance agree on similar species for most of the top ten (S. affine, S. monticolum, S. intermedium, S. biddulphi and S. lamjungense).

5 Conclusion

EPNs are one of the biological control agents. They are used in integrated pest management (IPM) programs. We aimed with this paper to help researchers identify the correct EPNs species. We utilized semantic web technologies such as Web Ontology Language (OWL) to build an ontology and provide semantic information for the nematode community. Further, we introduced a method for identifying EPNs by adopting morphometric characteristics. We used cosine similarity and Euclidean distance to compare different EPNs species and identify similar species.

Euclidean distance appears to be more effective than cosine similarity in identifying the most closely related species. We built a mobile application reads and parses a developed ontology to display EPNs species details and enrich researchers with a
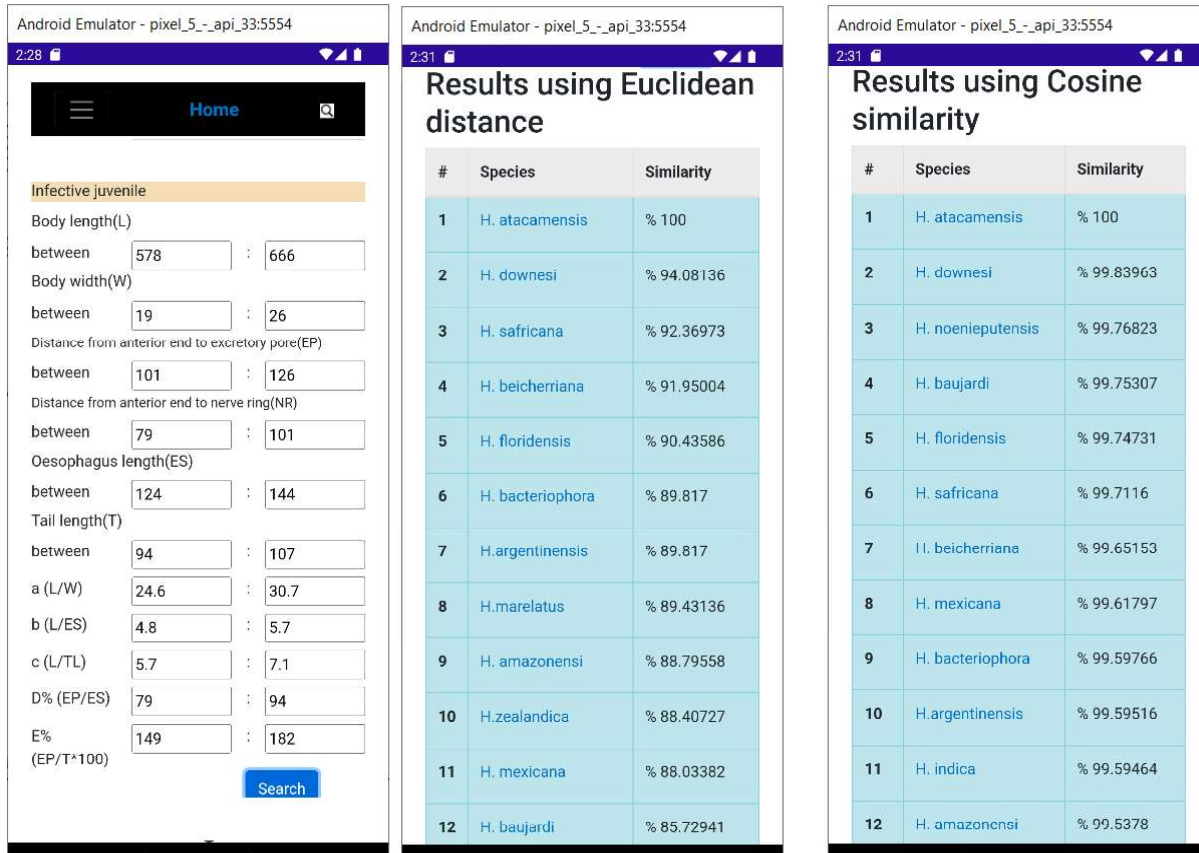
Figure 4: System results for *H.atacements* nearest species

Table 4: The results of running the system on some species of Steinernema using Cosine similarity

| Species	Similar species	Cosine similarity * 100
S. eapokense	*S. eapokense*	100 %
	S. backanense	99.97615 %
	S. surkhetense	99.94342 %
	S. balochiense	99.90489 %
	S. minutum	99.89507 %
	S. sasonense	99.89184 %
S. apuliae	*S. apuliae*	100 %
	S. pui	99.98583 %
	S. aciari	99.98195 %
	S. ethiopiense	99.95362 %
	S. thanhi	99.94365 %
	S. brazilense	99.92453 %
S. glaseri	*S. glaseri*	100 %
	S. arenarium	99.77076 %
	S. affine	99.65601 %

	S. pwaniensis	99.57247 %
	S. lamjungense	99.48499 %
	S. sandneri	99.43186 %

Table 5: The results of running the system on some species of Steinernema using Euclidian distance

Species	Similar species	Euclidean distance
S. eapokense	S. eapokense	100 %
	S. minutum	97.40327 %
	S. surkhetense	97.26441 %
	S. cumgarense	96.99397 %
	S. asiaticum	96.85899 %
	S. backanense	96.4893 %
S. apuliae	S. apuliae	100 %
	S. aciari	94.41532 %
	S. khoisanae	91.4565 %
	S. bakwenae	89.82047 %
	S. pui	89.36111 %
	S. guangdongense	88.29194 %
S. glaseri	S. glaseri	100 %
	S. arenarium	86.28402 %
	S. aciari	79.97972 %
	S. brazilense	79.60566 %
	S. apuliae	78.06147 %
	S. vulcanicum	77.63134 %

Table 6: Location of species

Species	Location
S. minutum	Thailand
S. surkhetense	Nepal
S. balochiense	Pakistan
S. sasonense	Vietnam
S. cumgarense	Vietnam
S. asiaticum	Pakistan
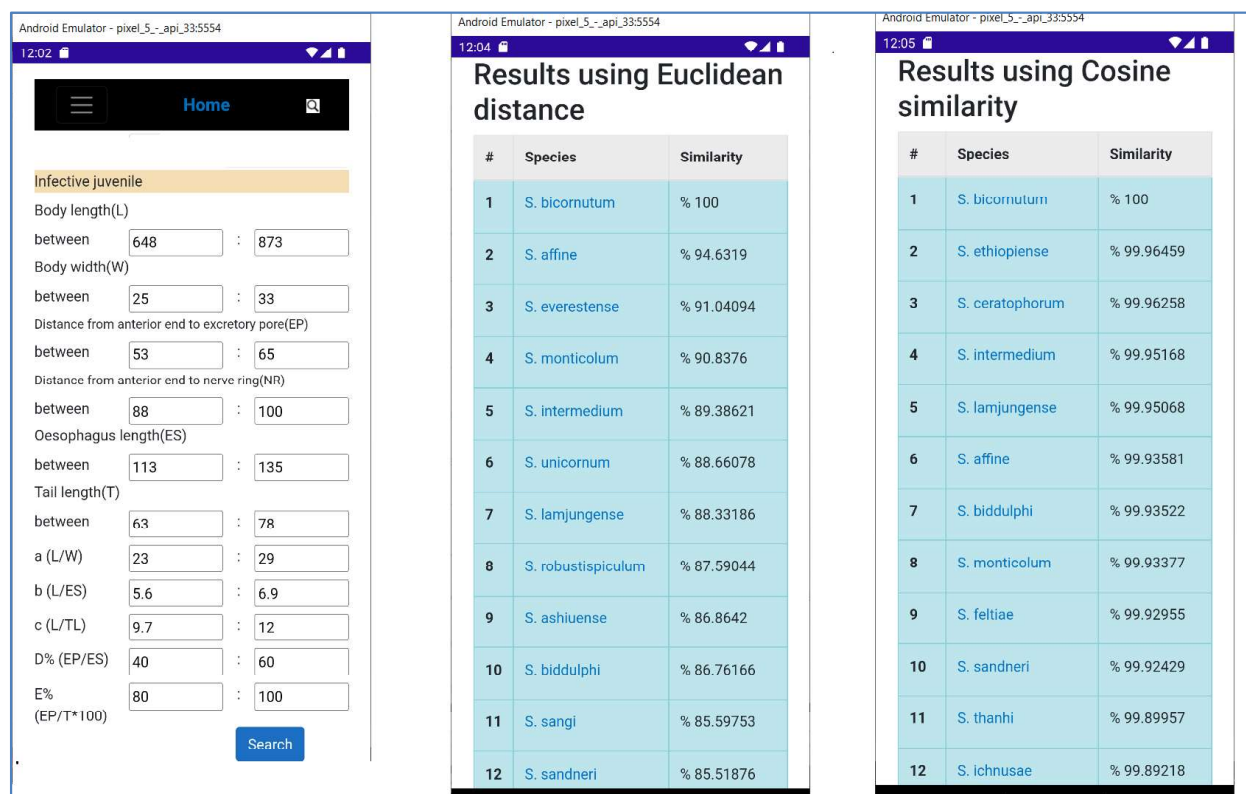
Figure 5: System results for *S. bicornutum* nearest spec

tool to search and find similar species. The result explained the strength of the proposed method in finding similarities between different species. One of the limitations of this research is that it doesn't include male morphometric characteristics in identifying similar species due to lack of time and system simplification. For future work, we can apply morphometric characteristics of males in comparison between species and automatically identify the most similar species for known and newly discovered EPNs species. Furthermore, integrating image identification techniques with similarity may enhance sytem performance and results.

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