A Method based on Ontologies to Support the Automatic Management of Knowledge about Covid-19

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***Abstract*—The importance of integration and retrieval of data is growing more and more in the context of post-COVID-19 analysis because of the increased generation of data in research and resources for studying COVID-19. In this context, the analysis of contagion groups that share some specific feature (for example, people that work together, people with the same clinical manifestation, etc.) may offer remarkable insights about COVID-19. For instance, it can be helpful to recognize the behavior of this disease in accordance with the unique characteristics of a group of people. In this regard, ontologies are a widely accepted alternative for representing and analyzing knowledge. Given their benefits, this paper introduces an ontology-based method to formally describe and analyze information about specific groups of people with COVID-19. Since the ontology was specified in OWL, a formal language based on description logics, it enables the consistency of the represented information to be verified and use automatic reasoning to deduce new knowledge. This approach allows modeling a wide variety of characteristics (symptoms, comorbidities, treatments, etc.) of the individuals and consequently use it to infer the general characteristics of the groups that they belong to. Hence, a reasoner can be applied to perform advanced analysis either to identify patterns in these groups or to find similarity with other groups. To demonstrate the applicability of this method, a case study is described. In addition, the ontology was used to represent and analyze the information of a sample of patients extracted from a public dataset. The results demonstrate the capability of the ontology to represent and analyze information about specific groups of people with COVID-19.**

Link to graphical and video abstracts, and to code: https://latamt.ieeer9.org/index.php/transactions/article/view/9707

***Index Terms*—Ontology, knowledge representation, COVID-19, automatic reasoning, decision making.**

I. INTRODUCTION

COVID-19 is a communicable disease that has impacted all the world with catastrophic consequences [1, 2]. A significant number of people have suffered from this disease and unfortunately a huge number of them have died. Due to the severity of this disease and its expansion around the world, it caused a world pandemic. Because of the growing generation of data in research and resources for analyzing COVID-19, as well as the requirement to properly manage it, ontology-based solutions might be critical in post-COVID-19 analysis. Plenty of researchers have been working tirelessly to alleviate the problems caused by this disease. A wide number of research has been carried out to deal with different perspectives of this disease and its consequences. For example, a previous work described the benefits of analyzing contagion chains [3]. This approach demonstrated how this type of analysis can provide interesting insights to know more about this disease. For example, identifying contagion chains with a specific behavior enables researchers to focus on them for finding the reasons of this behavior. In spite of the advantages of this approach, the way of transition and the high transmissibility of the virus make difficult the tracking of contagion chains. Hence, a more general approach that considers infected people grouped by different criteria may be more applicable and provide interesting insights as well. For example, the groups may be defined taking into account people that share certain characteristics (symptoms, age, sequels, vaccines, etc.). In this regard, we exploit an ontology to describe the knowledge related to groups of contagions and to perform automatic analysis to aid the efforts of those (researchers, medical professionals, local and national authorities, etc.) that are studying COVID-19. Knowledge is represented in an ontology in the form of a set of ideas that pertain to a specific area. Common terminology for describing

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the nature, history, and interconnections of a domain's concepts is a standard component of every ontology [4]. Effective transmission of biomedical knowledge is enabled by biomedical ontology [5]. Numerous biomedical ontologies explain a similar body of information in real-world applications. Ontologies expressed in Web Ontology Language (OWL) [6] are a type of Artificial Intelligence, AI, technique to represent and automatically analyze knowledge. Because of its foundation in description logics, OWL is a formal language that can be used with reasoners to ensure data accuracy and facilitate inferential reasoning that leads to the discovery of previously unknown information.

Given the benefits of using ontologies, the purpose of this work, which is a component of the advancements of the post-COVID-19 research, is to present an ontology-based method to formally describe and analyze information about specific groups of people with COVID-19. This study's key contributions are as follows:

- An ontology-based method is introduced for representing the contagion chains and evaluating data pertaining to communities of COVID-19-infected individuals
- Identifying groups of infectious individuals exhibiting a certain pattern by considering the infected sick people categorized in a variety of ways.
- The usage of an instance-matching mechanism to find related groups.
- The proposed ontology-based approach was conceived through the application of a reliable technique, ontological engineering process Methodology [7].
- Different techniques were used to ensure the ontology's quality; for example, a reasoner was used to evaluate its conditions as a logical-formal system.
- A case study is introduced to prove the applicability of this approach.

The rest of the paper has the following structure. The related works are examined in section II. The methods and materials used to develop and evaluate our approach are described in section III. This section includes the results of the ontological approach to represent and evaluate data pertaining to communities of COVID-19-infected individuals. The results after implementing the ontology are presented in section IV. A discussion about the results and the future work are presented in section V. Finally, the article's conclusions are provided.

II. RELATED WORK

Plenty of researches have been developed to analyze the spread of the coronavirus disease (COVID-19) and foretell its future development [8-15]. Although COVID-19 infections have been largely managed in certain countries by home quarantine, vaccination, and other measures, COVID-19 transmission has a repetitive nature, and still some countries are dealing with periodic waves of epidemic provoked by imported diseases [16]. In this regard, it is useful to model the contagion chains of COVID-19 infections in order to elucidate international transmission channels and regulate the infection of foreign epidemics. This study aims to identify chains of infectious people exhibiting a specific pattern by looking at infected patients with different characteristics. The modeling of COVID-19 dissemination has been widely studied. The majority of the existing investigation concentrates on the adoption of AI and machine learning methodologies for modeling and predicting the global spread of COVID-19 [17-21].

Modeling of pandemic data, ontological study of pandemic, and COVID-19 analytics are the three categories that best describe the relevant existing literature [22]. Some of these studies are detailed in this section. Research that models pandemic data provide answers for modeling pandemic scenarios based on data as well as decision processes to overcome certain implications that the epidemic has on health care, traditions, and economic disasters. Studies on simulating COVID-19 contagion can look at a variety of topics, including the contagion tracing, rates of spread, and social distance, for instance [14, 23-25]. The study on analytics of COVID-19 is currently in its beginning stages and focuses mostly on empirical studies assessing current systems and presenting data-driven approaches for sensing, mining, and visualizing healthcare data [26-28]. Various ontology-based approaches have been proposed for automatic reasoning about COVID-19 information, by conceptualizing its core ideas (such as infection symptoms or patient health) and defining the critical links between them [29, 30]. Astghik et al. developed an ontology for representing relevant information related to COVID-19 [31]. The authors aim to combine this ontology with text mining technique for the Covid 19 context. Since this ontology is based on the knowledge of experts in different fields, it includes an extensive diversity of concepts; for example, concepts related to epidemiology, virology and chemical biology. Besides, this ontology reuses a significant number of concepts from other ontologies.

Based on Infectious Disease Ontology (IDO) [32], several ontologies have been developed; for example, Coronavirus Infectious Disease Ontology (CIDO) and IDO-COVID-19. CIDO [33] has been used to describe a wide number of drugs and vaccines for COVID-19. CIDO has been used to identify potential vaccines for COVID-19 as well. CIDO reuses concepts from several ontologies; for example, ChEBI [34], UBERON [35], Vaccine Ontology [36] and NCBITaxon.

CODO allows to represent information about COVID-19 [29]. CODO is focused mainly on representing information about patients. Besides, it includes other concepts; for example, about available resources and actual needs (medical equipment, intensive therapy beds, etc.) and trend reports. CODO was used in the Ping COVID-19 risk detection system. This demonstrates the applicability of CODO.

Similarly to CIDO and CODO, other ontologies allow to describe different data about patients. For example, [37] and [38] are ontology-based approaches that include a wide variety of concepts to describe the aspects/dimensions of COVID-19. However, these approaches do not include mechanisms to conduct analysis about the groups.

Other ontologies are not focused on representing patient information but other dimensions. For example, COVID -19

Ontology (https://bioportal.bioontology.org/ontologies/COVID-9) covers the role of molecular and cellular entities in virus-host-interactions, as well as several medical and epidemiological concepts linked to COVID-19. But, the representation of information about patients is not in the scope of this ontology. ROC [39] focuses on country measures and enables the integration of data from heterogeneous data sources. Likewise, the COVID-19 Vocabulary (COVoc, https://www.ebi.ac.uk/ols/ontologies/covoc) is an ontology containing terms related to the research of the COVID-19 pandemic. This includes host organisms, pathogenicity, gene and gene products, barrier gestures, treatments and more. However, it does not include mechanisms to describe the information about patients. VODANA-COVIDTERMS (https://bioportal.bioontology.org/ontologies/vodanacovid) includes terms to collect and report general information about the countries related to COVID-19.

In a previous work we proposed an approach to represent and study information about COVID-19 contagion chains [3]. The benefits of this approach were discussed previously. However, its main limitation is related to the difficulties to track a COVID-19 contagion chain due to the high transmissibility of the virus and the way that it is transmitted.

These approaches demonstrate the potentialities of the ontologies to represent and analyze the knowledge related to COVID-19. These ontologies are focused mainly on representing information of individual patients. However, we are interested in focusing our analysis on the groups, instead of individual cases. This type of analysis can provide interesting insights to study the behavior of COVID-19. On the other hand, since we will deal with the groups as instances, it is possible to apply instance matching algorithms to enhance the analysis.

III. METHODS

A. *Technologies and Methodology for the Ontological Engineering Process*

Several prominent languages to implement ontologies have been proposed [40-45]. Slimani [44] carried out a comparison of the most notable languages by taking into account 21 requirements. This work yielded that OWL 2 reached the best performance, meeting 20 indicators.

OWL 2 is a formal language based on description logics. Hence, it allows checking the consistency of the information represented. In this regard, a reasoner is used to do it automatically. Taking into account its benefits, our ontology was implemented in OWL 2.

On the other hand, Protégé [46] was adopted to create the ontology. Protégé is an open-source and multiplatform tool that is widely used to manage ontologies in OWL. Protégé enables the option of using different reasoners to automatically analyze the ontologies.

Choosing a suitable methodology is an essential factor to create a high-quality ontology. After the examination of some methodologies [47], the proposal of Noy and McGuinness was selected. This methodology has been adopted for a significant number of initiatives to create ontologies [7]. The methodology proposes the following steps: define the domain and scope of the ontology, consider reusing existing ontologies, identify the relevant terms, define the classes and the class hierarchy, define the properties, define restrictions on slots or relationships and define instances.

B. *HMATCH(I): An Instance Matching Algorithm*

Our approach adopts an instance matching technique to analyze the groups. Since we focus the analysis on groups, it is suitable to include mechanisms to identify similar groups or simply to verify the similarity of specific groups. We studied several approaches for the problem of instance matching [48]. The approach of Castano et. al [48] will allow us to analyze the similarity based on different factors. The instance matching algorithm of HMatch(*I*) includes two approaches: syntactic and semantic. In this body of work, we followed the semantic approach, which involves a collection of explicit instance statements with a set of implicit assertions that are generated using an inference mechanism.

HMatch(*I*) relies on two functions known as Instance Affinity (IA) and Filler Similarity (FS). These two functions are detailed further down in this article. The primary principle of the Instance Affinity may be broken down into the following: given two individuals i_1 and i_2, that are instances of the same (or matching) concept, the Instance Affinity function $IA(i_1, i_2) \rightarrow 0$ provides a measure of their affinity in the range [0,1]. For each individual i, the Instance Affinity is calculated by taking into account all the properties $p_1^i, \ldots, p_n^i$ featuring i together with their corresponding property fillers $f_1^i, \ldots, f_n^i$. Each property p_j, is associated with a weight $W_{pj} \in [0,1]$ expressing the capability of p_i for the goal of univocally identifying the individual i in the domain of interest. Given two individuals i_1 and i_2, the Instance Affinity function $IA(i_1, i_2)$ between them is calculated as depicted in (1).

$$IA(i_1, i_2) = \frac{2.\sum_{k=1}^{k=n} F_S\left(f_k^{i_1}, f_k^{i_2}\right).W_{p_k^{i1}}}{\sum_{k=1}^{k=n} W_{p_k^{i1}} + \sum_{k=1}^{k=n} W_{p_k^{i2}}} \qquad (1)$$

Whereas the Filler Similarity function, $F_S(f_1, f_2)$ can be defined as shown in (2). Given two property fillers f_1 and f_2 and a threshold t, the filler similarity function $F_S(f_1, f_2) \rightarrow \{0,1\}$ is defined as:

$$F_S(f_1, f_2) = \begin{cases} 1, if\ sim(f_1, f_2) \geq t; \\ 0, otherwise \end{cases} \qquad (2)$$

Where $Sim(f_1, f_2)$ is a value in the range [0,1] and it is obtained depending on the type of the role fillers f_1 and f_2 and applying four rules defined by the authors in [48].

C. *The proposed ontology-based method to represent and analyze information about groups of people infected with COVID-19*

An ontology-based proposal to analyze information about groups of people infected with COVID-19 is described in this section. Here, we present the stages of our proposal.

Stages of the Proposed Method

1) **Creating the groups**

Based on the purpose (needs) of the analysis, the relevant characteristics of the groups will be defined. We have identified two types of groups: *natural groups* and *temporary groups*. People sharing some feature(s) are grouped in *natural groups*. For example, people with the same symptoms, vaccinated with a specific vaccine, etc. Natural groups can combine these features with predefined classifications of the patients; for example, adults, children, pregnant, etc. On other hand, *temporary groups* are composed of people who have been grouped under specific circumstances. For example, people who coincided in a physical space (social event, school, workplace, etc.). Members of *temporary groups* should be intentionally defined. Thus, analysts might study people that simultaneously belong to several interest groups.

2) **Defining the scope or hypothesis of the analysis**

We have identified two type of analysis. The goal for the first type of analysis is to identify groups with a high similarity based on certain features. Then, this result can be combined with other approaches to predict the behavior of other features for one of the groups. For example, if two groups have a high similarity taking into account the symptoms, and we know the sequels of one of the groups, it might be expected that the other group has similar sequels. However, it is important to mention that the scope for the current approach is to identify the groups with a high similarity. To conduct a predictive analysis, other aspects that are beyond the scope of this current approach should be considered. The second type of analysis is focused on finding groups with similar values for some features, but at the same time different values for other features. For example, groups with the same symptoms but with totally different sequels. With this last type of analysis, the experts can focus their attention on finding the reasons for these differences. To ensure the flexibility of this approach, the size, diversity, and source of the groups should be defined for the experts taking into account their needs.

3) **Exploiting the expressivity richness of OWL to support the analysis**

Based on the previous stage results, diverse constructs of OWL will be used to support the analysis. The algorithm described in section *III. B* is applied to estimate the similarity of groups. After implementing the mechanisms to support the analysis, the results will be examined by a reasoner which can provide useful inferences.

Results of the Ontological Process

The results after completing the steps defined in the adopted methodology to develop our ontology are described below.

Scope of the ontology

Competence questions (CQs) provide a method for precisely articulating an ontology's scope. In addition, the study's competence questions will be a crucial checkpoint for determining whether or not the ontology met its function. We anticipate that the ontology's needs will continue to evolve on a regular basis as our method moves toward widespread adoption. Nevertheless, this ontology can be expanded to accommodate novel needs. This corresponds to the second stage of the procedure outlined above. To demonstrate the versatility of our method, we defined the following six CQs.

- *CQ 1*. What are the characteristics of a certain person?
- *CQ 2*. Who are the members of a certain group?
- *CQ 3*. What are the main symptoms of the members of a certain group?
- *CQ 4*. What are the main sequels of the members of a certain group?
- *CQ 5*. What are the main adverse reactions of the members of a certain group?
- *CQ 6*. What is the similarity between two groups?

In this ontology, several concepts were reused from our previous work [3]. Likewise, the previous ontology reuses various concepts that are found in other ontologies stored in the Bioportal repository [49]. The competence questions were evaluated by two specialists, who work in a Cuban health institution. Specifically they work in the area of epidemiology at the Provincial Center for Hygiene, Epidemiology, and Microbiology in Cienfuegos, Cuba. After two iterations, they were satisfied with the proposed competence questions.

Classes and the Class Hierarchy

Classes are one of the key components of an ontology. As Fig. 1 depicts, for this new ontology we have added classes to represent the groups and other concepts (highlighted with a dotted red line form). For example, we have added the class **Natural_Group** and **Temporary_Group** to differentiate the type of groups that we mentioned in the previous section. The class **Similarity_Analysis** was created to represent the similarity of two groups. It is noteworthy that the class **Contagion_Chain** is subsumed by the class **Natural_Group** given that a **Contagion_Chain** can be analyzed as a specific type of a **Natural_Group.** In addition, we have added classes to represent other concepts; for example, the class **Sequel** for representing the sequels that a person that was infected with COVID-19 has. This concept is relevant to study the Long-COVID-19. Likewise, we added the class **Adverse_Reaction** for representing the reactions of a person that was vaccinated.

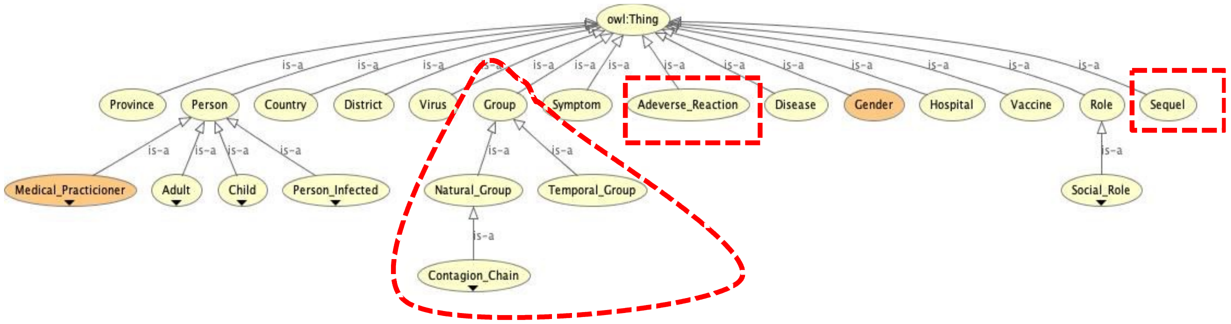


Fig. 1. Class Hiereарchy in the proposed ontology.

Object Properties

Object properties are one of the essential components in an ontology. They allow to describe how two individuals are related. For example, we have created the property *Belongs_To_Group* to specify that an instance of the class **Person** belongs to an instance of the class **Group**. Likewise, we have defined the object property *Has_Sequel* to relate instances of the classes **Sequel** and **Person**. Table I depicts several of the most relevant object properties.

TABLE I

SET OF OBJECT PROPERTIES

Domain	Object Property	Range
Person	*Has_Sequel*	Sequel
Person	*Has_Symptom*	Symptom
Person	*Has_Adverse_Reaction*	Adverse_Reaction
Person	*Has_Comorbidity*	Comorbidity
Group	*Is_Group_Of*	Person
Groups	*Members_Have_Symptom*	Symptom
Groups	*Members_Have_Sequel*	Sequel
Groups	*Members_Are_Vaccinated_With*	Vaccine
Groups	*Members_Have_Adverse_Reaction*	Adverse_Reaction
Groups	*Members_Have_ Comorbidity*	Comorbidity

Each object property in OWL has an inverse property. For instance, the property *Is_Symtom_Of* is the inverse of *Has_Symptom*. Thus, if an instance of the class **Person** is related to an instance of the class **Symptom** *through the* property *Has_Symptom*, the reasoner can infer the inverse relation between these two individuals. Fig. 2 depicts the relation between several properties.

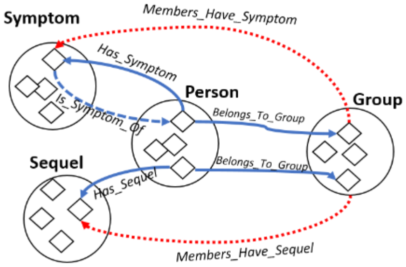


Fig. 2. Graphical representation of a set of object properties.

We want to remark those object properties related to the class **Group**. We are interested to automatically infer the values of these properties based on the information from the group members. In this case, the *Semantic Web Rule Language* (SWRL) was used to represent complex relations connected to the class **Group**. Table II depicts the rules to infer the values of the properties *Is_Sequel_Of_Group* and *Is_Adverse_Reaction_Of_Group*. Similar rules were defined for *Is_Symptom_Of_Group* and *Is_Vaccine_Of_Group*. In addition to these properties, the object property *Is_Similarity_Analysis_Of* was created to define the similarity between two groups. The specific value of the similarity is represented by the data property *Has_Similarity_Ratio*.

TABLE II

RULES IN SWRL TO INFER KNOWLEDGE OF GROUPS

	Rule
1	**Group**(?G)^**Person**(?P)^*Is_Group_Of*(?G,?P)^**Sequel**(?S)^*Is_Sequel_Of*(?S,?P)->*Is_Sequel_Of_Group(?*S,?G)
2	**Group**(?G)^**Person**(?P)^*Is_Group_Of*(?G,?P)^*Adeverse_Reaction*(?S)^*Is _Adverse_Reaction_Of*(?S,?P)->*Is_Adverse_Reaction_Of_Group*(?S, ?G)

Ontology Evaluation

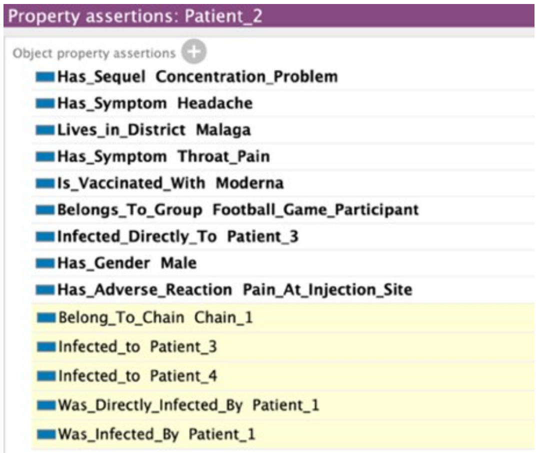
To evaluate the ontology, the authors checked if the prerequisites (a) for a formal-logical system and (b) for the purpose for which it was developed were complied. A reasoner was used for checking whether or not the requirements of the formal–logical system have been satisfied. In this particular instance, we used the reasoner Pellet, which provided conclusive evidence about the consistency of the ontology. It is important to keep in mind that the evaluation of the ontology is a process that is both iterative and progressive. The reasoner was used throughout the entire ontology development process in order to ensure that the ontology remained consistent.

In addition to that, the *Ontology Pitfall Scanner* (OOPS!) was used to evaluate the most recent version of the ontology [50]. After two iterations, OOPS reported that all of the issues had been resolved. This evaluation helped us to detect and fill in a number of holes in the developed ontology. We designed a case study in order to provide evidence that the ontology was successful in meeting the goals for which it was developed. In this case study, we made sure that the ontology had provided accurate responses to all the competency questions.

IV. RESULTS

This section describes the results after implementing the proposed ontology for a COVID-19 patient in order to demonstrate how personal information can be represented. In this particular use case, information about patient's symptoms, complications, vaccine, and reactions are related. Fig. 3 depicts how this information was represented in the ontology for the individual *Patient_2*, an instance of the class **Person**. In this example, we have used the object property *Has_Symptom* to express that *Patien_2* has the symptoms *Headache* and *Throat_Pain* which are instances of the class **Symptom**. Likewise, we have used the property *Has_Sequel* to express that *Patient_2* has the sequel *Concentration_Problem* that is an instance of the class **Sequel**. In addition, we represented that *Patient_2* is vaccinated with *Moderna (*instance of the class **Vaccine***)* and had reaction *Pain_At_Injection_Side (*instance of the class **Adverse_Reaction***)*. It is noteworthy that this person was included in the group *Football_Game_Participant* (Instance of the class **Group**) through the property *Belongs_To_Group*. Additional information related to the contagion chain has been included as well. CQ. 1 is answered with these specifications.

Fig. 4 depicts the way that the information about the groups is represented. This example includes several instances of the class **Person** (P1, P2, P3, P4 etc.). We defined several groups to classify these people according to their characteristics. For example, P1 and P2 belong to G1; P3 and P4 belong to G2 and P5 and P6 belong to group 3. To include a person in a group, the property *Belongs_to_Group* is used. Since the property *Is_Group_Of* is the inverse of *Belongs_to_Group,* if we use *Belongs_to_Group* then the reasoner will infer the members of a group. As example to answer CQ 2, Fig. 4 shows the members of G1, G2, G6 and G7.


Property assertions: Patient_2

Object property assertions

Has_Sequel Concentration_Problem
Has_Symptom Headache
Lives_in_District Malaga
Has_Symptom Throat_Pain
Is_Vaccinated_With Moderna
Belongs_To_Group Football_Game_Participant
Infected_Directly_To Patient_3
Has_Gender Male
Has_Adverse_Reaction Pain_At_Injection_Site
Belong_To_Chain Chain_1
Infected_to Patient_3
Infected_to Patient_4
Was_Directly_Infected_By Patient_1
Was_Infected_By Patient_1

Fig. 3. Information of Patient_2.

A feature of this approach is the possibility to obtain information about the individuals who make up a group. Consequently, the information about the groups is inferred from their members.

As an example to illustrate the answer to CQ. 3, Fig. 5 a) and Fig. 5 b) show, through the property *Members_Have_Symptom,* the symptoms that the members of the groups G1 and G2 have. Similarly, Fig. 5 a) shows, via the property *Members_Have_Sequel*, the sequels that the members of the group G1 have, thus providing an illustration of the solution to CQ. 4.

To answer CQ. 5, in Fig. 5 c) and Fig. 5 d), the properties *Members_Are_Vaccinated_With* and *Members_Have_Adverse_Reaction* reveal the vaccines and the reactions that the members of the groups G6 and G7 have. The rules depicted in Table II are important to infer this information. Similar rules can be implemented to infer more information about the groups taking into account the information of their members.

Using the same data as in Fig. 4, we can apply the instance matching algorithm to determine which groups are most similar to one another. Fig. 6 shows how the similarity of the groups G7 and G8 was represented. In this case, an instance of

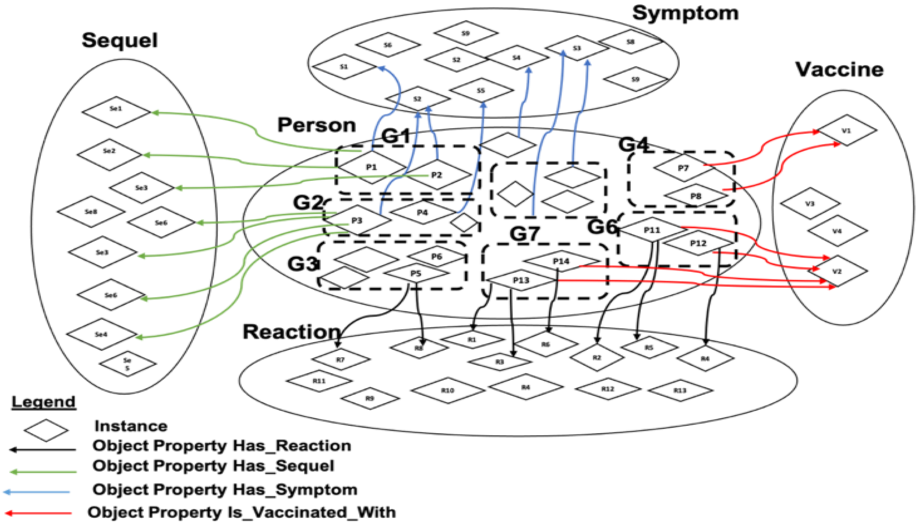
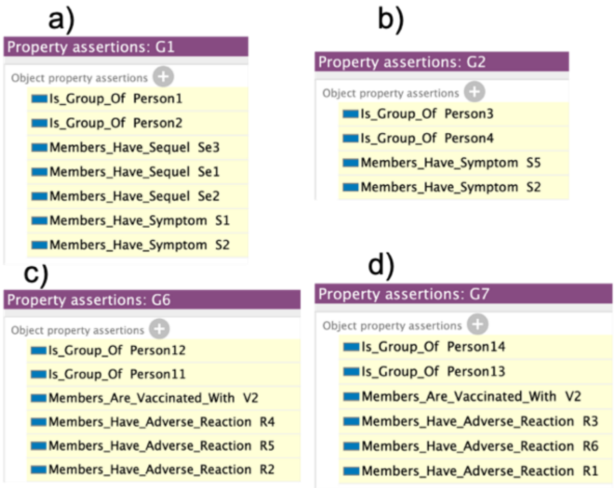


Fig. 4. Relations among individuals of different classes.


a)

Property assertions: G1

Object property assertions
- Is_Group_Of Person1
- Is_Group_Of Person2
- Members_Have_Sequel Se3
- Members_Have_Sequel Se1
- Members_Have_Sequel Se2
- Members_Have_Symptom S1
- Members_Have_Symptom S2

b)

Property assertions: G2

Object property assertions
- Is_Group_Of Person3
- Is_Group_Of Person4
- Members_Have_Symptom S5
- Members_Have_Symptom S2

c)

Property assertions: G6

Object property assertions
- Is_Group_Of Person12
- Is_Group_Of Person11
- Members_Are_Vaccinated_With V2
- Members_Have_Adverse_Reaction R4
- Members_Have_Adverse_Reaction R5
- Members_Have_Adverse_Reaction R2

d)

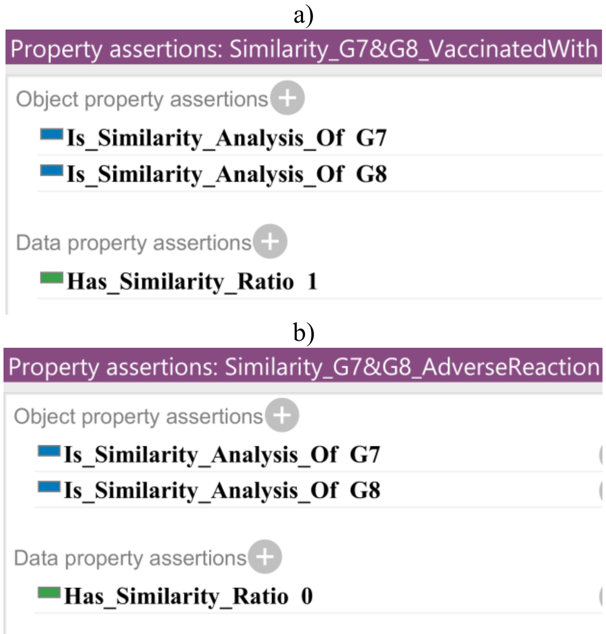
Property assertions: G7

Object property assertions
- Is_Group_Of Person14
- Is_Group_Of Person13
- Members_Are_Vaccinated_With V2
- Members_Have_Adverse_Reaction R3
- Members_Have_Adverse_Reaction R6
- Members_Have_Adverse_Reaction R1

Fig. 5. Knowledge inferred for the groups: a) G1; b) G2; c) G6; d) G7.

the class *Similarity_Analysis* was created and the groups G7 and G8 were specified as the values for the property *Is_Similarity_Analysis_Of*. Then, the value of the similarity, by the data property *Has_Similarity_Ratio,* was specified. As the Fig. 6 a) shows, when comparing G7 and G8, the similarity ratio is 1 if we only look at the property *Members_Are_Vaccinated_With*. Whereas, comparing objects based only on the *Members_Have_Adverse_Reaction* property yields a similarity ratio of 0, as Fig. 6 b) depicts. This may suggest that there are explanatory factors here. Assuming, for the sake of the argument, that the people in these two groups are all residents of different cities who received the same vaccine. To a large extent, we anticipate that the negative effects are comparable. Since the outcome was unexpected, the expert can dig in to figure out why the phenomenon occurred. This analysis exemplifies how to answer CQ. 6 and demonstrates the usefulness of this approach. This strategy might contribute, as was mentioned before, to the process of making predictive analyses. For instance, the ontology includes information regarding the signs and symptoms as well as the consequences of the group G1. We can use this information to locate other groups that share symptoms with G1, and then we can predict that the members of those other groups will experience sequels that are comparable to G1. In a similar way, we can use the algorithm to look for signals regarding the appearance of new variants. For instance, if we find that two groups have an important difference in their symptoms, this might be an indication that they are not infected with the same strains of the virus.

In addition to these examples, we have used the ontology to describe real data about patients stored in a public dataset (https://www.kaggle.com/datasets/meirnizri/covid19-dataset). This dataset gathered anonymized patient-related information; for example, the comorbidities and the received treatments. To demonstrate the potentiality of the ontology, we have used it to represent the information about 5000 patients. Once the information was represented, interesting analysis could be carried out.


a)

Property assertions: Similarity_G7&G8_VaccinatedWith

Object property assertions
- **Is_Similarity_Analysis_Of G7**
- **Is_Similarity_Analysis_Of G8**

Data property assertions
- **Has_Similarity_Ratio 1**

b)

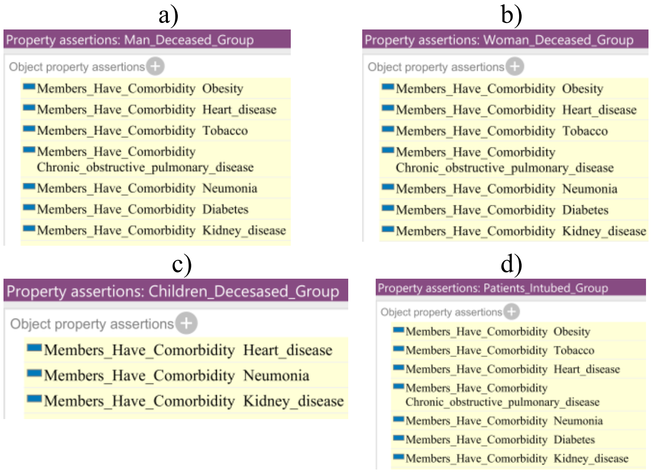
Property assertions: Similarity_G7&G8_AdverseReaction

Object property assertions
- **Is_Similarity_Analysis_Of G7**
- **Is_Similarity_Analysis_Of G8**

Data property assertions
- **Has_Similarity_Ratio 0**

Fig. 6. Representation of the similarity between the groups G7 and G8 based on: a) vaccine b) adverse reaction.

For example, we were interested in knowing the set of comorbidities of the deceased patients. Hence, we created the groups *Man_Deceased_Group, Woman_Deceased_Group and Children_Deceased_Group*. Fig. 7 depicts the comorbidities that were inferred by the reasoner for these groups. We can notice that there is not difference among the comorbidities of the *Man_Deceased_Group* and *Woman_Deceased_Group*. However the *Children_Deceased_Group* has only three comorbidities.


a)

Property assertions: Man_Deceased_Group

Object property assertions
- Members_Have_Comorbidity Obesity
- Members_Have_Comorbidity Heart_disease
- Members_Have_Comorbidity Tobacco
- Members_Have_Comorbidity Chronic_obstructive_pulmonary_disease
- Members_Have_Comorbidity Neumonia
- Members_Have_Comorbidity Diabetes
- Members_Have_Comorbidity Kidney_disease

b)

Property assertions: Woman_Deceased_Group

Object property assertions
- Members_Have_Comorbidity Obesity
- Members_Have_Comorbidity Heart_disease
- Members_Have_Comorbidity Tobacco
- Members_Have_Comorbidity Chronic_obstructive_pulmonary_disease
- Members_Have_Comorbidity Neumonia
- Members_Have_Comorbidity Diabetes
- Members_Have_Comorbidity Kidney_disease

c)

Property assertions: Children_Decesased_Group

Object property assertions
- Members_Have_Comorbidity Heart_disease
- Members_Have_Comorbidity Neumonia
- Members_Have_Comorbidity Kidney_disease

d)

Property assertions: Patients_Intubed_Group

Object property assertions
- Members_Have_Comorbidity Obesity
- Members_Have_Comorbidity Tobacco
- Members_Have_Comorbidity Heart_disease
- Members_Have_Comorbidity Chronic_obstructive_pulmonary_disease
- Members_Have_Comorbidity Neumonia
- Members_Have_Comorbidity Diabetes
- Members_Have_Comorbidity Kidney_disease

Fig. 7. Knowledge inferred for the groups: a) *Man_Deceased _Group*; b) *Woman_Deceased _Group*; and c) *Children_Deceased _Group*; d) *Intubed_Patients_Group*.

Likewise, it could be interesting to know the comorbidities of the patients that were intubed. For this case, we created the group *Intubed_Patients_Group* with these patients and the reasoner inferred the comorbidities of its members. Fig. 7 d) shows this inference. We carried out other analysis; for example, to know the difference of comorbidities among the patients that received intensive care assistance and those that did not need it. A similar analysis might be carried out considering other factors such as symptoms or sequels. In general, all these results can be used for the experts as significant insights to carry out deepest studies.

The described examples prove the applicability and value of our strategy. The used dataset includes 21 features to describe the patients. With our ontology, it was possible to represent all the features. This is an evidence about its applicability. However, we are working to evaluate the scalability of our method, for instance, when we evaluated the similarity, we only used one property, but we can use the same algorithm to evaluate multiple properties at the same time. This evaluation will provide new evidence about the benefits of this proposal.

Similarly to the competence questions, two specialists who work in a Cuban health institution evaluated the ontology.

V. DISCUSSION

As we mentioned in the related work section, there are plenty of ontology-based approaches to deal with some dimensions of COVID-9. Table III summarizes the analysis of the related ontologies considering their scope. Only [51] presents an ontology-based approach with a scope very similar to our research. That work describes a domain ontology that is used to discover interesting facts by using the association rule mining algorithm. The authors present promising results of this approach. However, the application of the association rule mining algorithm is different to the line that we have adopted in our approach. Nevertheless, some ideas of this approach will be considered to be implemented in our future work. For example, they found out the fact that Hypertension, Hypothyroid, breathing problems and asthma are commonly seen for age group of 45-55. We will create this group in our ontology to examine the comorbidities and verify if the results have coincidence.

In our approach is possible to conduct analysis based on the similarity of different groups. Then, according to the results, deeper analysis can be carried out by the experts. Likewise, to compare the characteristics of an individual with respect to the general characteristics of their groups is possible. If the experts find important differences, then they can carry out further analysis to find the reasons for this behavior.

The way that the similarity applying (1) and (2) is developed currently might be a limitation of our approach. In this regard, we are designing a plugin for Protégé that will allow to calculate the similarity in an easier way. This feature will enhance the applicability of our approach. Thus, the experts can concentrate their attention only on the results that the plugin will provide and consequently design new analysis to find the reasons for certain behaviors.

TABLE III
SUMMARY ON THE SCOPE OF SOME EXISTING ONTOLOGIES

Approach	**Represent and analyze patient data**	**Represent and analyze Groups**
COVID-19 Ontology https://bioportal.bioontology.org/ontologies/COVID-9	X	X
ROC [39]	X	X
CoVoc https://www.ebi.ac.uk/ols/ontologies/covoc	X	X
Vodana-Covidterms https://bioportal.bioontology.org/ontologies/VODANACOVID	X	X
CODO [29]	✓	X
CIDO [33]	✓	X
CovidO [37]	✓	X
Common data model [38]	✓	X
Ontology-based method [51]	✓	✓
Proposed ontology	✓	✓

VI. CONCLUSIONS

An ontology-based approach to study the knowledge held by groups of people infected with COVID-19 was presented in this article. For the purpose of guiding the implementation of this approach, we have defined five stages. A reasoner can be used to automatically validate the ontological model because the ontology is expressed in OWL, a formal language based on description logics. This enables the process to be carried out in a more efficient way. We included some interesting analyses that could be performed, but others could also be implemented according to the requirements of the experts who make use of this ontology. The ontology was subjected to validation, which demonstrated that its design is sound, that it satisfies the prerequisites for functioning as a formal–logical system, and that it accomplishes the objectives for which it was developed. Because we work with the groups as instances, an algorithm to determine the degree to which the groups are comparable to one another was used. Several analyses can be conducted based on the outcomes of applying this algorithm.

As future work, we will continue testing the ontology by using other datasets that include different data. Taking into account the data, we can define diverse groups and study the results that the ontology provides. Thus, we can evaluate the performance of the ontology with different data. Likewise, we will evaluate the alternatives to extend our approach in order to support predictive analysis.

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