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Exploiting an Ontological Model to Study COVID-19 Contagion Chains in Sustainable Smart Cities

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Abstract: The COVID-19 pandemic has caused the deaths of millions of people around the world. The scientific community faces a tough struggle to reduce the effects of this pandemic. Several investigations dealing with different perspectives have been carried out. However, it is not easy to find studies focused on COVID-19 contagion chains. A deep analysis of contagion chains may contribute new findings that can be used to reduce the effects of COVID-19. For example, some interesting chains with specific behaviors could be identified and more in-depth analyses could be performed to investigate the reasons for such behaviors. To represent, validate and analyze the information of contagion chains, we adopted an ontological approach. Ontologies are artificial intelligence techniques that have become widely accepted solutions for the representation of knowledge and corresponding analyses. The semantic representation of information by means of ontologies enables the consistency of the information to be checked, as well as automatic reasoning to infer new knowledge. The ontology was implemented in Ontology Web Language (OWL), which is a formal language based on description logics. This approach could have a special impact on smart cities, which are characterized as using information to enhance the quality of basic services for citizens. In particular, health services could take advantage of this approach to reduce the effects of COVID-19.

Keywords: COVID-19; ontology; artificial intelligence

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1. Introduction

Coronaviruses are a family of viruses found in certain animals, which become infection agents capable of causing serious diseases to humans through mutations, such as severe acute respiratory syndrome (SARS), Middle East respiratory syndrome (MERS) and SARS-CoV2 discovered in China in 2019. SARS-CoV2 causes the COVID-19 disease. The World Health Organization (WHO) declared COVID-19 a world pandemic due to the high number of infections and deaths that this disease had caused around the world.

The high transmissibility of SARS-CoV2 and the existence of asymptomatic patients are factors that considerably complicate its containment. An exhaustive analysis of chains of contagion can provide new findings that may be useful for epidemiological and virological studies. For example, it might be possible to identify the symptoms in a chain of contagion and make a comparison with the symptoms in other chains. If notable differences are found, further analysis may be necessary to find the source of those differences, which could be either biological, social or environmental. For example, the differences might be due to either different variants of the virus or to different human behaviors.

Likewise, the analysis of contagion chains might help to identify the points where the virus starts to change its behavior or its effects. On the other hand, it could be possible to measure how long a chain has been active. This information could be useful to define strategies to reduce the options for contagion. However, the high number of infections means that the chains are long, which considerably slows down the work of researchers. This situation makes it difficult to perform an in-depth analysis. Moreover, the lack of tools to support the efforts of researchers means that their work cannot be carried out with the agility that the current pandemic demands. Therefore, this study addresses the problem of how to represent the information related to the chains of contagion of COVID-19 in such a way that its analysis is expedited and traits that contribute to characterizing the disease can be obtained.

Seeking approaches to deal with the aforementioned problem, we found that the adoption of ontologies is a suitable option to represent and analyze knowledge of different domains [1–7]. The semantic representation of information by means of ontologies enables the consistency of the information to be checked, as well as automatic reasoning to infer new knowledge.

This paper aims to present an ontological model to represent information regarding sick patients with COVID-19 to improve the analysis of the characteristics of the disease. The main contribution of this research lies in the fact that the analysis focuses fundamentally on the chains of contagion, unlike previous studies that have focused on other perspectives. The results of this approach could be useful for epidemiological work, especially in countries where rigorous monitoring of contagion chains has proven to be an effective strategy to contain the virus. Likewise, this ontology could be a useful instrument to support the work of researchers during experimental studies. The ontology was developed following a sound methodology that is recognized and widely used in the scientific community. In addition, its conditions were validated as a logical–formal system by means of reasoners.

The rest of the article is organized as follows. The next section presents the analysis of related works. The following section describes the ontological model developed to represent and analyze the information of patients with COVID-19 disease. A case study is presented next, which shows the applicability of the proposal. Finally, the conclusions of the article are presented.

2. Related Works

Through a literature review, we found some works that analyzed contagion chains to characterize COVID-19. For example, Wang studied the contagion chains in Tianjin, a Municipality in China [8]. This study yielded useful results and identified some features of the contagion chains, for example transmission from a family member constituted 42% of infections, usually at the end of the transmission chain. Schwarz analyzed a contagion chain related to an 11-year-old girl that was infected by her father [9]. Although this was a small contagion chain, it illustrated the advantages of this kind of analysis. Cheng covered information on contagion chains in an analysis of the two COVID-19 outbreak waves in Hebei Province, China [10]. Likewise, Hu et al. analyzed a chain of transmission involving 52 linked patients with COVID-19 in three separate hospitals in Wuhan [11].

Furthermore, we found other ontologies focused on representing specific information related to COVID-19. The Long COVID Phenotype Ontology (https://bioportal.bioontology.org/ontologies/LONGCOVID) (accessed on 20 September 2021) represents information to analyze long COVID-19 patients. The COKPME-COVID-19 Ontology (https://bioportal.bioontology.org/ontologies/COKPME) (accessed on 20 September 2021) describes the relative and precautionary measures that can be put in place to control the spread of COVID-19. The COVID-19 Impact on Banking Ontology (https://bioportal.bioontology.org/ontologies/COVID19-IBO) (accessed on 20 September 2021) provides semantic information about the impacts of COVID-19 on the banking sector of India.

On the other hand, several studies applying ontologies in the domain of epidemiology were identified. We found two ontologies [12,13] that represented and analyzed information about COVID-19. The first ontology aimed to represent COVID-19 patient data [13]. Despite the multiple benefits of this ontology, an analysis of contagion chains was outside of its scope. Likewise, the other ontology [12] included a huge number of classes, properties and relations to present and analyze COVID-19 information, although we did not find specifications to analyze contagion chains.

Other studies adopted ontological approaches to analyze infectious diseases or virus behavior in plants and animals [14–16]. The reviewed studies confirmed the potential of ontologies to represent and analyze information from the area of epidemiology or virological analysis. We believe that an ontology that can be used to analyze contagion chains could be useful in supporting the work of those researchers and specialists who are studying the behavior of this disease.

3. Ontology for Representing and Analyzing Contagion Chains

3.1. Tools and Methodology

Among the languages used to specify ontologies [17–22], the following stand out: Loom, CycL, Ontolingua, XML Schema, RDF (Resource Description Framework), RDF Schema (or RDF-S) and OWL 2 (Web Ontology Language). Slimani compared how the most popular languages manage to meet attribute criteria, facet, taxonomy, function and general issue criteria [21]. This analysis showed that OWL 2 had the best results, satisfying 20 of the 21 requirements.

OWL 2 is based on a logic model that makes it possible to define and describe concepts. The OWL 2 model is distinguished by its set of intersection, union and negation operators. It is based on a logic model that defines the concepts as they are described. Furthermore, the possibility of using reasoners allows the consistency of the represented models to be checked automatically. Taking into account its advantages, OWL 2 (hereinafter OWL) was adopted to represent our ontology.

To implement the ontology, the Protégé tool [23], which is an open-source and multiplatform editor developed at Stanford University, was used. It has a flexible and extensible architecture and is recognized as one of the most used tools for ontological engineering. Ontologies created in Protégé can be exported in various syntax, such as RDF/XML and OWL/XML. On the other hand, FaCT ++, Hermit and Pellet reasoners can be used in the inference process.

The adoption of a solid methodology is crucial to obtaining a quality ontology. Therefore, several methodologies were analyzed [17,24,25]. The development of the ontology presented in this research was guided by the methodology proposed by Noy and McGuinness, which has been widely adopted [26]. This is the most used or cited methodology for designing an ontology [27]. It includes the following steps: determine the domain and scope of the ontology, consider reusing existing ontologies, list the relevant terms of the ontology, define the classes and the class hierarchy, define the properties (called relationships or slots) of the classes, define facets or restrictions on slots or relationships and finally define instances.

3.2. Results of the Ontology Development Process

The execution of the methodology described in the previous section allowed us to obtain an ontology to describe and analyze COVID-19 contagion chains. Below the main results of the otology development process are described.

Step 1. Define the domain and scope of the ontology.

The ontology has the objective of providing the mechanisms to represent and analyze information regarding sick patients with COVID-19. Emphasis is placed on the chains of contagion to find information that could be useful in the studies that are developed on the disease. It is based on the premise that certain information on patients in isolation could be of little relevance, although if the analysis is carried out on a chain of contagion, conclusions of interest for the scientific community and for health and government authorities could be obtained. Patterns were identified, the presence of which might warrant a more detailed study to consider possible causes or implications. To specify the objective of the ontology, ten competency questions (CQ) were formulated:

CQ 1. What patients belong to a chain of contagion?
CQ 2. Who has directly or indirectly infected another person?
CQ 3. Which chains include deceased people?
CQ 4. Which chains include people of only one sex exist?
CQ 5. Which chains include patients from different cities?
CQ 6. Which chains include pediatric patients?
CQ 7. Which are long chains?
CQ 8. Which chains exist in which all the members have recovered from the disease?
CQ 9. Which chains include only asymptomatic people?
CQ 10. How long has a certain chain been active?

Step 2: Reuse existing ontologies.

Although we did not find ontologies focused on representing the chains of contagion, we reused several concepts from different ontologies. We used the Bioportal repository (https://bioportal.bioontology.org/) (accessed on 10 September 2021) to search and analyze several ontologies. From the *Semantic Science Integrated Ontology* (https://bioportal.bioontology.org/ontologies/SIO) (accessed on 20 September 2021), we reused the *Medical_Practicioner* class, which is a subclass of the *Person* class. A *Medical_Practicioner* can be a Doctor or Nurse according to the role. We also adopted the *Role* class, *Medical_Role* class and the subclasses of *Medical_Role*. From the ontology Pediatric Terminology (https://bioportal.bioontology.org/ontologies/PEDTERM) (accessed on 20 September 2021), the hierarchy of the *Child* class was adopted. The identification of new concepts that could be reused to enhance our ontology is a future line of our research.

Step 3: List the relevant terms of the ontology.

From the review of the literature and the continuous monitoring of the information regarding the disease, a set of terms that are essential for modeling the ontology was identified. Among the most relevant terms were *person*, *patient*, *chain of contagion*, *classification of patients*, *date of infection* and *symptoms*, among others. These terms of reality constitute the basis for defining the structural elements of the ontology.

Step 4. Define the classes and class hierarchy.

In this step, we carried out an analysis to determine which of the terms defined in the previous step are modeled in the ontology as classes. Finally, 52 classes in the ontology were defined. The classes *Person* and *Contagion_Chain* are two of the main classes in the ontological model. Each of these classes subsumes other classes in order to characterize the individuals that compose it and offer analyses of interest. In Figure 1, the hierarchy of the class *Person* is shown. A diagnosed person with the disease can be classified as *Person_Deceased*, *Person_Recovered* or *Patient_Active*. An active patient can be classified as either *Stable_Patient* or *Severe_Patient*. In addition, a patient in a state of significant seriousness, with danger to their life, is classified as *Critical_Patient*. Additionally, the class *Patient_Asymptomatic* was included due to the high number of patients with this behavior and precisely because it is one of the characteristics that considerably influences the high transmissibility of the virus.

On the other hand, the hierarchy of the class *Contagion_Chain* that is shown in Figure 2 is also interesting. The defined classes in OWL (highlighted in the figure with the darker background) are a type of class to which necessary and sufficient conditions are defined. Therefore, a reasoner can automatically infer the individuals that belong to these classes. Taking advantage of these potentialities, several classes were defined to classify the contagion chains. The expressive richness of OWL 2 made it possible to define the necessary and sufficient conditions for various types of contagion chains, which will be explained in step 6.

Step 5: Define properties.

There are two types of properties in an ontology, *object properties* and *data properties*. Object properties are relationships between two individuals. In OWL, to restrict the classes that can use a property, the domain and range must be defined. For example, an individual of the class *Contagion_Chain* *Is_Chain_Of* individuals of the class *Person*. In this case, the property *Is_Chain_Of* has the classes *Contagion_Chain* and *Person* as the domain and range, respectively. Due to space limitations, only the properties of the classes *Person* and *Contagion_Chain* are included in Table 1, although the ontology includes 29 object properties in total. Furthermore, since object properties allow binary relationships to be established between individuals, each property has an inverse property. For example, the property *Was_Directly_Infected_By* has the inverse property *Infected_Directly_To* which allows one to establish that whether A *Infected_Directly_To* B then B *Was_Directly_Infected_By* A.

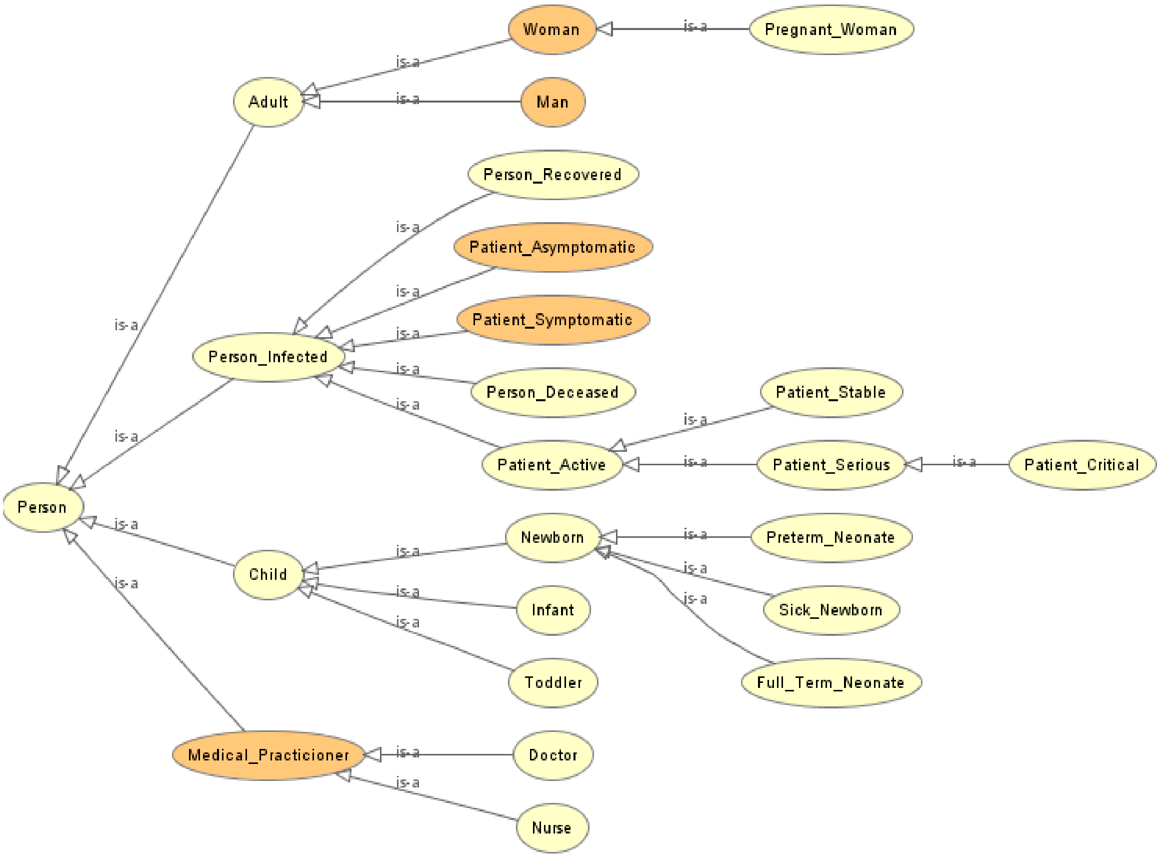


Figure 1. Hierarchy of the class *Person*.

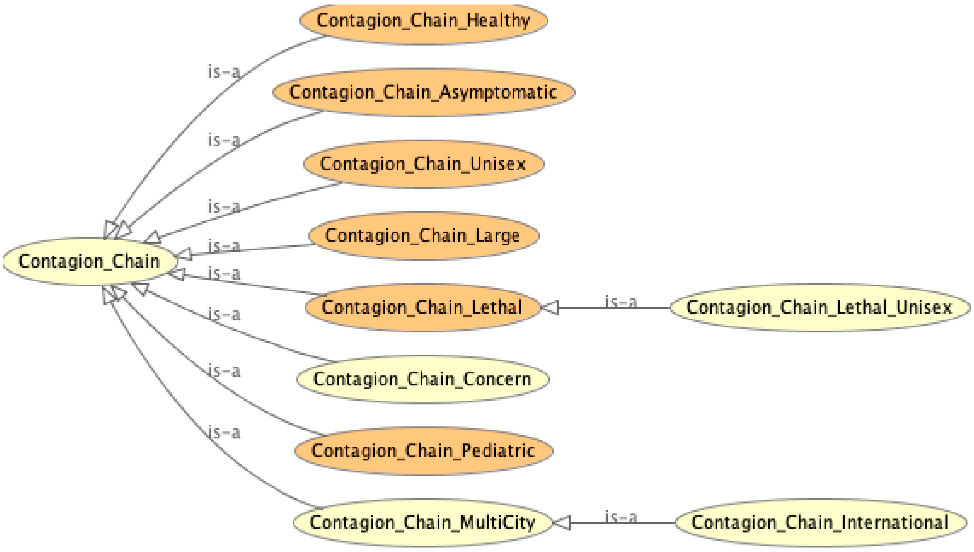


Figure 2. Hierarchy of the class *Contagion_Chain*.

Table 1. Object properties of the classes *Person* and *Contagion_Chain*.

Domain	Property	Range
Contagion_Chain	*Is_Chain_Of* *Has_First_Case* *Has_Last_Case*	Person
Person	*Was_Directly_Infected_By* *Was_Directly_Infected_By*	Person
Person	*Has_Sympton*	Sympton
Person	*Lives_In_Municipality*	Municipality
Person	*Is_Infected_With*	Virus

On the other hand, some data properties were also specified. Table 2 depicts the data properties of the classes *Person* and *Contagion_Chain*.

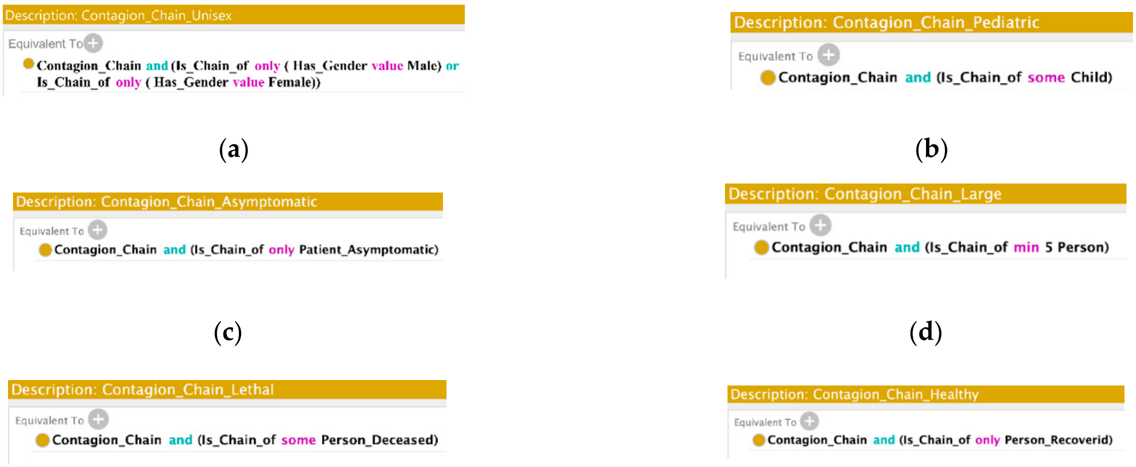
Table 2. Data properties of the classes *Person* and *Contagion_Chain*.

Domain	Data Property	Range
Contagion_Chain	*Has_Date_Start* *Has_Date_End*	DateTime
Person	*Has_Name*	String
Person	*Has_Birth_Date*	DateTime
Person	*Has_Contagion_Date*	DateTime

Step 6. Define restrictions.

In this step, a set of existential, universal and cardinal constraints was defined. The set of restrictions for some defined classes are described below.

As a necessary and sufficient condition for the class *Contagion_Chain _Unisex*, it was defined that it could only have people of the same sex. In this case, a universal restriction was defined, characterized in OWL by the expression *only*, as shown in Figure 3a. For the class *Contagion_Chain_Pediatric*, it was defined that there should be at least one child in the chain. This was modeled from an existential constraint, identified in OWL by the expression *some*, as shown in Figure 3b.



Description: Contagion_Chain_Unisex
Equivalent To
Contagion_Chain and (Is_Chain_of only (Has_Gender value Male) or Is_Chain_of only (Has_Gender value Female))

(**a**)

Description: Contagion_Chain_Pediatric
Equivalent To
Contagion_Chain and (Is_Chain_of some Child)

(**b**)

Description: Contagion_Chain_Asymptomatic
Equivalent To
Contagion_Chain and (Is_Chain_of only Patient_Asymptomatic)

(**c**)

Description: Contagion_Chain_Large
Equivalent To
Contagion_Chain and (Is_Chain_of min 5 Person)

(**d**)

Description: Contagion_Chain_Lethal
Equivalent To
Contagion_Chain and (Is_Chain_of some Person_Deceased)

(**e**)

Description: Contagion_Chain_Healthy
Equivalent To
Contagion_Chain and (Is_Chain_of only Person_Recoverid)

(**f**)

Figure 3. Definition of different types of *Contagion_Chain*: (**a**) *Contagion_Chain_Unisex*; (**b**) *Contagion_Chain_Pediatric*; (**c**) *Contagion_Chain_Asymptomatic*; (**d**) *Contagion_Chain_Large*; (**e**) *Contagion_Chain_Lethal*; (**f**) *Contagion_Chain_Healthy*.

For the class *Contagion_Chain _Asymptomatic*, it was defined that all members of the chain should be asymptomatic. For this, a universal restriction was defined, as shown in Figure 3c. For the class *Contagion_Chain _Large*, a cardinal constraint was created, which defines that a chain must have at least 5 people, as illustrated in Figure 3d. This threshold was established as an example; in a real environment it would be higher. The *Contagion_Chain _Lethal* includes at least one deceased person among its members. Therefore, it was defined as an existential constraint, as shown in Figure 3e. Additionally, it was defined that in a *Contagion_Chain_Healthy*, all members are recovered people. Therefore, it was also defined by a universal relation, as shown in Figure 3f.

A *Contagion_Chain_Multi_City* has members of different cities. To identify the instances of the class *Contagion_Chain_Multi_City*, certain rules in Semantic Web Rule Language (SWRL) were stated. The time of a chain can be known through the dates of its first case and its last case. This was modeled with SWRL as well.

Step 7. Define instances.

In this step, individuals were defined for the specified classes and the corresponding axioms were established. The results of this step are explained in the next section by means of a case study. Through the case study, the applicability and usefulness of the developed ontology is demonstrated.

3.3. Ontology Validation

To validate the ontology, we checked that (a) it met the specifications as a formal–logical system and (b) it satisfied the requirements for which it was created. To verify that the specifications as a formal–logical system are fulfilled, a reasoner is used. In this case, we used the reasoner Pellet, which confirmed that the ontology was consistent. It should be noted that the evaluation of the ontology is an iterative and progressive process. Throughout the life cycle of ontology development, we continually used the reasoner to verify the consistency of the ontology.

In addition, the last version of the ontology was evaluated using the OntOlogy Pitfall Scanner (OOPS!) (http://oops.linkeddata.es/index.jsp) (accessed on 10 November 2021) [28]. After three iterations, all problems detected by OOPS were addressed. This evaluation helped us to detect and correct certain pitfalls in our ontology.

To demonstrate that the ontology satisfied the requirements for which it was created, we carried out a case study. In this study case, we verified that all competency questions were answered correctly by the ontology. This study case, described in the next section, also illustrates the usefulness and applicability of our ontology.

4. Case Study

To illustrate the usefulness and applicability of the ontology, a case study is presented below. The contagion chains shown in Figure 4 will be modeled in the ontology. *Patient_1* infected to patients 2, 5 and 9. In the figure, the color of the number of patients shows their sex (red for male and blue for female). There are three chains: 1-2-3-4, 1-5-6-7-8 and 1-9-10-11-12. Additionally, as the caption of Figure 4 shows, some patient information is indicated. The modeling of this information in the ontology is illustrated below. Likewise, how the reasoning capacity of this ontological model is exploited to answer the competency questions defined in step 1 of the Section 3 is explained.

In Figure 5, different views of Protégé indicating how the information from Figure 4 was represented in the ontology are shown. Figure 5a shows the patients belonging to the class *Man*, Figure 5b illustrates that *Patient_3* belongs to the class *Patient_Deceased* and Figure 5b shows the patients that belong to the class *Patient_Asymptomatic*. Finally, Figures 5c and 5e show the municipalities of *Patient_2* and *Patient_3*, respectively.

In addition to the individual information for each patient, certain mechanisms to identify the contagion chains were defined. Through the property *Directly_Infected_To*, it is specified that *Patient_1* infected to patients 2, 5 and 9. Subsequently, direct transmission of the rest of the patients can be established. After those statements, the reasoner is able to infer that *Chain_1* contains patients 1, 2, 3 and 4, responding to CQ 1. In Figure 6a, the inference of the reasoner is shown (inferences in Protégé are shown with the yellow background). To achieve this inference, the property *Infected_To* is defined as transitive, exploiting the expressive richness of OWL. Furthermore, as a subtype of this property, *Directly_Infected_To* is defined. In this way, the traceability of all the people who indirectly infected a specific patient is achieved, as shown in Figure 6b for *Patient*_8.

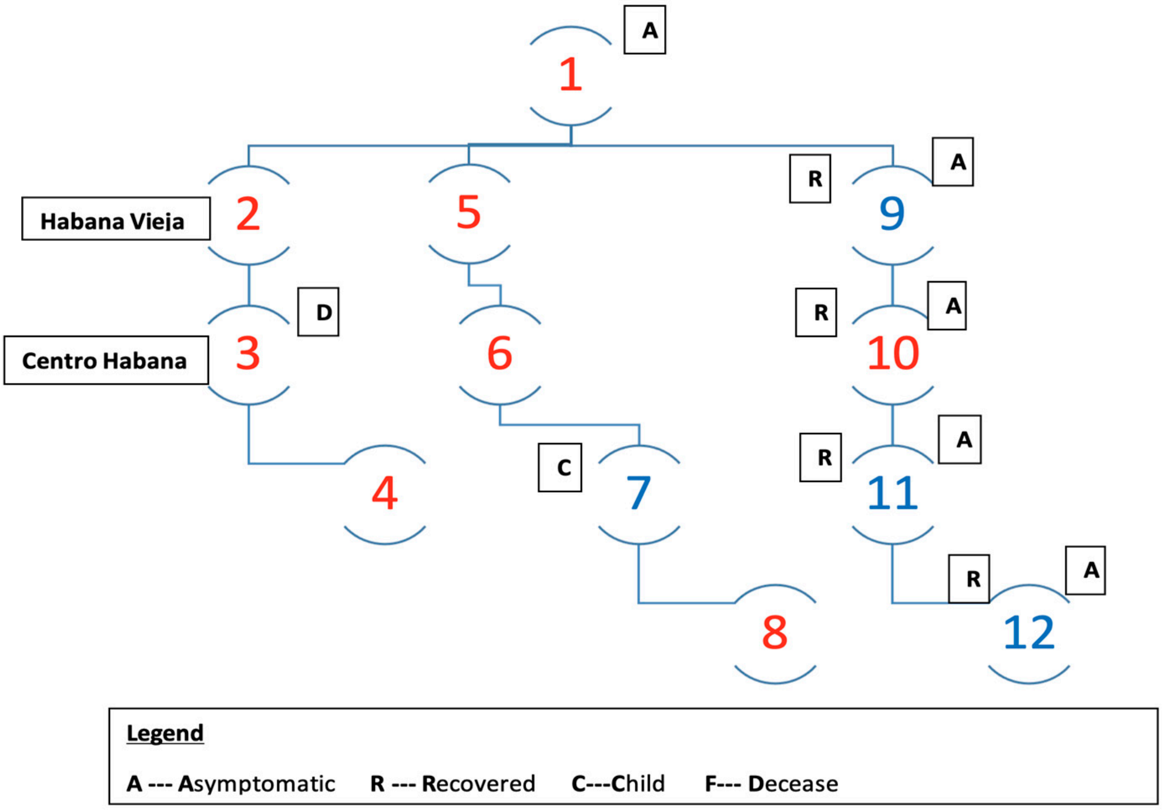
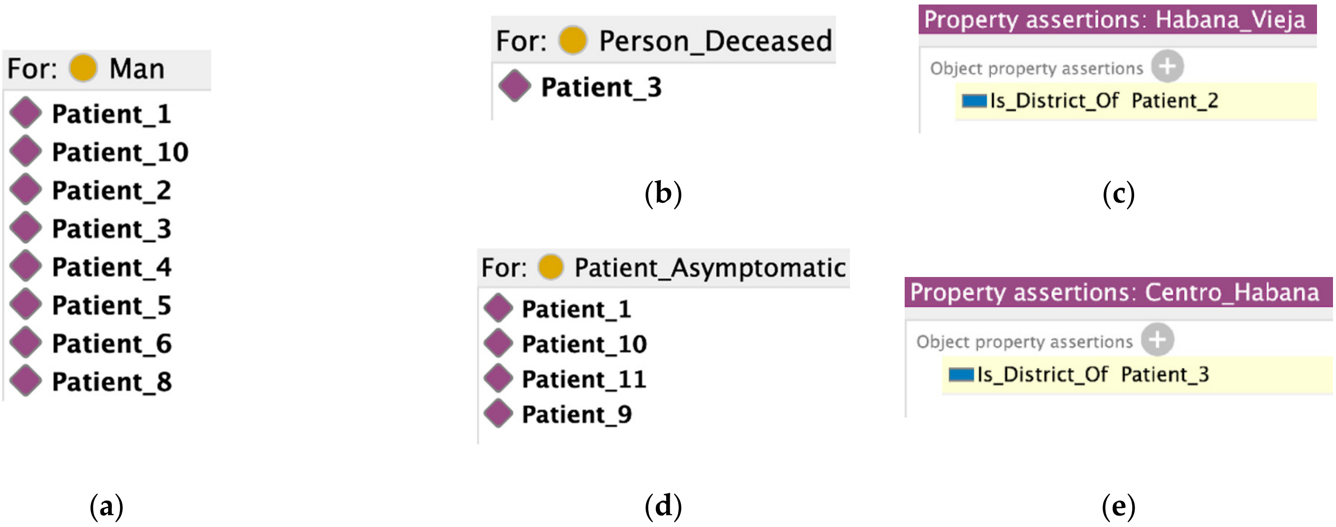


Figure 4. Example of contagion chains.



For: Man

- Patient_1
- Patient_10
- Patient_2
- Patient_3
- Patient_4
- Patient_5
- Patient_6
- Patient_8

(a)

For: Person_Deceased

- Patient_3

(b)

Property assertions: Habana_Vieja

Object property assertions

Is_District_Of Patient_2

(c)

For: Patient_Asymptomatic

- Patient_1
- Patient_10
- Patient_11
- Patient_9

(d)

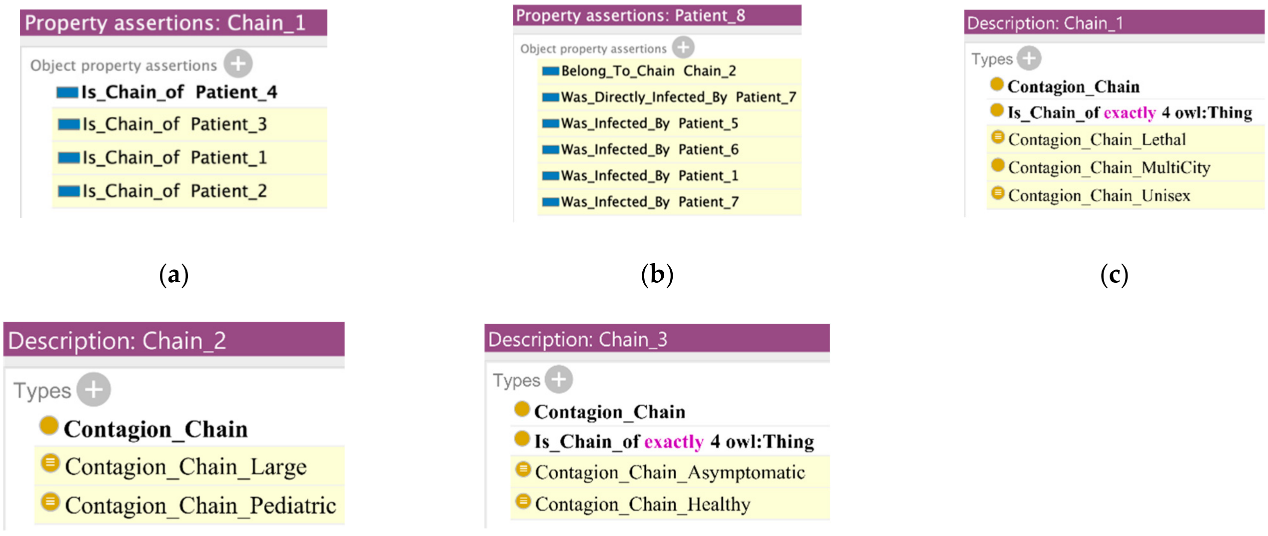
Property assertions: Centro_Habana

Object property assertions

Is_District_Of Patient_3

(e)

Figure 5. Representation of patient information: (**a**) Individuals of the class *Man*; (**b**) Individual of the class *Person_Deceased*; (**c**) District of *Patient_2*; (**d**) Individuals of the class *Patient_Asymptomatic*; (**e**) District of *Patient_3*.



Property assertions: Chain_1

Object property assertions

Is_Chain_of Patient_4

Is_Chain_of Patient_3

Is_Chain_of Patient_1

Is_Chain_of Patient_2

(**a**)

Property assertions: Patient_8

Object property assertions

Belong_To_Chain Chain_2

Was_Directly_Infected_By Patient_7

Was_Infected_By Patient_5

Was_Infected_By Patient_6

Was_Infected_By Patient_1

Was_Infected_By Patient_7

(**b**)

Description: Chain_1

Types

Contagion_Chain

Is_Chain_of exactly 4 owl:Thing

Contagion_Chain_Lethal

Contagion_Chain_MultiCity

Contagion_Chain_Unisex

(**c**)

Description: Chain_2

Types

Contagion_Chain

Contagion_Chain_Large

Contagion_Chain_Pediatric

(**d**)

Description: Chain_3

Types

Contagion_Chain

Is_Chain_of exactly 4 owl:Thing

Contagion_Chain_Asymptomatic

Contagion_Chain_Healthy

(**e**)

Figure 6. Inferences about the contagion chains: (**a**) Members of *Chain_1*; (**b**) Assertions of *Patient_8*; (**c**) Classifications of *Chain_1*; (**d**) Classifications of *Chain_2*; (**e**) Classifications of *Chain_3*.

Since all members of *Chain_1* are male, the chain should be classified as *Contagion_Chain_Unisex*. After modeling it in ontology, as shown in Figure 5a, it can be inferred that *Chain_1* is classified as *Contagion_Chain Unisex*, as illustrated in Figure 6c, thereby responding to CQ 4.

Since it was defined that *Patient_3* belongs to the class *Patient_Deceased*, as shown in Figure 5b, the reasoner classifies *Chain_1* as *Contagion_Chain_Lethal*, thereby responding to CQ 4. It was also defined that patients 2 and 3 live in the district *Habana_Vieja* and *Centro_Habana*, respectively, as shown in Figures 5c and 5e. Therefore, as shown in Figure 6b, *Chain_1* is also classified as *Contagion_Chain_MultiCity*, thereby responding to CQ 5.

The chains that include members that belong to the class *Child* are automatically classified as *Contagion_Chain_Pediatric*. For example, it was defined that Patient_7 is a child, hence, as shows Figure 6d, *Chain_2* is classified as *Contagion_Chain_Pediatric* because it includes *Patient_7*, thereby responding to CQ 6. As explained above, an extensive transmission chain has at least 5 patients. Therefore, since *Chain_2* has 5 members (Figure 4), it is also classified as *Contagion_Chain _Large*, which answers CQ 7.

If all members of a chain are asymptomatic, it is classified as *Contagion_Chain _Asymptomatic*. In this case, as shown in Figure 5d, it is defined that patients 1, 9, 10 and 11 belong to the class *Patient_Asymptomatic*. In addition, since they are all *Patient_Recovered*, *Chain_3* is classified as *Contagion_Chain_Healthy* and *Contagion_Chain _Asymptomatic*, which responds to CQ 8 and CQ 9. Figure 6e shows these inferences.

During the investigation, a group of chains with interesting behavior was identified. The detection of these chains of contagion would allow a more in-depth analysis to be carried out and for possible causes of that behavior to be was created. Additionally, the chains in which a group of patterns are combined could be the ones that should receive the most attention. For example, a chain that consists of patients of only one sex and where all of them are asymptomatic would require an in-depth study.

In this study, a group of chains that could be interesting has been identified. However, the contribution is not in these chains, but in the exploitation of the benefits of OWL to establish the mechanisms to characterize the chains and verify their capacity for analysis. Therefore, this ontology could be enriched with the definition of other types of chains. For example, it would be of interest to verify the behavior of pregnant women who contract the disease or those who have recently had a child.

The results of the automated analysis of the contagion chains could contribute to epidemiological work or to drawing up new strategies by governments considering social behavior. For example, it is possible to analyze the source of contagion of children under one year. Then, according to the results, new communication campaigns could be carried out to reinforce awareness about the care of children or to provide good practices to mothers to keep their children out of danger.

Similarly, an indicator that considers the members of a chain and the time elapsed between the first and the last case could be stated. Thus, a chain with a high value in this indicator could reveal that the appropriate actions for containment are not being followed or that the virus is spreading rapidly for some reason. Additionally, it is possible to incorporate useful indicators for epidemiological work; for example, the basic reproductive index of each patient and the average cases of a chain. These analyses could provide inputs to epidemiological work and could be used to evaluate the actions that have been applied.

Although this study has focused mainly on illustrating the potential of the ontological model to find interesting information for the analysis of contagion chains, some mechanisms have also been defined to perform analyses on individual patients. For example, the class *Disease* was defined, meaning for each patient one can verify which previous diseases they had. Likewise, the class *Symptom* was defined in order to represent the symptoms that a patient may have. In addition, some specifications were established to represent information regarding the vaccines. The correlation of these concepts is planned for our future work.

On the other hand, this ontological model can be queried by several types of software agents that support OWL to find relevant information. Furthermore, some languages to query the ontology can be exploited, for example SPARQL [29]. The ontology can be downloaded at [30].

5. Conclusions

In this work, an ontology developed for representing and analyzing information on COVID-19 infection chains has been described. The way that the expressive richness of OWL is exploited to represent different aspects of the chains of contagions has been illustrated. From this ontological model, an automated analysis of the information can be carried out and inferences of interest can be reached for the follow-up of the disease. The ontology was developed following a solid methodology that helped to ensure its quality. The validation of the ontology confirmed that it is correctly designed, it meets the specifications as a formal–logical system and it satisfies the requirements for which it was created. We illustrated by means of a study case the applicability of this ontological model. This approach could be a useful tool to support epidemiological work, especially in countries where rigorous monitoring of contagion chains has proven to be an effective strategy to contain the virus.

It is not the objective of this work to substitute other approaches. The main objective is to provide the community with a new alternative and to contribute to the struggle against COVID-19. We plan to continue this research plans in two directions. First of all, the ontology will be integrated with others that share concepts regarding epidemiology and diseases, for example Infectious Disease Ontology (IDO) [31] and others [12,32–34]. Then, the development of an information system based on the ontological model will be proposed. Although the motivation for this research is the study of COVID-19, the resulting ontology can be used to represent and analyze the behavior of other transmitted diseases between humans, for example HIV.

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