

The role of Ontology Matching in Ontology Network Development

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Abstract

Ontology networks (ON) have been arising as robust frameworks for organizing, linking, and managing vast amounts of information across different domains. However, the development of an ontology network requires the establishment of accurate and robust intra-domain and inter-domain relationships. Intra-domain relationships refer to connections between concepts from different ontologies from the same domain, while inter-domain relationships involve connections across different domains. We believe that ontology matching can play a crucial role when creating these relationships, as ontology matching serves as a pivotal mechanism for aligning and integrating ontologies to enable meaningful interactions between various domains. Through ontology matching, disparate ontologies can be harmonized and linked, thereby facilitating effective knowledge sharing and interoperability. In this paper, we focus on constructing intra-domain links using a voting-based matching approach. In particular, these links are generated using a voting system using the alignments generated by a number of well-known matching systems.

Keywords

Ontology matching, Ontology network, Alignment, Voting

1. Introduction

In the rapidly evolving landscape of knowledge representation and data integration, ontology networks (ON) have emerged as powerful frameworks for organizing, linking, and managing vast amounts of information. An ontology network or a network of ontologies is a collection of individual ontologies interconnected through various relationships, including alignment, modularization, and dependency relationships [1]. These networks, comprised of foundational, core, and domain ontologies, play a pivotal role in facilitating interoperability between diverse domains and bridging the gaps between domain-specific knowledge bases [2]. ONs can also help to overcome the limitations of single ontologies, such as the lack of coverage of a particular domain or the lack of interoperability with other ontologies. By leveraging existing ontologies rather than developing them from scratch, the creation and expansion of ontology networks can be significantly streamlined, resulting in accelerated progress and increased adaptability.

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Our work has been motivated by several perceived needs in the research community:

In contemporary scientific research, interdisciplinary studies often span multiple domains, incorporating diverse data sets, experiments, computational processes, and machine learning techniques. Provenance, which captures the origin and history of scientific data and processes, plays a critical role in ensuring research reproducibility and transparency. Consequently, researchers need to incorporate provenance representations to provide a comprehensive account of the entire scientific study. To facilitate reproducibility, ontologies are utilized to describe the provenance of data, steps, intermediary, and final results [3]. Given the complexity of reproducibility and the diverse requirements for describing provenance and metadata in various research projects, constructing a large monolithic domain to encompass all these aspects is unfeasible. Consequently, we propose organizing ontologies for describing scientific studies as an Ontology network.

A second current use case for ontology development can be observed within different NFDI (National Research Data Infrastructure)¹ consortia in Germany. The NFDI aims to create a common, sustainable infrastructure for research data management in Germany. It is composed of around 30 discipline-specific consortia. In the following, we focus on NFDI-MatWerk, the consortium for material sciences and engineering. Similar issues exist in many of the other domains, though. NFDI-MatWerk, explicitly addresses the significant role of ontology matching². Ontology matching is the process of identifying and aligning concepts and relationships between two or more ontologies [4]. One crucial use case involves establishing connections between domain-specific ontologies and application ontologies with more general or foundational ontologies. This process plays a vital role in enabling interoperability between various sub-domains and is essential for linking different sub-domains within the NFDI-MatWerk framework. Furthermore, ontology matching serves as a prerequisite for creating a well-connected “network” of ontologies across different NFDI consortia. The successful alignment and integration of ontologies from various consortia enable the establishment of strong intra-domain and inter-domain relationships, enhancing the overall coherence and comprehensiveness of the NFDI infrastructure. This is essential, as many scientific questions require integration of data in the responsibility of several different NFDI consortia.

The primary aim of this study is to explore the inherent potential of ontology matching techniques in developing ontology networks. Our proposed ON is based on a three-level architecture comprising foundational, core, and domain ontologies. We curate ontologies from various domains, utilize multiple well-known matching systems for generating alignments, and adopt a voting-based matching approach to create intra-domain links.

2. Related Work

Ontology networks establish connections between multiple ontologies, utilizing various relationships such as mapping, modularization, and versioning [5]. Recent literature showcases numerous studies implementing diverse methodologies to develop ontology networks across

¹<https://www.nfdi.de/>

²<https://nfdi-matwerk.de/infrastructure-use-cases/iuc12-alignment-of-application-and-higher-level-ontologies>

multiple domains [2, 6, 7, 8, 9, 10]³.

A comprehensive Ontology Network for Diabetes Mellitus in Mexico was developed, incorporating six distinct domains and introducing new classes by leveraging ontological and non-ontological resources, resulting in 1367 classes, 20 object properties, 63 data properties, and 4268 individuals sourced from seven different ontologies [9]. The methodology comprises several steps, commencing with defining network elements and participating domains, along with their scope, and performing ontological engineering tasks such as design, reuse, population, and evaluation, with a particular emphasis on the concept of ON. In their approach, the ontology integration process involves several steps: determining the base ontology for enrichment, identifying elements with similar names, conducting semantic verification, analyzing the representation of common elements (classes, instances, and properties), determining the final structure, and evaluating the resulting ontology. In analyzing the representation of common elements, they found that the best option is to convert the lowest classification levels to instances and to instance them from the immediate superior class. Our approach emphasizes on voting-based matching for intra-domain links, while their work explores ontology integration and new class introductions in specific domains.

SEON, a software engineering ontology network (ON) [2], consists of a foundational ontology, two core ontologies, and several domain-specific ontologies pertaining to subdomains within software engineering. The alignment process of SEON involves integrating ontologies grounded in the foundational ontology and linking concepts based on their shared base type. They have implemented *NeOn* methodological guidelines [1], specifically focusing on ontology modularization, evaluation, and adopting a pattern-based design approach. Simone et al. [8] present a recent approach called HCI-ON, which focuses on developing an ontology network specifically for human-computer interaction. HCI-ON is integrated with SEON, leveraging its existing structure and capabilities. In this approach, new ontologies are incorporated into the ontology network and aligned using their own annotation properties. While SEON and HCI-ON are centered around specific domains (software engineering and human-computer interaction, respectively), our work aims to provide a broader approach to ontology network development across diverse domains.

Ontology matching techniques play a crucial role in ontology network development. OM provides a solution to the issue of semantic heterogeneity by identifying correspondences between semantically related entities across ontologies [4]. A number of ontology matching systems have been developed in the past, demonstrating effective performance in real-world scenarios [11, 12, 13, 14, 15]. These systems typically use a combination of automated and manual techniques to identify correspondences between ontologies. Silva et al. [16] employ ontology matching (OM) techniques to create a network of 28 integrated ontologies, forming a knowledge graph for Explainable AI in personalized oncology. Their approach introduces a novel holistic ontology alignment strategy, using AML [17], which clusters ontologies based on semantic overlap measured by fast matching techniques with a high confidence level, followed by applying more sophisticated matching techniques within each cluster. In contrast, our approach concentrates on developing ontology networks by establishing intra-domain and inter-domain links through a voting-based matching approach, utilizing multiple well-known

³<https://github.com/spice-h2020/SON>, <https://bimerr.iot.linkeddata.es/>, <https://github.com/rapw3k/glosis>

matching systems, including AML, for generating required alignments. They also provide challenges of integrating 28 ontologies to form a KG at three levels: biomedical ontology matching, holistic ontology matching, and holistic ontology integration, in addition to quality, coverage, and scalability. High-quality mappings are vital, considering the minimal human involvement in large-scale tasks. Sufficient coverage of all domains is imperative to ensure comprehensive data description, supporting AI model training and explanations. Lastly, the scalability of the system must be considered due to the extensive processing of a large number of classes and properties from various ontologies. Balancing quality, coverage, and scalability is essential in building a high-quality network of biomedical ontologies.

Santos et al. [18] propose a different approach by utilizing random walks and frequent item sets algorithms to mine data from the networks, identifying relevant candidate entities and then pruning the networks using an algebraic method to remove identical entities, and subsequently reintegrating the relevant nodes to preserve essential correspondences. Foundational ontologies, a part of ONs, also play a crucial role in ontology matching by offering a well-founded reference model that can be shared across diverse domains. In the paper [19], the authors provide an overarching perspective on the various tasks involved in ontology matching, taking into account the incorporation of foundational ontologies. In this paper, we do not currently employ foundational ontologies for matching, but it is a potential avenue for future research. Another paper [20] addresses the problem of adding new information in networks of ontologies based on belief revision using the semantics of networks of ontologies.

A recent work focuses on developing a framework for classifying ontologies that provides a homogeneous environment for ontology network development [21, 22]. It classifies ontologies into reference ontologies, operational ontologies, operational ontologies with a previous reference ontology, and well-grounded ontology. Compared to our proposed ON, we propose a three-layered network, including foundational, core and domain ontologies. The framework investigates different kinds of relationships between ontologies, such as *groundover*, *drive*, *reuse*, and *subontology* relations [21, 22]. It is very important to identify these kind of relationships between ontologies in the ON, but we need first to determine which concepts from different ontologies participate in these different kinds of relationships.

3. Voting-based matching approach

To construct intra-domain and inter-domain connections across given sets of ontologies, we develop a voting system that makes use of at least three well-known matching systems. The general architecture of the voting system has a number of components as shown in Fig. 1, including *data ontology curating*, *matching*, *voting* and *validating*. In the following, we are going to describe these components. Throughout the description we will use the creation of an ontology network for provenance information as a running example. The motivation for establishing this ontology network is elaborated in our previous work [23].

3.1. Ontology curation

Our study aims to develop an ontology network for seamlessly integrating data from diverse scientific studies within an interdisciplinary research project. To achieve this, we integrate

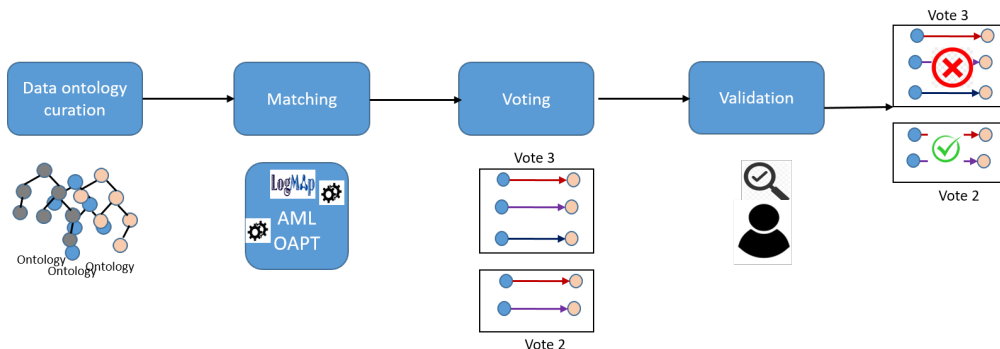


Figure 1: General pipeline of the proposed approach.

existing ontologies from various domains rather than building them from scratch. Our proposed architecture adopts a three-layer view, comprising foundational, core, and domain ontologies, with the aim of integrating diverse aspects of provenance of scientific study, which includes both computational and non-computational aspects across multiple applications [3], thus promoting reproducibility support. We identified existing ontologies in various domains through a systematic literature review based on our research requirements [3, 23]. Utilizing Google Scholar, we specifically focused on the areas of *Scientific Experiments*, *Machine Learning*, *Microscopy*, *Computational*, *Scientific Workflows*, and *Provenance* to compile a comprehensive list of ontologies in addition to foundational ontologies. In this process, we added additional ontologies to our existing collection⁴.

We found nine ontologies in *Provenance*, seven in *Scientific Experiments*, three in *Microscopy*, nine in *Computational*, six ontologies (thirteen with sub ontologies) in the *Machine Learning* domain, and four foundational ontologies. We collected the year of creation and the last update of each ontology. Furthermore, we conducted checks to verify the current availability and accessibility status of each ontology mentioned in the collected publications. In the next step, we excluded certain ontologies due to their unavailability or being in a format different from the standard ontology format. The resulting list of ontologies from *Scientific Experiments*, *Microscopy*, *Computational* and *Machine Learning* domains⁵, along with their version, number of classes, and properties, is presented in Table 1.

The cumulative number of classes across these domains are **10,259**, while the number of properties amounts to **1659**. Frequently, ontologies undergo regular modifications and are not static. This evolution involves incorporating new domain knowledge, rectifying design errors, or adapting to revised requirements. The active development of certain ontologies is evident in their version or release updates, reflecting ongoing improvements and enhancements (e.g., SMART Protocols, CMPO, EDAM); others remain stable over time (e.g., EXPO, MEX). Additionally, it is worth noting that certain ontologies lack version information. Furthermore, the number of classes varies significantly, ranging from 1 (CSO) to 3473 (EDAM), and the

⁴<https://github.com/fusion-jena/ReproduceMeON>

⁵In this paper, foundational ontologies and ontologies from *Scientific Workflows* and *Provenance* domains are not included in the matching step, but will be taken into consideration in future work.

Table 1

Ontology Dataset used in different domains

Domain	Ontology	Version	No. classes	No. prop.
Machine Learning	MEX	1.0.2	349	265
	MLSchema	1.0	25	14
	BigOWL	6	75	68
	DMOP	5.4	697	193
	OntoDM	1.0	593	40
	OntoDT	1.0	144	7
Computational	Function ontology	1.0	15	16
	WICUS	2.0	35	45
	REPRODUCE-ME	1.1	345	78
	Computer Science Ontology (CSO)	3.2	1	0
	EDAM	1.25	3473	12
	Dockeronto	-	54	62
	Dockerpedia ontology	0.1	29	52
	PAV	2.3.1	2	40
Microscopy	SWO	1.7	1845	48
	CMPO	1.3	1058	28
	OME	v0.2	17	34
	OMERO-RIKEN	-	181	217
	OME-Core	-	107	195
Experiment	REPRODUCE-ME	1.1	345	78
	EXPO	-	325	78
	Investigation, Study Assay (ISA)	1.0	73	29
	SMART Protocols Document Module	4.0	399	43
	SMART Protocols Workflow Module	4.0	417	17
	REPRODUCE-ME	1.1	345	78

number of properties varies from 0 (CSO) to 265 (MEX). In the context of Microscopy, the ontologies exhibit class counts ranging from 17 to 1058, presenting challenges when performing the ontology matching task.

3.2. Matching

In the following, we first analyze our example domain to motivate the need for matching and then introduce our approach to it.

3.2.1. Motivation for matching

Each ontology within the collected set of ontologies models a part of the domain it represents. However, frequently the same piece of information is represented in different ontologies. Sometimes, these representations are similar, sometimes they differ significantly. For example, as shown in Table 1, we collected six ontologies from the ML domain with a number of concepts ranging from 25 concepts (in the MLSchema ontology) to 697 (in the DMOP ontology). Investigating this set of ontologies, we found that it has a number of semantic heterogeneities that must be

<pre> <!-- http://www.w3.org/ns/mls#Dataset --> <owl:Class rdf:about="http://www.w3.org/ns/mls#Dataset"> <rdfs:subClassOf rdf:resource="http://www.w3.org/ns/mls#Data"/> <owl:disjointWith rdf:resource="http://www.w3.org/ns/mls#Feature"/> </owl:Class> </pre>
<pre> <!-- http://www.openmicroscopy.org/rdf/2016-06/ome_core/Dataset --> <owl:Class rdf:about="http://www.openmicroscopy.org/rdf/2016-06/ome_core/Dataset"> <rdfs:subClassOf rdf:resource="http://www.w3.org/2002/07/owl#Thing"/> <rdfs:comment xml:lang="en">Class "Dataset" is collections of images that are always processed together. <rdfs:label xml:lang="en">Dataset</rdfs:label> </owl:Class> </pre>
<pre> <!-- https://w3id.org/reproduceme#Dataset --> <owl:Class rdf:about="https://w3id.org/reproduceme#Dataset"> <rdfs:subClassOf rdf:resource="http://www.w3.org/ns/prov#Collection"/> <rdfs:comment xml:lang="en">An element specifying a collection of images that are always processed together.</rdfs:comment> <rdfs:isDefinedBy rdf:resource="http://www.openmicroscopy.org/Schemas/Documentation/Generated/OME-2016-06/ome_xsd.html#Dataset"/> <rdfs:label xml:lang="en">Dataset</rdfs:label> </owl:Class> </pre>
<pre> <!-- http://www.e-lico.eu/ontologies/dmo/DMOP/DMOP.owl#DataSetClass --> <owl:Class rdf:about="http://www.e-lico.eu/ontologies/dmo/DMOP/DMOP.owl#DataSetClass"> <rdfs:subClassOf rdf:resource="http://www.e-lico.eu/ontologies/dmo/DMOP/DMOP.owl#DM-DataClass"/> </owl:Class> </pre>
<pre> <!-- http://purl.org/isaterms/ISA dataset --> <owl:Class rdf:about="isaterms:ISA dataset"> <rdfs:label>ISA dataset</rdfs:label> <rdfs:subClassOf rdf:resource="isaterms:information"/> <terms:description>An ISA dataset is contains the metadata corresponding to the description of an experiment and it The ISA dataset has to comply with the ISA specification available at the ISA tools website (http://isa-tools.org/). <isaterms:is_a>dctypes:Dataset;http://purl.org/dc/dcmitype/Dataset</isaterms:is_a> </owl:Class> </pre>

Figure 2: Definition of the term "Dataset" in different domains.

aligned before the construction of the ontology network. For example, the term "parameter" has been modeled in all six ML ontologies using different IRIs. It is defined using the ID "http://www.e-lico.eu/ontologies/dmo/DMOP/DMOP.owl#Parameter" in the BigOWL and DMOP ontologies, while different IDs have been used to represent it in the other four ontologies. Indeed, to establish the accurate links between ontologies from the ML domain, it is first required to identify these differently modelled concepts as the same or different object. This is a perfect task for ontology matching.

The situation becomes worse when we attempt to construct links between similar concepts across different domains, as shown in Fig. 2. For example, the term "data" which is commonly used and needed in our use case, is defined using different terms across the five domains, "data", "dataset", "data item", and "datatype". Considering the term "dataset" which is modeled in four domains⁶. In SWO Computational ontology, there is a class called "data item". Also, in EDAM ontology, it is "data", as shown in Fig. 2. The term dataset is defined using IRI <http://www.e-lico.eu/ontologies/dmo/DMOP/DMOP.owl#DataSetClass> in the ML domain, and another IRI <https://w3id.org/reproduceme#Dataset> for the experimental domain. Another example is the term "model". The class "model" has a different meaning in Machine Learning than the term in Microscopy. In Microscopy, the class *model* is a manufacturer specification for a device, while in ML, it is a file created from ML algorithms that has been trained to recognize

⁶We are expecting it to be also modeled in the computational domain if we consider more ontologies from the domain

certain types of patterns based on previous experience or data.

The diversity of representations for ontology elements poses a significant challenge to ontology integration, encompassing issues like synonyms (representing the same thing with different names), homonyms (elements with the same name but different meanings), and varied correspondences between concepts in different ontologies. Without a well-defined strategy for integrating ontologies, inconsistency problems can arise that can alter the operation of ontologies.

3.2.2. Matching Approaches

Once we collected relevant ontologies to construct the ontology network, the arising question is how to establish links between similar concepts from the same domain, *intra-domain links* and links between related concepts from ontologies across different domains *inter-domain links*. In this paper, we focus on the intra-domain connections. To this end, we make use of available matching systems. However, as a matching system exploits specific features from input ontologies to generate alignments, we propose to use not only one matching system but at least three (or any larger uneven number of) available and well-known matching systems to generate the required alignment: *LogMap* [24], *AML* [17], and *OAPT* [12, 14].

Matching tasks: There are two different options to generate matching tasks across ontologies from the same domain, namely *pair-wise matching* and *holistic matching* [16, 25]. In the pair-wise matching scheme, every ontology pair is uploaded, and a matching algorithm is applied; in the holistic matching technique, a matching algorithm is applied to the whole set of ontologies from the same domain. It is unclear which matching outperforms the other, and as our proposed method is based on existing matching systems classified as pair-wise matching systems, we selected the pair-wise matching scheme. This results in $\frac{n \times (n-1)}{2}$ matching tasks for n ontologies in a domain.

Alignment candidate generation: A first step to construct the intra-domain links is to determine similar entities from different ontologies from the same domain. To this end, we generate match candidates using at least three ontology matching systems. We make use of *logMap* [24] and *AML* [17] as they are performing the best for OAEI (Ontology Alignment Evaluation Initiative)⁷ during the last ten years. Furthermore, we use our tool *OAPT* [12], the light version of *LogMap* [15] and *PoMap++* matching system that participated in OAEI 2020 [13]. We run a matching system using one matching task according to the pair-wise scheme we consider. We save the matching result for each task for further investigation. Fig. 3 shows a match result example between two concepts from the REPRODUCE-ME ontology and the CMPO ontology.

This example is taken from the *Microscopy* domain. The figure shows that only four out of the five systems used identify the mentioned correspondence at all. Furthermore, matching systems that are able to discover the same correspondences, assign different similarity values. For example, the two concepts in Fig. 3 are "http://purl.obolibrary.org/obo/PATO_0000140/" with a position as a label and "http://www.w3.org/ns/prov#Location/" with Location as a label. Both *PoMap++* and *LogMapLite* are able to discover this correspondence with a similarity value of 1.0, while the main *LogMap* system can achieve a similarity value of 0.51. The interesting

⁷<http://oei.ontologymatching.org/>

AML	<pre> <map> <Cell> <entity1 rdf:resource="http://purl.obolibrary.org/obo/PATO_0000140"/> <entity2 rdf:resource="http://www.w3.org/ns/prov#Location"/> <measure rdf:datatype="http://www.w3.org/2001/XMLSchema#float">0.8613</measure> <relation>=</relation> </Cell> </map> </pre>
LogMap-lite	<pre> <map> <Cell> <entity1 rdf:resource="http://purl.obolibrary.org/obo/PATO_0000140"/> <entity2 rdf:resource="http://www.w3.org/ns/prov#Location"/> <measure rdf:datatype="xsd:float">1.0</measure> <relation>=</relation> </Cell> </map> </pre>
LogMap	<pre> <map> <Cell> <entity1 rdf:resource="http://purl.obolibrary.org/obo/PATO_0000140"/> <entity2 rdf:resource="http://www.w3.org/ns/prov#Location"/> <measure rdf:datatype="xsd:float">0.51</measure> <relation>=</relation> </Cell> </map> </pre>
POMap	<pre> <map> <Cell> <entity1 rdf:resource="http://www.w3.org/ns/prov#Location"/> <entity2 rdf:resource="http://purl.obolibrary.org/obo/PATO_0000140"/> <measure rdf:datatype="http://www.w3.org/2001/XMLSchema#float">1.0</measure> <relation>=</relation> </Cell> </map> </pre>

Figure 3: An example of the matching result between two concepts from the REPRODUCE-ME ontology and the CMPO ontology.

finding from Fig. 3 is that LogMapLite is not able to determine the correspondence between the mentioned two entities. The example shown in Fig. 3 highlights the importance of using several matchers to increase the chance of finding all relevant correspondences, but also the need to find a way to combine results from different matchers. In our approach, this is achieved via voting.

3.3. Voting

The consensus alignments will be generated by making use of a voting algorithm utilizing alignments generated by different matching systems[26, 27]. A vote considers the number of times a mapping appears in the set of generated alignments by different matching systems. For example, the consensus of vote 3 means that a mapping is proposed by at least three matching systems. In general, the more the votes, the smaller the size of the consensus alignment.

Tables 2 and 3 show the sizes of the consensus alignments for the ML and Experiment matching tasks, respectively, as well as each systems family mappings ratio contribution.

3.4. Validation

After generating different sets of alignments, we carried out a validation process based on our knowledge and experience. Two authors of the paper have manually looked at different alignments. We plan to extend the validation process by involving more domain experts from

System	Vote 2	Vote 3	Vote 4
Total mapping	97	50	28
AML	67	38	28
LogMap	53	30	21
LogMap-Lt	51	43	28
OAPT	52	45	28
POMap	65	48	28

Table 2
Voting for ML domain

System	Vote 2	Vote 3	Vote 4
Total mapping	97	50	28
AML	67	38	28
LogMap	53	30	21
LogMap-Lt	51	43	28
OAPT	52	45	28
POMap	65	48	28

Table 3
Voting for Experiment domain

each domain to cross-validate our initial validation.

4. Resources availability

The resources related to the paper are published on GitHub ‘<https://github.com/fusion-jena/ReproduceMeON>’. This includes the ontology dataset, the methodology used to extract the ontology dataset, matching system results, and the output of the voting algorithm.

5. Conclusion

In conclusion, our paper presents a novel approach for developing ontology networks through the integration of ontology matching techniques, with a specific focus on establishing accurate and robust intra-domain links. By adopting a voting-based matching approach and leveraging multiple well-known matching systems. Even we achieved good progress to establish intra-domain links of ON, however, we plan to extend the validation process to involve more domain experts. Furthermore, once we settle intra-domain links, we will investigate how to use them to establish inter-domain links.

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