

# Biomedical Ontology Matching as a Service

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**Abstract.** Ontology matching is among the core techniques used for integration and interoperability resolution between biomedical systems. However, due to the excess usage and ever-evolving nature of biomedical data, ontologies are becoming large-scale, and complex; consequently, requiring scalable computational environments with performance and availability in mind. In this paper, we present a cloud-based ontology matching system for biomedical ontologies that provides ontology matching as a service. Our proposed system implements parallelism at various levels to improve the overall ontology matching performance especially for large-scale biomedical ontologies and incorporates third-party resources UMLS and Wordnet for comprehensive matched results. Matched results are delivered to the service consumer as bridge ontology and preserved in ubiquitous ontology repository for future request. We evaluate our system by consuming the matching service in an interoperability engine of a clinical decision support system (CDSS), which generates mapping requests for FMA and NCI biomedical ontologies.

**Keywords:** Biomedical Ontologies, Ontology Matching, Cloud Computing, Software as a Service

## 1 Introduction

Over the recent years, semantic web technologies especially ontologies are contributing in biomedical systems for greater benefit. These ontologies are getting used for annotation of medical records [1], standardization of medical data formats [2], medical knowledge representation and sharing, clinical guidelines (CG) management [3], clinical data integration and medical decision making [4]. As a consequence of this vast usage, biomedical researchers are investing more time in generating more and comprehensive biomedical ontologies. Therefore, biomedical community has in depth ontology repository like Open Biomedical Ontologies (OBO) [9]; furthermore, biomedical ontologies like the Gene Ontology (GO) [5], the National Cancer Institute Thesaurus (NCI) [6], the Foundation Model of Anatomy (FMA) [7], and the Systemized Nomenclature of Medicine (SNOMED-CT) [8] have emerged.

Biomedical ontologies are complex in nature and contain overlapping information. Utilization of this information is necessary for the integration, aggregation, and interoperability; for example, the plethora of web-based medical

information resources provides related information over the Internet. If these resources are annotated by ontologies, software agents can automatically aggregate information for biomedical professionals and biomedical querying systems. For example, NCI ontology defines the concept of “Myocardium” related to the concept “Cardiac Muscle Tissue”, which describes the muscles surrounding the human heart. Concept “Cardiac Muscle Tissue” is defined in FMA ontology; therefore, a biomedical professional or a system integrating knowledge regarding human heart requires mappings between candidate ontologies FMA and NCI [10]. Likewise, GO is a highly organized structure of medical knowledge facilitating medical genetics. It is widely used by biomedical researchers in numerous genetical research fields including gene group-based analysis for discovering the hidden links overlooked by the single-gene analysis [11]. Finding mappings between GO ontology and FMA ontology can be used by molecular biologist in understanding the outcome of proteomics and genomics in a large-scale anatomic view [12]. Moreover, mappings by ontology matching have also been used for heterogeneity resolution among various health standards [13].

Ontology matching systems developed over the years have taken biomedical ontologies into consideration and have implemented possible resolutions. However, these resolutions are more focused on optimization of the matching algorithms and partitioning of larger ontologies into smaller chunks for performance benefits [14]. In case of biomedical ontologies, matching algorithms utilize third-party resources like Unified Medical Language System (UMLS) [15] and WordNet [16]. Slow and comprehensive nature of these resources adds onto the performance bottlenecks during matching. Ontology matching being a quadratic complexity problem with an addition of slow third-party resources can go to a certain extent in gaining performance by optimizing only the algorithms over localized computational resources. Furthermore, these ontology matching systems are tools with confined deployments, which can be utilized locally with very limited computational ability and scalability over time. Therefore, an opportunity emerges of building a biomedical ontology matching system that can improve or sustain the ontology matching performance. Such system should not only be confined as a localized deployment; it should be a shareable resource of ontology matching that is available for biomedical researchers and biomedical systems to benefit from. So far in ontology matching, the performance improvement based on exploitation of newer hardware technologies has largely been missed. Among these technologies are affordable parallel systems which are easily available as distributed platforms [17]. One such platform is Cloud Computing.

This paper presents a biomedical ontology matching system that benefits from the cloud resources and provides biomedical ontology matching as a service to the consumer. Our proposed system avails the opportunity of multicore nature of cloud instances and performs parallel ontology loading and matching to improve overall ontology matching performance. Even with utilization of slow third-party resources, the performance fall is far less due to its parallel nature. Matched results are returned to the consumer as a bridge ontology and preserved in a centralized ontology repository for the same matching requests in future.

Due to the ubiquitous nature of the cloud, matching services are available for researchers and biomedical systems without downtime.

The rest of the paper is organized as follows. In Section 2 we describe the related work in the field of biomedical ontology matching. Section 3 provides the details of our proposed system. Section 4 describes a preliminary evaluation of our system performed by consuming the matching service in an interoperability engine of a Clinical Decision Support System (CDSS). Section 5 concludes this paper.

## 2 Related Work

Among the systems for biomedical ontology matching, SAMBO [18] is a pioneering system which provides a framework for aligning and merging ontologies. SAMBO's implementation is focused towards its matcher algorithms which integrates WordNet, UMLS, and PubMed [19] as third-party resources. Despite the fact that this integration is highly beneficial for accuracy, slow nature of these resources creates performance bottlenecks while matching. To overcome this bottleneck, SAMBO fails to provide any resolution.

Similar to SAMBO, ASMOV [20] with its computational performance directly associated with its matching algorithms, authors of [20] acknowledged that effort is required to improve the computational complexity of the system. With high coupling between ASMOV's performance and computational complexity of matching algorithms, and its sequential execution, it is unlikely for ASMOV to avail any performance benefits from parallel platforms.

ServOMap [21] is another biomedical ontology matching system, but built with the motivation of matching large-scale biomedical ontologies. Instead of using lexical resources like WordNet and UMLS, ServOMap relies on information retrieval and ontology repository technique. ServOMap does not implement any performance gain techniques that can exploit parallelism over available multicore platforms for the benefit of biomedical ontology matching.

In current state-of-the-art generic ontology matching systems, i.e., AgrMaker [22], LogMap [23], and GOMMA [24], performance has been given a considerable focus to complement accuracy of these systems. AgrMaker with its tightly integrated implementation between matching algorithms and the system's user interface, relies on user interactions and feedback. Performance of AgrMaker depends upon the iterative execution of matching algorithms as sample set for the following matching algorithms gets reduced. LogMap, is claimed as highly scalable from the perspective of ontology matching; however, this scalability is not of any parallel or distributed nature. After further research, it was found that one of the LogMap's associated research group has proposed a concurrent classification approach for reasoning over ontologies; nonetheless, its utilization for improving performance during ontology matching in LogMap is unclear. GOMMA on the other hand, implements parallelism with its techniques mentioned in [25] and [14]. In [25], authors acknowledge the fact that very little research has been performed in devising parallelism for matching problems; furthermore, it de-

scribes size-based partitioning scheme to perform parallel matching. Research presented in [25] discusses entity matching in general with no concentration or evaluation over ontologies. In [14] however, authors specifically discuss parallelism techniques pertaining to life science ontologies. They propose inter- and intra-matcher parallelism techniques, which uses parallel and distributed infrastructure for ontology matching to achieve better performance.

In contrast with above-mentioned techniques and systems, the focus of our proposed system is on facilitating the consumers with ontology matching as a service. Instead of localized implementation, it is deployed over cloud platform and scales according to the usage needs. To provide a performance efficient solution it implements parallelism at various levels. As the performance gain in our system is achieved by exploiting the parallelism from the multicore cloud instances, our system contributes largely to overcome performance bottlenecks encountered by using slow third-party biomedical resources and thesauri (e.g., UMLS, PubMed, and WordNet).

### 3 Methodology

Overall stack-like architecture of our proposed system is illustrated in Fig 1. The primary objective of our system is to exploit the available resources of cloud platform and provide a service-based interaction to our system, taking the benefit of the ubiquitous nature of the cloud computing.

Request of matching biomedical ontologies can be generated from several resources including, biomedical professionals and researchers, biomedical and bioinformatics system, or even third-party healthcare information services running over cloud platforms. Match request encapsulates the ontologies to be matched as source and target ontologies. Matched results are returned to the consumer as bridge ontology.

Starting from the top of the stack illustrated in Fig. 1, Consumer Interaction component provides an ontology matching RESTful web service for clients to consume. The matching service provides four trivial arguments as service bindings for consumption.

1. *match ( sourceOntologyURI/File, targetOntologyURI/File )*
2. *match ( sourceOntologyURI/File, targetOntologyURI/File, returnEmail)*
3. *match ( sourceOntologyURI/File, targetOntologyURI/File, matchingAlgorithms [ ])*
4. *match ( sourceOntologyURI/File, targetOntologyURI/File, matchingAlgorithms [ ], returnEmail)*

Among the arguments, collection of matching algorithms and return email are extended parameters used for matching request customization. In case of first request, all the algorithms present in the matching library will execute. This matching will take more time; however, will have higher accuracy. In case of trivial and far less complicated ontologies, consumer can select the matching algorithms to be executed as collection of matching algorithms (Request 3 and 4).

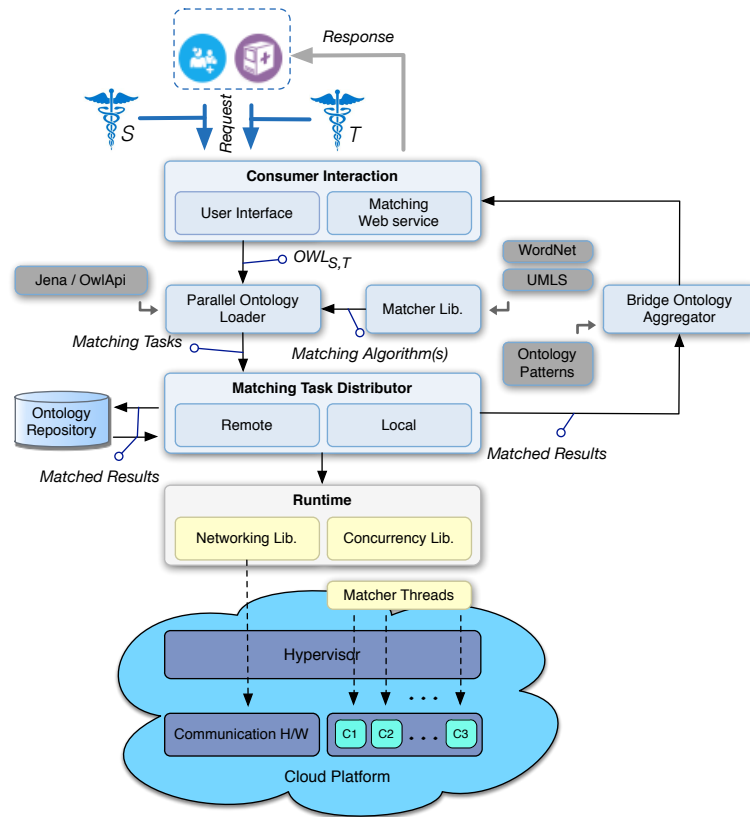


Fig. 1. Proposed architecture

For large-scale ontologies, where the evaluation time can exceed from 20 minutes or later, URL of the bridge ontology to-be is provided and can be returned over a particular email address (Request 2 and 4). After matching, the active URL will reference the bridge ontology.

Adjacent to the Web service, Consumer Interaction component encapsulates the matching web service in a user interface (UI). This UI provides a web-based direct interaction between a biomedical professional or a researcher who wants to benefit from matching service and our system.

Parallel Ontology Loading component benefits from the multicore nature of cloud instances and loads the source and target ontologies by thread-level parallelism. These ontologies are parsed in parallel and populated in multiple thread-safe ontology model objects. Each object encapsulates the information required by a single matching algorithm during runtime. Furthermore, redundancy like URI based names of concepts etc., is removed during this process. This keeps the system to load un-necessary and redundant information in main memory during

execution, preventing memory strains at runtime. For ontology parsing, available OWL frameworks, Apache Jena and OWLAPI are used. Although these frameworks provide comprehensive ontology models; due to these models not being thread-safe, our system provides its own ontology model implementation.

Matcher Library component provides a library of ontology matching algorithm. These algorithms are classified into primary, secondary, and complementary type. Primary algorithms execute for every matching request, secondary algorithms execute for higher accuracy, and complimentary algorithms execute with respect of ontology scope. Matcher Library also utilizes external third-party resources, i.e., WordNet and UMLS for higher accuracy in secondary and complementary type algorithms.

Matching Task Distributor component partitions the candidate ontologies as subsets and assigns over to the computing cores available. Several partitioning schemes including size-based and complexity-based partitioning are used. For local resources, matcher threads are assigned to perform parallel matching invoking available cores. For remote resources, control messages are generated for participating nodes regarding their chunk of partition to work and matching algorithm to execute. Each node after receiving the control message loads performs parallel matching over their available computing cores.

Every participating node(s) generates their respective matched results. Bridge ontology aggregator, accumulates these results and generate a bridge ontology file. Bridge ontology aggregator provides an interface to bridge ontology patterns to be used for pattern-based bridge ontology generation. Bridge ontology file is returned as a response or a URL to physical file to the consumer. This ontology is also be persisted in ontology repository for future use in case of same matching requests.

## 4 Evaluation

We have evaluated our system over a tri-node private cloud platform. Each Virtual Machine is equipped with 4 cores, 4 GB RAM, and Windows 7 based guest OS. These VMs are hosted over a Xen Hypervisor using Intel(R) Core(TM) i7 CPU, and 16 GB of memory as infrastructure.

For execution scenario, matching web service is consumed by an interoperability engine of a clinical decision support system (CDSS). Matching requests encapsulates small and whole versions of FMA and NCI biomedical ontologies for small and large matching requests respectively. All primary matching algorithms with quadratic or higher computational complexity were executed for this evaluation and the results are described in the following table.

As it can be seen from results, a substantial amount of time is taken by ontology loading in contrast with matching which is a more complicated task. Although source and target ontologies are loaded and parsed in parallel, the time taken is due to the slow single-threaded nature of Jena. If Jena is replaced with a performance-based ontology parser, a substantial improvement in performance can be seen, especially in case of large matching requests.

	Parameter	Small Request	Large Request
	Loading Time	11.2s	52.2m
	Matching Time	19.3s	228m
<b>Total Time</b>		30.47s	4.65hr
<b>F-Measure</b>	Refined UMLS	0.857	0.710
	Original UMLS	0.863	0.715

Table 1: FMA with NCI evaluation

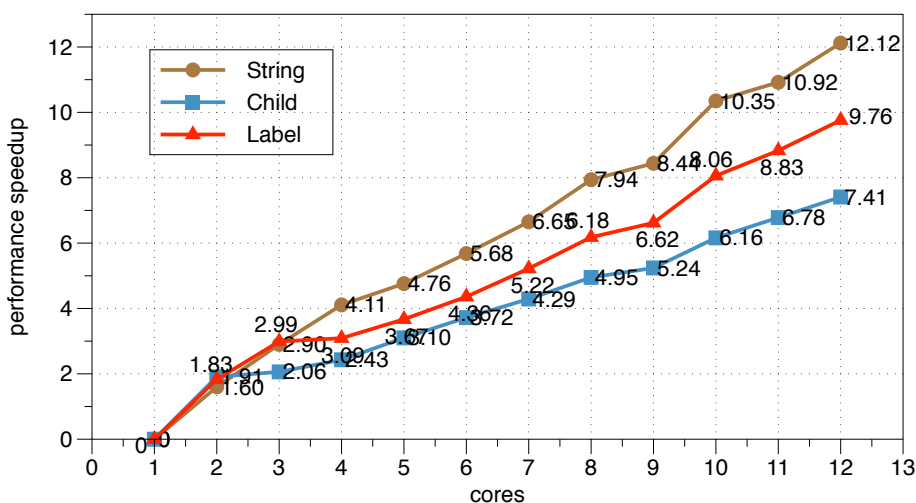


Fig. 2. Matching request scaling over cloud

To evaluate the scaling of the larger volume of matching tasks over cloud platform, the matching web service receives whole versions of FMA and NCI ontologies. The matching task distributor scales this large matching request from single-node sequential to tri-node parallel. Results are illustrated in Fig. 2. String-based, child-based and label-based matching algorithms are used from the matching library and after scaling it over all the available computing resource we observe a performance speedup of 12.12, 7.42, and 9.76 times respectively.

## 5 Conclusion

In this paper, we presented biomedical ontology matching system as a service that utilizes clouds computational resources and its ubiquitous nature for service availability. Our system provides a RESTful matching service for biomedical ontologies and provides comprehensive results by using UMLS and WordNet in the form of a bridge ontology. Matched results are preserved in a centralized reposi-

tory for future use. Our system implements parallelism during ontology loading and matching over multicore cloud instances; consequently, improving the ontology matching performance. The ontology matching service is currently being used in our lab by various biomedical systems with ontology matching needs and have shown promising results. Our current system scales single matching request at a time over cloud platform; however, in future we plan on evaluating our platform with multiple matching requests constituting various sizes and requiring various matching algorithms. We plan on extending our work by implementing a performance based ontology parser and exploring several other methods of parallelization to further improve the overall performance.

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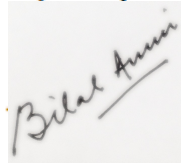
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