Aligning Medical Ontologies by Axiomatic Models, Corpus Linguistic Syntactic Rules and Context Information

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Abstract

We investigate formal semantics, as well as corpus linguistics and context based rules for ontology alignment in the medical domain. Semantic image retrieval should provide the basis for help in clinical decision support and computer aided diagnosis. Medical image and data retrieval for anatomy, diseases, or other patient-centric information require a comprehensive mapping of medical ontologies. We enhanced previous approaches of ontology matching for supporting collaboration by incorporating domain-specific context information of the application domain. The evaluation shows that axiomatic models in combination with syntactic rules and context information are very effective in terms of precision, recall, and F1 measure.

1 Introduction

To improve the access of medical images and their content information, several challenges need to be tackeled, e.g., efficient methods for flexible ontology alignment approaches. Therefore, in this work, our goal is to identify and post-process the correspondences between the concepts of different medical ontologies that are relevant to the semantic description of medical image contents.

A variety of methods for ontology alignment have been proposed [10, 3, 5, 2, 7, 6]. The objective of the state-of-the-art in ontology mapping research includes the development of scalable methods (e.g., by combining very efficient string-based methods with more complex structural methods), and tools for supporting users to tackle the interoperability problem between distributed knowledge sources (e.g., editors for iterative, semi-automatic mapping with advanced incremental visualisations [8]). In addition, cognitive support frameworks for ontology mapping really involve users [4], or try to model a natural language dialogue for interactive semantic mediation [9]. However, complex methods for ontology alignment in the medical domain turned out to be unfeasible because the concept and relation matrix is often on the scale of 100000×100000 alignment cells and appropriate subontologies cannot be created with state-of-the-art methods because of complex interdependencies. There exist pragmatic approaches for handling the complexity of the medical domain. For instance, [1] take an information retrieval approach to discover relationships between different medical ontologies by indexed ontology concept using Lucene (http://lucene.apache.org/) and by matching them against the search queries which contain the concepts from the second ontology. Although this approach is efficient and easy to implement and can therefore be successfully applied to large medical ontologies, it does not account for the complex linguistic structure typically observed in the concept labels of the medical ontologies and therefore often results in inaccurate matches.

Most medical ontologies can be summarized as: (a) they are very large models, (b) they have extensive is-a hierarchies up to ten thousands of classes which are organized according to different views, (c) they have complex relationships in which classes are connected by a number of different relations, (d) their terminologies are rather stable (especially for anatomy) in that they should not differ too much in the different ontologies, and (e) their modeling principles are well defined and documented.

Furthermore, medical ontologies are typically rich in linguistic information. For example, the Foundational Model of Anatomy (FMA)[1] contains concept names as long as "Anastomotic branch of right anterior inferior cerebellar artery with right superior cerebellar artery". Such long multi-word terms are usually rich in implicit semantic relations. Ontology alignment approaches for the medical domain need to incorporate the described common characteristics of the medical ontologies.

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[1] http://sig.biostr.washington.edu/projects/fm/FME/index.html

2 Composite Medical Ontology Alignments

The proposed medical ontology alignment framework has three main aspects: it suggests a combined strategy that is based on a) the automated linguistic-based pre-processing of ontology concepts to be aligned, b) the fine-tuning of correspondences by formulating context-specific axioms, and c) the continuous evaluation of user feedback for composing effective and context-specific ontology alignments.

In the following, we will introduce our formal approach exemplified in a concrete application scenario: medical image search in the context of the diagnosis and treatment of patients that suffer from lymphoma, a type of cancer affecting the lymphocytes (a systematic disease with manifestations in multiple organs). The available image data consist of many medical images in different formats, which additionally need to be associated with the corresponding patient data. The improved access to medical images can be used for searching and browsing patient records, clinical decision support, or quality control applications (e.g., the automated staging of lymphoma patients [11]).

Characteristics of Medical Ontologies As medical ontologies are quite large in size, we restricted the scope of the mapping. The established 'ontology modules' need to cover all concepts for describing the particular scenario. In this scenario, we aim to advance the diagnosis and treatment of lymphoma patients by improving medical image search. As the diagnosis and staging of lymphoma patient relies on the number and location of lymphatic occurrences, we require medical vocabularies that encompass concepts for describing lymphatic occurrences. Therefore, we restricted the scope of the ontology mapping to concepts that relate to lymph node occurrences. We use text mining methods for extracting all Radlex (http://www.rsna.org/radlex), the radiology term index, concepts containing the string "lymph", or "node" in their preferred name. The resulting list encompasses 151 concepts representing relevant lymph node occurrences. We do not capture the structural information of the Radlex Taxonomy.

Although the structural information of Radlex and FMA captures valuable information, we are—due to the large size of both knowledge models— not able to process this information. Radlex contains 11,962 domain related terms (e.g., *anatomy pathology* or *imaging techniques*). FMA covers 71,202 distinct anatomical concepts and about 1.5 million relation instances from 170 relation types. In addition, we are dealing with ontologies of different levels of details. For instance, Radlex contains 151 concepts that encompass the string 'lymph' or 'node' in their preferred names, whereas FMA contains more than 3000 concepts. To cope with the different levels of detail, we don't restrict the ontology alignment on the equivalence relationship but also consider hyponym/hypernym relationships. Due to the large size of the FMA ontology, it was not possible to deduce the more specific FMA concepts by means of reasoning over FMA's structural information. Moreover, a detailed analysis of FMA revealed that it contains closely related concepts such as "Anterior cervical lymph node" and "Set of anterior cervical lymph nodes", that are located at very different branches of the knowledge model without explicitly indicating the relationships.

Information Retrieval (IR) Approach We take an information retrieval approach to discover relationships between the FMA and the Radlex Taxonomy. Therefore, we treat FMA ontology concepts[2] as documents which we indexed using Lucene and match them against the search queries, which are the concepts from the Radlex taxonomy. We consider the ranked list of the "hits" related to a search as similarity measure: the higher the rank/score, the higher the similarity between the preferred name of the index term (FMA concept) and the preferred name of the search query (Radlex concept) obtained by the Lucene search engine. Whenever a match could be found, we took the rank/score as evidence of a correspondence. Although this initial mapping approach is efficient and easy to implement (and is therefore quite successful with large medical ontologies), it does not account for the complex linguistic structure typically observed in the concept labels of the medical ontologies and often results in inaccurate matches.

Linguistics Rules To cope with complex linguistic phrase structures, we enhanced the IR approach by incorporating mapping rules that reflect linguistic features of the phrases which describe a particular concept by using corpus statistics. Our assumption is that common patterns in the multi-word terms that are typical for the concept labels in the medical ontologies can be made explicit. We assume that the multi-word terms of the medical ontology encompass implicit semantics and aim to exploit this for the identification the correspondences. Thus, the initial ontology mapping uses linguistic features of the preferred names of the ontology concepts. In addition, the analysis of user feedback results provides us guidance in fine-tuning the initial mapping results in terms of context-dependent filter functions.

Evaluation with User Involvement The evaluation of ontology mapping requires the involvement of medical experts. At the same time, as medical ontology are large in size, the manual mapping of medical ontologies is cumbersome and impracticable. To support clinical experts in establishing ontology mappings, we require some automatic

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[2] We used the SAX parser to extract the concept names into a text file that we could use for the subsequent processing steps.

pre-processing steps enhanced by means for continuously integrating user/clinical feedback in an intelligent manner. For enabling the efficient and transparent processing of user feedback, we need to provide explanations of the matching results: each established ontology mapping instance need to incorporate the arguments of its derivation. To represent explanations in a simple and clear way to the user and knowledge engineer is key to facilitate informed decision making. As the medical domain is complex and sensitive, we require an ontology alignment approach that allows to seamlessly merge automated and user-interactive matching and evaluation processes; the alignments need to go through an interactive evaluation loop (cf. [9]) .

3 Formal Definitions

We will introduce the mapping functions to establish the ontology alignments (later exemplified in the lymphoma use case). To reflect the requirements of an specific application scenario, we need to enhance the established mapping functions by context-specific filtering axioms. We will provide some formal definitions with regard to the terminology we use.

Definition 1 (Ontology and Ontology Module) *An ontology O is a tuple $O = (C^O, R^O)$, such that C^O is the set of all concepts and R^O is the set of all binary relations between the concepts. An ontology module $M = (C^M, R^M)$ of O is itself an ontology such that $C^M \subseteq C^O$, $R^M \subseteq R^O$ and $C^M \neq \emptyset$.*

Definition 2 (Ontology Alignment Correspondence) *Given a source ontology $O_1 = (C^{O_1}, R^{O_1})$, a target ontology $O_2 = (C^{O_2}, R^{O_2})$, then an ontology alignment correspondence ω between O_1 and O_2 is a five-tuple $\omega = (id_\omega, s_\omega, t_\omega, r_\omega, \pi_\omega)$, where $id_\omega \in I$ a set of unique identifer, $s_\omega \in C^{O_1}$ denotes the source concept, $t_\omega \in C^{O_2}$ the target concept, and $r_\omega \in \{eq, \subset, \supset\}$ the type of relationship holding between s_ω and t_ω, and π_ω denotes the mapping function that lead to the ontology alignment correspondence. Ω denotes the set of all ontology alignment correspondences.*

Definition 3 (Mapping Function) *Given a source ontology $O_1 = (C^{O_1}, R^{O_1})$ and a target ontology $O_2 = (C^{O_2}, R^{O_2})$, we denote π mapping function between O_1 and O_2, if π is a function, such that $\pi : C^{O_1} \times C^{O_2} \longrightarrow P(\Omega)$ with $P(\Omega)$ the powerset of 0 Ω.*

A mapping function helps to identify a set of ontology alignment correspondences. In accordance with the requirements of the application domain, different mapping functions yield more or less valuable alignment results. In Section 4 we will evaluate the impact of the different mapping functions.

The final ontology alignment between two ontologies is established by a composition of different mapping functions.

Definition 4 (Ontology Alignment) *Given two ontologies $O_1 = (C^{O_1}, R^{O_1})$ and $O_2 = (C^{O_2}, R^{O_2})$ and a set of mapping functions $\pi_1, \ldots \pi_n$ between O_1 and O_2, then the ontology alignment Θ between O_1 and O_2 is defined as $\Theta(O_1, O_2) = \bigcup_{i=1}^{n} \{\pi_i(s,t) \mid s \in C^{O_1} \wedge t \in C^{O_2}\}$.*

In order to establish an ontology alignment between two ontologies, we have to find a suitable set of mapping functions that helps us to extend the set of valid alignment correspondences and, thus, improves the recall of the overall alignment process. In the following, we will describe the composition of different mapping functions (Section 3.1) to achieve an ontology alignment customized for the lymphoma application scenario. To reflect the requirements of this domain, we need to adjust the established mapping functions by context-specific filtering functions (Section 3.2) that establish a mechanism to improve the precision value of the mappings by sorting out incorrect mappings.

Throughout the following definitions, let $O_1 = (C^{O_1}, R^{O_1})$ denote the source ontology (e.g., the Radlex Taxonomy) and $O_2 = (C^{O_2}, R^{O_2})$ denote the target ontology (e.g., the FMA Ontology).

3.1 Mapping Functions

3.1.1 Equal Mapping Function

The *equal mapping function* π_{equal} helps to find equal matches: a concept of the source ontology (e.g., a Radlex concept) matches equal a concept of the target ontology if and only if each word of the preferred name of the source concepts occurs in the preferred name of the target concepts and the preferred name of source and target concept have the same length.

Definition 5 (Predicate Equal) *Let $s = [s_1, \ldots, s_n]$ and $t = [t_1, \ldots, t_m]$ with $n, m > 0$ be a multi-term expression, then the predicate $\sigma_{equal}(s,t)$ is true if and only if for all $i \leq n$ exists $j \leq m$ such that $s_i = t_j$ and $n = m$. Otherwise $\sigma_{equal}(s,t)$ is false.*

Definition 6 (Equal Mapping Function) *Let $s \in C^{O_1}$, $t \in C^{O_2}$, then the equal mapping function $\pi_{eq} : C^{O_1} \times C^{O_2} \longrightarrow P(\Omega)$ is defined as $\pi_{eq}(s,t) = \{(id, s, t, \subset, \{\pi_{eq}\}) \mid \sigma_{equal}(s,t)\}$.*

3.1.2 Trigram Mapping Function

As medical concepts are long multi-term expressions, exact matches are rare. However, Radlex and FMA concepts follow a similar linguistic structure that provides us guidance

in identifying the most meaningful terms of the multi-term expressions: medical concepts (in Radlex and FMA) consist of a noun or compound noun (e.g.,"lymph node") that is often described in more detail by a list of accompanying adjectives ("right lower paratracheal"). The adjective which is adjacent to the head noun is more discriminative than the remaining adjectives. Therefore information about nouns and adjacent adjectives needs to be considered when aligning medical concepts. This special head-modifier relationship can be detected without a complex syntactic parse tree; instead a trigram mapping function, following the medical concepts that match equally a) the noun or compound noun, b) the adjacent adjective, and c) in sum at least three terms, will be aligned. Thus, the trigram mapping function π_{tri} establishes a basic pattern that we use when searching for ontology alignment correspondences. The trigram pattern ensures that the search string (partial Radlex term) carries the relevant information.
The formal definition of the *trigram mapping function* relies on the predicate $\sigma_{trigram}$ which is defined as follows:

Definition 7 (Predicate Trigram) *Let* $s = [s_1, \ldots, s_n]$ *and* $t = [t_1, \ldots, t_m]$ *with* $n, m > 0$ *be multi-term expressions, then the predicate* $\sigma_{trigram}(s, t)$ *is true if and only if*

- *for all* $i \leq n$ *with* s_i *of type noun, there exists* $j \leq m$ *such that* $s_i = t_j$ *and*
- *for all* $i, j \leq n$ *with* s_i *of type adjective and* s_j *of type noun and* $i + 1 = j$*, there exists* $k, l \leq m$ *such that* $s_i = t_k$ *and* $s_j = t_l$
- *there exists* $i_1, i_2, i_3 \leq n$ *and* $j_1, j_2, j_3 \leq n$ *such that for all* $k \leq 3$ *holds* $s_{i_k} = t_{j_k}$

Otherwise $\sigma_{trigram}(s, t)$ *is false.*

Definition 8 (Trigram Mapping Function) *Let* $s \in C^{O_1}$, $t \in C^{O_2}$*, then the trigram mapping function* $\pi_{tri} : C^{O_1} \times C^{O_2} \longrightarrow P(\Omega)$ *is defined as* $\pi_{tri}(s, t) = \{(id, s, t, \subset, \{\pi_{tri}\}) \mid \sigma_{trigram}(s, t)\}$.

3.1.3 Generation of Linguistic Fullforms

In many cases, the correspondence between two concepts cannot be found because the source concept (e.g., "anterior cervical lymph node") is represented in singular form and the target concept (e.g., "Anterior cervical lymph nodes") in plural form. Even though the meaning of the concept is similar, the described mapping functions provide no means to capture the correspondance between these two concepts. Thus, we required a mapping function that integrates the linguistic fullforms of the ontology source concept labels. The *linguistic fullform mapping function* π_{full} is defined to transfrom multi-term expressions of the source ontology into their linguistic fullforms. (Stemming is not adequate since it denotes the opposite direction of application and results in equivalence sets for the source concepts instead of the target concepts). A standard linguistic fullform generator can be used, e.g., Mmorph[3].

Definition 9 (Plural Form) *Let* M *denote the set of multi-term expressions, then the plural form function* $\delta_{plural} : M \longrightarrow P(M)$ *returns for each multi term expression its plural form.*

Definition 10 (Linguistic Fullform Mapping Function) *Let* $s \in C^{O_1}$, $t \in C^{O_2}$*, then the linguistic fullform mapping function,* $\pi_{full} : C^{O_1} \times C^{O_2} \longrightarrow P(\Omega)$ *is defined as* $\pi_{full}(s, t) = \{(id, s, t, \subset, \{\pi_{full}\}) \mid s' \in \delta_{plural}(s) \wedge \sigma_{trigram}(s', t))\}$.

3.1.4 Syntactic Variants Function

Beside the syntactic fullform, we could extend the set of correct correspondences by using information about syntactic variants of source concepts in the search for alignments. Detecting syntactic variants of ontology source concept labels—for instance recognizing the term "anterior jugular lymphatic" as syntactic variant of the Radlex concept "anterior jugular lymph node"—helps to retrieve additional related FMA concepts (such as "Left anterior jugular lymphatic chain"). Therefore, we defined the *syntactic variants mapping function* that helps to transform multi-word expressions of the source ontology into their syntactic variants (e.g., by noun-to-adjective conversions) that nevertheless preserve their semantics. With the help of this function, the concept labels can be transformed into semantically equivalent but syntactically different word forms.

Definition 11 (Syntactic Variants) *Let* M *denote the set of multi-term expressions, then the syntactic variants function* $\delta_{syn\_variant} : M \longrightarrow P(M)$ *returns for each multi-term expression its set of syntactic variants.*

Definition 12 (Syntactic Variants Mapping Function) *Let* $s \in C^{O_1}$, $t \in C^{O_2}$*, then the syntactic variants mapping function* $\pi_{syn} : C^{O_1} \times C^{O_2} \longrightarrow P(\Omega)$ *is defined as* $\pi_{syn}(s, t) = \{(id, s, t, \subset, \{\pi_{syn}\}) \mid s' \in \delta_{syn\_variant}(s) \wedge \sigma_{trigram}(s', t)\}$.

3.2 Filtering Functions

Filtering functions aim to filter incorrect mappings; ths leads to improved precision at a certain recall level. We will introduce two filtering functions of great practical value:

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[3] http://www.issco.unige.ch/en/research/projects/MULTEXT.html

3.2.1 Antonym Filtering Function

For the declaration of an adequate filter function for antonyms in the medical scenario, we define an antonym set as follows:

Definition 13 (Antonym Set) *The medical antonym filter function's antonym set* Λ *is defined as* $\Lambda \subseteq \{$*(internal,external),(left,right),(deep,superficial), (internal,anterior),(external, anterior)*$\}$. *The antonym relationship is symmetric, i.e.,* $\forall(x, y) \in \Lambda \longrightarrow (y, x) \in \Lambda$.

The predicate $\sigma_{antonym}$ helps to identify ontology concepts that contain antonym terms.

Definition 14 (Predicate Antonym) *Let* $s = [s_1, \ldots, s_n]$ *and* $t = [t_1, \ldots, t_m]$ *with* $n, m > 0$ *be sets of multi-term expressions, then the predicate* $\sigma_{antonym}(s, t)$ *is true if and only if there exists* $i \leq n$ *and* $j \leq m$ *such that* $(s_i, t_j) \in \Lambda$. *Otherwise* $\sigma_{antonym}(s, t)$ *is false.*

The *antonym filtering function* δ_{ant} helps to filter out alignment correspondences that contain antonym terms.

Definition 15 (Antonym Filtering Function) *Let* $W \subset \Omega$ *be a set of ontology alignment correspondences, then the antonym filtering function* $\delta_{ant} : P(\Omega) \longrightarrow P(\Omega)$ *is defined as* $\delta_{ant}(W) = \{\omega \in W \mid \neg\, \sigma_{antonym}(s_\omega, t_\omega)\}$.

3.2.2 Hypernym Filtering Function

The analysis of alignment results showed that the integration of syntactic variants helped to increase the number of correct correspondances, but—at the same time—produced a large number of incorrect alignments (recall was enhanced at the cost of precision). By studying the clinical experts' feedback, we could formulate a special restriction on the variant generation process: nouns should only be conversed to their adjective form if the adjective is followed by a head noun that is a hyernym of the original head noun. For example, with the help of the *Hypernym Filtering Function*, the term "lymph node" can be replaced by the term "lymphatic chain" but not by the term "lymphatic vessel". As lymphatic chain consist of both a lymph node and a vessel, there is no hypernym relationship between the two terms "node" and "vessel". To implement it, we define the set of hypernym relationships that are of relevance as follows:

Definition 16 (Hypernym Set) *The Hypernym Set* Υ *is defined as* $\Upsilon \subseteq \{$*(node,chain),(node,trunk),(node,plexus), (node, tree),(vessel,chain)*$\}$. *The hypernym relationship is transitive, i.e.,* $\forall(x, y), (y, z) \in \Upsilon \longrightarrow (x, z) \in \Upsilon$.

The predicate $\sigma_{hypernym}$ allows us to identify syntactic variants of ontology concepts that are correct in the our application scenario.

Definition 17 (Predicate Hypernym) *Let* $s = [s_1, \ldots, s_n]$ *and* $t = [t_1, \ldots, t_m]$ *with* $n, m > 0$ *be multi-term expression, then the predicate* $\sigma_{hypernym}(s, t)$ *is true if and only if there exists* $i \leq n$ *and* $j \leq m$ *such that* $(s_i, t_j) \in \Upsilon$. *Otherwise* $\sigma_{hypernym}(s, t)$ *is false.*

The *hypernym filtering function* helps to remove the matches that could be identified by establishing syntactic variants that are not correct for our application scenario, i.e. that do not respect the set hypernym relations.

Definition 18 (Hypernym Filtering Function) *Let* $W \subset \Omega$ *be a set of ontology alignment correspondences, then the hypernym filtering function* $\delta_{hyp} : P(\Omega) \longrightarrow P(\Omega)$ *is defined as* $\delta_{hyp}(W) = \{\omega \in W \mid \sigma_{hypernym}(s_\omega, t_\omega)\}$.

4 Evaluation

We evaluated and compared different ontology alignments using our filters and axioms. For a comparision, we calculated the recall, precision, and F1-score (see Table 1). In order to obtain a reliable truth table for our test set, we relied on the user rating of our clinical experts (thereby relying upon inter-annotator agreements).

With the help of the *equal mapping function* π_{eq}, we can align the Radlex concept "thoracic lymph node" with the FMA concepts "Thoracic lymph node". The first evaluation showed that the equal mapping function produced a rather small set of alignment correspondences, i.e., 64 out of 151 Radlex concepts could be mapped onto FMA concepts. By analyzing the Radlex concepts without hits to FMA concepts (false negatives), we noticed a large number of Radlex multi-term expressions that consist of more than three terms, e.g., "right lower paratracheal lymph node". The longer the multi-term concepts, the more detailed becomes their meaning and the more difficult it is to find equal correspondances. Although FMA contains 11 different concepts that encompass the string "paratracheal lymph node" in the preferred name (e.g., "set of paratracheal lymph nodes"), no equal counterpart could be found in FMA.

Strategies for improving the recall value: We used our linguistic methods to enhance the number of alignment correspondences. For instance, by applying the *trigram mapping function* π_{tri}, we could enhance the numer of mappings by number 6.9 (starting from $64 = |\pi_{eq}|$), and by applying the *linguistic fullform* and the *syntactic variants mapping function* it was possible to enhance the number of mappings from 309 to 1409 ($|\delta_{ant} \circ (\pi_{tri} \cup \pi_{syn} \cup \pi_{full})|$). With the linguistic methods we could continously improve the recall of the alignment mappings at the cost of the precision measure: The evaluation of the results revealed that about 30% of the established mappings were not correct because the corresponding concepts contained antonym terms,

Ontology Alignment	Recall	Precision	F1-Score	# found alignments
π_{eq}	0,063	1	0,118	64
π_{tri}	0,303	0,693	0,422	446
$\delta_{ant} \circ \pi_{tri}$	0,303	1	0,465	309
$\delta_{ant} \circ (\pi_{tri} \cup \pi_{full})$	0,678	1	0,808	692
$\delta_{ant} \circ (\pi_{tri} \cup \pi_{syn})$	0,626	0,621	0,624	1026
$\delta_{ant} \circ (\pi_{tri} \cup \pi_{syn} \cup \pi_{full})$	1	0,722	0,838	1409
$\delta_{hyponym} \circ \delta_{ant} \circ (\pi_{tri} \cup \pi_{syn} \cup \pi_{full})$	1	0,997	1,992	1020

Table 1. Evaluation Results

e.g., "*Right* buccinator lymph node" and "*Left* buccinator lymph node". Therefore, we required some mechanism for filtering those incorrect correspondences.

Strategies for improving the precision measure: For improving the precision value, we incorporated context information. We used the filter functions to avoid uncorrect alignments. For instance, we used the *antonym filtering function* δ_{ant} in combination with the trigram mapping function, which yields a mapping function $\delta_{ant} \circ \pi_{tri}$. The evaluation showed that the combination of the two functions helps to improve the precision and F1-Score of the alignments significantly. It should be noted that the quality of these filters is directly influenced by the declaration of a suitable antonym set Ω. For each domain, a different set of antonyms has to be created. The analysis of incorrect mappings produced by the trigram mapping function in addition to the use of an antonym thesaurus[4] can provide useful guidance in determining the required antonym pairs. However, in order to cope with the particular meaning of medical antonym terms, a clinical expert-based evaluation of medical antonym pairs was required.

By combining the *hypernym filtering function* δ_{hyp} with the antonym filtering function and the trigram-based linguistic fullform and syntactic variants mapping functions, i.e., $\delta_{hyp} \circ \delta_{ant} \circ (\pi_{tri} \cup \pi_{syn} \cup \pi_{full})$, we could significantly increase the F1-Score from 0,83 to 1,99 (confidence level 0.01). Similar to the declaration of the antonym set, the declaration of the hypernym set is one of the essential influencing factors for improving the quality of mapping results. The definition of filter axioms relies on the domain-specific interpretation and analysis of the evaluation results (though discussions with medical experts) and the study of the expressiveness and coverage of the applied medical ontology relations.

5 Conclusions

We introduced a formal composite approach for medical ontology alignments which makes use of corpus linguistic rules, context information, and continuous expert user feedback. The evaluation shows that the incorporation of the context information paves the way for optimized F1 measures. In our future work, we plan to extend our approach to further (medical) use case domains. Moreover, we plan to establish an ontology alignment exchange format as the basis for a seamless integration of alignments into medical applications.

Acknowledgments This research has been supported in part by the THESEUS Program in the MEDICO Project, which is funded by the German Federal Ministry of Economics and Technology under grant number 01MQ07016. The responsibility for this publication lies with the authors.

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