RESEARCH

A sample article title

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Abstract

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Introduction

Data and Information modeling in the healthcare domain have witnessed significant improvements in the last decade owing to advances in the development of state-of-the-art information and communication technologies (ICT) and formalization of storage and messaging standards. Subsequently, the scope of Healthcare Management Information Systems (HMIS), medical ontologies, and Clinical Decision Support Systems (CDSS) has broadened, beyond the operational capabilities of traditional rule based systems. One of the major reasons behind this limitation is due to the numerous heterogeneities in healthcare at data, knowledge, and process level. Thus, healthcare interoperability which aims to provide a solution to this problem, can be compartmentalized into data interoperability, process interoperability, and knowledge interoperability. Data interoperability resolves the heterogeneity between data artificats, to enable, seamless and interpretable communcation among source and target organizations, while preserving the data's original intention during storage, communication, and usage (as defined by IEEE 610.12 [1], Health Level Seven International HL7, and Healthcare Information and Management Systems Society HIMSS [2]). On the other hand, process interoperability regulates the communication among organizational processes to provide compatability between process artifacts within and seamless transformations across different organizations[3]. Lastly, knowledge interoperability provides a sharing mechanism for reusing interpretable medical knowledge, acquired through expert intervention and other mechanisms, across decision support systems [4]. In more tangible terms, healthcare interoperability at data, process, and knowledge level can be exemplified within the healthcare constraints experienced due to the emergence of Covid 19. The operational capabilities of the current healthcare service delivery infrastructure has gone under tremendous stress due to Covid 19. World over, large primary healthcare units have managed to create separate units for managing patients, suffering from extreme cases of the novel coronavirus. For secondary and tertiary care units, government involvement has become necessary to filter coronavirus patients and adhering to a national pandemic response policy. These complex circumstances have enhanced the need for sharing patient data and state-of-the-art medical knowledge in real-time, to provide the medical experts with a tool to

make accurate and timely decisions. Data interoperability can enable the front line medical workers to fetch, understand, and use patient data, especially comorbidities, across organizational and physical boundaries, without suffering from societal taboos that may prevent the patient from sharing their complete and accurate medical histories. Knowledge interoperability can improve the knowledge acquisition and sharing protocols to provide the medical experts such as epidieomologists and vaccinologist, with latest information on affected population trends, disease diagnosis, treatment, and followup procedures, and interpretable decisions leading to positive or negative outcomes. Process interoperability can help reduce and in some cases remove the operational redundancies between health centers. In this way, successive healthcare treatments can take benefit from earlier diagnosis, treatment, and followup procedures, thereby reducing the stress on healthcare experts and systems. Standards such as Health Level Seven (HL7) Fast Healthcare Interoperability Resources (FHIR), and openEHR provide the foundations for storing and communicating medical data, through the use of well defined protocols. While systematized nomenclature of medicine—clinical terms (Snomed-CT) [5] and logical observation identifiers names and codes (LOINC) [6] provide a standard definition for clinical terminologies and laboratory tests, respectively. Similarly Medical Logic Module (MLM) provides a standardized way for expressing medical knowledge. However, the plethora of standards, necessitates the creation of bridging standards, that can resolve the heterogeniety between the medical standards. Substantial effort has gone into this endeavor with the Clinical Information Modeling Initiative (CIMI) [7] taking the lead in bridging the gap between HL7v3 and openEHR. Similarly, SNOMED CT and LOINC are working to resolve the redundancies between the two terminological standards since 2013. This healthcare interoperability solution follows a formal, albiet long process, which is greatly dependent on the human factor. However, the current healthcare scenario, requires a quick solution to create a scaffolding of an interoperable bridge between various healthcare providers. It is also important to ensure that this scaffolding should be able to support the formal standardization processes of the future. In [8]we have presented the Ubiquitous Health Platform (UHP), which provides semantic reconciliation-on-read based data curation for resolving data interoperability between various schema. This methodology is based on the creation and management of schema maps, that can provide the framework for transforming a source schema into a target schema. In the current manuscript, we will present our research work to build and manage the schema map knowledge base. Overall, our methodology is based on the creation, evaluation, and application of a novel schema matching technique to identify the relationships between attributes of the participating medical data schema. These will be presented in detail, with following flow:

- Section contains the details of our methodology
- Section provides the experimental setup
- Section presents the results
- Section presents the related work
- Section 6 concludes the paper.

Related Work

Althubait et al. [9] proposed an ontology expansion methodology that identifies and extracts new class from text articles using word embedding and machine learning techniques. The authors identified the similarity of tokens and phrases of the text articles with the exiting classes of the ontology. The target ontology is expanded with classes from text articles having greater similarity with that of already added classes. A similar word embedding technique was also used by Nozaki et al. [10], where the authors used instance based schema matching technique to identify the semantic similarity between two instances. The results of the study showed the possibility of detecting similar string attributes of different schemas. Yousfi et al. [11] also utilized semantic base techniques and proposed xMatcher XML schemas matching approach. xMatcher transforms schemas into a set of words, followed by measuring words context, and relatedness score using WordNet. The terms from different schemas having similarities greater or equal to 0.8 are considered similar. Bylygin et al. [12] devised an ontology and schema matching approach by combining lexical and semantic similarity with machine learning approaches. The authors used lexical and semantic measures as features and trained various machine learning algorithms including Naive Bayes, logistic regression, and gradient boosted tree. The result achieved showed that the combination of algorithms outperformed the single modal.

Martono et al. [13] provided overview of previous studies related to linguistic approaches used for schema matching. Linguistic methods focused on finding strings and evaluate there similarity in different schemas. The string are normally normalized before to align both the strings before similarity comparison. The normalized strings are categories based on the information relatedness and element with similar category are compared using various similarity measure including Jaro-distance, Lavenstein (edit-distance), and many more. Alwan et al. [14] have summarized the techniques used in the literature for schemas and instances based schema matching. The information used for schema matching is categories into schema information, instance and auxiliary information. Most of the searchers have used syntactic techniques (including n-gram, and regular expression), semantic techniques (including Latent Semantic Analysis, WordNet/Thesaurus and Google Similarity) for schema level and instance level matching to achieve the final goal of data/information interoperability. Kersloot et al. [15] performed a comprehensive systematic review to evaluate natural language processing (NLP) algorithms used for clinical text mapping onto ontological concepts. The findings of the studies were evaluated with respect to five categories; use of NLP algorithms, data used, validation and evaluation performed, result presentation, and generalization of results. The authors revealed that over one-fourth of the NLP algorithms used were not evaluated and have no validation. The systems that claimed generalization, were self evaluated and having no external validation.

Xu et al. [16] presented a framework for discovering indirect links besides direct links among schema elements. The indirect matches were detected for relations such as union, composition, decomposition, selection, and boolean. The indirect links are useful to handle concepts merge, split, generalization, and specialization.

The matching techniques utilized in the study considered terminological relationships (word synonym and hypernym), structural characteristics, data-value characteristics, and expected data values. The experimental results revealed framework effectiveness by achieving more than 90% precision and recall for direct and indirect link matching.

A comprehensive survey from 176 experts including physicians and nurses was conducted by Moll et al. [17] to check their perspectives regarding patient accessible electronic health record (PAEHR). The authors discovered that the PAEHR positively effect after six years of operations despite negative expectations. The primary concerns revealed was logger meeting time, change in documentation practices, and increasing varies of patients regarding their health conditions. However, attitude of both healthcare service providers and patients are changing positively with respect to PAEHR and its benefits.

Methodology

Healthcare interoperability, with a focus on non-standard compliant medical schema, is dependent on the generation and validation of schema maps, as discussed above. To this end, the creation of a cohesive workflow is of utmost importance. In our earlier work [8] we used maximum sequence identification and suffix tress based matching for syntactic matching of two distinct data schemas. This was followed by semantic concept enrichment and subsequently concept matching, for creating rules in the form of schema maps. The simplified mapping functions, thereby created, provided a simple methodology for converting semi-structured medical data, into an interpretable, model form. In our current methodology we have utilized state-of-the-art natural language processing (NLP) techniques to extract the schema mapping rules from semi-structured data schemas. This methodology is based on identifying similarity between vector representations of two attributes, belonging to different medical schemas. **Traditional NLP techniques such as WordNet are able to convert a word into an embedded vector, while Bidirectional Encoder Representations from Transformers (BERT) extracts an embedded vector from a sentence.** However, the terms forming the attribute names are bigger than a word (combination of multiple words) and smaller than a sentence. In order to resolve this problem, we extracted the set of suffixes from the terms forming the attribute names. The bidirectional nature of BERT, allows the creation of contextual embedded vectors, where each target word is affected by its neighboring words. Hence to convert the set of suffixes into a sentence, we collected the set of concepts corresponding to each suffix, from Unified Medical Language System (UMLS). This operation has two effects, firstly it is used to remove any suffix, which does not have a corresponding concept and secondly the extracted concepts are used to add context to each suffix and produce a contextual sentence. The following subsections provide the practical details for our methodology, from schema acquisition, to attribute name expansion, and finally schema map generation.

Schema acquisition

In the first step of our semantic reconciliation methodology, we simulate medical data acquisition from five distinct EMR storage systems (S). These include patient

reports from OpenEMR (s_1), 100,000 patient records from EMRBOTS (s_2) [18], custom database design by Pan et. al(s_3) for supporting regional clinics and health care centers in China [19], clinical knowledge discovery tool MedTAKMI-CDI (s_4) [20], and our custom implementation (s_5). Each of these medical systems as shown in **figSchema**, follows the relational database design, with logical entities, such as demographics, diagnosis, medicine or others, placed into tables which can be further linked to one or more tables. While the database design implemented by each of these systems, fulfills the need of their respective information processing applications, the lack of interoperability, in terms of identifying similar attributes or exchanging the medical data is very much evident here. A similar notion of data heterogeneity, in terms of medical data schema, is evident across the healthcare domain. This is caused by various factors, including the lack of one all-encompassing, and universally applicable terminological standard and different normalization level for representing attributes.

In the former case, while SNOMED-CT provides a mechanism for identifying the standard codes for clinical terms and LOINC can be used for laboratory related terms, most attribute names are created based on the gut feeling of the database designer. Additionally, while these codes can be used to represent data instances, the data schema, achieves no benefit from the same. Consider the terms "name" and "patientName", which refer to the same attribute of the patient entity. However, since there is no standard way to represent this attribute, both are considered correct (s_1 and s_3 use the former representation, while s_2 and s_5 use the latter).

In the later case, differences in normalization cause semantic differences, due to which some data could be available in one schema but absent in others, such as OpenEMR demographics identifying the patient's residential location using specific attributes like "Address", "City", "State", "Postal Code", "Country", and others. Similarly, "EncounterDate" from s_5 is semantically similar to "BeginDate" of "openemr_MedicalProblems" table in s_1, "AdmissionStartDate" of "LabsCorePopulatedTable" in s_2, "time" in "Diagnosis" table of s_3, and "dateOfAdmission" in "Diagnosis" and "CareHistory" tables of s_4. Finally, s_1 and s_3 have separate tables containing the medicinal prescription details, however the same details are unavailable in s_2, s_4, s_5. Once again, this is not an incorrect behavior since this information, might not be a part of the context or the requirements for these EMR storage systems. In fact, the change in context of the EMR storage system from the initial time of development to a later stage of collaborative processing systems, is the main cause of heterogeneity. In order to provide an interoperable solution, it is therefore necessary to enhance the semantics of each EMR attribute by its contextually equivalent sentence.

From Attribute to Sentence

In order to process the EMR schema set S and produce a set of corresponding semantically enriched sentences, we use the data representation s_i, generated through the process explained in sequence acquisition to collect the various medical fragments in memory. We then iterate over these fragments, building a set of attributes, distinguished by their name, schema's name, table's name, schema's version, source, and recorded data. This entails that "PatientID" from each of the four tables in s_2,

and "patientID" from five tables in s_4, would result into nine attributes (assuming, as in the current case, of no differences in versions of these systems). For each attribute, we then generate the suffix array, which provides all possible substring representations contained within the attribute name. In order to generate the set of suffixes, we employ three strategies, forward suffix generation, whereby for a word w of length n, $n-1$ suffixes of size 2 to $n-1$ are produced, backward suffix generation, to produce $n-1$ suffixes in reverse order with size $n-1$ to 2, and regular expression based suffix generation, which splits each word on, change of case, special characters(such as -, _, !, and others), and numbers. An example of this suffix generation process is shown in **figSuffixAttribute**. Here, the attribute "DOB" in s_1, "PatientDateOfBirth" appears in s_2, "birthday" appears in s_3, "DateOfBirth" in s_5, and "birthDate" in s_4. These attributes refer to the same attribute of the patient entity, however, with the suffix generation process, our aim is to identify all words within these strings. While the forward and backward generation process, generates all possible sequences of characters as suffix, the regex based method, only identifies the changes in the string. In this way a large list of suffixes is generated, which is combined using a "TreeSet" data structure of Java, which internally sorts this list as well.

Similarly the attribute, "dateOfAdmission" appears in s_4, while "AdmissionStartDate". "diseaseNameOnAdmission", and "AdmissionEndDate" appear in s_2. As evident within these strings, while they refer to semantically different entity attributes, syntactically they contain similar elements. The suffixes generated from these strings are shown in **figSuffixAttribute (b)**. The suffix generation process, identified thus far, is only able to generate syntactic suffixes, producing many incoherent and unrelated suffixes. In order to counter this problem, and to limit the list of suffixes within the domain, we then query UMLS, with exact search strategy, looking for the existence of any concepts, against each suffix. In case, no semantic concept is found for a particular suffix, it is removed from the final Suffix Array. On the other hand, if atleast one semantic concept is found against the queried suffix, it is retained. Meanwhile the process continues for the next attribute, then the next table, and finally the next system, till no further processing is possible. The set of suffixes and their corresponding concepts are then used to build the sentence, where by each concept, corresponding to a suffix is appended next to the suffix. An example of the resultant sentence for the attribute "DateOfAdmission" is shown as follows:

"Date Value type - Date date allergenic extract Date in time Data types - Date Date Fruit;Of SPI1 wt Allele SPI1 gene TAF1 wt Allele BRIP1 gene Within Degrees fahrenheit Oral contraception BRIP1 wt Allele;Da Displacement of abomasum dalton Anterior descending branch of left coronary artery deca units cytarabine/daunorubicin protocol Dai Chinese Asymptomatic diagnosis of Drug Accountability Domain;ion Iontophoresis Route of Drug Administration Ions;on SPARC wt Allele Osteonectin SPARC gene On (qualifier value) Upon - dosing instruction fragment;Admission Admission activity Hospital admission;Dat SLC6A3 gene SLC6A3 wt Allele dopamine transporter Direct Coombs test SLC6A3 protein, human Test Date cytarabine/daunorubicin/thioguanine Alzheimer's Disease;mission Religious Missions;"

Here the various suffixes and their concepts are seperated by the symbol ";", however together they form one sentence, for which an embedded vector is generated.

Schema Map generation

Schema Maps, provide an interoperable bridge between two medical systems ($s_i \wedge s_j$), by identifying the semantic relationship between their participating attributes. This identification is based on the similarity between the embedded vectors, of the semantically enriched sentences, corresponding to each EMR attribute. While the embedded vectors can be generated using any methodology (we tested 11 methodologies, with WordNet and 10 models of BERT further detailed in section), the large/STSb version of the Siamese BERT-Networks [21], commonly known as **stsb-roberta-large** provides the best results. The pair of embedded vectors thus produced are then used to calculate cosine similarity, which is based on the inverse cosine distance between them. For our classification, we used the raw results (unnormalized) of cosine similarity, which produces a score between -1, and 1. Cosine similarity score of 0 indicates orthogonal relationship between the two vectors, which in our scenario indicates that the two sentences, and by extension their attributes are not related to each other. -1 indicates, inverse relationship between the attributes, while 1 indicates the two attributes are very much the same. For producing our schema maps, we are interested in three types of relationships, "equal" (the two attributes are same), "related" (the two attributes are related to each other), and "unrelated" (no relationship between the attributes). In order to classify the similarity results, into one of these three classes, we then calculated the best thresholds, using Matthews Correlation coefficient (MCC) [22] for classifying each instance as "equal", "related", and "unrelated". Finally on a test dataset we evaluated our multi-class classification approach, to identify the relationships between each pair of attributes.

Experimental Setup

In our earlier work [8] s_1, s_2, and s_5 were used to generate over 115 million patient records, which are converted into a semi-structured form and stored in Hadoop Distributed File System (HDFS). We extended the same setup to create an additional 100,000 records, for 1000 patients with 3 medical fragments for s_1, s_2, and s_4, and 97 randomly selected and generated medical fragments amongst s_1, s_2, s_3, s_4 and s_5.

These fragments, follow various design elements, supporting a variety of valid relational storage architectures. Such as, s_1, s_2 and s_4 are represented by creating a separate medical fragment for each participating table, s_3 utilizes its medical fragment to generate a linked record (from a linked object graph), where by the attributes can refer to other objects besides the elements of t, mimicking the application of explicit foreign keys, and s_5 is a flat table structure. The code to generate this data set is available at "uhp_map_generation"[1]. This application produces three custom formatted files, containing an index for patients, an index for their medical fragments, and the medical fragment, corresponding to the EMR data. Using the medical fragments file, we then generate the semantically enriched attribute [2], which contains the suffixes and their concepts corresponding to each EMR data attribute. The resulting set of enriched attributes are temporarily stored in a "json" file, which is then read by the same application to partially generate the schema maps. This process, is used to create 20,349 distinct pairs of attributes, across s. Each pair also contains the "relationshipList", which stores the results of fuzzy string matching[23] [3] between the attribute names. The "json" file thus produced, is then used by a python script to generate the semantically enriched sentences and their embedded vectors using WordNet, and 10 pre-trained BERT NLI models [21]. The BERT models include 'bert-base-nli-stsb-mean-tokens', 'bert-large-nli-stsb-mean-tokens', 'roberta-base-nli-stsb-mean-tokens', 'roberta-large-nli-stsb-mean-tokens', 'distilbert-base-nli-stsb-mean-tokens', 'bert-base-nli-mean-tokens', 'bert-large-nli-mean-tokens', 'roberta-base-nli-mean-tokens', 'roberta-large-nli-mean-tokens', and 'distilbert-base-nli-mean-tokens'. The embedding vectors are then compared using cosine similarity, which produces a score between -1 and 1. The rationale behind switching the applications at various stages, is to cache the results and create checkpoints for restarting any failed stages, easily. Additionally, since python provides better support for easy generation of embedding vectors, it was thus preferred over the Java based implementation, which is otherwise very beneficial for other tools. These applications were executed on a workstation running Ubuntu 20.04.2 LTS on top of AMD Ryzen 3 2200G, and 32GB ram.

In order to compare our computed models with ground truth, and to identify the best thresholds for classifying each instance as "equal", "related", or "unrelated" 4 human annotators were utilized, to anonymously, score the similarity of each pair of attribute names. In order to support this process, we first repurposed one of our generated data matrix, by marking all attribute pairs belonging to the same schema with the symbol "-". Following this, the annotators, marked each cell corresponding to a pair of attributes, by determining the similarity in terms of dissimilar as "0", exactly similar as "1", row attribute as child of column attribute as "¡", row attribute as a parent of the column attribute as "¿", and finally, unknown as " ". The data sheets generated after this extensive human effort, have been made available for other researchers[4]. These sheets, additionally contain some missing values, which were left out by the annotators, but in order to maintain their originality,

[1] https://github.com/desertzebra/UHP_v4/tree/main/uhpr_storage
[2] https://github.com/desertzebra/UHP_v4/tree/main/uhp_map_generation
[3] Java Library: https://github.com/xdrop/fuzzywuzzy
[4] https://github.com/desertzebra/EMR-Interoperability/tree/master/Implemenation/Data/Annotated

these values were not filled; instead during our evaluation for these datasets, the missing values were considered as having the score "0". Using **Cohen's Kappa score (d)**, we evaluated the inter-rater agreement of these annotations, which have been visualized in **figKappaScore**. The 7 permutations, amongst the 4 annotators, generate 261 kappa scores, where each individual score corresponds to the correlation of agreement between two annotators. Further, each score identifies the agreement in terms of scoring a set of paired attributes, while keeping the row attribute constant, and moving along the 261 column attributes. Finally we produced a consolidated dataset, using mode scores of all annotators, for each attribute pair. This dataset is then split into development and testing partitions with a ratio of 70:30. The development partition is used for threshold selection, based on the best MCC score for identifying class "equal", followed by best scores for class "related" and finally best of class "unrelated". The optimal threshold thus achieved is used to classify the instances of the test dataset, which is finally evaluated on its MCC and F-1 score.

Results

The validity of our proposed approach has been evaluated using several techniques, including comparison of the proposed syntactic and semantic matching process with fuzzy string matching, only semantic matching of attribute names using sentence embedding, and with multiple human annotated versions of the schema map. Using the 21,873 AA pairs, we created a two dimensional matrix, of AA identifiers, whereby each cell refers to a "SchemaName_TableName_AttributeName" element. All nodes, for which the SchemaName part of the name is same, are then marked with "-", and these are omitted from further processing. This various versions of this dataset (D) are available at **url**.

The results of fuzzy string comparison (D_f) on the attribute names of each pair, can be visualized using the heatmap shown in **figFuzzyWuzzy**. Similarly, the results of comparison using BERT based word embedding of the attribute names (D_b), is shown in **figBase**. Finally, the heatmap of the syntactic and semantic matching of the AA's using our proposed Algorithm **??** (D_p), is shown in **figSynAndSemMatching**. The values, for each cell range between "0" and "1", with higher values indicating a larger match between the elements, in each of these cases. The black areas of these heatmaps, indicate missing values, while white indicates a matching value of "0". The few areas with red color, indicate the values above "0.9", while blue areas indicate values above "0.8".

Threshold Selection Overall, the number of similarities above the threshold values of "0.8" are greatly increased from D_f, to D_b, and then to D_p (proposed methodology). Changing the threshold value in D_p to "0.9", brings it relatively closer to D_b. This is due to our proposed similarity matching methodology, which gives an equal score (0.5) to the values obtained from both syntactic and semantic matches. Since the decision made at the syntactic evaluation is binary (0 or 1), thus for a similarity score of "0.8", in D_p, "0.5" represents the syntactic similarity, and "0.3" semantic similarity. The semantic similarity value, obtained from this rescaling process, would in turn represent an original value of "0.6" from D_b. Therefore, for an equal semantic representation, the value of semantic similarity

after rescaling (between 0 and 0.5) should be "0.4", and originally "0.8". **figSynAndSemMatching0.9** shows the heatmap, of similarity matrix, obtained from D_p with the threshold values as "0.9".

Generally, a comparison of these heatmaps, indicate an increase in the recall rate of the methodology. This is due to the fact, that our proposed methodology is able to match a larger number of AAs, providing 50% of the score to the syntactic match, thereby increasing the count of cells without a missing value. This approach is also able to reduce the impact of semantic matching from names, which might contain repeated words, such as "patient" but in reality refer to disparate concepts, such as "PatientName" and "PatientDateOfBirth". Another important aspect of our matching process is the inclusion of semantic concepts and suffixes, as a sentence before its conversion to an embedded vector. As discussed earlier, this process is used to reduce the impact of syntactic matches alone, which would give a higher score to the attributes "PatientName" and "PatientGender", which refer to different concepts. The inclusion of concepts behind "Name" and "Gender" part of these names, allow for an improved comparison.

In order to evaluate the accuracy and precision rates of these methodologies, we then compared the results of our computed methods D_f, D_b, and D_p, with the average scored datasets by the human annotators. A visualization of the resultant Cohen's Kappa score for the 261 participating attributes, is shown in **figComputedComparisonKappaScore**. The bar chart shown in this visualization, indicates, an overall greater positive agreement between our proposed methodolody D_p, and the average scores of the annotators. The same is shown by the **orange** colored peaks in this dataset, which in all cases is either equivalent to the other approaches (D_f and D_b), or better than them.

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Figures

Figure 1 Schemas used for knowledge interoperablity.

Figure 2 Sample figure title

Figure 3 Sample figure title

Tables

Table 1 Sample table title. This is where the description of the table should go

	B1	B2	B3
A1	0.1	0.2	0.3
A2	...	..	.
A3	..	.	.

Additional Files

Additional file 1 — Sample additional file title
Additional file descriptions text (including details of how to view the file, if it is in a non-standard format or the file extension). This might refer to a multi-page table or a figure.

Additional file 2 — Sample additional file title
Additional file descriptions text.