Semantic-based Data Integration and Mapping Maintenance: Application to Drugs Domain

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Abstract: In recent years, the number of data sources and the amount of generated data are increasing continuously. This voluminous data leads to several issues of storage capacities, data inconsistency, and difficulty of analysis. In the midst of all these difficulties, data integration techniques try to offer solutions to optimally face these problems. In addition, adding semantics to data integration solutions has proven its utility for tackling these difficulties, since it ensures semantic interoperability. In our work, which is placed in this context, we propose a semantic-based data integration and mapping maintenance approach with application to drugs domain. The contributions of our proposal deal with 1) a virtual semantic data integration and 2) an automated mapping maintenance based on deep learning techniques. The goal is to support the continuous and occasional data sources changes, which would highly affect the data integration. To this end, we focused mainly on managing metadata change within an integrated structure, refereed to as mapping maintenance. Our deep learning models encapsulate both convolutional, and Long short-term memory networks. A prototype has been developed and performed on two use cases. The process is fully automated and the experiments show significant results compared to the state of the art.

1 INTRODUCTION

Big data has become a great phenomenon in the modern industry, especially with the availability of enormous amounts of data. The benefits of such data sparkled the curiosity of multiple companies and researchers.

Nevertheless, although it offers such benefits, managing the different data sources remains a challenging problem. Indeed, data size, heterogeneity, variety, etc, make it hard to manage and interlink data sources. Accordingly, to overcome this problem, it has been suggested to add semantics to data. Ontologies, as a knowledge representation formalism, continue to be a promising solution for the semantic interoperability between this data. Indeed, they allow representing data following a semantic model, which permit a better understanding of data. In this regard, in terms of heterogeneity, variety and volume, drugs data are one of the targeted fields by big data techniques. In effect, big biomedical data has grown exponentially during the last decades and a similar growth rate is expected in the next years, resulting into different interoperability conflicts among data collections with entities being dispersed across different datasets. Each data source can likely get a change of structure and metadata, which compromises the whole integration (Maria-Esther and al., 2019). As aforesaid, the data sources being numerous and varied, this issue impacts consistency in virtual data integration and its maintenance. This latter, namely, mapping maintenance is defined as the task aiming to keep existing mappings in an updated and valid state, reflecting the changes affecting a source's entities at evolution time (Cesar and al., 2015).

Therefore, this work aims to integrate data sources based on ontologies with an application to drugs' domain. Our proposal takes into account both the data sources integration changes and associated metadata. To do so, the study focuses on automatically manipulating mappings generated from virtual data integration, in order to adapt them to the observed changes. Thus, the study responds to two main research questions: (i) which data integration is suitable for the

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mentioned problem, and (ii) how to adapt and update mappings to handle data sources' changes. The originality of our work is the novel automated mapping maintenance that we propose, based on deep learning techniques. This article is organized as follows: Section 2 presents related works. Our proposal is detailed in section 3. Section 4 presents the implementation and discusses the evaluation of our proposal. Lastly, we conclude and deliver the future works in section 5.

2 STATE OF THE ART

Our study of recent works has focused on schema matching and mapping maintenance as a solution for change in the metadata of data sources.

Schema matching makes use of name, description, type of data, constraint, and schema structure in order to identify the match between two attributes of data source's schema. (Do, 2007) describes the architecture, functionality, and evaluation of the schema matching system COMA++ (Combining Matchers). COMA++ represents a generic and customised system for semi-automatic schema matching, which combines different match algorithms in a flexible way. But even though the work shows good results, it stays limited due to the unavailability of metadata and schema of all data-sources. Furthermore, the use of metadata is not always appropriate to schema matching process. This issue has been related in many works. That being said, work on schema matching has shifted towards Instance based matching. This approach employs the available instances as a source to identify the correspondences between schema attributes. (Munir and al, 2014) focuses on finding similarities/matchings between databases based on the instance approach. It uses the databases' primary keys. The proposed approach consists of two main phases : Row Similarity and Attribute Similarity. This work shows significant results in terms of matching accuracy. However, it remains limited by its applicability to only databases.

While working on databases, (Sahay and al, 2019) and (Mehdi and al, 2015) use a hybrid approach, using schemas and data provided to manage matchings, by using machine learning. They try to work on one-to-one matchings, and introduce a dictionary for one-to-many matchings. The results seem sufficient for simple use cases, but show mediocre performance in a complex mappings while supporting only databases.

Concerning other formats, (Mohamed-Amine and al, 2017) work on Json datasets. They focus solely on schema inference, but they show great potential for schema matching. They deal with the problem of inferring a schema from massive JSON datasets, by identifying a JSON type language which is simple and expressive enough to capture irregularities and to give complete structural information about input data. (Ahmad Abdullah Alqarni, 2017) introduces two approaches to improve XML Schema matching efficiency: internal filtering and node inclusion. In the former, it detects dissimilar elements at all schema levels at early stages of the matching process. And In the latter, it detects dissimilarity between elements on leaf nodes only using their ancestor degree of similarity and then exclude them from the next phase of matching process.

In another context, several researches focused on mappings maintenance to fix data availability. This means manipulating and updating mappings to handle data sources' and ontologies' change.

In that matter, (Cesar and al, 2015) and (N. Popitsch, 2018) take into account the definition of established mappings, the evolution of Knowledge Organization Systems (KOS) and the possible changes that can be applied to the mappings. they define complete frameworks based on formal heuristics that drives the adaptation of KOS mappings. These studies show great results in terms of mappings maintenance, but they require a lot of human intervention, with a repeated the integration process, which re-value the need for a mapping maintenance solution.

(Khattaka and al., 2015) proposes an other approach towards mappings evolution regeneration. It focuses on finding alignments between ontologies. The paper proposes a mapping reconciliation approach between the updated ontologies that have been found to take less time to process compared to the time of existing systems when only the changed resources are considered and also eliminates the staleness of the existing mappings. Even though this work presents intresting work concerning mappings maintenance, it focuses only on ontology descriptions, without taking into consideration the data change.

2.0.1 Synthesis

The literature revue on schema matching and mapping maintenance shows that the existing works focused either on manipulating ontologies or by changing data sets. But since our focus is on mapping files, no study has tried to manipulate the files directly. That being said, our aim is to focus on how to manipulate and update mapping files, following a change in data sources' metadata.

3 SEMANTIC-BASED DATA INTEGRATION AND MAPPING MAINTENANCE APPROACH

In this section, we describe our proposed approach for drug integration. The aim is to provide a virtual semantic data integration of heterogeneous multiple data sources in drugs domain. As aforementioned, the proposed approach focuses on two main functionalities: Federated data integration and mappings update.

Figure 1 presents the global architecture of the proposed approach. The layered architecture is composed of 6 components:

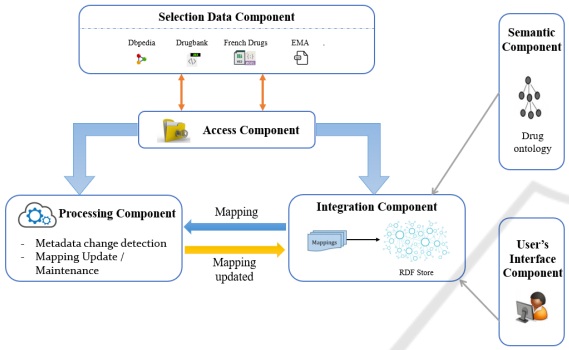


Figure 1: The proposed data integration architecture.

- **Selection Data Component:** It encompasses the selection of different data sources with different contents and data types (XML, CSV, TXT, etc).
- **Access Component:** It contains all the necessary implementations allowing the access to multi-source data.
- **Integration Component:** The purpose of the integration component is to combine data coming from multiple data sources to provide a unified, single view of data. The integration process is based on a drug ontology (concepts). The output of the integration is a file of mappings. This component takes as input, the data sources and the domain ontology. As output, it returns the mappings file for the virtual integration. We point out that a virtual integration approach means that data remains in local sources and is accessed through an intermediate infrastructure called a mediator (Masmoudi and al, 2021).
- **Processing Component:** The aim of this component is to maintain an integration system up-to-date. It checks changes in data sources, and updates accordingly the mapping file, as presented in figure 2.

  We perform this processing by following three basic functionalities:

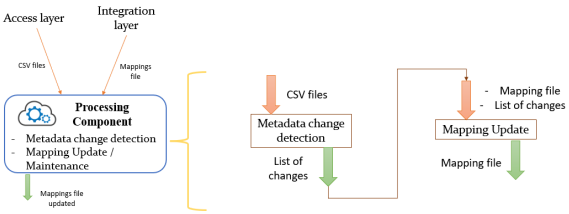


Figure 2: Processing component.

  - **Metadata Changes Detection:** an algorithm is proposed to detect changes occurred in the sources' metadata. The changes are taken into account by the algorithm, to classify them into the corresponding metadata: matching between and new data sources/metadata.
  - **Mappings Update:** for this functionality, we develop an algorithm to update the previous mapping file to match the new changes. It takes as input the list of changes resulted from the first algorithm, and outputs the updated mapping file.

    According to the list of changed attributes, we use a classification algorithm to match data with the corresponding attribute (figure 3).

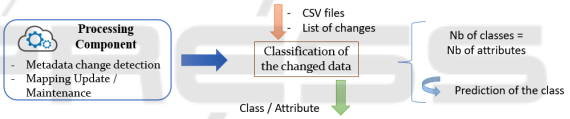


Figure 3: Classification.

  - **Integration Update:** After generating the updated mapping file, this latter gets transferred to the integration component once more, in order to maintain the integration process with the new changes.
- **Semantic Component:** This component contains the domain ontology allowing the semantic integration.
- **User's Interface Component:** It represents the front-end interface allowing to dialog with the proposed system. Through this interface, users are able to query the integrated data.

3.1 Data and Algorithms' Description

This section describes the algorithms developed for our approach, as well as a presentation of the drugs dataset used for the prototype.

3.1.1 Drug Dataset Overview

As aforementioned we applied our approach to the drugs domain, thus we used the DrugBank dataset [1]. It is a comprehensive online database containing information on drugs and drug targets. DrugBank combines detailed drug (i.e. chemical, pharmacological and pharmaceutical) data with comprehensive drug target (i.e. sequence, structure, and pathway) information. The database contains 9591 drug entries including 2037 FDA-approved small molecule drugs, 241 FDA-approved biotech (protein/peptide) drugs, 96 nutraceuticals and over 6000 experimental drugs. It contains 55 attributes, each attribute describing a characteristic of the drugs. We enumerate some of them : the drug identifier (Drugbank-id), the drug's name, the drug's Chemical Abstracts Service number (CAS number).

3.1.2 Data Integration

The proposed approach starts with semantically integrating data and generating the corresponding mapping files. Indeed, it matches the attributes of the data source (metadata) with the ontology concepts. To do so, we used **Onto-Kit** (Masmoudi and al, 2021), an automatic ontology-based data integration tool. By importing the drug ontology and the dataset to the tool, we generate an RML mapping document 1. We point out that RML is a mapping language that describes mapping rules between any form of data to RDF (A triple based graph model language) (Masmoudi and al, 2021).

```
@prefix rr: <http://www.w3.org/ns/r2rml#>.
@prefix  rml: <http://semweb.mmlab.be/ns/rml#> .
@prefix xsd: <http://www.w3.org/2001/XMLSchema#>.
@prefix rrx: <http://www.w3.org/ns/r2rml-ext#>.
@prefix rrxf: <http://www.w3.org/ns/r2rml-ext/functions
/def/>.
@prefix drugbankvocab: <http://bio2rdf.org/drugbank_
vocabulary:>.
@base <http://example.com/base> .

<#DrugBankMapping> a rr:TriplesMap;
rml:logicalSource [
        rml:source "C:\Users\marmo\OneDrive\Bureau
        \TEST\drugbank.csv";
        rml:referenceFormulation ql:CSV;
];

rr:subjectMap [
        rr:template "http://example.com/{drugbank-id}";
        rr:class drugbankvocab:drugbank-id;
];
rr:predicateObjectMap [
        rr:predicate drugbankvocab:name;
        rr:objectMap [
rml:reference "name"; ];
        ];
rr:predicateObjectMap [
        rr:predicate drugbankvocab:description;
        rr:objectMap [
rml:reference "description"; ];
        ];
```

Listing 1: Mapping file.

[1]Drugbank dataset, https://go.drugbank.com

This file defines links as a triple map format, between a concept of the ontology and an attribute of the data source.
Onto-kit maps each class of the ontology to the corresponding attribute of the dataset. Then, running through all the attributes, Onto-kit generates the predicate-object mapping file, in which the number of maps corresponds to the number of attributes of the data source.

3.1.3 Metadata Change Detection

While ensuring the data integration, the work of the processing component comes in play, when a change is detected in the data source. We try periodically to check change in the metadata following the algorithm 1. This detection is based on the old metadata previously registered of the data source and the new one.

Algorithm 1: Metadata change detection.

$Old.file \leftarrow read-CSV(old.file)$
$New.file \leftarrow read-CSV(new.file)$ ▷ Read the data
$List.changes \leftarrow []$
$Old.attributes \leftarrow metadata-of(Old.file)$
$New.attributes \leftarrow metadata.of(New.file)$ ▷ Get the metadata / attributes
for *attribute*.1 in $Old.attributes$ **do**
  for *attribute*.2 in $New.attributes$ **do**
    while *attribute*.1 and *attribute*.2 have the same index **do**
      if *attribute*.1 is not similar to *attribute*.2 **then** ▷ Check for changes
        Add *attribute*.2 to $List.changes$
      end if
    end while
  end for
end for
return $List.changes$

The algorithm 1 compares the old and the new data source's metadata, and returns a list of the changed attributes. The next step is to determine the corresponding attributes of these changes in the new data source.

3.1.4 Metadata Matching

With the algorithm 1, we got to detect the attributes that have been changed in the new data source. But the problem is that we don't know to which attributes correspond these changes.

For example, we know that the metadata $drugbank-id$ and *description* have been changed, but how can we match the new changes to them? a bad scenario would be to correspond the data *" DB00105 "* to the attribute *description*, and the data *" Lepirudin is used to break up clots and to reduce thrombocytopenia. It binds to thrombin ... "* to

$drugbank - id$.

Such a bad matching would have bad impact on the mapping file, and thus, it would result a wrong data integration.

Thus, the problem we are facing now, is a classification one. This means that we want to classify the data to a corresponding attribute. In other words, we consider each attribute of the dataset as a class, and based on the data, we predict the corresponding class.

Therefor, the purpose of the algorithm 2 is to match the old changed attributes with the new ones. This is done by training learning models to predict which class an attribute's data corresponds to. The algorithm returns the attribute of the new data which enables the resulting matching.

Algorithm 2: Metadata matching.

$Data.Frame \leftarrow read - CSV(old.file)$
▷ transform the dataframe to a two column data frame of attributes and values
$Data.Frame \leftarrow Re - map(Data.Frame)$
▷ Delete NULL values
$Data.Frame \leftarrow Drop.Null.Values$
$Dictionary \leftarrow []$
$i \leftarrow 0$
for $attribute$ in $dataframe.attributes$ **do**
    add $[attribute : i]$ to $Dictionary$
    $i \leftarrow i + 1$
end for
▷ We replace the attributes by numerical values
Data.Frame[attributes] ← Data.Frame[Dictionary]
$Labels \leftarrow Data.Frame[attributes]$
$Vocab \leftarrow words$ in $Data.Frame[values]$
$Vocab.int \leftarrow to - int(Vocab)$
▷ We create a matrix of data in numerical values
$Feature \leftarrow matrix(Vocab.int(Data.Frame[values]))$
▷ We split the data to training set and test set
$train_x, test_x, train_y, test_y \leftarrow train_test_split(features, labels)$
$train_y, test_y \leftarrow one.hot.encoding(train_y, test_y)$
$model \leftarrow model.train(train_x, train_y)$
$Precision \leftarrow model.precision$
$New.Data \leftarrow Data.change$ from $List.changes$
$Prediction \leftarrow model.predict(New.Data)$
return $Prediction$

In terms of data processing, we transform all data to strings. In the neural network, we use an embedding layer, which purpose is compressing the feature space of the input into a smaller one.

We use afterwards layers of LSTM (long short-term memory) to conceptualize semantics in data, and CNN (Convolutional neural network) layers to well extract features of data.

For optimisation purposes (time execution and precision), we decided to train the model on the attributes (classes) changed. The predictions made will be therefore applied to update the mappings.

3.1.5 Mapping File Update

In the integration process, the generated output is a file of mappings connecting the metadata of the data source with the ontology concepts. Our aim is to change this file according to the predictions made by the previous algorithm.

We perform this by replacing the changed attributes in the mapping file, with the new ones predicted by the metadata matching algorithm.

4 IMPLEMENTATION AND RESULTS

We present in this section the execution of our solution, as well as it's application on different use cases.

4.1 Tools of Development

To manage the implementation of our approach, we used the following tools :

- Google Colab[2] : We used Google colab as a python platform to develop the proposed algorithms and to build the prediction models of the system.
- Keras[3] : We used the keras library to create, train and test the prediction models of our system.
- Protégé[4] : An open source ontology editor and a knowledge management system. We used it to explore the ontology of drugbank available online.

4.2 Evaluation Metrics

To evaluate the classification models, we used the confusion matrix. This latter is a table used to describe the performances of a classification model on a set of data. It differentiates between the true and false positives and negatives. It allows us to compute the metrics of Precision, Recall, F-mesure and Accuracy.
TP / TN: True Positive / True Negative.
FP / FN: False Positive / False Negative.

- Accuracy : It's the ratio between the total correct predictions and the total predictions. $Accuracy = \frac{TP+TN}{TP+TN+FP+FN)}$

[2]Google Colab, https://colab.research.google.com
[3]Keras, https://keras.io
[4]Protégé, https://protege.stanford.edu

- Precision: Proportion of well classed elements in a particular class.
  $Precision = \frac{TP}{TP+FP}$
- Recall: Proportion of well classed elements over the number of elements of a given class. $Recall = \frac{TP}{TP+FN}$
- F1-score: Mesures the compromise between the precision and the recall.
  $F1-score = \frac{2*(Recall*Precision)}{(Recall+Precision)}$

Regarding the model's calculated loss, we use the Mean Square Error, to determine how much is the difference between the actual values and the predicted values: y (Actual values), y_p (Predicted values).
$Loss = MSE = \frac{1}{n} * \sum_{i=1}^{n} (y_i + y_{p_i})^2$

4.3 Classification Model

As for the classification model, we use two architectures and compare the results. Te first architecture depends on LSTM layers and the second depends on CNN layers. The figure 4 presents these architectures.

We explore 2 use cases: *4 classes (4 attribute changes)* and *6 classes (6 attribute changes)*. We run our approach in these cases, and capture the results.

4.4 Study Cases

The approach, and specifically the processing component starts by detecting changes in files metadata. It works by comparing lists of strings corresponding to the metadata. The result is the list of changes with attributes of the old file.

For the drugbank data we're working with, we have 55 attributes in the metadata. To illustrate the result of the algorithm, we display changes over 10 attributes shown in table 1.

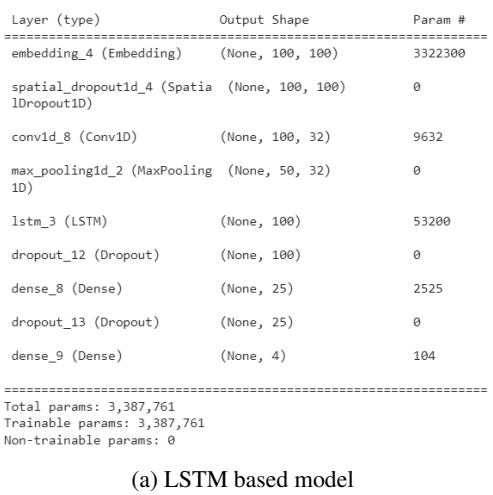
Table 1: Metadata change.

Old metadata	drugbank-id	name	description	cas-number	unii
	state	groups	general-references	synthesis-reference	indication
New metadata	drug	name	specification	cas-number	unii
	state	groups	general-references	source	indication

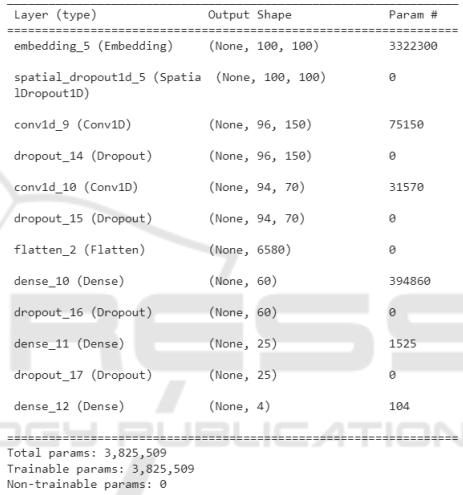
As we can see, some attributes have been changed (colored attributes), others did not. The algorithm returns the list of attributes that have been changed [drugbank-id, description, synthesis-reference]. We train therefore the models, and we present the results as study cases.

4.4.1 Case of 4 Classes

We plot the training-validation accuracy and loss throughout the whole training of the model. These



(a) LSTM based model



(b) CNN based model

Figure 4: Classification models.

plots (figure 6 a/b) describe the training phase of both models. This phase has a training sub-phase in blue, and a validation sub-phase in orange. We can see that the LSTM model has a steady training accuracy, but in contrast, it has a growing loss regarding the validation.

As for the CNN model, even though it lacks consistency, it shows better results over the loss and accuracy in training.

But these results do not fully represent the models capacity, that's why we test (test phase) them on a test dataset, to compute the actual accuracy and recall.

Using the corresponding confusion matrices, we compute the precision, recall, f1-score and accuracy in table 2.

The test results show that, although the fact that the LSTM model struggled and had poor results in training, it has performed well. This is annotated by

Table 2: Metrics of the models for 4 classes.

Model	Accuracy	Precision	Recall	F1-score
LSTM Model	0.93	0.859	0.855	0.86
CNN model	0.90	0.80	0.80	0.81

the accuracy reaching 93%.

But overall, both models got good results by reaching an accuracy of 90%

4.4.2 Case of 6 Classes

We plot again the training-validation accuracy and loss throughout the whole training of the model (figure 6 c/d).
The plots show that both models do train well, but have trouble to well predict the classes in the validation. As validation loss, once again, the CNN model show better results, but it lacks consistency.

We execute therefore the models on a test dataset and compute evaluation metrics as shown in table 3.

As test results, LSTM model gives better performance, even though it lacked a bit in the training phase. These good results are due to it's consistency in the training, which is not the case for the CNN model, who, the more it loses consistency, the more poorly it performs.

Table 3: Metrics of the models for 6 classes.

Model	Accuracy	Precision	Recall	F1-score
LSTM Model	0.93	0.891	0.894	0.89
CNN model	0.85	0.74	0.72	0.70

But in general, the performance of both models is good, by attending 85% for the CNN model and 93% for the LSTM model.

4.4.3 Optimization

For both models, we have observed that they suffer from an over-fitting problem. This problem means that the model has a bad generalisation (Brownlee, 2018). It has learned too much that it performed well on the training but poorly on a new data (test data).

So, to overcome this issue, we have applied some regularisation techniques throughout our process to get better results. Specifically, we used dropout and early stopping.

By using both techniques, we managed to raise the accuracy of both models to nearly 80%.

4.5 Mappings Update

As previously said, the classification algorithm takes as input the data corresponding to the changes discovered, and it outputs the attribute (class) of each set of data. To update the mappings file, we take list of changes and update the file correspondingly.

The final updated file (shown in figure 5) will ensure that the data integration approach works without any issues, regardless of the metadata change of data sources.

```
@prefix rr: <http://www.w3.org/ns/r2rml#>.
@prefix  rml: <http://semweb.mmlab.be/ns/rml#> .
@prefix xsd: <http://www.w3.org/2001/XMLSchema#>.
@prefix rrx: <http://www.w3.org/ns/r2rml-ext#>.
@prefix rrxf: <http://www.w3.org/ns/r2rml-ext/functions/def/>.
@prefix drugbankvocab: <http://bio2rdf.org/drugbank_vocabulary:>.
@base <http://example.com/base> .

<#DrugBankMapping> a rr:TriplesMap;
rml:logicalSource [
        rml:source "C:\Users\marmo\OneDrive\Bureau\TEST\drugbank.csv";
        rml:referenceFormulation ql:CSV;
];

rr:subjectMap [
        rr:template "http://example.com/{drugbank-id}";
        rr:class drugbankvocab:drugbank-id;
];
rr:predicateObjectMap [
        rr:predicate drugbankvocab:name;
        rr:objectMap [
rml:reference "name"; ];
        ];
rr:predicateObjectMap [
        rr:predicate drugbankvocab:description;
        rr:objectMap [
rml:reference "description"; ];
        ];
rr:predicateObjectMap [
        rr:predicate drugbankvocab:state;
        rr:objectMap [
rml:reference "state"; ];
        ];
rr:predicateObjectMap [
```

(a) Old mappings

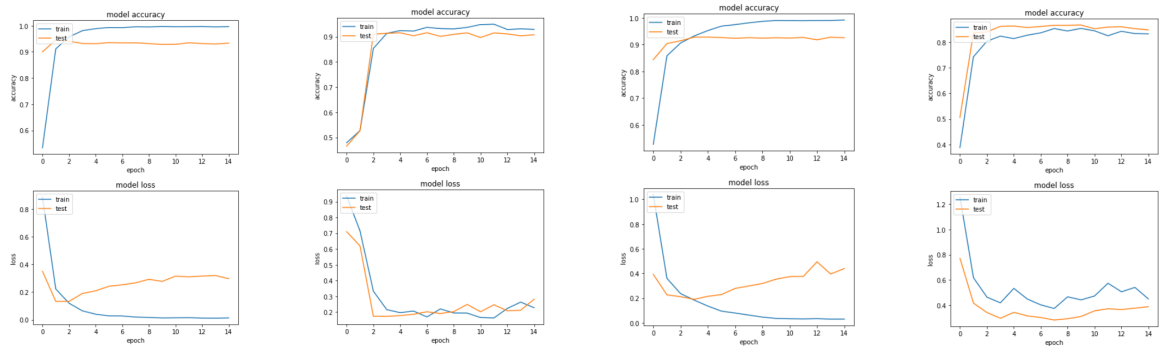
```
@prefix rr: <http://www.w3.org/ns/r2rml#>.
@prefix  rml: <http://semweb.mmlab.be/ns/rml#> .
@prefix xsd: <http://www.w3.org/2001/XMLSchema#>.
@prefix rrx: <http://www.w3.org/ns/r2rml-ext#>.
@prefix rrxf: <http://www.w3.org/ns/r2rml-ext/functions/def/>.
@prefix drugbankvocab: <http://bio2rdf.org/drugbank_vocabulary:>.
@base <http://example.com/base> .

<#DrugBankMapping> a rr:TriplesMap;
rml:logicalSource [
        rml:source "C:\Users\marmo\OneDrive\Bureau\TEST\drugbank.csv";
        rml:referenceFormulation ql:CSV;
];

rr:subjectMap [
        rr:template "http://example.com/{drug}";
        rr:class drugbankvocab:drugbank-id;
];
rr:predicateObjectMap [
        rr:predicate drugbankvocab:name;
        rr:objectMap [
rml:reference "name"; ];
        ];
rr:predicateObjectMap [
        rr:predicate drugbankvocab:description;
        rr:objectMap [
rml:reference "specification"; ];
        ];
rr:predicateObjectMap [
        rr:predicate drugbankvocab:state;
        rr:objectMap [
rml:reference "state"; ];
        ];
rr:predicateObjectMap [
```

(b) Updated mappings

Figure 5: Results of the mappings update.



(a) LSTM based model (4 classes) (b) CNN based model (4 classes) (c) LSTM based model (6 classes) (d) CNN based model (6 classes)

Figure 6: Test cases' models training.

5 CONCLUSION AND LIMITATIONS

In this paper, we give a response to the problem of how to ensure the maintenance of the virtual data integration and metadata changes. Indeed, we present a semantic-based data integration and mapping maintenance approach with an application to drugs domain. The proposed approach contains two main components: a virtual semantic data integration component, and a mapping update component. Both of them ensure the fully automated mapping maintenance of the data integration. The proposal includes deep learning techniques for the mapping maintenance. We have performed our solution on two use cases, 4 and 6 changes in the data sources' metadata. In each case, we detect changes, and train a deep learning model to classify the corresponding attribute based on its' data. We used also two types of models, an LSTM-based model and a CNN-based model.

In terms of results, the models showed interesting performances, as the accuracy reached 90%. Although, the models did suffer from an over-fitting problem, which is due to the similarity between the different classes (attributes) in the dataset. Overall, our solution is fully automated, which represents huge benefits compared to the existing solutions that require human intervention. In matters of time execution, training models do not surpass the limit of 10 minutes for the worst-case scenario. This time execution is indeed long for an automated system, but compared to the state of the art (human intervention), it shows significant optimal result. We are currently working on the number of classes that the model needs to deal with. Indeed, as we handle data sources changes, the data within these sources doesn't contain high rate of change. So, basically, the models work on the same data that they were trained on, which will enable high performance results. We intend also, to manage not only one-to-one changes (one class corresponding to only one class), but one to many changes, which will improve the mapping maintenance. We also plan, to improve our proposal to support different multimodal data.

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