Relational Learning and Feature Extraction by Querying over Heterogeneous Information Networks

Parisa Kordjamshidi † Sameer Singh‡ Daniel Khashabi‡ Christos Christodouloupolos§
Mark Summons‡ Saurabh Sinha‡ Dan Roth¶
† Tulane University ‡ University of Illinois at Urbana-Champaign § University of California, Irvine ¶ Amazon Research Cambridge, UK
† pkordjam@tulane.edu § sameer@uci.edu ¶ chrchrs@amazon.co.uk ‡ {khashab2,mssammon,sinhas,danr}@illinois.edu

Abstract

Many real world systems need to operate on heterogeneous information networks that consist of numerous interacting components of various types. Examples include systems that perform data analysis on biological information networks; social networks; and information extraction systems processing unstructured data to convert raw text to knowledge graphs. Many previous works describe specialized approaches to perform specific types of analysis, mining and learning on such networks. In this work we propose a unified framework consisting of a data model - a graph with a first order schema- along with a declarative language for constructing, querying and manipulating such networks in ways that facilitate relational and structured machine learning. In particular, we provide an initial prototype for a relational and graph traversal query language where queries are directly used as relational features for structured machine learning models. Feature extraction is performed by making declarative graph traversal queries. Learning and inference models can directly operate on this relational representation and augment it with new data and knowledge that, in turn, is integrated seamlessly into the relational structure to support new predictions. We demonstrate this system’s capabilities by showcasing tasks in natural language processing and computational biology domains.

1 Introduction

Many real world systems need to operate on heterogeneous information networks (Shi et al. 2015) that consist of multiple interacting components of various types. Examples include biological networks containing genes and proteins along with experimental genomic and clinical data of the patients; social networks, such as citation networks relating authors and papers; or even more complex networks such as knowledge graphs, which can contain a large variety of types of entities and relationships (Nickel et al. 2015).

Although previous research extensively addresses the challenges of working with such networks for various mining tasks (see for example (Sun and Han 2013; Kuck et al. 2015)), a general solution for easily constructing such networks or systematically manipulating them by various analysis units has not yet been worked out. In other words, mostly specialized approaches are proposed to perform specific types of analysis over a network design and the implementations are mostly dependent on the type of tasks and the type of analysis (for an overview, see (Shi et al. 2015)).

Data representation and flexible intelligent data analysis, as well as the evolution of these networks based on the analysis outcomes, need to be placed in a well-defined framework. A complex version of such networks are instantiations of knowledge graphs and as Nickel, et al. put it: “Representing, learning, and reasoning with [knowledge graphs] remains the next frontier for AI and machine learning.” (Nickel et al. 2015). In this work, we move closer to this frontier by: 1) proposing a unified framework for integrating data from heterogeneous resources in one relational graph structure; 2) proposing a query language for constructing, manipulating and evolving this graph; 3) providing the capability of performing relational machine learning and feature extraction on this graph using the same query language. The novelty of our work, which is in progress, is in the integration of the learning-based analysis with the above components in one system, and allowing the proposed graph query language to be used consistently for preparing learning examples, extracting relational features, and processing the results of the learning models.

Our proposal is different from the conventional usage of query languages in the context of information networks, which are either standard retrieval queries (He and Singh 2008) or designed for a specialized task (Kuck et al. 2015). Here, relational and structured machine learning models are declared using a succinct definition language, and are directly applied on the graph. The resulting predictions can be integrated into the same graph in a seamless manner. Our model can be seen as an information extraction model that can make declarative queries from unstructured data by expressing them in a relational graph structure. This combines the aspirations of existing works that have tried to combine information extraction modules with relational database systems and use standard querying languages for retrieving the information (Krishnamurthy et al. 2009a) with those of systems that are designed for processing textual data and which provide a regular expression language to directly query from text (Broda et al. 2013). Comparatively, our first order graph query language provides the flexibility and expressivity to extract relational and global patterns from unstructured data for various kinds of data analysis, including feature extraction as well as basic search and retrieval from the network.
In a complete system, the data is read using programs called data readers. The user declares the schema of the data as a graph in which data items are collections of nodes, edges and properties, which are defined using Sensors, succinct specifications in Saul’s definition language. The data from the reader is mapped into the data-model and a populated graph containing all the data is generated. After population, all the operations such as example generation, feature selection, querying, and learning are defined using user-specified graph queries expressed in terms of data-model components. The predictions of the learning models can be incorporated into the data-model and the outcomes are integrated into the generated data graph, allowing them to be queried by the feature extraction and learning components. Basically, these components are used to put the raw data into the graph structure and capture domain-specific knowledge, including learned representations of the data itself (e.g. a collection of raw image data can be used to train to recognize an object node).

3 Data Modeling

One main goal of our framework is to facilitate using heterogeneous information from various domains in a unified framework. For example, raw data can be textual documents, a collection of images or videos or spreadsheets describing patients, drug responses. The basic notions that we use including readers, baseTypes, sensors, etc and using these to build an arbitrary graph structure provide an abstraction that paves the way for achieving this goal.

The data-model is a graph schema that is used to explicitly represent the structure of the data and contains typed nodes, edges and properties. The node types are domain’s basic data-structures, called base-types. The base-types are pre-established for each application domain. The Saul base-types for NLP domain are discussed in (Kordjamshidi et al. 2016) and include for example base-types for representing documents, sentences, phrases, etc, referred to as linguistic units. Our computational biology data-model is augmented by necessary base-types to represent genes, patients, etc.\(^3\)

We use the notion of data readers which are programs that can read the data into the base-types. Each domain is equipped with a set of sensors that are black-box functions applied on the base-types and can generate new nodes, connect them by edges or generate properties of the nodes. The graph schema is a first order graph that is based on types of nodes instead of representing all individual objects. The programmer declares the schema of the data, which later, will be populated with the actual data instances in the program and used for feature extraction and learning. A node of type T is declared as in line 1 below and a property for node nodeName is declared as in line 2:

```scala
val nodeName = node[T]
val propName = property(nodeName) /*body*/
```

In the body of the property declaration we use a sensor that operates on type T and returns a value of property type. The property type can take any of Scala’s basic

\(^1\)Saul code: [https://github.com/CogComp/saul](https://github.com/CogComp/saul)

\(^2\)Data from the KnowEng: [http://www.knoweng.org/](http://www.knoweng.org/)
data types or a standard collection. A property sensor associates each object with a property type. An edge that connects a source node node1 of type T to a destination node node2 of type U is defined as edge(node1, node2). The edge declaration defines the type of edge; sensors will populate the instances with actual edges. A sensor that defines how a node is connected to another node is called an edge sensor. We can easily add sensors to edges as 

val phraseToRelations=edge(phrase,relations)

val relations=node[Relation]
val phrases=node[Phrase]
val sentences=node[Sentence]

flexibility of working with a relational model.
connections in both directions automatically and provide the
tokenization edge, generates tokenized token nodes, upon
connection between the source and destination. For example, a
of destination nodes and at the same time establish a con-
Generating sensors

3.1 Populating the data model

Once a data-model is specified, we can populate it with the actual data instances to get a propositionalized data graph. For example, given a data reader that provide collections of objects for all declared nodes, we can populate the node, nodeName as: 

val connectedPhrases = phrase(x)\rightarrow\text{phraseToRelation}^{-1}\rightarrow\text{phraseToRelation}

Explicit joins. Though the graph traversal operations provide the functionality that is expected from classic relational join operations, the user can join nodes explicitly and add complex relational nodes to the graph. This can be done as follows:

val joinNode = join(node1, node2)(/*body*/)

Algorithm 1 shows the steps needed for declaring the data-model. For example, a typical NLP data-model can have the following nodes and edges,
where the body is a logical expression based on the properties of the nodes that indicates which node instances should be joined together. For example, \( \_ . \text{posTag} \equiv \_ . \text{posTag} \) indicates that we need to join the nodes which have the same posTag property values. The outcome node is represented as a tuple of the two nodes and gives access to all their properties, edges and instances.

Filtering. The Scala’s `filter` is used to Select a set of nodes that meet a specified condition. For example, `words().filter(x=>pos-tag(x).equals("NN"))` selects a set of `words` nodes whose `pos-tag` is `NN`.

4.2 Pattern-matching and graph-isomorphisms

The `data-model` provides the advantage of finding patterns of data instances as well as meta patterns according to the type of nodes and edges in the data graph or its schema i.e. `data-model`. These kinds of queries are not easy to formulate in standard relational data models.

Contextual queries. We provide functions that help explore the context of a node and its neighborhoods for more flexible pattern matching and accessing global patterns. The edges provide only one step access from one node to another node that is directly connected to it. The command `node(x).neighborAt(n)` gives the collection of nodes that are exactly `n` edges away from node instance `x`. We also provide a `neighborWithin(n)` variant that provides the collections of nodes that are at least `n` edges away, and for both these functions the users can include an optional set of edges to restrict the neighborhood by. Like the rest of the queries, neighborhood queries allow composition via chaining: it can be applied to a result of another query, and other operations such as filtering, aggregation, or traversal can be applied on its result.

Path queries. In order to identify the shortest path between two data instances, we provide the `path` function that can be applied to node queries, `node(x).path(y)`. In particular, this function searches for an instance `y` that is reachable from a path of edges starting from instance `x`, and returns the sequence of edges that connect these two nodes (which is empty if a path does not exist). Optionally, the query can contain a maximum length `n` of the path `node(x).path(y,n)`, i.e. an empty path is returned if a path of size `<=n` is not found.

These neighborhood and path queries can be used to define features that capture the local graph context in the data. For example the size of the neighborhood `neighborWithin(n).size` or its diversity `neighborWithin(n).groupBy(_._tag).size` may be used to represent an instance, while the length of the path between two instances `path(y).size` captures the similarity. It should be noted that such queries can get computationally very complex in large graphs. In order for such queries to be efficient, this function is implemented using breadth-first search over the nodes in the graph. More sophisticated optimization techniques are to be investigated in the future.

4.3 Aggregation functions

We can apply various aggregation functions on a collection of properties:

```scala
t.propertyName.aggregationFun()
```

Since the property values have Scala’s basic types, a large number of aggregation functions are available to `Saul` via built-in Scala functionality. Hence, depending on the type of the collection, various functions may be applied. In case of numeric property types, for example, we can apply aggregations such as `sum`, `product`, and `max`. A number of aggregation functions are available for any type of instances, such as `size` and `mkString` for customized concatenation, and further, users can also implement their own aggregation functions by using `filter`, `map`, `reduce`, and `groupBy`. In `Saul`, such native Scala aggregation functions can be applied on the nodes and properties of the graph.

5 Querying for learning models

One main goal of basing `Saul` around a graph based data modeling language is to provide the facility and flexibility for relational learning models to extract complex features. Formally, in supervised learning, given a set of examples i.e. pairs of input and output, \( E = \{ (x^{(i)}, y^{(i)}) \in X \times Y : i = 1 \ldots N \} \), learning is defined as a mapping \( h : X \rightarrow Y \). In general both inputs \( (X) \) and outputs \( (Y) \) can be arbitrary complex structures. In `Saul` both \( x \) and \( y \) are sub-graphs of the `data-model`. Each input \( x \) is a set of nodes \( \{ x_1, \ldots, x_K \} \) and each node has a type \( p \). Each \( x_k \in x \) is described by a set of properties relevant to its type; this set of properties will be converted to a feature vector \( \phi_p \). For instance, an input type can be a word (atomic node) or a pair of words (composed node), and each type is described by its own features (e.g. a single word by its part of speech, the pair by the distance of the two words). The output space \( y \) is represented by a set of labels \( l = \{ l_1, \ldots, l_P \} \) each of which is another property of a node in the graph. The labels can have semantic relationships to each other, so that they can represent complex output concepts for any arbitrary task. The main components that must be declared for the learning models are learning examples \( x \) and \( y \) and the features. In structured output prediction tasks the background knowledge about the output space should also be declared. Here, we describe how our graph data modeling and various graph queries are used in defining the components of the learning models.

5.1 Learning examples

Classically, each machine learning example has an input which has a feature vector representation and an output label which is a single variable. A label can be a binary or a multi-valued variable in the classification setting, and a real valued variable in the regression setting. Classic learning models are the basic building blocks for composing `Saul`’s complex learning model configurations.

Example representation. In our integrated feature extraction and learning environment, each learning example is a rooted sub-graph. Each learning model is applied on a specific root node. The input feature types and the label type
of the learning examples are a set of graph queries returning direct or contextual properties of the root node. In other words, the root node is the pivot of all the queries that are used for extracting features for a learning example. Consequently, we can define a learning example with a node and a set of pivoted queries, one of which is the label query and the rest of which are feature queries. All these queries return a property or a collection of properties.

The signature for defining a learning model, called modelName, is as follows:

```scala
object modelName extends Learnable(rootNodeName) { /* body */}
```

where rootNodeName is the name of the root node (in the typed graph) of the examples that the learning model takes. Different kinds of properties related to the root node or its connected nodes can be used to define features in the form of queries. These queries define the feature types and the label type of this learning model. As described in Section 4, queries can be declared and named as properties in the data-model and used in the body of the learners or they can be declared directly when defining the learning model. The following snippet shows how the feature information can be provided in the body of the learning model:

```scala
def label = queryLabel
def feature = using(query1, query2, ...)
```

In this snippet we assume all queries are declared and the learner refers to a list of query names to be used as features.

**Example selection.** The examples used by a learner are instances of a single node in the graph and can be retrieved from the graph. It is often the case that the programmer needs to filter the data items and use only a subset of examples for training. A common use case is filtering the negative examples in an unbalanced data set. This can be declared as a part of the learning model. Alternatively, it can be defined elsewhere and set as the example selection filter for the learning model when populating the training data into the data graph. The default filter uses all instances of the learner’s type that exist in the instantiated graph.

**Constraints.** Constraints may be used in structured learning models to incorporate domain knowledge by explicitly linking some output predictions. Constraints are implemented using queries to specify the relevant properties in the data graph and using a logical expression to impose restrictions on the sets of values they can take. For example,

```scala
(sentences(s) ~ sentenceToPhrase)._forall{x =>
  isPredicate on x is "True" ==>
  isArgument on x isNot "True"
```

indicates that all phrases in a sentence can be labeled as a predicate or as an argument not both.

The constraints are defined in terms of the outputs of the classifiers and their primary usage is to impose structural restrictions on the output values of classifiers while making joint predictions. The constraints can be used for structured learning models for joint training too. The details about the underlying computational model for using global constraints in learning and prediction in Saul is provided in (Kordjamshidi, Wu, and Roth 2015). A constrained classifier can always be used in the body of the properties to generate the property values of the nodes in the data-model and called via graph traversal queries. This implies, the answer to such queries is found by performing global inference and finding the best assignments under the user specified constraints.

### 6 Biological networks Application

In this section, we show the value in integrating heterogeneous data coming from various resources in a unified data model for the computational biology domain and the way it facilitates performing various kinds of analysis by querying, learning and inference. Figure 2 shows the conceptual model of the employed data in terms of entities and relationships. In Saul all the entities and relationships are declared as nodes in a graph and there is no distinction between them.

#### 6.1 Data description

Our experimental data includes various spreadsheets. One spreadsheet is about patients, including an identifier for each patient and some clinical properties of the patients such as age, race and type of cancer. This data is shown in the diagram with the patient box and the type of properties of the patients are connected to this box. There is another spreadsheet that contains the response of each patient to different drugs. This is shown in the patient-drug diamond (relation symbol in relational data models) in the figure. The drug response is a real-valued property of this relation. The genomic information of the patients shown with the patient-gene diamond. This is a spreadsheet that shows the gene expression levels in each patient. The actual data contains the expression values of ~ 20k genes, typically for a few thousands of patients. The left part of the diagram shows the schema of our biological knowledge graph, which contains the information about genes and their relationships. This is used as background knowledge when performing analysis on patients’ data. The Gene box shows the individual properties of each gene, such as the pathways that it belongs to, biological processes (from Gene Ontology) it is active in, etc. The Gene-Gene diamond shows relationships between genes, e.g., their sequence similarity, their protein-protein interactions, etc.

#### 6.2 Data model declaration

Given the conceptual model of the data, we can declare the data-model at the same conceptual level using Algorithm 1:

```scala
val patients = node[Patient]
val genes = node[Gene]
val patientGene = node[PatientGene]
val patientDrug = node[PatientDrug]
val geneGene = node[GeneGene]
val geneGenes = edge(geneGene, genes)
```

---

^see KnowEng project [https://knoweng.org/research/analytics/](https://knoweng.org/research/analytics/)
Figure 2: This graph represents the type of entities and relationships that are involved in our biological network.

The properties are assigned to nodes, e.g., the response of a patient to a drug given base-types and sensors, is defined as,

```scala
val drugResponse = property(patientDrug) { 
  x: PatientDrug => x.response }
```

Similarly the KEGG property is defined as the set of pathways (catalogued in the public KEGG database) that are known to contain that gene,

```scala
val KEGG = property(gene) { 
  x: Gene => x.pathways }
```

### 6.3 Querying the biological network

Given the properties, genes can be grouped by the pathways. This results in lists of genes per pathway.

```scala
val geneGroupedPerPathways = 
  genes.SGroupBy(KEGG, GeneName)
```

The `geneGroupedPerPathways` is a mapping between pathway names and lists of gene names. Using this mapping we can get a set of genes using a pathway name as a key.

```scala
val myPathwayGenes = 
  geneGroupedPerPathways.get("hsa01040")
```

This would return all the genes in our genomic data that belong to pathway “hsa01040”. Biologists might need to retrieve the subsets of genes that belong to a specific pathway as described above and seek all the genes connected to this subset by a specific type of edge. For example, one edge in our experimental knowledge graph is PPIBioGrid edge (protein-protein interaction edge catalogued in the BioGrid database). To obtain all genes connected by such an edge type to any gene in a specific pathway, the following query can be made:

```scala
val pathwayNeighbors = 
  myPathwayGenes.map (gen => 
    geneGenes(genes(gen)) -> PPIBioGrid(rel).equals(1)))
```

This query maps each gene in `myPathwayGenes` to all the genes that are connected to it via `geneGenes` relation inverse edge, then filters these pairwise gene relations to be limited to a specific class of relations, viz., all relations whose `PPIBioGrid` property is equal to one. The goal of this query and the previous one is to obtain a specific subset of genes to be used, for example, in learning or in computing the correlation between the gene expression values and drug responses across all patients. Towards this goal, one may obtain the expression values of a given subset of genes after usage of a specific drug, by defining a property based on joining patient-drug and patient-gene information, as follows,

```scala
val PWgeneExpression=property(patientDrug) { 
  pd: PatientDrug => 
    patientDrug().filter(_.pid == _.pid). 
    filter(myPathwayGenes.contains(GeneName(_))). 
    map(_.gExpression) }
```

This definition, given a patient identifier, it retrieves its gene expression measurements and filters them using the subset of genes selected in the previous query above.

### 6.4 Learning and regression

A user can define a machine learning model that uses the just-obtained subset of gene expression values for each patient and measures its correlation with the drug response, using a multi- regressor. The multi-regressor is a learner that is defined as described in Section 5.1.

```scala
object DrugResponseRegressor extends 
  Learnable(patientDrug){ 
  def label = drugResponse override 
  def feature = using(PWgeneExpression) 
  def classifier = new 
    StochasticGradientDescent() }
```

This learner defines the expression of the above-mentioned subset of genes as the input features and the drug response as the target label. The user can upload the data into the knowledge graph as: `KnowEngDataModel.populateWithKnowengdata()`. This will read the data from files to nodes and edges in the graph. Then the data for each patient will serve as training examples and the regressor can be trained and then tested easily with a few lines of code as follows:

```scala
DrugResponseRegressor.learn( 
  patientDrugTrainingInstances) 
DrugResponseRegressor.testContinuous( 
  patientDrugTestingInstances)
```

The `testContinuous` method reports the regressor’s evaluation using various metrics including sum-square of residuals, Pearson correlations, etc.

### 6.5 Meta analysis based on learning results

`Saul` facilitates meta analysis of the results of various learning models. In the previous problem, the user can easily define a set of learners by parameterization of the input properties. For example, a property (called `PWgeneExpression`) can receive the name of a pathway as an input parameter and return the expression of the genes of that specific pathway for a specific patient.

```scala
val pathWayGExpression= (pathway: String) => 
  property(patientDrug) { 
    pd: PatientDrug => 
      patientDrug().filter(_.pid == _.pid). 
      filter(myPathwayGenes.contains(GeneName(_))). 
      map(_.gExpression) }
```

This definition, given a patient identifier, retrieves the gene expression measurements and filters them using the subset of genes selected in the previous query above.
Assume that we have 100 pathways in our data graph and the biologist wants to define a separate regressor each of which uses the genes of each pathway as input features. This can be done by defining a class of learners, parameterized with the pathway property:

```scala
class DrugResponseRegressor(pathway: String) extends Learnable(patientDrug) {
  def label = drugResponse
  def feature = using(PWgeneExpression(pathway))
}
```

Given this class of models, we can create as many regressors as the number of distinct pathways in our data.

```scala
val myLearners=(genes() prop gene_KEGG).
  flatten.distinct.map(new DrugResponseRegressor(_:))
```

`myLearners` is a collection of regressors, each of which is created based on a set of gene expression values corresponding to a specific pathway. Now we can apply train, test, etc on all learners on this collection at once:

```scala
myLearners.map {_.train()}
val testRslts = myLearners.map {_.test()}
val sortedRgrs = testRslts.SortWithAccuracy
val bestRegressor = testRslts.maxAccuracy
```

The first line in the above snippet trains all the regressors. The second line shows how to test the regressors according to a specific evaluation metric, for example accuracy. For a different task on the same data, the user can seamlessly define new nodes, properties and classifiers and reuse the existing data model.

### 7 Related Work and Discussion

Our proposed model is related to many existing systems from various perspectives. We highlight the differences and similarities and the new advantages of our data-model in the context of Saul (Kordjamshidi, Wu, and Roth 2015).

**Comparison to machine learning tools.** Most of the commonly used ML tools such as WEKA (Witten et al. 1999) or Mallet (McCallum 2002) provide easy access to learning algorithms. However, a common characteristic of these tools is that a flat data structure in a specific file format should be provided. This is a major disadvantage for relational learning when a) the data domain is structured and features should be extracted from parts of the structure b) there are several learning models involved that interact with each other and use multiple feature generation tools (potentially from different sources) c) the user needs to do experimentation and feature engineering, which is often the case when designing machine learning models. One goal of Saul’s data modeling language is to address these issues on top of machine learning models.

**Comparison to feature extraction languages.** Feature extraction is very challenging in relational data domains such as computational biology, or when the data is raw with a complex and implicit structure such as natural language or computer vision. There are some tools available in the latter two domains which facilitate feature extraction by providing generic data structures appropriate for those domains and set of tools applicable on those data structures (i.e. readers and sensors). A recent example in NLP domain is Fextor (Broda et al. 2013). This tool provides an internal representation for textual data and provides a library to make queries, relying on its fixed internal representation. Prior to Fextor, Fex (Cumby and Roth 2003) views feature extraction from a first order knowledge representation perspective, and it is closer to our view here. However, their formalization is based on Description Logic (Baader 2003) where each feature extraction query is answered by logical reasoning. While having similar perspective, we solve queries using graph traversal over the propositionalized graph instead of logical reasoning. We are able to run the same type of queries given our graph-based formulation (Shastri 1991). Unlike Fex, our data model declaration provides the flexibility of working with arbitrary types of objects—e.g. we are not limited to having sentence level features, or tokens level features, etc. Saul’s data modeling language enables the user to declare the graph and plugging in any arbitrary data structures and arbitrary external sensors.

**Information extraction tools.** With the ability to work on unstructured data, our system has many common features with the information extraction tools. To facilitate working on unstructured data, there has been efforts in designing unified data structures for processing textual data and preparing tools (i.e. sensors) that can operate on those data structures (Sammons et al. 2016). A well-known example of such universal data structure is UIMA (Ferrucci and Lally 2004) that can be augmented with NLP tools. Similarly, there are some well-known software that focus on providing NLP sensors, such as NLTK (Loper and Bird 2002), GATE (Cunningham et al. 2011). These frameworks, focus on providing a specific internal representation and do not allow for a declaration of a model based on arbitrary structures and using arbitrary external sensors easily in one data model. Though some of these information extraction systems are equipped with very well designed and efficient query languages such as SystemT (Krishnamurthy et al. 2009b), we argue for a generic framework for information extraction in the context of heterogeneous information networks while addressing learning and inference in a same framework.

**Relational and graph based query languages.** The concept of graph queries and using first order logical languages for querying from structured data is well-established for relational and graph database technologies. Along the same line, our data modeling language facilitates querying form structured data. Graph traversal approaches are known to be more efficient for performing join operations and there are scalable implementations available for working on graph structures (Gonzalez et al. 2014). Our goal is integrating such capabilities with learning based programming.

**In the context of Saul.** Our proposed feature language currently implemented as a part of Saul (Kordjamshidi, Wu, and Roth 2015), that does structured-learning based on Constrain Conditional Models (Chang, Ratinov, and Roth 2012).
but can be integrated with any JVM-based languages which are designed for advanced machine learning models such as probabilistic graphical models e.g. WOLFE (Riedel et al. 2014) and FACTORIE (McCallum, Schultz, and Singh 2009). Using such a data modeling language, structured output prediction models can exploit the expressive power of relational feature representation to easily handle the issues of representation of the structured inputs and outputs, and define relational features over them. In contrast to our proposed representation of the structured inputs and outputs, and de-lational feature representation to easily handle the issues of prediction models can exploit the expressive power of relational learning language kLog (Frasconi et al. 2014) has the same input structure and format. However, kLog is more flexible from the feature extraction point of view, because it uses Prolog and provides the possibility of logical reasoning for feature extraction. These systems are not designed to be integrated with various sources of information and building an information network is not their concern. The feature extraction is treated as an external prepossessing component in such frameworks.

8 Conclusion

In this work we propose an initial prototype for a new integrated graph-based data-modeling and feature extraction language as a part of declarative learning language, Sail, to facilitate building end-to-end learning based systems for real world applications. We address the issue of building a heterogeneous information network based on both structured and unstructured data from various resources. Our language combines the power of relational, graph-based feature extraction, with the flexibility to exploit previously established resources such as data readers, annotators, sensors, and data structures in a given domain. We describe examples in NLP and computational biology domains. In summary our prototype, similar to the existing data modeling languages, provides the capability of declarative querying from data using relational operations; in contrast to existing systems, a) provides the possibility of seamless integration of unstructured and heterogeneous data from various domains into a unified data model; b) connects the relational graph directly to the analysis units which are relational machine learning models; c) facilitates on-the-fly integration of the output of the analysis units into an evolving graph.

Acknowledgements

The authors would like to thank all the students who have helped in the implementation of this project, as well as the anonymous reviewers for helpful comments. This research is supported by NIH grant U54-GM114838 awarded by NIGMS through funds provided by the trans-NIH Big Data to Knowledge (BD2K) initiative (www.bd2k.nih.gov). This material is based on research sponsored by DARPA under agreement number FA8750-13-2-0008. The U.S. Government is authorized to reproduce and distribute reprints for Governmental purposes notwithstanding any copyright notation thereon. The views and conclusions contained herein are those of the authors and should not be interpreted as necessarily representing the official policies or endorsements, either expressed or implied, of DARPA or the U.S. Government or NIH.

References

[Baader 2003] Baader, F. 2003. The description logic handbook: Theory, implementation and applications. Cambridge university press.

[Bio 2015] 2015. Pathway and network analysis of cancer genomes. Nat Meth 12(7):615–621.

[Broda et al. 2013] Broda, B.; Kedzia, P.; Marciniuk, M.; Radziszewski, A.; Ramocki, R.; and Wardyński, A. 2013. Fextor: A feature extraction framework for natural language processing: A case study in word sense disambiguation, relation recognition and anaphora resolution. In Computational Linguistics. Springer. 41–62.

[Chang, Ratinov, and Roth 2012] Chang, M.-W.; Ratinov, L.; and Roth, D. 2012. Structured learning with constrained conditional models. Machine learning 88(3):399–431.

[Cumby and Roth 2000] Cumby, C., and Roth, D. 2000. Relational representations that facilitate learning. In Proc. of the International Conference on Principles of Knowledge Representation and Reasoning (KR), 425–434.

[Cumby and Roth 2003] Cumby, C., and Roth, D. 2003. On kernel methods for relational learning. In Proc. of the International Conference on Machine Learning (ICML), 107–114.

[Cunningham et al. 2011] Cunningham, H.; Maynard, D.; Bontcheva, K.; Tablan, V.; Aswani, N.; Roberts, I.; Gorrell, G.; Funk, A.; Roberts, A.; Damjlanovic, D.; Heitz, T.; Greenwood, M. A.; Saggion, H.; Petrak, J.; Li, Y.; and Peters, W. 2011. Text Processing with GATE (Version 6).

[Ferrucci and Lally 2004] Ferrucci, D., and Lally, A. 2004. UIMA: an architectural approach to unstructured information processing in the corporate research environment. Natural Language Engineering 10(3-4):327–348.

[Frasconi et al. 2014] Frasconi, P.; Costa, F.; De Raedt, L.; and De Grave, K. 2014. Klog: A language for logical and relational learning with kernels. Artificial Intelligence 217:117–143.

[Gonzalez et al. 2014] Gonzalez, J. E.; Xin, R. S.; Dave, A.; Crankshaw, D.; Franklin, M. J.; and Stoica, I. 2014. Graphx: Graph processing in a distributed dataflow framework. In 11th USENIX Symposium on Operating Systems Design and Implementation (OSDI 14), 599–613. Broomfield, CO: USENIX Association.

[He and Singh 2008] He, H., and Singh, A. K. 2008. Graphs-at-a-time: Query language and access methods for graph databases. In Proceedings of the 2008 ACM SIGMOD International Conference on Management of Data, SIGMOD ’08, 405–418. New York, NY, USA: ACM.
Better call saul: Flexible programming for learning and inference in nlp. In Proc. of the International Conference on Computational Linguistics (COLING).

Saul: Towards declarative learning based programming. In Proc. of the International Joint Conference on Artificial Intelligence (IJCAI).

Systemt: A system for declarative information extraction. SIGMOD Rec. 37(4):7–13.

Systemt: A system for declarative information extraction. SIGMOD Rec. 37(4):7–13.

Query-based outlier detection in heterogeneous information networks. In Proceedings of the 18th International Conference on Extending Database Technology, EDBT 2015, Brussels, Belgium, March 23-27, 2015., 325–336.

Nltk: The natural language toolkit. In Proceedings of the ACL-02 Workshop on Effective Tools and Methodologies for Teaching Natural Language Processing and Computational Linguistics - Volume 1, ETMTNL02 ’02, 63–70. Stroudsburg, PA, USA: Association for Computational Linguistics.

McCallum, Schultz, and Singh 2009] McCallum, A.; Schultz, K.; and Singh, S. 2009. FACTORIE: Probabilistic Programming via Imperatively Defined Factor Graphs. In The Conference on Advances in Neural Information Processing Systems (NIPS).

McCallum, A. K. 2002. Mallet: A machine learning for language toolkit. http://www.cs.umass.edu/~mccallum/mallet.

A review of relational machine learning for knowledge graphs: From multi-relational link prediction to automated knowledge graph construction. CoRR abs/1503.00759.

Markov logic networks. Machine Learning Journal 62(1-2):107–136.

WOLFE: strength reduction and approximate programming for probabilistic programming. Statistical Relational Artificial Intelligence.

Weka: Practical machine learning tools and techniques with java implementations.