國立政治大學資訊科學系

Department of Computer Science
National Chengchi University

碩士論文

Master’s Thesis

利用馬可夫邏輯網路模型與自動化生成的模板加強生醫文獻之語意角色標註

Biomedical Semantic Role Labeling with a Markov Logic Network and Automatically Generated Patterns

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中華民國一百零一年七月

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摘要

背景: 生醫文獻語意角色標註（Semantic Role Labeling, SRL）是一種自然語言處理的技術，其可用來將描述生物過程的語句以 predicate-argument structures（PASs）表示。SRL 經常受限於 arguments 的 unbalance problem 而且需要花費許多的時間和記憶體空間在學習 arguments 之間的相依性。

方法: 我們提出一 Markov Logic Network (MLN) -based SRL 之系統，且此系統使用自動化生成之 SRL 模板同時辨識 constituents 與候選之語意角色。

結果及結論: 我們的方法在 BioProp 語料上來評估。實驗結果顯示我們的方法勝過目前最先進的系統。此外，使用 SRL 模板後，在時間及記憶體之花費上亦大幅的減少，而且我們自動化生成之模板亦能幫助建立這些模板。我們認為本論文提出之方法可以透過增加新的 SRL 模板例如：由生物學家手動寫的模板，而得到進一步的提升，而且本方法也為於需要處理大量 SRL 語料時，提供一種可能的解法。

Biomedical Semantic Role Labeling with a Markov Logic Network and Automatically Generated Patterns

Abstract

Background: Biomedical semantic role labeling (SRL) is a natural language processing technique that expresses the sentences that describe biological processes as predicate-argument structures (PASs) . SRL usually suffers from the unbalanced problem of arguments and consuming time and memory on learning the dependencies between the arguments.

Method: We constructed a Markov Logic Network (MLN) -based SRL system, and the system uses SRL patterns, which utilizes automatically generated approaches, to simultaneously recognize the constituents and candidates of semantic roles.

Results and conclusions: Our method is evaluated on the BioProp corpus. The experimental result shows that our method outperforms the state-of-the-art system. Furthermore, after applying SRL patterns, the costs of the time and memory are greatly reduced, and our automatically generated patterns are helpful in the development of these patterns. We consider that our method can be further improved by adding new SRL patterns such as biological experts manually written patterns and it also provide a possible solution to process large SRL corpus.

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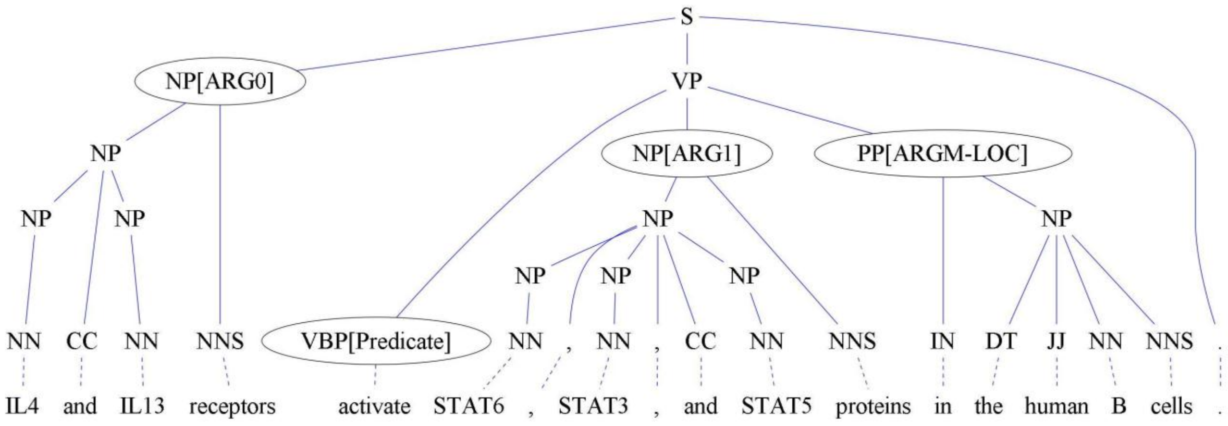
CHAPTER 1

Introduction

1.1 Background

The volume of biomedical literature available on the World Wide Web has experienced unprecedented growth in recent years. Automatically processing biomedical literature has been receiving lot attentions. Many information extraction (IE) researches[1] have shown their interested in the challenges of the biomedical text mining. Because of the difficulties on processing natural language texts, many biomedical relation-extraction systems only consider the main relation targets and the verbs linking them. However, they frequently ignore phrases describing location, manner, timing, condition, and extent[2]. In the biomedical field, these modifying phrases are especially important. Biological processes can be divided into temporal or spatial molecular events, for example activation of a specific protein in a specific cell or inhibition of a gene by a protein at a particular time. Having comprehensive information about when, where and how these events occur is essential for identifying the exact functions of proteins and the sequence of biochemical reactions. Detecting the extra modifying information in natural language texts requires semantic analysis tools.

Figure 1.1: A parsing tree annotated with semantic roles.



1.2 Biomedical Semantic Role Labeling (SRL)

Semantic role labeling (SRL) , also called shallow semantic parsing[3], is a popular semantic analysis technique. On SRL, sentences are represented by one or more predicate argument structures (PASs) , also known as propositions[4]. Each PAS is composed of a predicate (e.g., a verb) and several arguments (e.g., noun phrases) that have different semantic roles, including main arguments such as an agent and a patient, as well as adjunct arguments, such as time, manner, and location. Here, the term argument refers to a syntactic constituent of the sentence related to the predicate; and the term semantic role refers to the semantic relationship between a predicate (e.g., a verb) and an argument (e.g., a noun phrase) of a sentence. For example, in Figure 1.1, the sentence "IL4 and IL13 receptors activate STAT6, STAT3, and STAT5 proteins in the human B cells." describes a molecular activation process. It can be represented by a PAS in which "activate" is the predicate, "IL4 and IL13 receptors" and "STAT6, STAT3, and STAT5 proteins" comprise the ARG0 and ARG1 respectively, and "in the human B cells" is the location. ARG0 and ARG1 have different defines on different predicate, and describe agent and patient respectively. Thus, the agent, patient, and location are the arguments of the predicate.

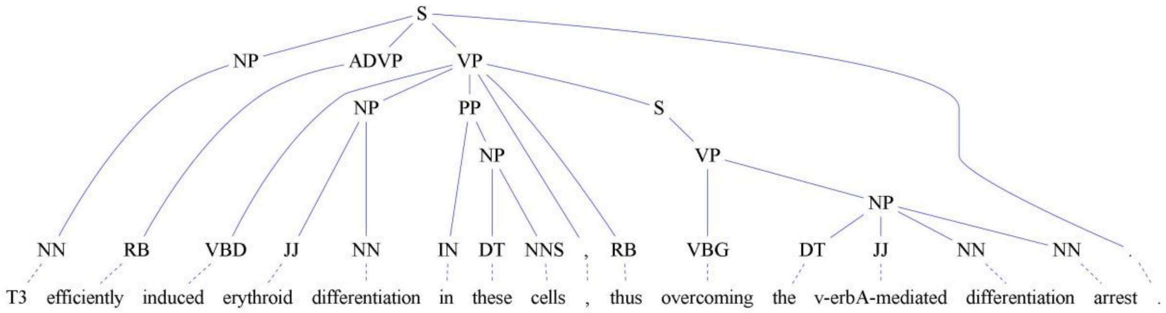
1.3 Traditional Formulation of SRL

SRL has being formulated as a classification problem in which supervised machine learning methods can be applied [2, 5, 6]. In order to constructing such a classifier, it is essential to select an annotated corpus and a PAS standard, such as PropBank[7]. Figure 1.2 shows the most general formulation of SRL, a pipeline method [8]. As shown in Figure 1.2.a, SRL usually starts with accepting a syntactic structure of a sentence (parse tree), because the structure encode more information such as the headwords [9]. The second step (Figure 1.2.b) is *predicate identification* that identifies the verb on the sentence. This step can be achieved by using a part-of-speech (POS) tagger with some filtering rules. Figure 1.2.c and Figure 1.2.d shows the two major tasks of SRL. Figure 1.2.c is called *argument identification* that identifies the word boundaries by determining whether the constituents, the nodes on the syntactic tree, contain semantic roles or not. Figure 1.2.d refers to as the *argument classification* step that assigns appropriate semantic role labels to the constituents. Finally, Figure 1.2.e checks whether the semantic roles are legal or not[10] by checking constraints such as word boundaries cannot be overlapped and determines the final semantic roles of the sentence. This step has been shown as an importance step in SRL [10].

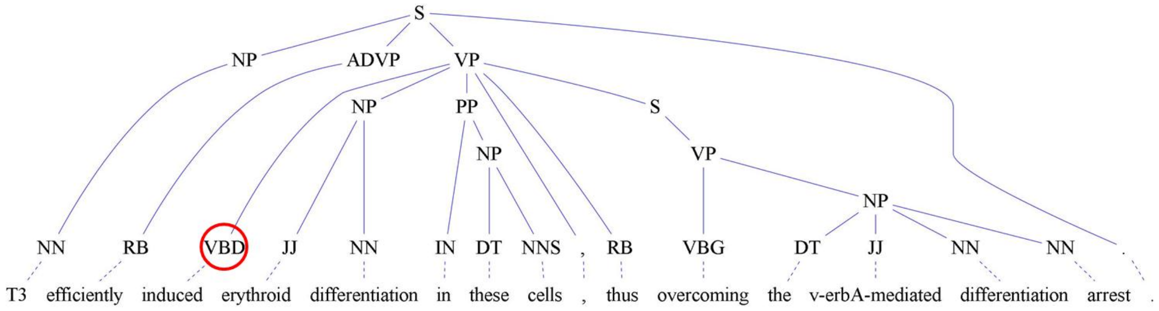
Some systems, such as BIOSMILE[2], treat *argument identification* and *argument classification* as a single step, and recognize word boundaries and semantic roles simultaneously. However, the formulation usually suffers from the unbalanced problem of semantic role labels, because there are many kinds of semantic role labels for instance BioProp defines thirty-two kinds of semantic role labels. Furthermore, SRL is a non-i.i.d (individual and identical distribution) problem. Following the formulation, the dependencies between semantic roles could not be known immediately until the last step. In the next section, we will describe our observations on both problems on the current biomedical SRL approaches.

Figure 1.2: The pipeline methods of the SRL.

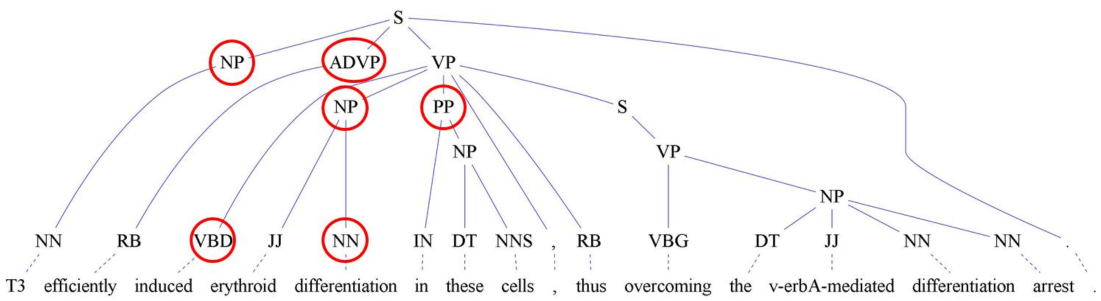
a. The input of SRL is the syntactic tree of the sentence, and the nodes of the syntactic tree are called constituents.



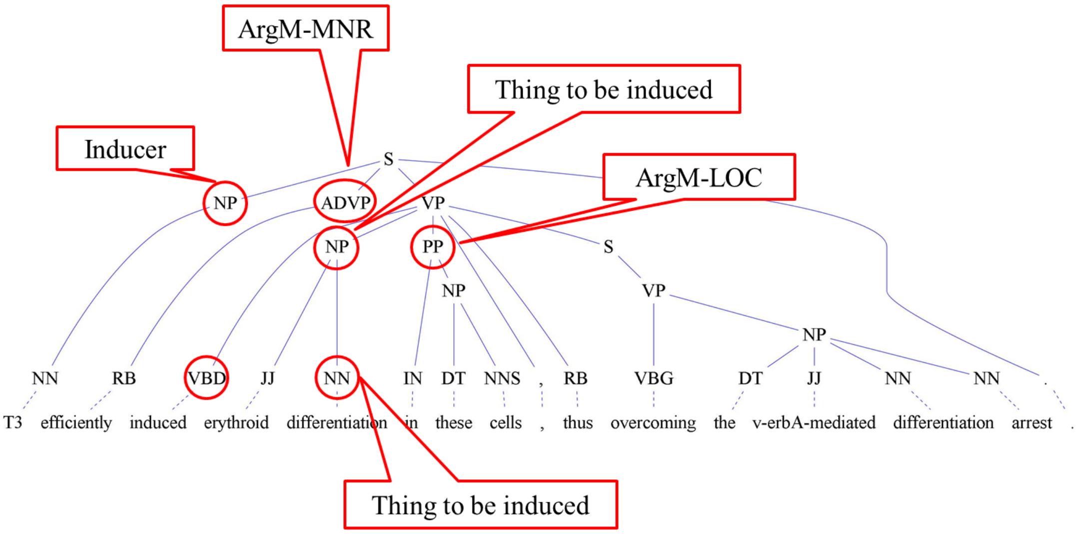
b. *Predicate identification* identifies the predicate constituent.



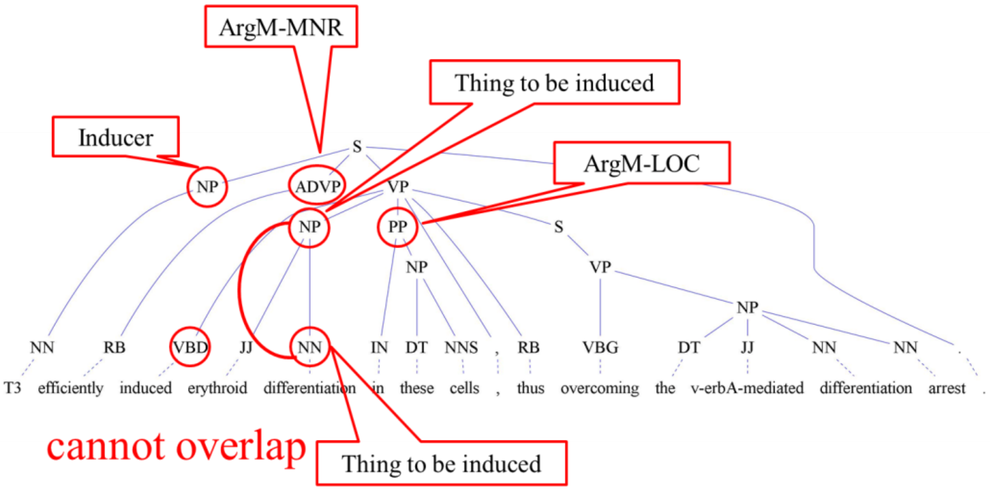
c. *Argument identification* identifies the argument constituents.



d. ***Argument classification*** **assigns appropriate the semantic role labels to the constituents.**



e. **Checking whether the semantic role labels violate the linguistic constraints.**



1.4 Problems

1.4.1 Unbalanced Problem

At first, we found the major reason causing unbalanced semantic roles comes from the stages of *argument identification* and *argument classification*. Table 1.1 shows our statistics of the constituents that possess semantic role labels on BioProp. As shown in Table 1.1, about 93.55% of the constituents in the syntactic tree do not have any semantic role label, meaning that these constituents are labeled with the NULL label in the dataset. By further analyzing these semantic roles, we observed that some of them can be found by simple patterns such as their syntactic path. For instance, in Figure 1.2, the *inducer* “T3” can be recognized by the syntactic path from the constituent to the verb “NP>S<VP<VBD”. However, most systems take all constituents as the input, and spend a lot time on tuning the weights for features of the NULL label and ignore the semantic roles with few instances.

Table 1.1: The statistic of the constituents and semantic roles.

Role	**#Constituents (total)**	**Coverage**
Arg0	0.69 (1333)	1.56%
Arg1	0.99 (1941)	2.21%
Arg2	0.16 (310)	0.33%
Arg3	0.01 (10)	0.01%
ArgM-NEG	0.05 (102)	0.12%
ArgM-LOC	0.19 (373)	0.44%
ArgM-TMP	0.07 (138)	0.16%
ArgM-MNR	0.24 (470)	0.52%
ArgM-EXT	0.01 (23)	0.02%
ArgM-ADV	0.15 (298)	0.30%
ArgM-PNC	0.00 (3)	0.00%
ArgM-CAU	0.01 (15)	0.02%
ArgM-DIR	0.01 (22)	0.02%
ArgM-DIS	0.09 (179)	0.24%
ARGM-MOD	0.06 (121)	0.13%
ARGM-REC	0.00 (6)	0.01%
Overall	2.9 (5727)	6.45%
Overall (includes NULL)	53.57 (105121)	100%

1.4.2 Dependency Problem

Based on our error analysis on the output generated by BIOSMILE, some sentences failed to be expressed as PAS, which mainly results from incorrect SRL due to the complexity of the sentences. An example is shown in Figure 1.2.e. If we have enough knowledge of the linguistic constraints between semantic roles, it might help us in assigning the appropriate semantic role labels. This is also called collective learning. We think this observation emphasizes the importance of collectively learned semantic roles.

1.5 Our Goal

In this paper, we focus on 1) how to automatically select and assign initial semantic roles; 2) how to enhance SRL with collectively learned semantic roles through using a Markov Logic Network[11]. Following is an overview of this paper. In Chapter 2, we describe our method. The subsection 2.1 introduces MLN proposed by [12]. The implementation of our SRL system is described in subsection 2.2. The subsection 2.3 proposes the method of using SRL patterns to select and assign initial semantic role labels. Due to the difficulties for employing biological experts in manually writing the SRL patterns, we propose an automatic pattern generation method. In the subsection 2.4, we introduce the collectively learned semantic roles method that implements linguistic constraints. In Chapter 3, we detail the experiments designed for examining the effect of our methods. In Chapter 4, we show the experimental results and related analysis. Finally, Chapter 5 concludes the contributions of this paper.

CHAPTER 2

Method

2.1 Markov Logic

2.1.1 First-Order Logic

MLN combines first order logic (FOL) and Markov networks. In FOL, formulae consist of four types of symbols: constants, variables, functions, and predicates. *Constants* represent objects in a specific domain (e.g. Part-of-speech: NN, VB, etc.) . *Variable* is the range over the objects (e.g., PoS (Part-of-speech) , where $PoS = \{pos \mid pos \in \text{Part} - \text{of} - \text{speech}\}$) . *Functions* represent mappings from tuples of objects to objects (e.g., $ChildrenOf$, where $ChildrenOf(i) = \text{children of tree node } i$) . *Predicates* represent relationships among objects (e.g., PoS of headword) , or attributes of objects (e.g., Arg0) . Constants and variables may belong to specific types. An *atom* is a predicate symbol applied to a list of arguments, which may be constants or variables (e.g., $role(p,i,r)$) . A *ground atom* is an atom whose arguments are all constants (e.g., $event\_trigger = \{p \mid p \in \text{selected 30 frequent verbs}\}$) . A *world* is an assignment of truth values to all possible ground atoms. A *knowledge base* (KB) is a partial specification of a world; each atom in it is true, false or unknown.

2.1.2 Markov Networks

A Markov network represents the joint distribution of a set of variables $X = \{X_1, \ldots, X_n\} \in \mathcal{X}$ as a product of factors: $P(X = x) = \frac{1}{Z}\prod_k f_k(x_k)$, where each factor f_k is a non-negative function of a subset of the variables x_k , and Z is a normalization constant. The distribution is usually equivalently represented as a log-linear form: $P(X=x)=\frac{1}{Z}\exp\left(\sum_i w_i g_j(x)\right)$, where the features $g_i(x)$ are arbitrary functions of (a subset of) the variables' states.

2.1.3 Markov Logic Networks

An MLN is a set of weighted first-order formulae. Together with a set of constants representing objects in the domain, it defines a Markov network with one variable per ground atom and one feature per ground formula. The probability distribution over possible worlds is given by $P(X=x)=\frac{1}{Z}\exp\left(\sum_{i\in F}\sum_{j\in G_i} w_i g_j(x)\right)$ where Z is the partition function, is the set of all first-order formulae in the MLN, g_j is the set of groundings of the *i*-th first-order formula, and $g_j(x)=1$ if the *j*-th ground formula is true and $g_j(x)=0$ otherwise. Markov logic enables us to compactly represent complex models in non-i.i.d. domains. General algorithms for inference and learning in Markov logic are discussed in Richardson and Domingos[13]. We uses 1-best MIRA online learning method [14] for learning weights and employs cutting plane inference [15] with integer linear programming as its base solver for inference at test time as well as during the MIRA online learning process. To avoid the ambiguity between the predicates in FOL and SRL, we refer the predicate in SRL as "event trigger" from now on.

2.2 Implement Biomedical Semantic Role Labeling

2.2.1 Formulating SRL

Our SRL system incorporates three components: (1) SRL patterns; (2) collective learning formulae; (3) a MLN-based classifier.

SRL patterns: The SRL patterns are the patterns described in subsection 2.3. We use

$pattern\_match(p,i,r)$ to describe that there is an event trigger p and the constituent i has a semantic role r.

Collective learning formulae: The collective learning formulae are the formulae described in subsection 2.4.

MLN-based classifier: Our MLN-based classifier uses the features of BIOSMILE, transform them into the formulae. In subsection 2.2.2, we will propose our method about how to transform these features into the formulae and how to incorporate SRL patterns and the classifier. In section 2.2.3, we propose a method to automatically generate conjunction formulae using only annotated PAS information. In section 2.2.4, we further apply the collective learning on SRL.

In our formulation, we use $event\_trigger(p)$ to express a constituent p that is an event trigger; $event\_type(p,t)$ to express that the event type of p is t such *binding*; $role(p,i,r)$ to express that there is an event trigger p and a constituent i with the semantic role r.

2.2.2 Basic formulae

Basic formulae are derived from the features used on the SRL systems[5, 16-18] that are based on Maximum Entropy Model (ME), Support Vector Machine (SVM). As shown in Table 2.1. These features are also used on BIOSMILE. These features have been proved their contributions on SRL. To apply these features on our classifier, we transform the features into the formulae, since MLN only accepts the formulae rather than features.

A basic formula consists of two predicates, one corresponding to the event trigger and the other one is a feature of a constituent. For example, the headword feature could be expressed in FOL as $pattern\_match(p,i,+r) \wedge headword(i,+w) \Rightarrow role(p,i,+r)$, where w is the headword of the constituent i. If the "+" symbol appears before a variable, it indicates that each different value of the variable has its own weight.

Table 2.1: The features are used in previous SRL systems.

BASIC FEATURES
• Predicate – The predicate lemma • Path – The syntactic path through the parsing tree from the constituent being classified to the predicate • Constituent type • Position – Whether the phrase is located before or after the predicate • Voice – passive if the predicate has a POS tag VBN, and its chunk is not a VP, or it is preceded by a form of "to be" or "to get" within its chunk; otherwise, it is active • Head word – Calculated using the head word table described by Collins (1999) • Head POS – The POS of the Head Word • Sub-categorization – The phrase structure rule that expands the predicate's parent node in the parsing tree • First and last Word and their POS tags • Level – The level in the parsing tree
PREDICATE FEATURES
• Predicate's verb class • Predicate POS tag • Predicate frequency • Predicate's context POS • Number of predicates
FULL PARSING FEATURES
• Parent, left sibling, and right sibling paths, constituent types, positions, head words, and head POS tags • Head of Prepositional Phrase (PP) parent – If the parent is a PP, then the head of this PP is also used as a feature
COMBINATION FEATURES
• Predicate distance combination • Predicate phrase type combination • Head word and predicate combination • Voice position combination
OTHERS
• Syntactic frame of predicate/NP • Headword suffixes of lengths 2, 3, and 4 • Number of words in the phrase • Context words & POS tags

2.2.3 Conjunction formulae

In addition to the basic formulae described above, we also employ conjunction formulae. We use a similar approach described in the subsection 2.3 to generate conjunction formulae. However, unlike those patterns would like to achieve a higher recall and not care about the precision, the conjunction formulae should as possible as improving the recall and precision. Therefore we use Apriori algorithm to generate conjunction formulae.

Apriori algorithm has been described in the subsection 2.3, and to generate conjunction formulae we set the default minimum support and confidence are 15 times and 80%, and we believe the values could generate the reliable conjunction formulae.

Conjunction formulae are composed of three or more predicates, one is the event trigger and the others are the linguistic properties of a constituent. For instance,

$$\begin{gathered} event\_trigger\,(p) \wedge constituent\_type\,(i, \text{"PP"}) \wedge firstword\,(i, \text{"in"}) \\ \wedge\, lastword\,(i, \text{"cell"}) \Rightarrow role\,(p, i, \text{"ARGM-LOC"}) \end{gathered}$$

means that the constituent *i* should be labeled as "ARGM-LOC" when its constituent type is "PP", its first word is "in", and its last word is "cell".

2.2.4 Global formulae

Basic formulae and conjunction formulae are local formulae whose conditions only consider the observe predicates. That is the dependencies of the semantic roles do not take into considered. The global formula is the condition of the formula including hidden predicates or the constraints that cannot be violated. In our system the hidden predicate is $role\,(p, i, r)$. We use the global formulae described in subsection 2.4 to the collectively learned semantic roles with dependences including tree collective and path collective.

2.3 Patterns for SRL

2.3.1 Introduction of the Patterns

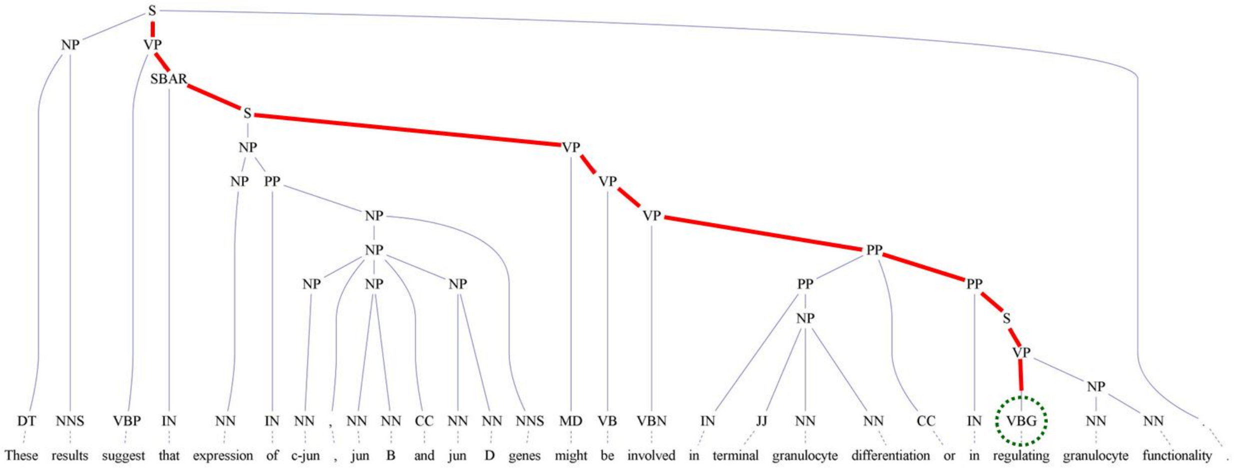
In this section, we propose the formal definition of our patterns. In ideal situation, the patterns of SRL can express the sentences as PASs. However, it is difficult without the help of the biological experts. For example, a pattern indicates that the noun phrase that appears in front of an active verb such as *bind* is the agent, but another pattern indicates that the protein before *bind* is the agent. It is difficult to determine which pattern is corrected. The first pattern might be wrong while the noun phrase describes the process about a protein. However the second pattern might be fail while the protein could not be recognized. Therefore, it requires to manually design the dependencies of the patterns. Because it is difficult for human to manually design the dependencies. Our patterns are designed to answer what are the candidate labels of the semantic roles on the sentences rather than what are the appropriate semantic role labels. Our patterns focus on removing the constituents that should not be assigned semantic role labels and recognizing the candidate labels of the semantic roles. Following sections describe our SRL patterns.

2.3.2 Tree Pruning

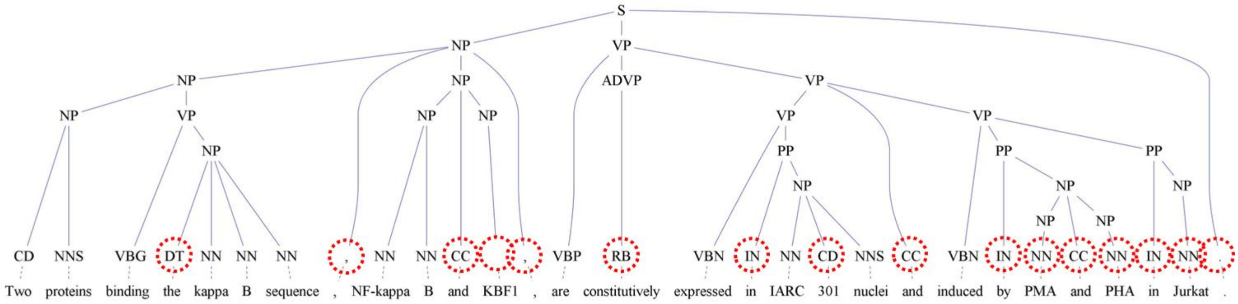
Since the ratio of the constituents with semantic roles is much lower than all constituents. The goal of tree pruning is to reduce the number of the constituents. Some SRL systems also use the pruning methods[17] or pre/post-processing filtering method[10] on the SRL to reduce the complexity or improve the performance. These methods are also used in our SRL patterns. We use two different tree pruning methods in our SRL. The first one is removing the constituents in the same path with the predicate. If a constituent overlaps with the predicate and it should not be assigned the semantic role. Removing these overlapped constituents before classification not only make sure they cannot be assigned the semantic roles but also make training/testing efficiently. Figure 2.1.a shows an example. The second one is that SRL prefer to annotate semantic roles on the phrase rather than the token, while the constituents 1) are leaves, 2) do not have any sibling 3) are stop words, they should be removed. Figure 2.1.b shows an example.

Figure 2.1: The examples show the tree pruning.

a. The constituents overlap with the predicate *regulate*.



b. The constituents are stop words or without the siblings.



2.3.3 Lexicon Pattern

Lexicon pattern assigns the semantic role label to the constituent. Like most of the SRL systems use lexicon features on argument identification/classification. Here we describe the semantic role labels could be found by their words, and we use the string match method to identify these semantic role labels.

Discourse (ARGM-DIS) : Discourse connects a sentence to a preceding sentence, it is not necessary to use classification to find them but a simple list.

Modals (ARGM-MOD) , *Negation* (ARGM-NEG): While the predicate next to these words, we would assign the words the semantic roles. We collect these words and semantic role pairs with the words list.

2.3.4 Temporal Pattern

The semantic roles with number or time are difficult to be recognized. These semantic roles also make the sentences much complex. Recognizing these semantic roles before classification could decrease the complexity of the sentences. We manually write the patterns to recognize these semantic roles

Extent Marker (ARGM-EXP) : Extent marker indicates the amount of change occurring from an action such as "… fold". We observe that extent markers usually are the siblings of the verb. Therefore, we design our pattern as following: if there is a trigger of the extent markers such as "%" or "fold", the constituent of the sibling of the verb which contains this trigger would be assigned the extent marker.

Temporal Marker (ARGM-TMP) : Temporal marker indicates when an action took place. Like extent marker, temporal markers usually are the siblings of the verb. Therefore, we use the same methods to find temporal markers. Furthermore, temporal markers sometimes appear in the head of sentence, we also assign the temporal marker to the constituent which has the trigger of temporal marker such as "hour" and is the start of the sentence.

2.3.5 Conjunction Pattern

In addition to all above patterns, there still have a lot of potential patterns could be used to annotate the semantic roles. Here we propose a method that uses the *association rule mining* and can automatically generate the patterns that conjunct several features of the constituents. For instance, *first_word* (*i*, "in") $\wedge$ *last_word* (*i* , "cell") => *role* (*p, i,* "ARGM-LOC"), this pattern means the constituent *i* started with "in" and ended with "cell" should be assigned the locative modifiers ARGM-LOC. In subsection 2.3.5.1, we introduce the association rule mining; in subsection 2.3.5.2, we propose our formulation of the transactions on SRL; in subsection 2.3.5.3, we describe our filtering methods to select the conjunction patterns.

2.3.5.1 Association Rule Mining

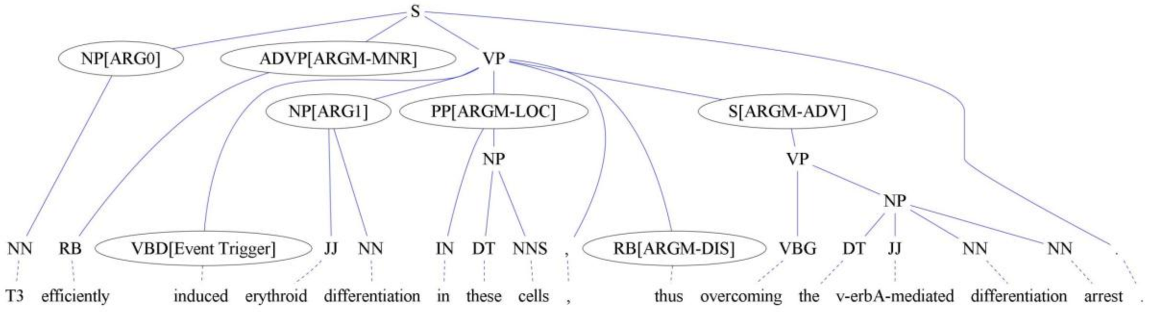
Association rule mining[19] is to discover the *interesting* relations, called association rules, from certain database, and it also is a popular research method. An association rule is a rule like “If a person buys wine and bread, he/she often buys cheese, too”. We found that the SRL patterns are very similar with the association rules. For an instance, a SRL pattern can be written as a rule like “If a constituent starts with the word **in** and ends with the word **cell**, it often plays an **ARGM-LOC**”. Therefore, we apply association rule mining to generate conjunction patterns. In order to discover the *interesting* relations, it is necessary to define four things including *item*, *transaction*, *support* and *confidence*. An *item* is the object participating in the rules, continuing the example, the started word **in**, the ended word **cell** and the semantic role **ARGM-LOC** are the items. The *transaction* is a collection of the items. The *support* is the number of the *itemset*, a subset of the *transaction*, appearing in the collection of the transactions. A *minimum support* could be used to make sure that the mined rules are not to overfit the database. The *confidence* is the number of the rule hold divided by the number of the condition hold. A *minimum confidence* could make sure that mined rules often are corrected in the database. A *maximum confidence* could make sure that mined rules are not obviously in the database. In our paper, we will focus on how to discover the rules instead of how to implement the association rule mining method.

2.3.5.2 Formulate the Transaction

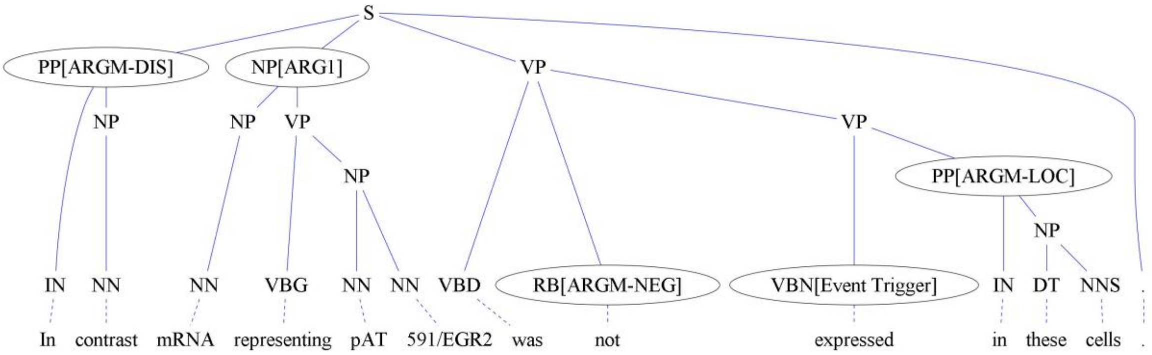
By observing the individual semantic role, we find sometimes the semantic role could be determined by its first and last words such as a phrase likes “in…cell” usually play a role ARGM-LOC. Therefore, we propose a method which could automatically generate the patterns like that, and the steps are below:

Figure 2.2: The examples for mining association rules.

a. T3 efficiently induced erythroid differentiation in these cells, thus overcoming the v-erbA-mediated differentiation arrest.



b. In contract mRNA representing pAT 591/EGR2 was not expressed in these cells.



Step 1: Extracts the information about all the arguments include constituent type, first word and last word, syntactic path from the predicate and the predicate. We treat these information as the items. For instance, in Figure 2.2.a, for ARGM-LOC, we could extract the information as following:

Table 2.2: The information extracted from ARGM-LOC on Figure 2.2.a.

Constituent type : PP

First word / *POS* : in / IN

Last word / *POS* : cells / NNS

Syntactic path from the predicate : VBD > VP < PP

Predicate : induce

Step 2: We treat each constituent with the semantic role as a transaction, and its information extracted in *Step 1* is its items. For instance, we have two sentences as shown in Figure 2.2, and we could transform them into the transactions:

Table 2.3: The transactions are transformed from Figure 2.2.

Itemset
FW (T3) , LW (T3) , CT (NP) , PATH (NP>S<VP<VBD) , event_trigger (induce) , ROLE (ARG0)
FW (efficiently) , LW (efficiently) , CT (ADVP) , PATH (ADVP>S<VP<VBD) , event_trigger (induce) , ROLE (ARGM-MNR)
FW (erythroid) , LW (differentiation) , CT (NP) , PATH (VBD>VP<NP) , event_trigger (induce) , ROLE (ARG1)
FW (in) , LW (cell) , CT (PP) , PATH (VBD>VP >S<PP) , event_trigger (induce) , ROLE (ARGM-LOC)
FW (thus) , LW (thus) , CT (RB) , PATH (VBD>VP<RB) , event_trigger (induce) , ROLE (ARGM-DIS)
FW (overcoming) , LW (arrest) , CT (S) , PATH (VBD>VP<S) , event_trigger (induce) , ROLE (ARGM-ADV)
FW (in) , LW (contrast) , CT (PP) , PATH (PP>S<VP<VP<VBN) , event_trigger (express) , ROLE (ARGM-DIS)
FW (mRNA) , LW (591/egr2) , CT (NP) , PATH (NP>S<VP<VBN) , event_trigger (express) , ROLE (ARG1)
FW (not) , LW (not) , CT (RB) , PATH (RB>VP<VBD) , event_trigger (express), ROLE (ARGM-NEG)
FW (in) , LW (cell) , CT (PP) , PATH (VBD>VP<S<PP) , event_trigger (express), ROLE (ARGM-LOC)

Step 3: Using association rule mining, we could generate the rule likes

$$\begin{gathered} event\_trigger\,(p) \wedge constituent\_type\,(i,\text{"PP"}) \wedge firstword\,(i,\text{"in"}) \\ \wedge\, lastword\,(i,\text{"cells"}) \\ \wedge\, lastword\_POS\,(i,\text{"NNS"}) \Rightarrow role\,(p,i,\text{"ARGM-LOC"}) \end{gathered}$$

2.3.5.3 Select the Patterns

However, the patterns generated in *Step 3* probably are not suite for the SRL. We observe the characteristics of different semantic roles, and we apply following the metrics to select SRL patterns:

a) The conjunction patterns for ARGX must contain “the syntactic path and the predicate type” and must appear more than 2 times, and the condition should only include these two items.

b) The conjunction pattern for ARGM-LOC should contain either “the first word and the last word” or “the first word and the syntactic path” and should appear more than

2 times.

c) The conjunction pattern for the other ARGM should contain “the word and the syntactic path” and should appear more than 2 times.

2.3.6 Syntactic Path Pattern

In addition to all above methods, we use the shortest syntactic path patterns, while the constituents have no candidate semantic role label, we check whether the constituent has similar syntactic path with semantic roles that appear in training set, if it exists, the constituent would be assigned the semantic role label.

2.4 Collective Learning for SRL

2.4.1 Collective Learning

Collective learning is also known as collective classification. In classification problems, they assign appropriate labels to the instances. For instance, the disease-gene related document classification problem distinguish disease-gene related document from other documents. In this problem, it assumes whether the document is disease-gene related or not, that is independent with other reference documents. However, there is rich information on its reference documents. Using collective learning can benefit from this information. And MLN also show that it performs well on collection learning[20].

2.4.2 Linguistic Constraints

The linguistic constraints[10] have shown their contributions on SRL. In our paper, we called the linguistic constraints as *tree collective* and *path collective*.

Tree collective indicates that two or more arguments in a sentence may be assigned the same semantic role, which contradicts PAS. To prevent this, we use the formula

$$event\_trigger(p) \wedge core\_arg(+r) \Rightarrow \left|role(p, i, +r)\right| \leq 1$$

This formula ensures that each semantic role is assigned to only one constituent. We called the formula as tree collective, since the formula limits an event trigger could not has more than one core argument (the number argument : ARGX).

Furthermore, the arguments may overlap when a node and it antecedent node(s) are all assigned semantic roles. The formula $overlap(i,\ j) \wedge role\,(p, i, r_1) \Rightarrow \left|role\,(p,\ j, r_2)\right| = 0$ ensures that if two or more constituents overlap, then only one can be assigned a semantic role. We called the formula as path collective, since the formula limits the argument could not appear in the same path on the syntactic tree.

CHPATER 3

Experiment

3.1 Dataset

To evaluate our SRL system, we select BioProp[9] as our dataset. BioProp is a semantic role labeling corpus, including 445 biomedical abstract labeled with the semantic roles and 30 predicates, which are most important or frequently appearing in biomedical literatures. Table 3.1 shows the statistics of the BioProp.

Table 3.1: The statistics on the BioProp corpus.

Role	**Number**
Core argument types	11
Adjunctive argument types	21
Feature	**Number**
Constituent types	17
Unique words	5258
Part-of-speech	34
Other	**Number**
Event types	30
Abstracts with Propositions	445
Sentences with Propositions	1622
Propositions	1962

Core arguments play the major semantic role of the event, including ARGX, R-ARGX and C-ARGX. ARGX usually plays the agent, patients and objects; R-ARGX indicates the start of the clause that describes ARGX; C-ARGX describes the continuous ARGX. Adjunctive arguments play the location, manner, temporal, extent used to indicate the state of the event.

3.2 Experiment Design

3.2.1 Experiment 1 – The Effect of Automatically Generated Patterns

In this experiment, we evaluate the effect of using SRL patterns. In order to evaluate the effect of automatically generated patterns. We compare three different configurations. 1) BIOSMILE : This only implements the *basic formulae* but with slightly difference is that $event\_trigger(p)$ replaces $pattern\_match(p, i, +r)$, which means the patterns are not used. 2) BIOSMILE + *pattern w/o auto* : To examine the effect of the patterns, another configuration implements the *basic formulae*. In this configuration, $pattern\_match\_wo\_auto\_gen(p, i, +r)$ replaces $pattern\_match(p, i, +r)$, which means automatically generated patterns are not used in this configuration. 3) BIOSMILE + *pattern* : The configuration implements all the patterns and the formulae including *basic formulae* and *conjunction formulae*. Comparing configuration 2 and configuration 3 could show the effects of using automatically generated patterns.

3.2.2 Experiment 2 – Improvement by Using Collective Learning

In this experiment, we examine whether the patterns incorporated with collective learning could further enhance SRL. We compare four different configurations. 1) BIOSMILE : BIOSMILE is the same configuration with that is used in *experiment 1*. 2) BIOSMILE + *pattern* : it is also the same with that is used in *experiment 1*. 3) BIOSMILE + *CL* : BIOSMILE incorporate with the collective learning. 4) BIOSMILE + *pattern* + *CL* : BIOSMILE + *pattern* incorporate with the collective learning.

3.3 Evaluation Metric

The results are given as F-score using the CoNLL-05[8] evaluation script and defined as $F = \frac{2 \times P \times R}{P + R}$, where P denotes the precision and R denotes the recall. The formulae for calculating precision and recall are as follows:

$$Precision = \frac{\text{the number of correctly recognized arguments}}{\text{the number of recognized arguments}}$$

$$Reacll = \frac{\text{the number of correctly recognized arguments}}{\text{the number of true arguments}}$$

Furthermore, we also evaluate the F-score with sentence-level F_s , which we denote P_s and R_s as follows:

$$Precision = \frac{\text{the number of correctly recognized Propositions}}{\text{the number of recognized Propositions}}$$

$$Reacll = \frac{\text{the number of correctly PASs}}{\text{the number of true PASs}}$$

3.4 t-test

In order to develop a much fairer environment, we apply a two-sample paired *t*-test, which is defined as following:

The null hypothesis, which states that there is no difference between the two configurations A and B, is given as

$$H_0 : \mu_A = \mu_B$$

where μ_A is the true mean F-score of configuration A, μ_B is the mean of the configuration B, and the alternative hypothesis is

$$H_1 : \mu_A > \mu_B$$

A two-sample paired *t*-test is applied since we assume the samples are independent. As the number of samples is large and the samples' standard deviations are known, the following two-sample *t*-test is suitable:

$$t = \frac{(\overline{X_A} - \overline{X_B})}{\sqrt{\frac{S_A^2}{n_A} + \frac{S_B^2}{n_B}}}$$

If the resulting *t*-score is equal to or less than 1.67 with a degree of freedom of 29 and a statistical significance level of 95%, the null hypothesis is accepted; otherwise it is rejected.

To get the average F-scores and their deviations required for the *t*-test, we randomly sampled thirty training sets (g_1, ..., g_{30}) and thirty test sets (d_1, ..., d_{30}) from the 500 abstracts. We trained the model on g_i and tested it on d_i. Afterwards, we summed the scores for all thirty test sets, and calculated the averages for performance comparison.

CHAPTER 4

Results and Discussion

4.1 Improvement by Using SRL Patterns

Table 4.1 shows the results of using SRL patterns on CoNLL evaluation metrics. There are three different configurations. First, the config. 1 is BIOSMILE. Secondly, the config. 2 is *SRL patterns* excluded *automatically generated patterns* and *basic formulae*. The config. 3 is *SRL patterns*, *basic formulae* and *automatically generated formulae*. We use '*' to indicate the configuration has statistically significant improvement with the config. 1 and 2.

The results show that the config. 2 outperforms the BIOSMILE by 0.44% on ARGX, and the config. 3 outperforms the BIOSMILE by 1.20% and 0.54% on ARGX and Overall ARG, respectively. The config. 2 and 3 decrease 2.39% and 0.25% on ARGM respectively.

As show in Table 4.1 that both the config. 2 and 3 perform better in recall but worse on precision. The reason might be that lacks negative examples that SRL patterns remove the constituents which were considered to be without semantic role labels.

Table 4.1: The performances of SRL using SRL patterns.

Configuration	ARGX				ARGM				Overall ARG			
	P	R	F	ΔF	P	R	F	ΔF	P	R	F	ΔF
1. BIOSMILE	90.62	84.55	87.48	-	82.96	62.65	**71.39**	-	88.59	77.78	82.83	-
2. 1 + Pattern w/o Auto	89.48	86.42	87.92	+0.44	76.63	62.76	69.00	-2.39	86.00	79.21	82.46	-0.37
3. 1 + Pattern	89.69	87.70	**88.68**	+1.20*	74.20	68.33	71.14	-0.25	85.10	81.71	**83.37**	+0.54*

Table 4.2: The distribution of ARGM on BIOSMILE and BIOSMILE + Pattern w/o Auto.

	BIOSMILE			BIOSMILE + Pattern w/o Auto		
ARGM	corr.	excess	missed	corr.	excess	missed
ARGM-ADV	639	332	1102	706	552	933
ARGM-LOC	1465	364	797	1546	494	693
ARGM-MNR	1952	341	811	2025	527	671
ARGM-MOD	696	11	49	709	29	36
ARGM-NEG	521	5	43	536	48	28
ARGM-TMP	286	93	527	327	140	483

Figure 4.1: An example: ARGM-MNR is failed to be labeled using BIOSMILE + Pattern w/o Auto.

Collectively , these data suggest that [NFAT$_{\text{ARG1}}$] [can$_{\text{ARGM-MOD}}$] be [activated$_{\text{Event Trigger}}$] and IL-2 can be produced [in a calcineurin independent manner$_{\text{ARGM-MNR}}$]

Furthermore, we analysis the possible reasons why the config. 2 uses the patterns could improve on ARGX, but decrease on ARGM. Table 4.2 shows the individual distribution of different semantic roles. After applying the patterns, the both number of corrected and excessed semantic roles on the ARGM increased. Figure 4.1 shows that the patterns of the config. 2 without automatically generated patterns are hardly on recognizing the ARGM such as ARGM-MNR which needs the other information such as the last word, the constituent started with “in” and ended with “manner” usually indicates ARGM-MNR.

4.2 Improvement by Using Collective Learning

Table 4.3 shows the performance of using collective learning on CoNLL evaluation metrics. Table 4.4 shows performance of using collective learning on sentence-wide evaluation metrics. We use ‘*’ to indicate the configuration has statistically significant improvement with BIOSMILE use ‘**’ to indicate the configuration has statistically significant improvement with both BIOSMILE and the config. 2. There are four different configurations. The config. 3 incorporates BIOSMILE with collective learning; the config. 4 incorporate BIOSMILE + *SRL patterns* with collective learning. Table 4.3 shows that the config.3 and 4 applying collective learning outperform BIOSMILE and BIOSMILE + *SRL pattern* by F-score 1.91% and 1.65% on overall ARG respectively. And, their improvements on sentence-wide evaluation, in Table 4.4, are F-score 6.93% and 4.43% on overall ARG respectively, especially on ARGX with 7.54% and 6.93%. These improvements indicate that uses MLN to collectively learned SRL can improve both individual arguments and the sentence-wide argument. Table 4.5 shows the costs of the time and memory. Despite, the performances of our system, the config. 4, is slightly lower than the config. 3, but costs are much lower than the config 3 on both time and memory.

Table 4.3: The performances of SRL using collective learning.

Configuration	ARGX				ARGM				Overall ARG			
	P	R	F	ΔF	P	R	F	ΔF	P	R	F	ΔF
1. BIOSMILE	90.62	84.55	87.48	-	82.96	62.65	71.39	-	88.59	77.78	82.83	-
2. 1 + Pattern	89.69	87.70	88.68	+1.20*	74.20	68.33	71.14	-0.25	85.10	81.71	83.37	+0.54*
3. 1 + CL	89.88	88.88	**89.37**	+1.89*	80.00	68.15	**73.60**	+2.21*	87.13	82.48	**84.74**	+1.91**
4. 2 + CL	90.90	88.44	**89.65**	+2.17*	77.81	66.93	**71.96**	+0.57	87.24	81.89	**84.48**	+1.65**

Table 4.4: The performances of SRL on sentence-wide evaluation metrics.

Configuration	ARGX				Overall ARG			
	P	R	F	ΔF	P	R	F	ΔF
1. BIOSMILE	71.83	70.41	71.11	-	51.78	51.41	51.60	-
2. 1 + Pattern	74.77	73.94	74.35	+3.24*	55.27	55.12	55.19	+3.59*
3. 1 + CL	78.75	78.54	**78.65**	+7.54**	58.58	58.57	**58.57**	+6.93**
4. 2 + CL	78.26	77.82	**78.04**	+6.93**	56.09	55.95	**56.02**	+4.42*

Table 4.5: The cost of time and memory.

Configuration	Train time	Test time	Memory
1. BIOSMILE	1 hr 10m	127.0ms	1130MB
2. 1 + Pattern	36 m	91.0ms	92MB
3. 1 + CL	2 hr 55m	143.0ms	1130MB
4. 2 + CL	1 hr 40m	103.0ms	92MB

4.3 Related Work

4.3.1 Biomedical Semantic Role Labeling Corpus

PASBio[21] is the first PAS standard used in the biomedical field, but it does not provide the SRL corpus. GREC[22] is an information extraction corpus focuses on gene regulation event. However, GREC do not support the Treebank format SRL annotations[23]. BioProp is the only corpus that provides SRL annotations and annotates semantic role labels on the syntactic trees. BioProp is created by [24]. BioProp selects 30 most frequently or important verbs appearing in the biomedical literatures, and defines the standard of the biomedical PAS. Furthermore, following the style of PropBank[7], which annotates PAS on Penn Treebank (PTB) [23], BioProp annotates their PAS on GENIA TreeBank (GTB) beta version[25]. GTB contains a collection of 500 MEDLINE abstracts selected from the search results with the following keywords: human, blood cells, and transcription factors and contains the TreeBank that follows the style of Penn Treebank.

4.3.2 Biomedical Semantic Role Labeling System

Most semantic role labeling systems follow the pipeline method, which includes *predicate identification*, *argument identification* and *argument classification*. However, in recent years, instead of using pipeline method, several researches have shown that using the collective learning method could outperform the pipeline method. [20] uses Markov Logic to collectively learned these stages on SRL. However, we found that there seem to be no SRL system using MLN in the biomedical field. [26] uses the domain adaption approaches to improve SRL in biomedical field. [27] considers SRL as token-by-token labeling problem and focuses on the SRL in the transport protein. BIOSMILE is the biomedical SRL system focus on 30 frequently appearing or important verbs in biomedical literatures and trained on the BioProp, and it is based on Maximum Entropy (ME) Model.

CHAPTER 5

Conclusion

We observe that some SRL ignore the complexity in classification and the dependencies between the semantic roles. These systems usually take all constituents as candidate semantic roles and use a post-processing step to deal with their dependencies. In this paper, to tackle both problems, we construct a biomedical SRL system that uses SRL patterns and a Markov Logic Network (MLN) to collectively learned semantic roles. However, SRL patterns are difficult to be manually written, and we use automatically generated approaches, to recognize the words boundaries and the candidates of semantic roles simultaneously. Our system is trained on BioProp corpus. The experimental results show that using SRL patterns can improve the performance by F-score 0.54% on overall ARG. Furthermore, using collective learning, which incorporated with linguistic constraints, can improve the result by F-score 1.65%. We show that uses SRL patterns can improve the efficiency of training model and predicate instances, and reduce the memory. Also, we show that our approaches can compete with current state-of-the-art approaches. The corpus used in our experiments is a small biomedical SRL corpus that only uses one out of four of GENIA TreeBank corpus and also focuses on 30 verbs. It is important to enable SRL to be trained on a large corpus in the future. We consider that our approaches provide a possible solution to process large SRL corpus.

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