Discovering Informative Syntactic Relationships between Named Entities in Biomedical Literature

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***Abstract*—The discovery of new and potentially meaningful relationships between named entities in biomedical literature can take great advantage from the application of multi-relational data mining approaches in text mining. This is motivated by the peculiarity of multi-relational data mining to be able to express and manipulate relationships between entities. We investigate the application of such an approach to address the task of identifying informative syntactic structures, which are frequent in biomedical abstract corpora. Initially, named entities are annotated in text corpora according to some biomedical dictionary (e.g. MeSH taxonomy). Tagged entities are then integrated in syntactic structures with the role of subject and/or object of the corresponding verb. These structures are represented in a first-order language. Multi-relational approach to frequent pattern discovery allows to identify the verb-based relationships between the named entities which frequently occur in the corpora. Preliminary experiments with a collection of abstracts obtained by querying Medline on a specific disease are reported.**

***Keywords*-Multi-Relational Data Mining; Frequent Pattern Discovery; Syntactic Text Structure; Biomedical Literature**

I. Introduction

The exponential increase in publication rate of new articles in biomedicine makes difficult for researchers to keep up with research progresses without the help of automatic knowledge discovery techniques. Over 16 million references to biomedical journal articles are currently contained in the Medline collection [15], the main online resource of biomedical research literature.

Textual data as Medline articles are generally unstructured and the available resources (e.g., PubMed, the search engine interfacing Medline) do not still provide adequate mechanisms for helping humans in "deeply analyze" very large amount of content. The need to analyze this volume of unstructured data has prompted the use of text mining tools to automatically extract key biological information.

Several successes may be attributed to text mining research in biomedicine and many methods have been presented so far [1], [4], [7], [11]. Most of the text mining methods provide keyword-based search functionalities, which are based on the frequencies of surface information such as words and parts of speech (e.g., sentences). These methods work well concerning similarity of topics or term-based contents of sentences, but ignore more abstract information such as syntactic structures: although the surface information of two sentences is similar, the syntactic structures may be completely different. By the way, syntax-based search methods have been investigated in text mining literature. In [5], [10], syntax-based search methods defined on the similarity between syntactic structures of sentences are presented. In [6], [18], sentences are parsed according to a user-defined structural pattern and sentences, whose parse trees match the given pattern, are returned. In [13], both a syntax-based search functionality and a keyword-based interface are used to retrieve subject-object relationships between user-defined keywords. The user is not required to edit a structural pattern, but to specify the keywords of interest. Relationships simply express the existence of a verbal interaction between subject and an object without distinguishing among different kind of interactions (e.g., the subject "causes" the object or the subject "inhibits" the object and so on).

An overview of main research on applying the syntax-based search methods to a biomedical corpus is reported by Page and Craven [17]: subject-object-verb relationships are extracted from the text in order to address the task of protein localization. Also in this case, the verb is used to isolate potentially meaningful part of speech. Manually-written rules which identify the common verb of expressing protein interactions in natural language are applied to isolate the part-of speech where proteins can be searched.

In this work, we investigate the problem of how to mine an unstructured biomedical text corpus in order to identify any syntactic structures of named entities which appear frequently in a text corpus retrieved by querying biomedical literature database on a specific topic. We propose a knowledge discovery framework, called BioSOV-FP (BIOlogical Subject-Object(s)Verb based Frequent Pattern discovery system), which automatically annotates the named entities in the training corpus, integrates these entities in syntactic structures, uses a first-order language to represent these structures and resorts to a multi-relational data mining approach for frequent pattern discovery to identify frequent syntactic structures. Similarly to the system proposed in [13], BioSOV-FP uses both keyword-based interface and syntax-based search functionality. Anyway, BioSOV-FP exhibits fundamental differences with the competitor system. First, BioSOV-FP is not a general purpose system, but it is appositely designed for biomedical domain, although it can be adapted to different domains by providing adequate domain knowledge (dictionary, domain specific named entities and so on). Biomedical keywords are the named entities in this paper. These entities are not apriori user-defined, but they are automatically annotated in the training corpus as they appear in the controlled dictionaries (e.g., MeSH (Medical Subject Headings) taxonomy). The MeSH taxonomy is a biological dictionary in form of a set of hierarchically related biomedical terms [16]. Second, the syntactic dependencies between biomedical keywords are 3-structures in the form of subject-object(s)-verb. Differently from most of works surveyed in [17], the verb is not used to only extract part of speech of interest, but it is also processed to discover *how* a subject entity is frequently related to its object entiti(es).

The first-order logic representation of these 3-structures allows to take advantage of the syntactical structure of text corpus according to the assumption that a more knowledge intensive technique is likely to perform better when applied on the tasks of text mining due to expressive power gained through relations [8]. The choice of the expressive power of first-order logic language is further motivated by the fact that it is so close to the human one that it is easy to guess the original sentence underlying this formal description. The first-order logic language allows to exploit a background knowledge such as the MeSH taxonomy, a domain specific knowledge as well as a language bias. In particular, hierarchical relations reported in the MeSH taxonomy allow to address the discovery task at multiple levels of abstractions. Discovered frequent patterns play the role of informative syntactic knowledge shared by the articles under study. In this work, the informativeness of a pattern is intended not only as the capability of capturing the existence of frequent co-occurrences among named entities in a text corpus, but also as the capability of "informing" on the syntactic role (subject or object) of each entity and the kind of relationship (verb) eventually connecting them.

These patterns can be employed to formulate new queries to biomedical search engines on the topic of interest.

The paper is organized as follows. Section II describes BioSOV-FP framework. Section III presents the extraction of syntactic structures from a biomedical text corpus. Section IV illustrates the discovery of frequent syntactic structures of named entities. Finally, an application is reported.

II. An overview of BIOSOV-FP Framework

The framework of BIOSOV-FP is reported in Figure 1. A biomedical text corpus is poured into the BioSOV-FP framework and the knowledge discovery process is triggered. Initially, the unstructured text corpus is allowed to express itself in a structured format. This transformation is in charge of a four-stepped job which includes acronym processing, stopword removing, syntactic structure extraction and named entities annotation. Transformation job uses acronym dictionary, stopword list and MeSH taxonomy as input. The structure is added to the training corpus in the form of the subject-objects(s)-verb tuples. Named entities are annotated in the nominal components (subject and object(s)) of these structures as they appear in MeSH taxonomy. The MeSH taxonomy allows the representation and management of named entities at different levels of granularity (from the most general, at the top level of taxonomy, to the most specific, at the bottom level of taxonomy). The subject-objects(s)-verb tuples which express verbal dependencies between named entities are represented in a first-order language and stored in the extensional part of a Datalog database. Domain specific knowledge is stored as a set of rules in the intensional part of the Datalog database to support qualitative reasoning. A language bias is used to specify constraint specifications for interesting patterns. Datalog database and language bias are passed down to the relational frequent pattern discovery module. The minimum support $\sigma[l]$ is given for each level of MeSH taxonomy before frequent pattern discovery starts.

Details on how the text corpus is transformed from the original unstructured format to the structured format and how the relational frequent pattern discovery is performed are reported in the next Sections.

III. Extracting Syntactic Structures

The text processor identifies verbal components and nominal components in the text, assigns each nominal component

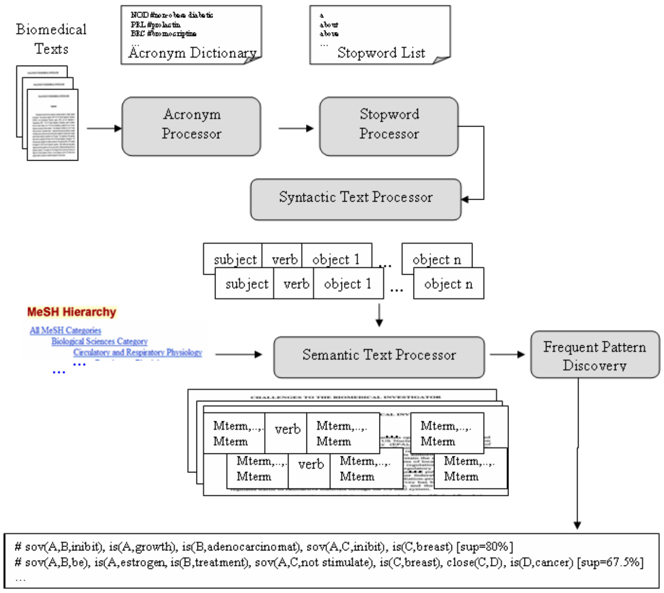

Biomedical Texts
NOD #non-obese diabetic
PRL #prolactin
BRC #bromocriptine
Acronym Dictionary
a
about
above
...
Stopword List
Acronym Processor
Stopword Processor
Syntactic Text Processor
subject
verb
object 1
...
object n
MeSH Hierarchy
All MeSH Categories
Biological Sciences Category
Circulatory and Respiratory Physiology
...
Semantic Text Processor
Frequent Pattern Discovery
Mterm,...,Mterm
verb
# sov(A,B,inibit), is(A,growth), is(B,adenocarcinomat), sov(A,C,inibit), is(C,breast) [sup=80%]
# sov(A,B,be), is(A,estrogen, is(B,treatment), sov(A,C,not stimulate), is(C,breast), close(C,D), is(D,cancer) [sup=67.5%]
...

Figure 1. BIOSOV-FP framework.

with either the role of subject or the role of object of the corresponding verbal component, and annotates the named entities in the nominal components. In this way, syntactic 3-structures, that is, subject-object(s)-verb structures, are extracted. For each subject-object(s)-verb structure, the subject is the modifier of the dependency expressed by the verb, while the object(s) are modifee(s) of the same verbal dependency. The syntactic 3-structures whose nominal components include named entities are output as a structured representation of the text and passed down to the frequent pattern discovery module together with the MeSH taxonomy. Details of steps of transformation job are described below.

Acronym processing. A dictionary-based approach is used to identify the occurrences of biomedical acronyms in the text corpus. Acronyms are replaced by the expanded definitions as in the dictionary. This allows to avoid part-of-speech tagging errors due to multi-worded nouns. The domain experts curate the dictionary of these long forms and their abbreviated forms as they appear in the literature.

Stopword removing. Stopwords (e.g., article such as "the" or modal verbs such as "can") reported in the stopword list are removed from the text.

Subject-Object(s)-Verb extraction. The text is considered as a sequence of (non stopwords) words which are analyzed by means of the generic text processor for English corpora, called MontyLingua [12]. Montylingua provides the functionalities to tokenize, part-of-speech tag, chunk, stem texts and transform corpora into a set of subject-object(s)-verb (SOV) 3-structures.

Definition 1: A subject-object(s)-verb (SOV) structure is defined as the extended BNF grammar in the followings.

⟨ SOV ⟩ ::= {⟨SUBJECT⟩ { ⟨OBJECT⟩ } ⟨ VERB⟩}
⟨ SUBJECT ⟩ ::= { ⟨ TERM ⟩ }
⟨ OBJECT ⟩ ::= { ⟨ TERM ⟩ }
⟨ VERB ⟩ ::= ⟨ INFINITIVE_FORM_OF_VERB ⟩

The text is firstly tokenized in individual sentences according to a regular expression recognizer of sentence delimiters (e.g., full-stop, ellipse, exclamation mark and question mark, at the end of a word) and then each sentence is atomized in words using white spaces as word delimiter. Common abbreviated words, such as "isn't" are expanded into the words "is" and "not". Each word is tagged by a Brill Tagger [3] which firstly tags each word according to a lexicon which contains the likely tag for each word and then corrects the original tags by using lexical and contextual rules. Some SOVs structures are reported in Example 1.

Example 1. Let us consider a fragment of a Medline article entitled "Hormone replacement therapy: the perspectives for the 21st century", that is:

"*Progestogens* can *modify* the *cellular response* of *normal* as well as *cancer breasts.* The *possible protective effect* of *continuous progestogen addition* is very *interesting* and *needs* further *investigation*."

The text without stopwords is in italics. SOV structures extracted from the text in italics by MontyLingua are listed below:

$$\text{SOV}=[\underbrace{\langle progestogen\rangle}_{subject}, \quad [\underbrace{\langle cell, response, normal\rangle}_{object}, \underbrace{\langle cancer, breast\rangle}_{object}], \underbrace{modify}_{verb}\ ]$$

$$\text{SOV}=[\underbrace{\langle continuous, progestogen, addition\rangle,}_{subject} [\underbrace{\langle interest\rangle}_{object}], \underbrace{be}_{verb}\ ]$$

$$\text{SOV}=[\underbrace{\langle continuous, progestogen, addition\rangle,}_{subject} [\underbrace{\langle investigation\rangle}_{object}], \underbrace{need}_{verb}\ ]$$

Named entity annotation. The BioTeKS Text Analysis Engine provided within the IBM UIM Architecture [9] is used to annotate the named entities which occur in the nominal components of the SOV structures and in the MeSH taxonomy. We use the "canonical" form of each MeSH term, which is available in the MeSH taxonomy. Terms without the MeSH tag are removed from the corresponding nominal environments of the SOV structure. A definition of a MeSH annotated subject-object(s)-verb structure (MeSH SOV) is reported in Definition 2.

Definition 2: A MeSH annotated subject-object(s)-verb (MeSH SOV) structure is defined as the extended BNF grammar in the followings.

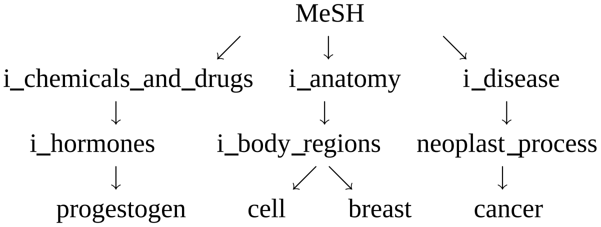
⟨ MESH SOV ⟩ ::= {⟨SUBJECT⟩ { ⟨OBJECT⟩ } ⟨ VERB⟩}
⟨ SUBJECT ⟩ ::= { ⟨ MESHTERM } ⟩
⟨ OBJECT ⟩ ::= { ⟨ MESHTERM } ⟩
⟨ VERB ⟩ ::= ⟨ INFINITIVE_FORM_OF_VERB ⟩

An example of MeSH SOV structure is reported in Example 2.

Example 2. Let us consider the SOV structure reported in Example 1, that is:

$[\ \langle progestogen\rangle,$
$[\langle cell, response, normal\rangle\ \langle cancer, breast\rangle],$
$modify\ ]$

Named entities (in italics) are annotated as leaves of MeSH taxonomy, that is,



Words which are not annotated as named entities are removed from the nominal components, thus the following MeSH SOV structure is constructed:

$[\langle progestogen\rangle,\ [\langle cell\rangle\ \langle cancer, breast\rangle],\ modify].$

IV. Frequent Pattern Discovery

The frequent pattern discovery is in charge of SPADA [14], which addresses the task of frequent pattern discovery from a Datalog database by dealing with taxonomy knowledge and language bias. In the followings, we present how to store MeSH SOV structures in a Datalog database and to express patterns which describe syntactic structures of named entities. The search strategy adopted by SPADA to discover frequent patterns is also reported.

Text corpus representation. Let t_i be a text in the corpus T. t_i represents a unit of analysis and it is represented by means of the MeSH SOV structures, which are extracted from t_i. These structures are stored as ground atoms in the extensional part D_E of a Datalog database D. The hierarchical relations between the nodes of Mesh taxonomy which involve the named entities in the corpus are also stored in D_E. Predicates used are the followings:

- **text**(t): t is a text in the corpus;
- **verb**(t, v): t is a text and v is a verb;
- **nominal**(t, n): t is a text and n is a nominal component;
- **mesh**(n, m): n is a nominal component and m is a named entity;
- **is_a**$(m1, m2)$: $m1$ and $m2$ are nodes of the MeSH taxonomy, there is a hierarchical relation between $m1$ and $m2$ in the taxonomy;
- **close**$(t, w1, w2)$: t is a text, $w1$ and $w2$ are named entities which appear to be close in the nominal component of t;
- **sbj_vb_obj**$(n1, v, n2)$: $n1$ (subject) and $n2$ (object) are the nominal components, v is the verb.

An example of the use of these predicates is reported in Example 3.

Example 3. The MeSH SOV structure [$\langle progestogen \rangle$, [$\langle cell \rangle$ $\langle cancer, breast \rangle$], $modify$] in Example 2 is extracted from a text t_1 and stored in D_E as follows:

text(t1). nominal(t1,n1). nominal(t1,n2). nominal(t1,n3).
mesh(n1,progestogen). mesh(n2,cell). mesh(n3,cancer).
mesh(n3,breast).
verb(t1,modify). close(t1,cancer, breast).
is_a(progestogen,i_hormones). is_a(cell, i_body_regions).
is_a(breast,i_body_regions).
is_a(cancer,i_neoplast_process).
is_a(i_hormones,i_chemical_and_drugs).
is_a(i_body_regions, i_anatomy).
is_a(i_neoplast_process,i_disease).
is_a(i_chemical_and_drugs, mesh).
is_a(i_anatomy, mesh). is_a(i_disease, mesh).
sbj_vb_obj(n1,modify,n2). sbj_vb_obj(n1,modify,n3).

where "is_a(_,_)" atoms express the hierarchical relations of MeSH taxonomy (BK) (see Example 2) which are used to annotate the named entities.

The domain knowledge is formulated as a normal logic program which defines the intensional part D_I. This intensional part allows deductions to be made (i.e. concluding additional atoms) from data stored in D_E. Example 4 shows the normal logic program stored in D_I and deductions made from atoms in D_E.

Example 4. The domain knowledge includes the intensional definition of the predicate "mesh_verb_mesh(_,_)", which expresses a verbal dependency between named entities(and not the nominal components):

mesh_vb_mesh(T, M1, V, M2): − text(T, N1), text(T, N2),
sbj_vb_obj(N1, V, N2), mesh(N1, M1), mesh(N2, M2).

By considering the extensional atoms reported in Example 3, this domain knowledge entails the atoms *mesh_vb_mesh(t1, progestogen, modify, cell), mesh_vb_mesh(t1, progestogen, modify, breast), mesh_vb_mesh(t1, progestogen, modify, cancer), mesh_vb_mesh(t1, cell, modify, cancer).*

Pattern representation. Relational patterns to express syntactic structures of named entities at a level l of the MeSH taxonomy are atomsets in which the form "$text(T), \mu_l(T)$ [s]", where text(T) is the atom that identifies each single text in the text corpus, while $\mu_l(T)$ is a conjunction of Datalog atoms which provide a description of a fragment of the text T at the level l of the MeSH taxonomy. Each atom in $\mu_l(T)$ describes either an extensionally/intensionally defined predicate in D. is_a atoms map each named entity with the granularity level l of the MeSH taxonomy. The support s estimates the probability p($\{text(T), \mu_l(T)\}$) on D. This means that s is the probability that a text matches the syntactic structure $\{text(T), \mu_l(T)\}$, that is, a substitution $\theta = T \leftarrow t$ exists such that $\{text(T), \mu_l(T)\}\theta \subseteq D$. The support of a pattern depends on the granularity level l. To be more precise, a pattern $P[s]$ is frequent at level l if $s \geq \sigma[l]$ and all ancestors of P with respect to the MeSH taxonomy are frequent at their corresponding levels. The definition of ancestor relation adopted in this work is based on the MeSH taxonomy as reported in Definition 3.

Definition 3: A pattern P at granularity level l of the MeSH taxonomy is an ancestor of the pattern P' at granularity level l' with $l' < l$, if P' can be obtained from P by replacing each variable X representing a MeSH term at the granularity level l with a variable X' which is more specific than X in the taxonomy and is mapped into the granularity level l'.

Patterns, which are related according to the ancestor relation in MeSH taxonomy, are reported in Example 5.

Example 5. A top-level relational pattern is in the form:

P1: text(T), mesh_vb_mesh(T, M1, reveal, M2),
is_a(M1, mesh), is_a(M2, mesh).

Both M1 and M2 are mapped with "mesh" that is the root of the taxonomy. By descending one level of taxonomy (from more general term to more specific terms), we can find the relational pattern

P2: text(T), mesh_vb_mesh(T, M1,reveal,M2),
is_a(M1, i_anatomy), is_a(M2, i_disease).

M1 is mapped with "i_anatomy", while M2 is mapped with "i_disease" and "mesh" is hierarchically related to both of them in the taxonomy. By descending to the bottom level of the MeSH taxonomy, M1 and M2 are mapped with the leaf nodes which contain the MeSH terms as they are annotated as named entities in the text,

P3: text(T), mesh_vb_mesh(T, M1, reveal, M2),
is_a(M2, breast), is_a(M2, cancer).

P1 is ancestor of P2 and P3, P2 is ancestor of P3.

Discovery. The set of ground atoms in D_E is partitioned into a number of non-intersecting units of analysis, that is, subsets $D[t]$ each of which includes atoms which describe the nominal components, verbal components, named entities which belong to a text t of the corpus. This partitioning of D_E is coherent with the individual-centered representation of training data [2], which has both theoretical (PAC-learnability) and computational advantages (smaller hypothesis space and more efficient search). SPADA mines frequent patterns across the different units of analysis by performing both an intra-level search and an inter-level search. Intra-level search is performed in the space of patterns where the *is_a* atoms refer to MeSH terms defined at the same level of MeSH taxonomy. Pattern space is ordered according to the θ-subsumption generality order between patterns. In the inter-level search, SPADA takes advantage of statistics computed at a level l when it searches in the space of more specific MeSH terms at level l + 1. By descending through the MeSH taxonomy it is possible to view the same term levels of abstraction (or granularity) and discover patterns at different levels of granularity. During the frequent pattern generation, patterns which do not satisfy pattern constraints defined in language bias are filtered out. A detailed description of SPADA can be found in [14].

V. The Application

BioSOV-FP has been evaluated over a corpus of abstracts of biomedical articles extracted by Medline. The dictionary used for the acronym processing is defined by a domain expert. The PubMed query "Alzheimer Drug Treatment Response" is formulated by biomedical researchers. The abstracts of twenty-five articles randomly selected in the retrieved article set are used as a training biomedical text corpus for BioSOV-FP. By processing the text corpus, BioSOV-FP identifies 1957 nominal components (on average 78.28 per abstract) and 834 verbal components (on average 33.36 per abstract) for a total of 834 SOV structures. By annotating the named entities, 164 MeSH SOV structures are extracted and stored in a Datalog database for a total of 25 "text(_)" atoms, 241 "verb(_,_)" atoms, 122 "close(_,_,_)" atoms, 311 "nominal(_,_)" atoms, 171 "sbj_vb_obj(_,_,_)" atoms, 374 "mesh(_,_)" atoms, 910842 "is_a(_,_)" atoms stored in extensional database and 241 "mesh_vb_mesh(_,_,_,_)" entailed by normal logic program in the intensional database. Multi-level frequent relational patterns are discovered with $\sigma[l] = 0.08$ for each level l of a six-level MeSH taxonomy. The maximum length of a pattern is set to 9. The language bias is used to ask for patterns containing only the atoms "mesh_vb_mesh(_, _)" and "close_to(_, _)".

A syntactic structure that is discovered at the top level of the MeSH taxonomy is reported below:

P1 [s=0.4]: text(T), mesh_vb_mesh(T, M1, cause, M2),
mesh_vb_mesh(T, M1, cause, M3), is_a(M1, mesh),
is_a(M2, mesh), is_a(M4, mesh), is_a(M3, mesh).

By descending to the second level of taxonomy we can find patterns whose ancestor is P1, but which provide a deeper insight in the nature of M1, M2 and M3. For example, the pattern:

P2 [s=0.12]: text(T), mesh_vb_mesh(T, M1, cause, M2),
mesh_vb_mesh(T,M1,cause,M3),
is_a(M1,i_biological_sciences),
is_a(M2,i_chemicals_and_drugs),
is_a(M3,i_chemicals_and_drugs).

By descending to the bottom level (level of leaves), we find the pattern P3 such that P2 is ancestor of P3 and M1, M2, and M3 are mapped to the named entities as they appear in the text corpora.

P3 [s=0.08]: text(T), mesh_vb_mesh(T, M1, cause, M2),
mesh_vb_mesh(T, M1, cause, M3).
is_a(M1, mutat), is_a(M2, protein), is_a(M3, amyloid).

Knowledge revealed by this bottom level pattern is the existence of a causal dependence (confirmed by domain expert) between mutations in Alzheimer disease and amyloid protein. The training corpora which match this syntactic structure (in italics) are reported below:

"....Presenilin *mutations* have been hypothesised to *cause* Alzheimer disease either by altering *amyloid* precursor *protein* metabolism or ..."

"... PS *mutations cause* the same functional consequence as mutations on *amyloid* precursor *protein* ..."'

For comparison, we consider the multi-level frequent patterns discovered by resorting to either a keyword-based representation (B1) or a subject-object based representation (B2) of the text corpus. In the former case, the boolean representation is adopted in order to represent only the occurrence of named entities in the text. In this case, patterns discovered as in [1] express similarity of MeSH term based content in the abstracts without considering differences of the grammatical environment. In the latter case, first-order language is used to represent only subject-object dependencies between named entities as in [13], the verb is not considered. Patterns are discovered by SPADA. They express similarity of named entity based content in the abstracts where named entity are provided as part of subject-object dependencies. The number of the discovered patterns and the elapsed time (in secs) of the learning job are reported in Table I. As expected, results show a great difference in the number (and elapsed time) of subject-object(s)-verb patterns discovered by BioSOV FP compared with both the number of named entity based frequent patterns and the number of subject-object(s) based frequent patterns. In general, for each pattern discovered in BioSOV-FP a pattern involving the same named entities is discovered both in B1 and B2. In this study, the following patterns:

P4$\leftarrow_{B1}$ *[s=0.12]: mutat, protein, amyloid*
P5$\leftarrow_{B2}$ *[s=0.08]: text(T), mesh_mesh(T, M1, M2), mesh_mesh(T, M1, M3), is_a(M1, mutat), is_a(M2, protein), is_a(M3, amyloid).*

are discovered, but both of them are less informative than P3 which informs not only on the meaning of each named entity, but also on the syntactic role of the entities and the verb which connect them.

Text representation	Patterns	Time
Named entities (B1)	78541	15710.985
MeSH subject-object(s) structures (B2)	1720	229.188
MeSH subject-object(s)-verb structures (BioSOV FP)	800	22.109

Table I
NUMBER OF PATTERNS AND ELAPSED TIME (SECS) OF LEARNING JOB ON AN INTEL CENTRINO (1.66 GHZ - 2GB RAM) RUNNING WINXP.

VI. CONCLUSIONS

We investigated how to combine syntax search functionality and keyword search functionality to detect subject-object(s)-verb structures of named entities in biomedical abstracts. Subject-object(s)-verb structures are represented in first-order logic language. Frequent syntactic structures are mined as relational frequent patterns. They provide an indication of the existence of interesting verbal based dependency among named entities. Some results are discussed. In the current study, we do not consider aspects related to the disambiguation/similarity of words (in particular verbs). As future work, we plan to extend the framework by integrating more sophisticate natural language processing techniques (e.g. word sense disambiguation by dictionary definitions or synonymy/hyponymy relation) in order to disambiguate a verb in the context of a given sentence/phrase. Additionally, we intend to analyze a larger corpus of biomedical texts.

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