COMPARISON OF SYNTACTIC PARSERS ON BIOMEDICAL TEXTS

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ABSTRACT

Syntactic parsing is an important step in the automated text analysis which aims at information extraction. Quality of the syntactic parsing determines to a large extent the recall and precision of the text mining results. In this paper we evaluate the performance of several popular syntactic parsers in application to the biomedical text mining.

Keywords Syntactic parser · biomedical text mining

1 INTRODUCTION AND RELATED WORK

Biomedical information extraction from text is an active area of research with applications to disease maps generation, construction of protein-protein interaction networks, and more. The backbone of such applications are semantic relations between relevant concepts, and this relational information is encoded in syntactic dependencies between the words representing the concepts. It means that proper understanding of the syntactic structure of a text is a precondition for correct interpretation of its meaning. In the last years many high quality syntactic parsers became publicly available leading to a natural question of choice of the best and most appropriate one for a specific task. The question calls for parser evaluation and comparison.

To date, parsers have been evaluated from a variety of perspectives. McDonald and Nivre (McDonald & Nivre, 2011) compared two prevailing dependency parsing paradigms, transition and graph-based, with the goal to connect error types with the theoretical aspect of each model. For the accuracy evaluation they consider sentence length, dependency distance, valency (the number of node’s siblings), part-of-speech and main dependency types: root, subject and object. Recently Choi (Choi et al., 2015) compared 10 state-of-the-art parsers in terms of their accuracy and speed in application to a number of genres covering newswire, broadcast news and conversation, web text and telephone conversation.

The most important metrics used in the parser evaluation CoNLL shared tasks are accuracies of unlabeled (UAS) and labeled (LAS) word attachments. The former check correctness of words’ syntactic head assignment while the latter controls also correctness of dependency label between the words’ pairs. Although these metrics give a feeling of overall parser performance, they do not shed light on how errors are propagated and affect parse components. Kummerfeld et. al. (Kummerfeld et al., 2012) implemented an alternative evaluation procedure aiming to estimate the downstream effect of each error. Pyysalo et. al. (Pyysalo et al., 2006) pointed out differences in parsing schemes which impose a challenge for reliable comparison of the results.

Another point of interest is evaluation of parser efficiency within specific domains and tasks. In the biomedical area, Clegg and Shepherd (Clegg & Shepherd, 2007) used manually annotated abstracts from GENIA corpus (Kim et al., 2003) to benchmark four parsers that have been applied in bioinformatic projects. They identified Charniak-Lease and Bikel parsers to perform the best overall and specifically on subtask of gene expression extraction. Miyao et. al. (Miyao et al., 2008) measured performance of eight parsers used as component of an information extraction pipeline aiming at protein-protein interactions. They found that retraining with domain-specific data improves parsers accuracy although to different extent.

Growing availability of full text articles for text mining called for comparison between article abstracts and article bodies. A few years ago Cohen et. al. (Verspoor et al., 2012b) analyzed 97 full text articles assembled in CRAFT corpus (Verspoor et al., 2012a) and evaluated performance of various text mining tools on their abstracts and bodies. They showed that article bodies have longer sentences, significantly higher usage of passives, negation and parenthesized material, compared to article bodies. Part-of-speech tagger and syntactic parser performed differently on abstracts and bodies, with the former significantly better on abstracts, while the latter insignificantly better on bodies.

In this work we evaluate performance of seven state-of-the-art parsers on biomedical texts. We pursue the following goals:

- compare parsers performance on abstracts and full texts;
- investigate main difference between these two types of text that influence parser performance;
- evaluate parsers suitability for biomedical event extraction and fine-grained contextualization;

1.1 Parsers and models for the comparison

For this study we used seven different statistical parsers. Four of these are Stanford parsers based on different linguistic paradigms: PCFG, Factored, RNN and SNN. The other three

²Most of this work was done in 2018 when the author was primarily affiliated with LCSB, Bioinformatic Core.

³Syntactic parser performance was measured in terms of bracket recall which shows how well a parser identified sentence constituent boundaries compared to gold standard.

⁴https://nlp.stanford.edu/software/
are BLLIP\footnote{https://github.com/BL莉/BL莉-parser} and McParseface\footnote{https://github.com/tensorflow/models/tree/master/syntaxnet} (referred to as Google throughout the paper), and Mate\footnote{https://nlp.stanford.edu/~mcclosky/biomedical.html}. The parsers are briefly introduced below:

- PCFG is an accurate unlexicalized parser based on a probabilistic context-free grammar (PCFG) (Klein & Manning, 2003).
- Factored parser combines syntactic structures (PCFG) with semantic dependencies provided by using lexical information (Klein & Manning, 2003). Lexicalization proved efficient when dealing with language ambiguities and helps correctly identify dependencies between sentence constituents.
- Recursive neural networks (RNN) parser (Socher et al., 2011) works in two steps: first it uses the parses of PCFG parser to train; then recursive neural networks are trained with semantic word vectors and used to score parse trees. In this way syntactic structure and lexical information are jointly exploited.
- Neural Network Parser (SNN) (Chen & Manning, 2014) is a greedy transition-based dependency parser with dense word embedding.
- BLLIP is a two-stage parser composed of generative PCFG-like constituent parser and discriminative maximum entropy reranker (Charniak & Johnson, 2005). This parser provided the basis for various self-training experiments aiming at parser domain adaptation (McClosky & Charniak, 2008), (McClosky et al., 2006).
- Parsey McParseface is a transition-based neural network parser with feature embeddings (Andor et al., 2016). The parser performs beam search for maintaining multiple hypotheses (as opposed to the 'greedy' approach), followed by global normalization.
- Mate (Bohnet, 2010) is a dependency parser which combines the second order maximum spanning tree and passive-aggressive perceptron algorithms to achieve high accuracy, high training and medium parsing speed.

All the parsers are distributed with pre-trained English models, and BLLIP has in addition separate models for less formal and medical slang. The scope of genres used to train English models varies among the parsers. The most diverse is that of Stanford, which combines medical model is trained on GENIA. Google is similar to newsgroups, emails, and weblogs (SANCL2012-Uniform). Its oriented model from that trained on reviews, question-answers, and encompasses newswire, abstracts of biomedical articles and biomedical slang. The scope of genres used to train English models and BLLIP has in addition separate models for less formal and

2 Corpora and Data sets

In our experiments, we used two gold standard in-domain corpora. One was released in the framework of Genia project (Kim et al., 2003). It consists of 2000 Medline abstracts in the area of molecular biology. Another corpus is known as "Colorado Richly Annotated Full Text Corpus" (CRAFT) (Verspoor et al., 2012a). It contains 67 full text articles in a wide variety of biomedical sub-domains. Both corpora are annotated from linguistic and semantic perspectives. In this work we use a portion of linguistic annotation, which concerns part-of-speech tagging and syntactic parsing.

2.1 Data sets

All the studied parsers were evaluated on the abstracts from Genia, and full texts from Craft. First of all, we used the parsers as they are distributed, typically trained on generic English language (see section \footnote{http://nlp.stanford.edu/software/dependency-parser-task-description.html} for the description). Next, we trained some of the parsers on biomedical texts, and evaluated their performance with the new models.

To obtain test and train data we used the Genia division as distributed by McClosky (McClosky & Charniak, 2008), and split Craft in a similar way. English models of BLLIP, Google and Mate have been evaluated on the "train and development" portions of Genia and Craft corpora. Genia model and English model of the Stanford parsers have been evaluated on "test and future use" section of Genia, and "train and development" of Craft. Similarly, Craft model was evaluated on "train and development" of Genia, and "test" set of Craft. The details of the corpora split for the training and evaluation tasks are shown in Table\footnotemark[11] "Mixed" model refers to our experiment with self-training of the Google parser (see subsection \footnotemark[12] for details).

Genia and Craft constituency trees (s-expressions) have been converted to Universal Dependencies (UD) CoNLL format using Stanford converters\footnotemark[11]. To evaluate Mate parser with its original CoNLL2009 model, we used the LTH Constituent-to-Dependency Conversion Tool\footnotemark[11] due to substantial differences between the parser output and UD format of the gold standard.

2.2 Training

For re-training we selected SNN because it showed, together with BLLIP, the best performance on both corpora and was the fastest of all parsers; Mate because it scored first of 10 leading (as of 2015) statistical parsers (Choi et al., 2015), and Google - the newest and the most accurate among the best performing parsers (as of 2016) (Andor et al., 2016). We trained the parsers following recommendations of the parsers’ authors. The original English model of SNN was trained with word embedding suggested by (Collobert et al., 2011). Given the domain orientation, we experimented with two different word embeddings - the
Table 1: Training and test data sets for parser evaluation (in thousands of sentences).

| Model | Test | \(N\) of sents | Train | Dev |
|-------|------|----------------|-------|-----|
| English | Genia-S | 12 – 15.5 | - | - |
| | Craft-B | 10 – 14.5 | - | - |
| Genia | Genia-S | 2.5 – 2.7 | 14.3 | 1.1 |
| | Craft-B | 10 – 14.5 | - | - |
| Craft | Craft-S | 0.6 – 0.8 | 17 | 2.1 |
| | Genia-B | 12 – 15.5 | - | - |
| Mixed | Genia-S | 2.7 | - | - |
| | Craft-S | 0.6 | 9.5 + 8.6 | 1.0 |

Suffixes ‘-B’ and ‘-S’ denote big and small test sets, respectively.

We apply head-dependency criterion when evaluating parsers’ performance on specific syntactic patterns (Tables 7, 8).

The first observation confirms a widespread belief that performance of statistical parsers depends on how close are the training and test domains. One of the reasons for that are out-of-domain words (Lease & Charniak, 2005; McClosky et al., 2010; Clegg & Shepherd, 2007) which have a higher chance to be assigned wrong part-of-speech tag and, as a consequence, make the parser generate erroneous dependency. CHECK WORDING: To estimate the influence of part-of-speech tagging on parser accuracy, we calculated, for all non-overlapping edges between the gold and test parses, the number of times when one or two words (end nodes) were wrongly tagged in the test set. Correlation between the part of speech error and edge mismatch varied from 10% to 36% depending on model. For curiosity, we calculated vocabulary overlap between GENIA and CRAFT corpora with 333,000 most frequent English words. The idea was to estimate the new vocabulary parsers have learned during the training of biomedically oriented models. It turned out that 68% lemmas from Craft and 47% lemmas from GENIA are among these frequent English words (Table 4). As can be seen in Table 3, domain acquaintance leads to up to 15% improvement of the part-of-speech tagging accuracy. An exception is SNN which achieves 98% already with its English multidomain model. It should not be unexpected as biomedical data makes part of the training corpus. In addition to the vocabulary, genre of the training corpora matters. Note that the News model of BLLIP performs slightly better than SANCL-2012 Uniform which is trained on less standard English from both, lexical and structural perspectives.

We compare parser results on entire full texts from CRAFT, and abstracts from GENIA and note much lower scores for CRAFT. On the one hand, it should not be surprising given substantial linguistic and structural differences between article abstracts and bodies demonstrated by Cohen et al. (Verspoor et al., 2012b) On the other hand, both belong to biomedical domain and share genre of scientific writing. McClosky et al. (McClosky & Charniak, 2008) noticed that reranking parser trained on LA Times achieved high accuracy in parsing WSJ despite, although small, differences in vocabulary and style. Unfortunately neither reranking parser, BLLIP, nor any other parser among the ones we tested demonstrate similar behavior. We try to investigate the reasons of such results in the following section.

With respect to the quantitative results, Stanford SNN trained on English model, BLLIP, trained on biomedical abstracts with GENIA reranker, Google and Mate trained by us on PubMed abstracts from GENIA corpus, reach almost the same scores on GENIA (+1%), and CRAFT (+3%). Note, that while being trained on the same English corpus, SNN outperforms by far all other Stanford’s parsers. Particularly low result of the Factorized parser, which is designed to take advantage of lexical information, runs against our expectations.

Training Craft models lets parsers reach higher scores on CRAFT, although impact of the training varies considerably between the parsers. Google and Mate turned to be responsive to the training, resulting in 16% gain in LAS for Google and 17% for Mate, compared to the results obtained with the models trained on Genia. Training SNN on Craft brought only 2% improvement, which might suggest that presence of common English from a large variety of genres in the training data is indispensable for that parser even though it is intended for biomedical domain. Here our observations on variable portability of training data and methods are similar to those made by Miyao et al. (Miyao et al., 2008) with respect to re-training of Stanford unlexicalized parser on GENIA data. The role of embeddings in
Table 2: Overall parsers performance

| Parser       | Model                               | Test        |
|--------------|-------------------------------------|-------------|
|              |                                     | WSJ | Genia | Craft |
| Stanford RNN | English multidomain                 | 0.90| 0.84 | 0.79 |
|              |                                     |     | 0.70 | 0.66 |
| Stanford PCFG| English multidomain                 | –  | 0.86 | 0.81 |
|              |                                     |     | 0.69 | 0.64 |
| Stanford Factored | –                             | –  | 0.87 | 0.78 |
|              |                                     |     | 0.67 | 0.62 |
| Stanford SNN | English multidomain                 | 0.92| 0.90 | 0.89 |
|              | Craft without embedding             |     | 0.89 | 0.74 |
|              | Craft with PubMed embedding         |     | 0.74 | 0.70 |
|              | Craft with PMC embedding            |     | 0.70 | 0.70 |
| BLLIP        | News                                | 0.92| 0.92 | 0.75 |
|              | SANCL-2012 Uniform                 |     | 0.92 | 0.70 |
|              | Genia+PubMed                        |     | 0.70 | 0.66 |
|              |                                     |     | 0.68 | 0.62 |
|              |                                     |     | 0.74 | 0.70 |
| Google       | English multidomain                 | 0.95| 0.93 | 0.57 |
|              | Genia                               |     | 0.95 | 0.57 |
|              | Craft                               |     | 0.88 | 0.74 |
|              | Bio Mixed                           |     | 0.86 | 0.70 |
| Mate         | English CoNLL 2009                  | –  | 0.90 | 0.57 |
|              | Genia                               |     | 0.88 | 0.86 |
|              | Craft                               |     | 0.82 | 0.79 |
|              |                                     |     | 0.68 | 0.62 |
|              |                                     |     | 0.72 | 0.68 |
|              |                                     |     | 0.87 | 0.85 |

Table 3: Accuracy of part of speech tagging

| Parser       | Model                               | Genia | Craft |
|--------------|-------------------------------------|-------|-------|
| RNN          | English multidomain                 | 0.83  | 0.71  |
|              |                                     | 0.82  | 0.71  |
|              |                                     | 0.98  | 0.90  |
| SNN          | English multidomain                 | 0.98  | 0.89  |
|              | Craft+PubMed emb.                   | 0.82  | 0.79  |
|              | Genia+PubMed                        | 0.82  | 0.77  |
|              |                                     | 0.98  | 0.88  |
| BLLIP        | English multidomain                 | 0.85  | 0.82  |
|              | Genia                               | 0.98  | 0.88  |
|              | Craft                               | 0.94  | 0.97  |
|              | Bio Mixed                           | 0.94  | 0.96  |
| Google       | English multidomain                 | 0.85  | 0.82  |
|              | Genia                               | 0.98  | 0.88  |
|              | Craft                               | 0.94  | 0.97  |
| Mate         | English CoNLL 2009                  | 0.94  | 0.97  |
|              | Genia                               | 0.94  | 0.97  |
|              | Craft                               | 0.94  | 0.97  |

the parser training had very little but negative influence: ≈ 0.5% loss in performance was observed with the PubMed and 2% with the PMC embeddings. It contradicts the parser’s results on WSJ test corpus, where the embedding brought ≈ 0.7% improvement (Chen & Manning, 2014). However the original word embedding was created from a vast English corpora which might have positive effect. The effect of the PMC-based embedding could probably be attributed to the quality of the word vector itself. Pyysalo et. al. suspect that it might be affected by either high proportion of noisy data in the training corpus, or aggressive trimming of the rare words performed by the word2vec implementation used to create the vector (Chiu et al., 2016).

3.2 Corpora comparison

As already mentioned, neither common English nor English from the biomedical abstracts provide adequate training sets for parsing full texts.

Table 4: Overview of the GENIA and CRAFT corpora

| Corpus       | Unique Tokens | Common with English | Corpora overlap | Sent. length |
|--------------|---------------|---------------------|-----------------|-------------|
| GENIA        | 15324         | 7257                | –               | 26.3        |
| CRAFT        | 12702         | 8733                | –               | 25.7        |
| BOTH         | –             | 4656                | 4924            | –           |

Figure 1: Sentence length distribution in GENIA and CRAFT corpora.

To understand what is so special about the full texts, we compare GENIA and CRAFT corpora from lexical and structural points of view. General corpora overview is given in Table 4. To calculate unique tokens we lemmatized the words, and excluded numbers and punctuation marks from computation. It turned out that the corpora share less than half of the vocabulary, and 94%...
of that common part are from the frequent English words list. Corpus-specific items are mostly names of proteins, chemicals, mutations, coding sequences, organs and organisms. To get an idea of how challenging corpus-specific words are for overall parsing we applied Google parser to CRAFT and GENIA test sets, using Genia model for CRAFT and Craft model for GENIA.\footnote{Among two parsers trained on CRAFT set, we choose Google because it showed slightly better performance than Mate.} We then calculated impact of mistagged words on edge mismatch. It turned out that CRAFT-specific words accounted for only 8% of all wrongly tagged words implicated in edge mismatch. Surprisingly, there was higher percentage of such words in the case of GENIA test set (16%). However the most problematic were not the names of in-domain concepts (e.g., proteins, chemicals etc.), but words with dashed prefixes and suffixes (e.g., "pre-activation", "gelatinase-associated") or words written with slash separator (e.g., "and/or" or "promoter/enhancer"). These orthographic phenomena are more diverse in GENIA than CRAFT. With the exception of molecule names and mathematical notation, dash occurrences in CRAFT are mostly limited to prefixes (e.g., "non-redundant", "re-introduce"), while slashes are found exclusively in URLs. Another frequent source of part-of-speech errors were 'ing'-ended words (e.g., "binding", "activating"), with the confusion between gerund, adjective and noun. This is an example of syntactic ambiguity rather than corpus-specific feature.

Next we looked at the structural characteristics of the corpora. Figure\footnote{The governor of the nsubj relation is not always a verb. When the verb is a copular verb (e.g., 'be' and its inflections), semantic predicate would be expressed by an adjective or noun. E.g., in "Reduction of IL-2 production is secondary to...", the nominal subject is "Reduction", while the predicate is an adjective "secondary".} shows normalized sentence length distribution in GENIA and CRAFT. As one can see, CRAFT has much bigger range of sentence lengths while the average is almost the same: 26.17 in GENIA vs 25.73 in CRAFT (Table\footnote{The governor of the nsubj relation is not always a verb. When the verb is a copular verb (e.g., 'be' and its inflections), semantic predicate would be expressed by an adjective or noun. E.g., in "Reduction of IL-2 production is secondary to...", the nominal subject is "Reduction", while the predicate is an adjective "secondary".}). Sentence length range in CRAFT is explained by the diversity of content types: captions, "Abstracts" and "Methods" sections are the shortest (mean 24.8 and 26.8), "Results" and "Discussion" - the longest (mean 31.17 and 30.35), and "Introduction" and "Conclusions" are in between (mean 26.80 and 26.49). Longer sentences have been suspected to decrease parsers performance on article bodies (Verspoor et al., 2012b). We measured parsers accuracies with respect to sentence lengths in bins of 10. We run the parsers with various models on GENIA and CRAFT test sets (Figure\footnote{The governor of the nsubj relation is not always a verb. When the verb is a copular verb (e.g., 'be' and its inflections), semantic predicate would be expressed by an adjective or noun. E.g., in "Reduction of IL-2 production is secondary to...", the nominal subject is "Reduction", while the predicate is an adjective "secondary".}\footnote{The governor of the nsubj relation is not always a verb. 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Among the remaining 3 parsers, SNN is the earliest to decline with respect to sentence lengths in bins of 10. We run the parsers on full texts. It is especially important for downstream tasks aiming at extraction of technical details provided in supplementary materials, methods sections, figure and table legends. From the practical point of view, it would be interesting to create a model which allowed a parser to perform equally well on either abstracts or full texts. Our experiment with self-training Google parser shows a promising trend. The created parser is more flexible than the ones trained on Genia or Craft individually: it performs better on Genia test set than its sibling, trained on Craft; it performs better on Craft than its sibling trained on Genia, and the difference in parsing accuracy between the Genia and Craft is also reduced. However, the absolute values leave room for training improvement.

3.3 Parser performance on syntactic patterns

In our applications we aim at finding so-called 'events': functional connections between various biomedical concepts such as proteins, chemicals, diseases, processes. At the very basic level, event is represented by the subject-predicate-object triplet which carries information about cause, action or change of state, and theme, respectively. The most typical syntactic dependencies which encode these relations are nominal and passive subjects ('nsubj' and 'nsubjpass'), and direct object ('dobj'). These in turn are syntactic arguments of a verb\footnote{The governor of the nsubj relation is not always a verb. When the verb is a copular verb (e.g., 'be' and its inflections), semantic predicate would be expressed by an adjective or noun. E.g., in "Reduction of IL-2 production is secondary to...", the nominal subject is "Reduction", while the predicate is an adjective "secondary".} whose role is to express event predicate. For example, in the sentence TGF-beta reduces Ig expression, 'reduces' is the verb which is also event...
Figure 2: Genia, small test set.

Figure 3: Craft, big test set

Figure 4: Craft, small test set

Figure 5: LAS versus sentence length in Genia and Craft corpora.
Table 5: Parsers’ performance on main event-related dependencies

| Parser          | Corpus  | nsubj | nsubjpass | dobj  | root   | compound |
|-----------------|---------|-------|-----------|-------|--------|----------|
| SNN + English   | Genia   | 0.92  | 0.93      | 0.93  | 0.94   | 0.87     |
|                 | Craft   | 0.78  | 0.83      | 0.87  | 0.86   | 0.64     |
| SNN + Craft     | Genia   | 0.81  | 0.86      | 0.83  | 0.83   | 0.67     |
|                 | Craft   | 0.81  | 0.87      | 0.86  | 0.89   | 0.56     |
| BLLIP           | Genia   | 0.95  | 0.96      | 0.92  | 0.95   | 0.88     |
|                 | Craft   | 0.92  | 0.95      | 0.92  | 0.95   | 0.87     |
| Google          | Genia   | 0.90  | 0.96      | 0.89  | 0.92   | 0.87     |
|                 | Craft   | 0.93  | 0.94      | 0.94  | 0.95   | 0.87     |
| Mate            | Genia   | 0.88  | 0.96      | 0.87  | 0.93   | 0.87     |
|                 | Craft   | 0.93  | 0.94      | 0.94  | 0.95   | 0.87     |

Table 6: Examples of syntactic patterns

| Patterns          | Examples                                                                 | Explanation                                                                 |
|-------------------|---------------------------------------------------------------------------|------------------------------------------------------------------------------|
| PP modifying      | Relief of cyclin A gene transcriptional inhibition                         | Attachment of a preposition to the head of a prepositional phrase            |
| PP modified       | Relief of cyclin A gene transcriptional inhibition                         | Attachment of the head of a prepositional phrase to the head of the phrase it modifies |
| Nominal coordination | IL1β, IL-8, and monocyte chemoattractant protein                           | Combining on an equal ground of multiple nominal or adjectival phrases      |
| acl               | activation triggered by either H2O2 or TNF-α                              | Clause that modifies a nominal which precedes it                             |
| acl:relcl         | bacterium that infects monocytes                                          | Clause introduced by a relative pronoun; modifies noun which precedes it    |
| advcl             | treatment of K562 cells increases γ-globin mRNA without affecting the expression of genes... | Clause which modifies a predicate (verb, adjective, etc.). Cares temporal, conditional, purpose information, etc. |
| xcomp             | Fos B expression is required to transactivate IL-2 promoter.              | Compliment of a verb or adjective without its own subject.                  |

predicate. Its syntactic arguments are subject 'TGF-beta', and direct object 'Ig expression'. Their semantic roles are cause and theme respectively. Inverting this sentence into passive voice would show how 'nsubjpass' comes into play. In Ig expression is reduced by TGF-beta, 'Ig expression' is the passive subject of the verb 'reduced'; its second argument, 'TGF-beta', is introduced by the preposition 'by'; arguments' semantic roles do not change.

Along with these three dependencies, we evaluate also 'root' and 'compound' relations. The former is selected because it is very often the way of introducing the main event predicate. Moreover, an error in tree root detection may come at expense of getting the whole parse wrong. With respect to 'compound' dependency, it is indispensable in multi-word entity names (e.g. in T cells receptor beta genes, 'genes' is the head of the nominal phrase, while all the remaining words are connected to the head by 'compound' relation) which are so abundant in biomedical slang. As any nominal event argument may be expressed by such multi-word construct, accurate identification of compound relations are important for finding complete event arguments.

The overview of the parser general performance indicates that for more accurate results it is better to use models trained on abstracts for processing the abstracts, and models trained on full texts for processing the full texts. Therefore, from now on, we evaluate the parsers with the corpus compatible models. However, since off-the-shelf state of the art parsers are trained on the abstracts, we include also results obtained by the SNN with English and BLLIP with GENIA+PubMed models on the CRAFT test set.

Table 5 helps us to get a feeling of how good our parsers are for extraction of major event components. On GENIA test set, scores of all the parsers for all but 'compound' dependency are between 93% and 96%, which is higher than their average performance. Accuracy of the 'nsubjpass' attachment is systematically higher than that of 'nsubj'. It can be explained by the presence of passive verb lexical cues (auxiliary and inflected verb, e.g., was induced'). Compound nouns are known to be syntactically and semantically difficult to process (Cohen et al., 2008). Although this relation is labeled with lower accuracy it is about the average of parsers performance. With respect to the individual results, BLLIP is the most accurate, reaching 1% − 3% more on all the dependencies except 'root', where all the parsers except SNN obtain the same score.

On CRAFT test set, Google and Mate with Craft models, outperform BLLIP and SNN with either models. It is in line with the discussion about the overall parsers performance in Subsection 3.1. Google reaches 2% more on 'nsubj' and 'dobj', while Mate has 1% more on 'root' dependency. Like in the case of
Table 7: Parsers’ performance on specific patterns

| Parser | Corpus | PP    | PP    | Coordination | acl  | acl:relcl | advcl | xcomp |
|--------|--------|-------|-------|--------------|------|-----------|-------|-------|
|        |        | modifying (‘case’) | modified (‘nmod’) |              |      |           |       |       |
| SNN + English | Genia | 0.94 | 0.89 | 0.68 | 0.82 | 0.81 | 0.69 | 0.86 |
|          | Craft  | 0.85 | 0.82 | 0.54 | 0.71 | 0.73 | 0.59 | 0.76 |
| BLLIP   | Genia  | 0.95 | 0.90 | 0.71 | 0.82 | 0.78 | 0.80 | 0.89 |
|          | Craft  | 0.87 | 0.82 | 0.54 | 0.68 | 0.68 | 0.66 | 0.73 |
| Google  | Genia  | 0.95 | 0.88 | 0.70 | 0.81 | 0.76 | 0.75 | 0.85 |
|          | Craft  | 0.94 | 0.86 | 0.70 | 0.70 | 0.68 | 0.81 | 0.86 |
| Mate    | Genia  | 0.94 | 0.87 | 0.69 | 0.79 | 0.75 | 0.70 | 0.86 |
|          | Craft  | 0.95 | 0.83 | 0.69 | 0.76 | 0.64 | 0.72 | 0.79 |

Table 8: Parser performance on prepositions in %

| Parsers | Preps | SNN | BLLIP | Google | Mate |
|---------|-------|-----|-------|--------|------|
|         | of    | 91  | 91    | 92     | 91   |
|         | by    | 88  | 80    | 87     | 86   |
|         | with  | 86  | 68    | 87     | 84   |
|         | to    | 84  | 75    | 81     | 81   |
|         | between | 81 | 64    | 83     | 84   |
|         | in    | 78  | 64    | 79     | 76   |

GENIA test set, the scores here are above average for all the parsers for all the dependencies. It is also so for 'compound' in the case of Google and Mate, while SNN and especially BLLIP score poorly. We have already mentioned that training of SNN on CRAFT was much less successful compared to Google and Mate. In the context of main event-related dependencies, results reached by SNN with English and Craft models are not conclusive: Craft-trained model is better in 'nsubj', 'nsubjpass' and 'compound', while 'dobj' and 'root' are more accurate with English model. With respect to 'nsubj', 'nsubjpass' and 'dobj', BLLIP achieves (almost) the same scores as the best SNN; it outperforms either SNN model on 'root' and is worst in 'compound' relation. With respect to 'root' dependency, SNN scores last on both test sets and with either model. It does not appear to be related to the domain orientation of our data. Choi et al. (Choi et al., 2015) noticed the same behaviour of the parser on the OntoNotes, and attributed it to the earliest reasonable choice of root node made by the parser.

In addition to detecting main event players, we are particularly interested in determining the event context: conditions and temporal order, coordination, mutual dependency and/or exclusion, location. Such relations are expressed via abundant use of coordination, prepositions, adverbial and relative clauses. This is the reason why, in addition to the main event-related dependencies, we look closely at parsers’ performance on the corresponding syntactic patterns.

Table 7 shows LAS scores obtained by the selected parsers on prepositional attachment, coordination, nominal and relative clause modifier (acl and acl:recl, respectively), predicate modifying clauses (advcl), and open clausal complements (xcomp). Examples for each relation can be found in Table 6.

On Genia, BLLIP wins in all the dependencies except relative clause ('acl:recl'), where SNN takes the lead. Google performs slightly better than Mate, but overall SNN, Google and Mate obtain similar results. On Craft test set, Google with Craft model shows the most stable performance, only being outperformed by Mate and SNN in nominal ('acl') and relative clause modifier assignments ('acl:recl').

- Prepositional attachment. Dependencies related to prepositional attachment reach the highest scores. 'case' scores better than 'nmod' (columns 1 and 2, respectively), which could be explained by shorter dependency distance between dependent and its parent: it is twice as much for 'nmod' compared to 'case'. Overall, accuracy of the prepositional attachment is equal or above average scores for all the parsers and test sets (except Mate, where it is 2% less in Craft). It is good news because prepositions are crucial in event argument detection and event contextualization. Table 8 shows parser performance on a selection of most relevant prepositions. The scores are listed as ranges, quoting results for Genia and Craft test sets. For Google and Craft, corpus-compatible models are used; for SNN and BLLIP we apply English and GENIA+PubMed models, respectively. The most accurate is the attachment of preposition 'of'. So, as far as the prepositions are concerned, unary events like inhibition of c-jun are nicely secured. Attachment of 'in' is the worst scored. It might have negative influence on finding arguments of regulatory events (e.g., PP1 may be involved in T cell activation) or location specification. One of the major challenges for automatic preposition processing is contextual ambiguity. Consider the phrase induction of cytokine expression in leukocytes: what would be the correct parse: induction of [cytokine expression] in leukocytes; [cytokine expression] in leukocytes; both or none of the two? Syntactically speaking, the first answer is the right one.

Importantly, experiments with Google and Mate parsers show that applying corpus-compatible model considerably improves prepositional attachment accuracies. When English or Genia models are used to parse Craft test set, SNN and BLLIP obtain fairly similar results.

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\[18\] We do not include results of SNN trained on Craft because they were lower than those obtained by the parser run with English model for all the dependencies.
Figure 6: Coordination example. Model parse.

Figure 7: Coordination example (a). (Google + Craft model.)

Figure 8: Coordination example (b). (Google + Mixed model)

Figure 9: Coordination example (c). (Google + Genia model.)

- Coordination. Identification of the coordination scope is not easy either, often for the same reason of semantic ambiguity. In the following fragment: No differences between the normal and KA mutant mice can be detected, are the coordinated components (1) [normal and KA mutant] mice, or (2) [normal and KA] mutant mice? The correct answer is (1) although all parsers except BLLIP yielded tree corresponding to (2). Ambiguity is not the only challenge; there are also complex constructions involving prepositions, complementary clauses and punctuation marks. In the sentence: In unstimulated THP-1, CRE-binding protein and, to a lesser extent, c-Jun complexes were found to bind to the CRE site., the coordinated elements are CRE-binding protein and c-Jun complexes; they participate in binding relation (Figure 6). None of the parser-produced trees corresponds to the model; yet, from the interpretation point of view, the errors are not equally harmful. Tree in Figure 7 captures the coordination and scope of binding. On the contrary, the one in Figure 9 consider THP-1 among the coordinated elements which participate in binding. It is wrong because THP-1 is a cell line while CRE and s-Jun are proteins. The outcome based on the tree in Figure 9 suggests that binding of
Figure 10: Coordination example (d). (Bllip + Genia and PubMed model.)

Table 9: Most frequent confusions between modifying dependency types.

| Gold dependency | Test alternatives          |
|-----------------|---------------------------|
| acl             | advcl, root, xcomp        |
| acl:relcl       | admod, acl, ccomp         |
| advcl           | xcomp, nmod, acl          |
| xcomp           | acl, advcl                |

a ccomp: clausal complement of a verb or adjective  
b nmod: nominal modifiers of nouns or clausal predicates

c-Jun complexes happens in THP-1 and CRE-binding protein, which is also wrong. This example is different from the previous ones in that the sentence does not offer multiple syntactic solutions. Yet, in-domain knowledge is nearly indispensable for finding the correct parse. Note the direct object ("dobj") dependency on Figure 8 instead of the expected adjectival modifier "amod". "dobj" results from the miss-attribute of Verb to "CRE-binding". Although morphologically wrong, such reading pertains to the functional meaning captured in the protein name.

- **Typical confusions.** Remaining dependencies in Table 9, 'acl', 'acl:relcl', 'advcl', 'xcomp', behave as modifiers. Table 9 shows typical edge label confusions between the gold and test parses. Naturally, the most "dangerous" swaps are the ones which wrongly identify the modified element. Take for example, adjectival (acl) → adverbial (advcl) clause modifiers. The former tells us about some properties expressed by a noun, while the latter conveys details about an action expressed by a verb. Exchange of these dependencies would most probably lead to an interpretation error. Consider the following examples:

  - acl → advcl. The capacity of curcumin to inhibit both cell growth and death strongly implies that... curcumin affects a common step, presumably involving a modulation of the AP-1 transcription factor. According to gold tree, what involves modulation of AP-1 TF is the step (step acl involving). On the contrary, all the parsers identified affects as dependency target of involving (affects advcl involving). As a result, we should understand that curcumin affects a common step by means of modulation of AP-1 TF. Syntactically speaking, both parses are legal. However they lead to two different interpretations and choosing the correct one may require domain expertise.

Figure 11: Adverbial clause modifier: correct (Google and Mate with Genia model.)

- acl → advcl. The capacity of curcumin to inhibit both cell growth and death strongly implies that... curcumin affects a common step, presumably involving a modulation of the AP-1 transcription factor. According to gold tree, what involves modulation of AP-1 TF is the step (step acl involving). On the contrary, all the parsers identified affects as dependency target of involving (affects advcl involving). As a result, we should understand that curcumin affects a common step by means of modulation of AP-1 TF. Syntactically speaking, both parses are legal. However they lead to two different interpretations and choosing the correct one may require domain expertise.

Figure 12: Adjectival clause modifier: wrong (Google with Mixed model and BLLIP)
- `advcl → acl`. Adverbial and adjectival clause modifiers express often so-called "long-distance" dependencies, when the modified and modifying words are separated by many other words in the sentence. Consider an example: *Cytomegalovirus infection induced interleukin-8 gene transcription in a human monocytic cell line, leading to IL-8 secretion*. When parsed correctly (Figure 11), 'advcl' dependency should be established between induced ➔ leading, thus showing that cytomegalovirus infection is the cause of IL-8 secretion. Nevertheless, some parsers suggested line ➔ leading edge instead making 'line' to be the cause of IL-8 secretion, which is wrong.

- 'root'. Erroneous attribution of 'root' dependency is often an artifact resulting from parsing titles and headings, which are in many cases not real sentences. For example, in *Rescue by cytokines of apoptotic cell death induced by IL-2 deprivation of human antigen-specific T cell clones*. The 'acl' dependency: death ➔ induced, is substituted by root ➔ induced dependency, which is wrong. It is not surprising that such substitutions occur much more often in Craft, which is composed of full texts and, in addition to article titles contains (sub)section headings and figure captions.

- Parsing scheme variability. Similarly to the dependency variability, different ways of attaching constituents lead sometimes to differences between gold and test trees while do not alter the meaning. Consider the following sentence: *We report that the mouse ortholog (Trip13) is required for completion of meiosis in both sexes*. The gold tree for the prepositional fragment (Figure 14) suggests serial attachment of prepositional phrases of meiosis and in both sexes such that the latter directly modifies the former which in turn is attached to completion. Some parsers adopt the same scheme, some others prefer parallel attachment (Figure 15) in which both dependencies 'required' ➔ mmod for mmod:for ➔ differentiation would lead to the same interpretation as necessary ➔ mmod for mmod:for ➔ differentiation.

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Figure 13: Alternative dependency labels: advcl (Model tree, SNN) or xcomp (BLLIP, Mate).

![Figure 13: Alternative dependency labels](image)

Figure 14: Attachment of a prepositional phrase; serial scheme. (Model tree, Bllip, Mate+Genia model.)

![Figure 14: Attachment of a prepositional phrase](image)
After having looked closely at parsers treatment of various dependency relations in a diversity of contexts, we conclude that multiple constituent attachment schemes and errors in gold standard annotation.

Gold standard specificity. Besides syntactic and parsing schemes flexibility, gold standard annotation itself is not always instructive. Such is the case of 'dep' relation - the most generic one, which only tells that the words are dependent but does not specify, how. A recurrent example from Genia corpus is coordination of premodifiers. Consider the following fragment: elements with NFkappaB, AP1 and ETS-like binding motifs have been identified.... The gold annotation suggests 'dep' relation between the motifs $\text{NFkappaB} \rightarrow \text{dep}$. On the contrary, all the parsers labeled the relation as conjunction which seems to be correct.

After having looked closely at parsers treatment of various dependency relations in a diversity of contexts, we conclude that differences between the gold and parse trees may result from parsers errors, input text ambiguity, certain flexibility in choice of the dependency relation, multiple constituent attachment schemes and errors in gold standard annotation.

4 Final notes: parsing time and recommendations

Since parsing is one of the steps in the information extraction pipeline, parser speed matters, especially when large amounts of texts must be processed. Table 10 shows times required by each of the four top-scored parsers to process GENIA small (2854 sentences) and CRAFT big (19128 sentences) test sets. As one can see, SNN is by far the fastest one, BLLIP - the slowest, Google and Mate are in the middle, with Google being three times faster than Mate. Now, with the detailed account of the parsers accuracy and time, we could provide a few recommendations on which parser to choose for information extraction from biomedical articles. If only abstracts are concerned, time is important, and the goal is to accurately identify main semantic roles in terms of subject-predicate-object triplets, SNN is the best option. Google with Genia model provides a respectable alternative for detecting main and context-related dependencies involved in event extraction, especially if time is a concern. If time is not a limiting factor, we would opt for BLLIP as the most accurate parser.

With regard to full text processing, models trained on CRAFT have obvious advantage. In our experiments, Google performs a little better in identification of main event-related dependencies and patterns involved in the event contextualization. If the choice is to be made between off-the-shelf parsers, BLLIP was more accurate in detection of most of the main event-related dependencies but had serious disadvantage in labeling 'compounds'. Each parser had its stronger and weaker points in labeling contextualization-related dependencies. Therefore, the best strategy here could be a combination of both parsers as long as there are no restrictions on parsing time.

5 Conclusions

In this paper we have studied performance of seven statistical syntactic parsers on biomedical texts. We evaluated the parsers from the point of view of the overall accuracy and identified four best performing ones. The latter have been further analyzed on a selection of syntactic patterns with the task of general and fine-grained event extraction in mind. While interpreting evaluation scores, we pointed out cases, in which formal scores do not pertain to quality of parses. We have compared portability of various models to abstracts and full texts and found that even within the same genre, models trained on abstracts do not perform respectably on full texts. We have also compared two main gold standards available for biomedical scientific writing, GENIA and CRAFT, and traced possible reasons why parsers trained on abstracts perform poorly on full texts. Finally, we compared the parser speed and provided a few recommendations on parser’s choice with respect to the task of event extraction.

As a future work, we see interest in finding optimal data and technique to train parsers such that they would work equally well on abstracts and full texts. In this light, SNN is attractive as it shows the highest speed. Mate is the one with the lowest time required for training, and thus is also worth exploration. Our experiment with self-training Google parser shows a promising start, and it might be interesting to investigate efficiency of this strategy with different parsers.

10 All the experiments are performed on 2,9 GHz Intel Core i5 MacBook Pro.
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