Double Layered Learning for Biological Event Extraction from Text

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Abstract
This paper presents our approach (referred to as BioEvent) for protein-level complex event extraction, developed for the GENIA task (Kim et al., 2011b) of the BioNLP Shared Task 2011 (Kim et al., 2011a). We developed a double layered machine learning approach which utilizes a state-of-the-art mini-mized feature set for each of the event types. We improved the best performing system of BioNLP 2009 overall, and ranked first amongst 15 teams in finding “Localization” events in 2011. BioEvent is available at http://bioevent.sourceforge.net/

1 Introduction
A biological event refers to a specific kind of interaction between biological entities. Events consist of two parts: event triggers and event arguments. Event extraction can be very challenging when dealing with complex events with multiple or nested arguments; for example, events themselves can be an argument for other events.

2 Methods
In general, to detect an event mentioned in text, the event trigger should be identified first, then complemented with event arguments. We divided the training and testing tasks into two phases: trigger detection and argument detection.

2.1 Event Trigger Detection
The trigger detection problem can be modeled as a multi-class classification of a word or combination of words (phrase). Instead of using all possible phrases in the training text as examples for the classifier, we only included those that were known triggers in the training set. For the official shared task submission we used SVMlight (Joachims, 1999). Detailed explanation of the trigger detection process includes three main steps: pre-processing, training of the SVM models, and combining SVM results.

Pre-processing. All tokenized documents provided by the shared task organizers (Stenetorp et al., 2011) were converted to database records. Then different sets of attributes were defined and calculated for words, sentences and documents.

Training SVM models and Combining Results. We trained 9 different binary SVM models using one-vs-many approach. One of the challenging tasks was to compare the results of different SVM models, given that each had different feature sets and their confidence values were not directly comparable and needed to be calibrated properly before comparing. We tried three approaches: 1) selecting the SVM result with highest positive distance to hyperplane, 2) using a trained decision tree and 3) using another SVM trained for voting. Model J48 from the WEKA library (Hall et al., 2009) was trained based on SVM distances for the training set examples and expected outputs. In the third approach, we tried SVM for voting, which generated better results than the decision tree. Last two approaches consist of two layers of classifiers which first layer includes event types classifiers and second layer generates final decision.
Table 1: F-Value from our BioEvent system compared to Turku09 (Bjorne et al., 2009) results, using Approximate Span/Approximate Recursive matching based on first layer outputs.

| Event type          | Bioevent | Turku09 |
|---------------------|----------|---------|
| Gene expression     | 71.88    | 70.84   |
| Transcription       | 47.62    | 47.14   |
| Protein catabolism  | 60.87    | 60.87   |
| Phosphorylation     | 75.14    | 73.39   |
| Localization        | 61.49    | 59.68   |
| Binding             | 34.42    | 35.97   |
| Regulation          | 24.03    | 22.26   |
| Positive regulation | 33.41    | 31.84   |
| Negative regulation | 18.89    | 18.58   |
| ALL-TOTAL           | 44.69    | 43.54   |

References

Jari Bjorne, Juho Heimonen, Filip Ginter, Antti Airola, Tapio Pahikkala, and Tapio Salakoski. 2009. Extracting Complex Biological Events with Rich Graph-Based Feature Sets. Computational Linguistics, (June):10–18.

M. Hall, E. Frank, G. Holmes, B. Pfahringer, P. Reutemann, and I.H. Witten. 2009. The WEKA data mining software: an update. ACM SIGKDD Explorations Newsletter, 11(1):10–18.

T. Joachims. 1999. Making large scale SVM learning practical. Advances in Kernel Methods - Support Vector Learning, (B. Schölkopf and C. Burges and A. Smola (ed.)).

Jin-Dong Kim, Sampo Pyysalo, Tomoko Ohta, Robert Bossy, and Jun’ichi Tsujii. 2011a. Overview of BioNLP Shared Task 2011. In Proceedings of the BioNLP 2011 Workshop Companion Volume for Shared Task, Portland, Oregon, June. Association for Computational Linguistics.

Jin-Dong Kim, Yue Wang, Toshihisa Takagi, and Akinori Yonezawa. 2011b. Overview of the Genia Event task in BioNLP Shared Task 2011. In Proceedings of the BioNLP 2011 Workshop Companion Volume for Shared Task, Portland, Oregon, June. Association for Computational Linguistics.

Pontus Stenetorp, Goran Topić, Sampo Pyysalo, Tomoko Ohta, Jin-Dong Kim, and Jun’ichi Tsujii. 2011. BioNLP Shared Task 2011: Supporting Resources. In Proceedings of the BioNLP 2011 Workshop Companion Volume for Shared Task, Portland, Oregon, June. Association for Computational Linguistics.