Detecting Relations in the Gene Regulation Network

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Abstract

The BioNLP Shared Task 2013 is organised to further advance the field of information extraction in biomedical texts. This paper describes our entry in the Gene Regulation Network in Bacteria (GRN) part, for which our system finished in second place (out of five). To tackle this relation extraction task, we employ a basic Support Vector Machine framework. We discuss our findings in constructing local and contextual features, that augment our precision with as much as 7.5%. We touch upon the interaction type hierarchy inherent in the problem, and the importance of the evaluation procedure to encourage exploration of that structure.

1 Introduction

The increasing number of results in the biomedical knowledge field has been responsible for attracting attention and research efforts towards methods of automated information extraction. Of particular interest is the recognition of information from sources that are formulated in natural language, since a great part of our knowledge is still in this format. Naturally, the correct detection of biomedical events and relations in texts is a matter which continues to challenge the scientific community. Thanks to the BioNLP Shared tasks, already in the third instalment, researchers are given data sets and evaluation methods to further advance this field.

We participated in the Gene Regulation Network (GRN) Task (Bossy et al., 2013), which is an extension of the Bacteria Gene Interactions Task from 2011 (Jourde et al., 2011). In this task, efforts are made to automatically extract gene interactions for sporulation, a specific cellular function of the bacterium bacillus subtilis for which a stable reference regulatory network exists. An example sentence can be seen below. Note that all entities (except for event triggers, i.e. action entities like transcription in figure 1) are given as input in both training and test phases. Therefore, this task makes abstraction of the entity recognition issue, putting complete focus on the subproblem of relation detection.

Figure 1: Example sentence: there is an Interaction: Requirement relation defined between entities GerE and sspG, through the action event of transcription. Full-line entities are given in the test phase, while dashed-lined ones are not.

As this is our first participation in this task, we have built a simple, yet adaptable framework. Our contributions lie therefore more in the domain of feature definition and exploration, rather than in designing novel machine learning models. Predictions could be given in two ways. Either all events and relations could be predicted, from which the regulation network would then be inferred (cfr. figure 1, detect all dashed-lined entities, and the relations between them). Or, a specification of the regulation network itself is directly predicted (in the example, this amounts to finding GerE \( \rightarrow \) sspG, and the type (Requirement)). We chose to implement the latter method. In section 2 we will lay out the framework we constructed, and the tools we used. In that section, we will also look at some of the design choices for our feature construction. Finally we discuss our results in section 3, and touch upon opportunities to exploit the available interaction hierarchy in this data.
2 Implementation

Basic Framework For this interaction detection task, we implement a Support Vector Machine (SVM) (Vapnik, 1995), with the use of the SVMLight (Joachims, 1999) implementation in the Shogun Machine Learning Toolbox. Per given sentence, we construct our data points to be all pairs of genic entities in that sentence, i.e., all possible interaction agent/target pairs. Note that since the regulation network is a directed graph, the order of the nodes matters; each such pair therefore occurs twice in the data. It is obvious from this construction that this leads to a great imbalance: there are a lot more negatively labelled data points than positive ones. To respond to this, we tried applying differential weighting (as seen in (Shawetaylor and Cristianini, 1999) and (Veropoulos et al., 1999)). This amounts to appointing a bigger regularisation parameter $C$ to the positive data points when training the SVM, thus tightening the boundary constraint on the margin for these points. The results of this were unconvincing however, so we decided not to implement it.

For each interaction type (there are 6 of them), we then train a separate binary (local, hence one-versus-all) SVM classifier$^1$, with a Gaussian Radial Basis Function (RBF) kernel as in (A˘izerman et al., 1964) and (Schölkopf et al., 1997). We evaluated several types of kernels (linear, polynomial, Gaussian) in a 25-fold cross-validation over the utilisation of these similarity measures how much of the beginning of the word is shared$^2$. In using a similarity scoring instead of a binary-valued indicator function, we want to respond to the feature sparsity, aggravated by the low amount of data (134 sentences in training + validation set). While this introduces some additional noise in the feature space, this is greatly offset by a better alignment of dimensions that are effectively related in nature. Also note that, due to the nature of the English language, this approach of scoring similarities based on a shared beginning, is more or less equivalent to stemming (albeit with a bias towards more commonly occurring stems). For our cross-validations, utilisation of these similarity scores attributed to an increase in F-score of 7.6% (mainly due to an increase in recall of 7.0%, without compromising precision) when compared to the standard binary vocabulary features.

- Part-of-speech information, using the Penn-Treebank (maximum entropy) tagger, through the NLTK Python library (Bird et al., 2009). These are constructed in the same fashion as the vocabulary features;

$$f_{ent}(e_{ij}) = \frac{1}{N_{ij}} \sum_{w \in e_{ij}} f_{base}(w) \circ f_{context}(w, i),$$

where $N_{ij}$ is the number of words in $e_{ij}$. This is an average over all words $w$ that make up entity $e_{ij}$, with the choice of averaging as a normalisation mechanism, to prevent a consistent assignment of relatively higher values to multi-word entities. Inside the sum is the concatenation of the local feature function on the words ($f_{base}$) with $f_{context}$, which will later be seen as encoding the sentence context.

The base feature function on a word is a vector containing the following dimensions:

- The entity type, as values $\in \{0, 1\}$;
- Vocabulary features: for each word in the dictionary (consisting of all words encountered), a similarity score $\in \{0, 1\}$ is assigned that measures how much of the beginning of the word is shared$^3$. In using a similarity scoring instead of a binary-valued indicator function, we want to respond to the feature sparsity, aggravated by the low amount of data (134 sentences in training + validation set). While this introduces some additional noise in the feature space, this is greatly offset by a better alignment of dimensions that are effectively related in nature. Also note that, due to the nature of the English language, this approach of scoring similarities based on a shared beginning, is more or less equivalent to stemming (albeit with a bias towards more commonly occurring stems). For our cross-validations, utilisation of these similarity scores attributed to an increase in F-score of 7.6% (mainly due to an increase in recall of 7.0%, without compromising precision) when compared to the standard binary vocabulary features.

$^1$There is a lot of scope for leveraging the hierarchy in the interaction types; we touch upon this in the conclusion.

$^2$Note that one entity can consist of multiple words.

$^3$To not overemphasise small similarities (e.g. one or two initial letters in common), we take this as a convex function of the proportion of common letters.
• Location of the word in its sentence (nor-
malised to be $\in [0, 1]$). Note that next to
being of potential importance in determining
an entity to be either target or agent, the sub-
space of the two location dimensions of the
respective entities in the data point $x_{ijk} = (e_{ijk}, e_{ijk})$ also encodes the word distance be-
tween these.

• Depth in the parse tree (normalised to be $\in [0, 1]$).

Adding contextual features On top of these ba-
sic features, we add some more information about
the context in which the entities reside. To this ef-
fact, we concatenate to the basic word features the
tree context: a weighted average of all other words
in the sentence:

$$f_{\text{context}}(w, i) = \frac{1}{Z} \sum_{w_j \in \text{sentence}_i} \alpha d_i(w, w_j) f_{\text{base}}(w_j)$$

with $f_{\text{base}}$ the basic word features described
above, and weights given by $\alpha \leq 1^4$ and $d_i(w, w_j)$
the parse tree distance from $w$ to $w_j$. The normal-
isation factor we use is

$$Z = \sum_{w_j \in \text{sentence}_i} \alpha d_i(w, w_j)$$

i.e., the value we would get if a feature would be
consistently equal to 1 for all words. This normal-
isation makes sure longer sentences are not
overweighted. For the inner parse tree nodes we
then construct a similar vector (using only part-
of-speech and phrasal category information), and
append it to the word context vector.

Note that the above definition of $f_{\text{context}}$ also al-
lowrs us to define $d_i(w, w_j)$ to be the word distance
in the sentence, leaving out any grammatical (tree)
notion. We designate this by the term sentence
context.

3 Results and Conclusion

Cross-validation performance on training data
Because we have no direct access to the final test
data, we explore the model performance by con-
sidering results from a 25-fold cross-validation on
the combined training and validation set. Table 1
shows the numbers of three different implementa-
tions\(^4\): one with respectively no $f_{\text{context}}$ concate-
nated, and the tree context (the official submission
method) and sentence context versions. We see
that a model based uniquely on information from
the agent and target entities already performs quite
well; a reason for this could be the limited amount
of entities and/or interactions that come into play
in the biological process of sporulation, augment-
ing the possibility that a pair can already be ob-
served in the training data. Adding context inform-
ation increases the F-score by 2%, mainly due to
a substantial increase in precision, as high as 7.5%
for the sentence context. Recall performs better in
the tree variant however, pointing to the fact that
grammatical structure can play a role in identify-
ing relations.

Note that we only considered the sentence alter-
ation after the submission deadline, so the better
results seen here could no longer implore us to use
this version of the context features.

| Context   | SER  | Prec. | Recall | F1   |
|-----------|------|-------|--------|------|
| None      | 0.827| 0.668 | 0.266  | 0.380|
| Tree      | 0.794| 0.709 | 0.285  | 0.406|
| Sentence  | 0.787| 0.743 | 0.278  | 0.405|

Table 1: Results of the cross-validation for several implementations of context features. ($C = 5, \sigma = 8.75$)

We can identify some key focus points to fur-
ther improve our performance. Generally, as can
be seen in the additional results of table 1, a low
recall is the main weakness in our system. These
low numbers can in part be explained by the lack
of great variation in the features, mainly due to
the low amount of data we have. Interesting to
note here, is the great diversity of performance of
the local classifiers separately: the SVM for Trans-
scription attains a recall of 42.0%, in part because
this type is the most frequent in our data. However,
the worst performers, Requirement and Regulation
(with a recall of 0.0% and 3.7% respectively) are
not per se the least frequent; in fact, Regulation
is the second most occurring. Considerable effort
should be put into addressing the general recall is-
sue, and gaining further insight into the reasons
behind the displayed variability.

\(^4\)For simplicity, we keep all other parameters ($C$, and the
RBF kernel parameter $\sigma$) identical across the different entries
of the table. While in theory a separate parameter optimisa-
tion on each model could affect the comparison, this showed
to be of little qualitative influence on the results.
Final results on test data  On submission of the output from the test data, our system achieved a Slot Error Rate (SER) of 0.830 (precision: 0.500, recall: 0.227, F1: 0.313), coming in second place after the University of Ljubljana (Zitnik et al., 2013) who scored a SER of 0.727 (precision: 0.682, recall: 0.341, F1: 0.455).

Exploring structure  One of the main issues of interest for future research is the inherent hierarchical structure in the interactions under consideration. These are not independent of each other, since there are the following inclusions:

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Regulation
  Inhibition  Activation
     Requirement  Binding
    Transcription
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So for example, each interaction of type Transcription is also of type Binding, and Regulation. This structure implicates additional knowledge about the output space, and we can use this to our benefit when constructing our classifier. In our initial framework, we make use of local classifiers, and hence do not leverage this additional knowledge about type structure. We have already started exploring the design of techniques that can exploit this structure, and preliminary results are promising.

One thing we wish to underline in this process is the need for an evaluation procedure that is as aware of the present structures as the classifier. For instance, a system that predicts a Binding interaction to be of type Regulation, is more precise than a system that identifies it as an Inhibition. Both for internal as external performance comparison, we feel this differentiation could broaden the focus towards a more knowledge-driven approach of evaluating.

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