A Graph-Search Framework for GeneId Ranking
(Extended Abstract)

William W. Cohen
Machine Learning Department
Carnegie Mellon University
Pittsburgh PA 15213
wcohen@cs.cmu.edu

1 Introduction

One step in the curation process is geneId finding—the task of finding the database identifier of every gene discussed in an article. GenelId-finding was studied experimentally in the BioCreatIvE challenge (Hirschman et al., 2005), which developed testbed problems for each of three model organisms (yeast, mice, and fruitflies). Here we consider geneId ranking, a relaxation of geneId-finding in which the system provides a ranked list of genes that might be discussed by the document. We show how multiple named entity recognition (NER) methods can be combined into a single high-performance geneId-ranking system.

2 Methods and Results

We focused on the mouse dataset, which was the hardest for the BioCreatIvE participants. This dataset consists of several parts. The gene synonym list consists of 183,142 synonyms for 52,594 genes; the training data consists of 100 mouse-relevant Medline abstracts, associated with the MGI geneId’s for those genes that are mentioned in the abstract; the evaluation data consists of an additional 50 mouse-relevant Medline abstracts, also associated with the MGI geneId’s as above; the test data consists of an additional 250 mouse-relevant Medline abstracts, again associated with MGI geneId’s; finally the historical data consists of 5000 mouse-relevant Medline abstracts, each of which is associated with the MGI geneId’s for all genes which are (a) associated with the article according to the MGI database, and (b) mentioned in the abstract, as determined by an automated procedure based on the gene synonym list.\(^1\) We also annotated the evaluation-data for NER evaluation.

We used two closely related gene-protein NER systems in our experiments, both trained using Minorthird (Min, 2004) on the YAPEX corpus (Franzén et al., 2002). The likely-protein extractor was designed to have high precision and lower recall, and the possible-protein extractor was designed to have high recall and lower precision. As shown in Table 1, the likely-protein extractor performs well on the YAPEX test set, but neither system performs well on the mouse evaluation data—here, they perform only comparably to exact matching against the synonym dictionary. This performance drop is typical when learning-based NER systems are tested on data from a statistical distribution different from their training set.

As a baseline for genelId-ranking, we used a string similarity metric called soft TFIDF, as implemented in the SecondString open-source software package (Cohen and Ravikumar, 2003), and soft-matched extracted gene names against the synonym list. Table 2 shows the mean average precision on the evaluation data. Note that the genelId ranker based on possible-protein performs statistically significantly better\(^2\) than the one based on likely-protein, even though possible-protein has a lower F score.

To combine these two NER systems, we represent all information as a labeled directed graph which in-

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1 The training data and evaluation data are subsets of the BioCreatIvE “devtest” set. The historical data was called “training data” in the BioCreatIvE publications. The test data is the same as the blind test set used in BioCreatIvE.

2 With \(z = 3.1, p > 0.995\) using a two-tailed paired test.
Table 1: Performance of the NER systems on the mouse evaluation corpus and the YAPEX test corpus.

|                      | Precis. | Recall | F   |
|----------------------|---------|--------|-----|
| mouse eval           |         |        |     |
| likely-protein       | 0.667   | 0.268  | 0.453|
| possible-protein     | 0.304   | 0.566  | 0.396|
| dictionary           | 0.245   | 0.439  | 0.314|
| YAPEX test           |         |        |     |
| likely-protein       | 0.872   | 0.621  | 0.725|
| YAPEX system         | 0.678   | 0.664  | 0.671|

Table 2: Mean average precision of several geneId-ranking methods on the 50 abstracts from the mouse evaluation dataset.

| mouse evaluation data | Mean Average Precision (MAP) |
|-----------------------|-----------------------------|
| likely-protein + softTFIDF | 0.450                       |
| possible-protein + softTFIDF | 0.626                       |
| graph-based ranking    | 0.513                       |
| + extra links          | 0.730                       |
| + extra links & learning | 0.807                       |

Figure 1: Part of a simplified version of the graph used for geneId ranking.

The graph includes the test abstracts, the extracted names, the synonym list, and the historical data. We then use proximity in a graph for ranking. The graph used is illustrated in Figure 1. Nodes in this graph can be either files, strings, terms, or user-defined types. Abstracts and gene synonyms are represented as file and string nodes, respectively. Files are linked to the terms (i.e., the words) that they contain, and terms are linked to the files that contain them.3 File nodes are also linked to string nodes corresponding to the output of an NER system on that file. (String nodes are simply short files.) The graph also contains geneId nodes and synonym string nodes created from the dictionary, and for each historical-data abstract, we include links to its associated geneId nodes.

Given this graph, gene identifiers for an abstract are generated by traversing the graph away from the abstract node, and looking for geneId nodes that are “close” to the abstract according to a certain proximity measure for nodes. Similarity between two nodes is defined by a lazy walk process, similar to PageRank with decay. The details of this are described in the full paper and elsewhere (Minkov et al., 2006). Intuitively, however, this measures the similarity of two nodes by the weighted sum of all paths that connect the nodes, where shorter paths will be weighted exponentially higher than longer paths. One consequence of this measure is that information associated with paths like the one on the left-hand side of the graph—which represents a soft-match between a likely-protein and a synonym—can be reinforced by other types of paths, like the one on the right-hand side of the figure.

As shown in Table 2, the graph-based approach has performance intermediate between the two baseline systems. However, the baseline approaches include some information which is not available in the graph, e.g., the softTFIDF distances, and the implicit knowledge of the “importance” of paths from an abstract to a synonym via an NER-extracted string. To include this information, we inserted extra edges labeled proteinToSynonym between the extracted protein strings x and comparable synonyms y, and also “short-cut” edges in the graph that directly link abstracts x to geneId nodes reachable via one of the “important” paths described above.

As Table 2 shows, graph search with the augmented graph does indeed improve MAP performance on the mouse evaluation data: performance is better than the simple graph, and also better than...
Table 3: Mean average precision of several geneId-ranking methods on the 250 abstracts from the mouse test dataset.

| Method                        | MAP  | Avg  | Max F |
|-------------------------------|------|------|-------|
| likely-prot + softTFIDF       | 0.368| 0.421|       |
| possible-prot + softTFIDF     | 0.611| 0.672|       |
| graph-based ranking           | 0.640| 0.695|       |
| + extra links & learning      | 0.711| 0.755|       |

In the most natural manner, the F-measure performance of an NER systems does not correlate well with MAP of the geneId-ranker based on it: rather, the NER system with higher recall, but lower overall performance, has significantly better performance when used for geneId-ranking.

We also present a graph-based scheme for combining NER systems, which allows many types of information to be combined. Combining this system with learning produces performance much better than either NER system can achieve alone. On average, 68% of the correct proteins will be found in the top two elements of the list, 84% will be found in the top five elements, and more than 90% will be found in the top ten elements. This level of performance is probably good enough to be of use in curation.

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4For instance, the test-set abstracts contain somewhat more proteins on average (2.2 proteins/abstract) than the evaluation-set abstracts (1.7 proteins/abstract).