Homework #2 report
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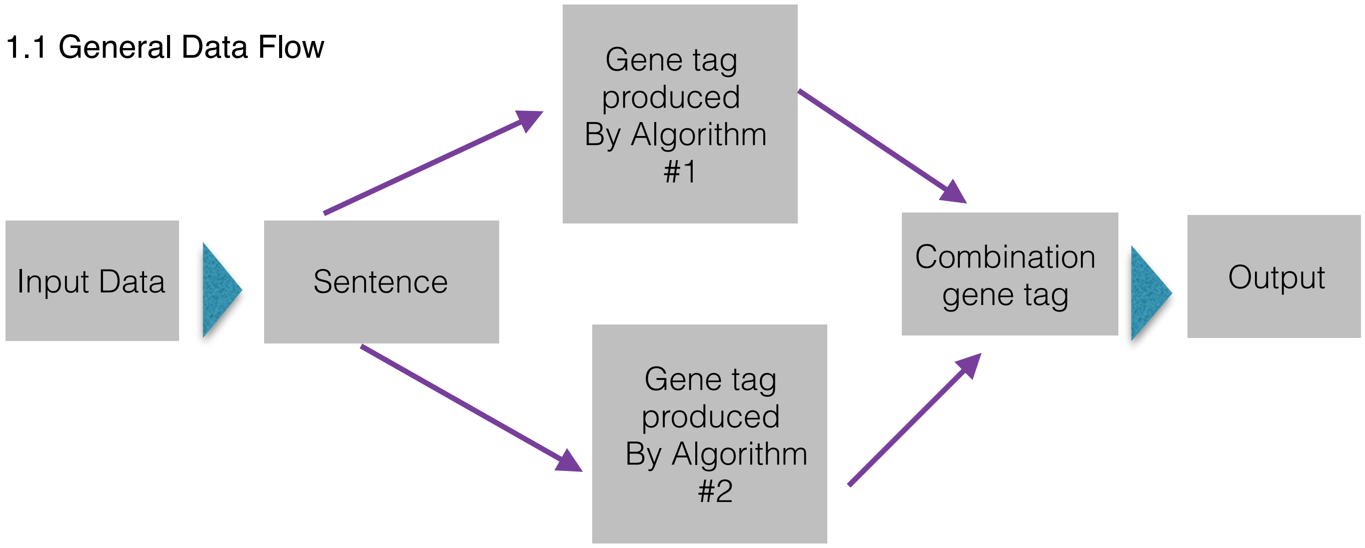
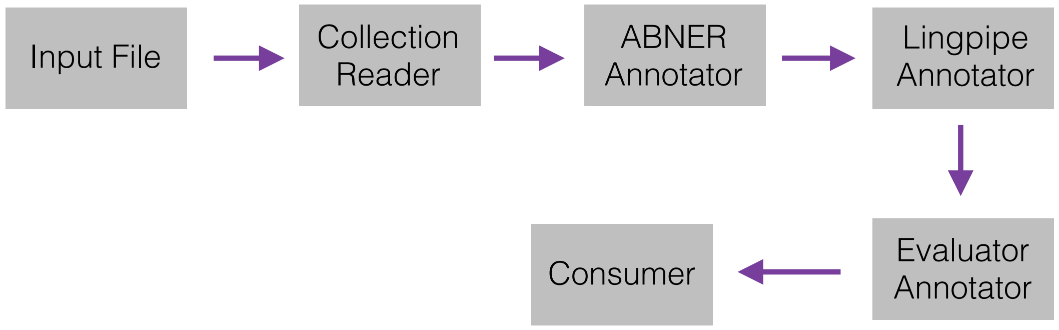
1. Logical Structure

1.1 General Data Flow


Input Data
Sentence
Gene tag produced By Algorithm #1
Gene tag produced By Algorithm #2
Combination gene tag
Output

Step 1: Read input file line by line and save by sentence annotation
Step 2: Process sentence annotations by two different NER model separately
Step 3: Evaluate the results of two models and combination them
Step 4: transfer combination gene tag to output format

1.2 NER Pipeline Design



1.3 Type Systems

GeneAnnotation. This annotation is inherited from edu.cmu.deiis.types.Annotation. It inherits casProcessID and Confidence features. And I also add two more features: entity and sentenceID. These GeneAnnotation is used in the main part of NER system. CasProcessID feature is for distinguish gene tag produced by different models. And Confidence is used to save lingpipe' confidence. Entity is for gene tag itself and sentenceID is for the sentence to which gene tag links.

SentenceAnnotation. This annotation is used for transforming original raw data into two parts (e.g. sentence id and sentence content). These annotation is not only provided to NER models to process, it also takes part in final output processing.

ABNERAnnotation (Not used). This annotation was mainly to save the intermediate result which was produced by ABNER.

LingpipeAnnotation (Not used) . This annotation was mainly to save the intermediate result which was produced by Lingpipe. This annotation was in charge of saving position, confidence and text of gene tag produced by lingpipe.

SDGeneEntity. Once SentenceAnnotation has been processed by ABNER and lingpipe. I will combine these two models' solution space based confidence. Some model specific gene tag may be dropped in this step.

1.4 Annotators

SDABNERAnnotator. This annotator utilizes ABNER, a Biomedical Named Entity Recognizer. ABNER's core is consist of statistical machine learning algorithms. Version 1.5 includes two models trained on the NLPBA and BioCreative corpora, respectively[1].

SDGeneAnnotator. This annotator utilizes lingpipe. Lingpipe has been trained by a new corpus and it turns out that this retrained model is reliable. As a two main model in my system, the output of lingpipe is very essential to final output. I use the confidence model which could be used in the flowing annotator to compare effectiveness of different models.

SDEvaluatorAnnotator. I use a few strategies in this annotator in order to measure correctness of output of two annotators above. Details will be discussed below.

2. Algorithms

2.1 Comparison strategy one

Since I use two models in my NER system, I should use some strategies to compare the output of these two models and expect a better final output. There are a few common strategies in comparison step. For example, if two models returns the same word, the we can compare their confidence. If confidences are both high, this word could be considered as a correct output. Such strategy is based on return confidence of models.

However, I have a challenge that ABNER doesn't produce a confidence for each gene tag it marks. This fact makes strategies above no longer available. In order to solve this problem, I make up with a strategy by which I can combine non-confidential and confidential data.

My strategy:

a) For a specific sentence, if ABNER and lingpipe mark the same gene tag. I think this is a strong confidence.
b) For a specific sentence, if lingpipe mark a gene tag but ABNER does not. I consider this is a suspicion, so I need to double check confidence of this gene tag. If lingpipe gives a confidence which is greater than my threshold, I think this tag should be correct. (I will discuss how to set this threshold in the following section)

[1] ABNER home page: http://pages.cs.wisc.edu/~bsettles/abner/

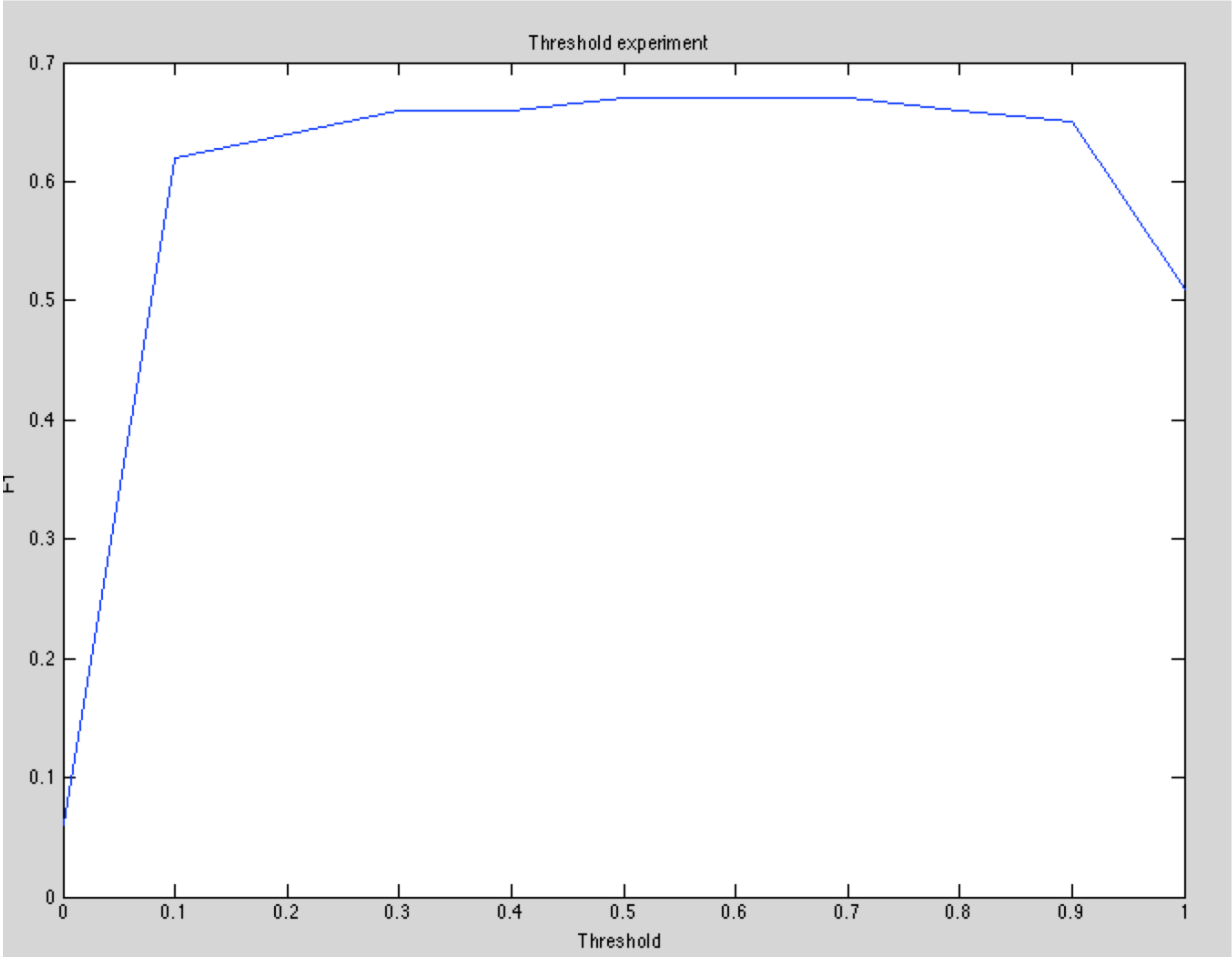
c) For a specific sentence, if ABNER mark a gene tag but lingpipe does not. I consider this is not a strong confidence. So I give this tag up.

2.2 How to decide threshold of Lingpipe

In order to decide what is the optimal threshold of Lingpipe, I made experiments in which I kept changing the threshold and observed precision, recall and F1 scores.

Threshold Experiments Record

Lingpipe Threshold	0.0	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1.0
Presicion	0.03	0.48	0.51	0.53	0.54	0.55	0.56	0.56	0.57	0.56	0.49
Recall	0.95	0.89	0.87	0.87	0.85	0.84	0.83	0.82	0.80	0.77	0.53
F1	0.06	0.62	0.64	0.66	0.66	0.67	0.67	0.67	0.66	0.65	0.51



From figure I conclude that the optimal value of threshold should be in range [0.4, 0.6]. So I finally use 0.6 in my program.

2.3 Comparison Strategy Two

Homework writeup mentions a vote strategy, which says giving confidence to all output of models. If a model does not return confidence, assign confidence to output manually. Here is my version:

a) For a specific sentence, if ABNER mark a gene tag, set a given confidence.
b) For a specific sentence, if ABNER and lingpipe mark the same gene tag, sum their confidence. If ABNER mark a tag but lingpipe does not, return confidence of ABNER. Similarly, if lingpipe mark a tag but ABNER does not, return confidence of lingpipe.

I tried to utilize this strategy but I was stopped by a problem. What confidence should I set manually for ABNER, and what evidence could support my choice?

It is really hard to choose this value. Of course I could test different values and to see which is best. However, it is a very difficult experiment because not only I need to consider the confidence of ABNER, I also need to adjust vote strategy every time I reset that value. Eventually, I gave this approach up.

2.3 Comparison Strategy Three

This strategy is the one I eventually use. The key core of this idea is still how to deal with the relationship with a non-confidential model and a confidential model.

As mentioned above, It is unreasonable to set a confidence to ABNER. So I decide to use a new idea, that is to combine rules and confidence.

There is what it is:

a) For a specific sentence, if ABNER marks a gene tag, I use rules to judge if this is a valid tag. For instance, a tag cannot contain a comma. So if ABNER return a tag which has commas, I drop it.
b) For a specific sentence, if Lingpipe makes a gene tag, I use a threshold to judge if this is a valid tag. If the confidence returned is less than 0.6, then drop it.
c) Finally, I do a union of these two output.

The reason I think this is a good idea is that It uses different approaches to filter those unbelievable results of two different models, and these filtering strategy make sense. On the one hand, this comparison could improve Recall, because it combines results of two models, on the another hand, this comparison could improve Recision, because it filters bad tags.