COMP90049 Project 2 Report: Identifying Tweets with Adverse Drug Reactions

1. Introduction

This project is aiming to assess on the performance of some supervised machine learning methods to determining whether a tweeter contains an ADR (Adverse Drug Reactions). By finding one or more non-word unigram features and generating the new train ARFF file and dev ARFF file, the quality of the newly found features could be judged using weka machine learning tool.

2. Dataset

The train, develop and test data provided from the teachers is from Twitter, and is an altered form of a dataset from the DIEGO Lab (Gonzalez, 2015).
In this project, the programs were implemented in Java and used some data from some websites, including Wikipedia and Medscape. The detailed usage would be introduced in the following pages and has been cited in the readme file as well as the reference section.

3. Classifier Selection

The classifier used in this project is Naïve Bayes. Naive Bayes classifier is based on the Bayes' theorem with strong naive independence assumption between features, it is simple to build also fast to make decision, also is easy to scale to large data size(Verspoor, 2017). By using the Naïve Bayes classifier embedded in the Weka tool, the classiffication process is accomplished accordingly.

4. Methodology and evaluation explanation

4.1. Methodology

As indicated in the specification, the main task is to find one or more new attributes and evaluate the performance. The whole logic was accomplished in the following three steps.

a. Generate new features.

The new features need to be non-word unigram, because the best 92 tokens which were selected by their frequencies has been selected and listed in the ARFF files, therefore there is no need to select features using the token frequency again.

The aim of the feature is to distinguish sentences that contain ADR from those not. By viewing the given TXT files, there is a common regularity for those sentences that labelled with 'Yes', that is they mostly contain one specific body part, or contain a kind of bad symptom, or contain a name of a medicine, or contains more than one of these elements. Therefore in this project, the firstly selected features are:

- isBodyPart: Whether body part is occured in the tweet
- isDrugName: Whether drug name is occured in the tweet
- isSymptom: Whether one symptom is occured in the tweet.

After firstly extracting these three profound features, the next step is to evaluate them and combine them to form a new feature then evaluate. The detailed process would be illustrated in the result section.

b. Update the train and dev files.

In this step, the new found features would be added into the train ARFF file and the dev ARFF file. Then the reduced VSM over the tweets need to be updated to adapt the new features.

This step is implemented in Java. The train ARFF file updating process is listed as the following steps and the dev ARFF file updating is in the same process.

i. Set three Arraylists(BodyParts, DrugName and Symptom) to store the word lists for judging whether one tweet could express this feature. The elements for body parts were extracted from http://www.enchantedlearning.com/wordlist/body.shtml, the drug names were found in http://www.medscape.com/viewarticle/825053 which indicates the top 100 saled drugs, the symptom word list is found in wekipedia.

ii. Read attributes from train.arff, write the header and attribute lines to the new ARFF file. Append new attributes behind.

iii. Read and update the VSM to the new ARFF file. Since the attributes are whether the attributes are expressed in the tweet, if the tweet contains one element of the Arraylist then the value is 'Y', otherwise 'N'.

By completing the three steps could these three attributes updated to the new train ARFF file and dev ARFF file.

c. Evaluate using Weka

Weka could help to train the model and analyse

the performance. . The evaluation result contains the number and rate of the Correctly Classified Instances and Incorrectly Classified Instances, and the detailed accuracy data including TP rate, FP rate, precision, recall, F-measure and so on for class N and class Y separately. The confusion matrix would also displayed to indicate the differences between the expectation and reality circumstance.

4.2. **Evaluation**

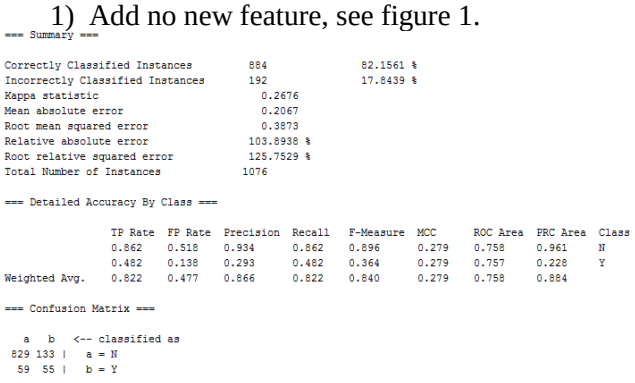
To assess whether the new features could improve the performance, one of the evaluation index is the correct rate. However in the given train.txt file, there are only 373 tweets that labelled with “Y” from 3166 tweets, the percentage of the class ‘Y’ and class ‘N’ are not balance so the accuracy is highly affected by the performance of class ‘N’.

Therefore the accuracy is insufficient to describe the performance, the precision for the two class are important as well. The TP rate is the true positive rate which value is the same with the recall rate, it could judge the performance of hit the correct class.

5. **Result**

By executing the Java programs and assessing the output ARFF files using Weka, the result for each features is list as the following captures.

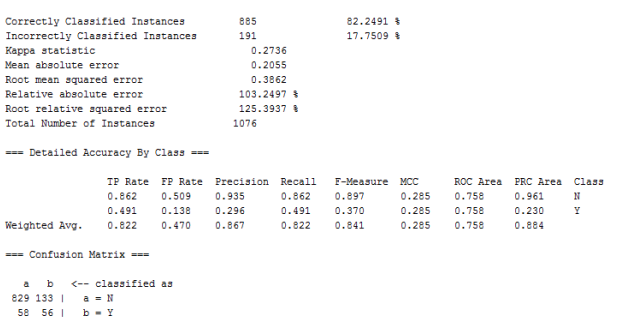
1) Add no new feature, see figure 1.



```
=== Summary ===

Correctly Classified Instances         884               82.1561 %
Incorrectly Classified Instances       192               17.8439 %
Kappa statistic                          0.2676
Mean absolute error                      0.2067
Root mean squared error                  0.3873
Relative absolute error                103.8938 %
Root relative squared error            125.7529 %
Total Number of Instances             1076

=== Detailed Accuracy By Class ===

               TP Rate   FP Rate   Precision   Recall  F-Measure  MCC      ROC Area  PRC Area  Class
                 0.862    0.518    0.934      0.862    0.896      0.279    0.758     0.961     N
                 0.482    0.138    0.293      0.482    0.364      0.279    0.757     0.228     Y
Weighted Avg.    0.822    0.477    0.866      0.822    0.840      0.279    0.758     0.884

=== Confusion Matrix ===

   a   b   <-- classified as
 829 133 |   a = N
  59  55 |   b = Y
```

Figure 1

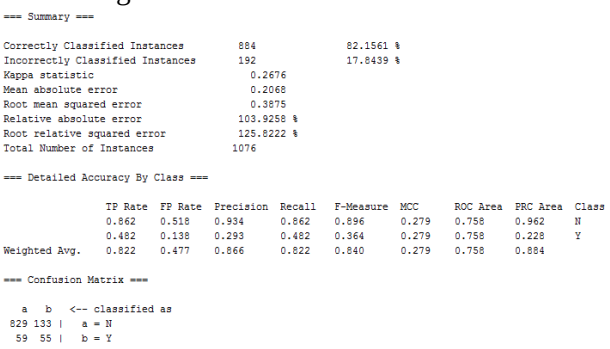
2)Only add the isBodyPart feature, see figure 2.



```
=== Summary ===

Correctly Classified Instances         885               82.2491 %
Incorrectly Classified Instances       191               17.7509 %
Kappa statistic                          0.2736
Mean absolute error                      0.2055
Root mean squared error                  0.3862
Relative absolute error                103.2497 %
Root relative squared error            125.3937 %
Total Number of Instances             1076

=== Detailed Accuracy By Class ===

               TP Rate   FP Rate   Precision   Recall  F-Measure  MCC      ROC Area  PRC Area  Class
                 0.862    0.509    0.935      0.862    0.897      0.285    0.758     0.961     N
                 0.491    0.138    0.296      0.491    0.370      0.285    0.758     0.230     Y
Weighted Avg.    0.822    0.470    0.867      0.822    0.841      0.285    0.758     0.884

=== Confusion Matrix ===

   a   b   <-- classified as
 829 133 |   a = N
  58  56 |   b = Y
```

Figure 2

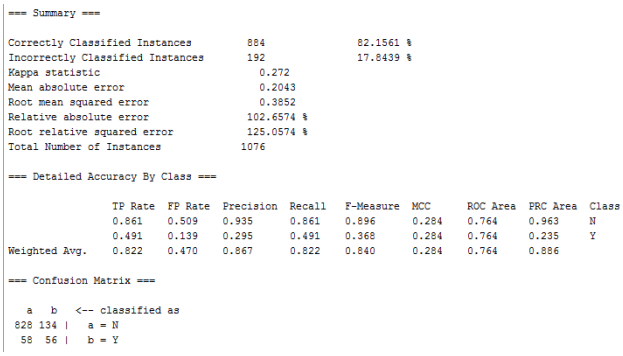
3) Only add the isDrugName feature, see figure 3.



```
=== Summary ===

Correctly Classified Instances         884               82.1561 %
Incorrectly Classified Instances       192               17.8439 %
Kappa statistic                          0.2676
Mean absolute error                      0.2068
Root mean squared error                  0.3875
Relative absolute error                103.9258 %
Root relative squared error            125.8222 %
Total Number of Instances             1076

=== Detailed Accuracy By Class ===

               TP Rate   FP Rate   Precision   Recall  F-Measure  MCC      ROC Area  PRC Area  Class
                 0.862    0.518    0.934      0.862    0.896      0.279    0.758     0.962     N
                 0.482    0.138    0.293      0.482    0.364      0.279    0.758     0.228     Y
Weighted Avg.    0.822    0.477    0.866      0.822    0.840      0.279    0.758     0.884

=== Confusion Matrix ===

   a   b   <-- classified as
 829 133 |   a = N
  59  55 |   b = Y
```

Figure 3

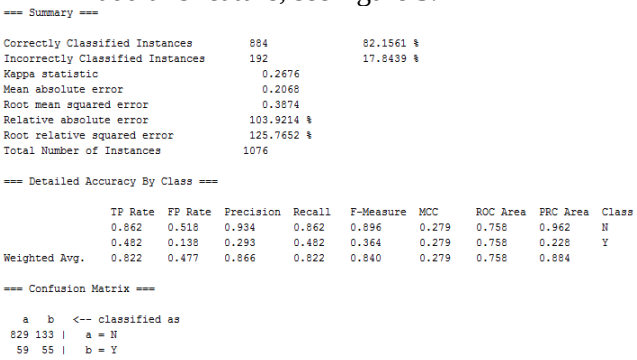
4) Only add the isSymptom feature, see figure 4.



```
=== Summary ===

Correctly Classified Instances         884               82.1561 %
Incorrectly Classified Instances       192               17.8439 %
Kappa statistic                          0.272
Mean absolute error                      0.2043
Root mean squared error                  0.3852
Relative absolute error                102.6574 %
Root relative squared error            125.0574 %
Total Number of Instances             1076

=== Detailed Accuracy By Class ===

               TP Rate   FP Rate   Precision   Recall  F-Measure  MCC      ROC Area  PRC Area  Class
                 0.861    0.509    0.935      0.861    0.896      0.284    0.764     0.963     N
                 0.491    0.139    0.295      0.491    0.368      0.284    0.764     0.235     Y
Weighted Avg.    0.822    0.470    0.867      0.822    0.840      0.284    0.764     0.886

=== Confusion Matrix ===

   a   b   <-- classified as
 828 134 |   a = N
  58  56 |   b = Y
```

Figure 4

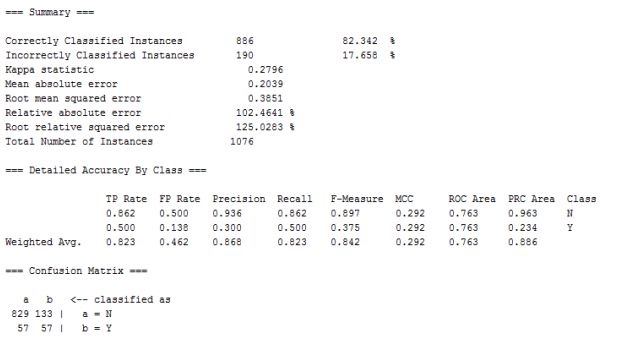
5) Combine isBody and isDrugName feature to the new isBody_Drug feature and only add this feature, see figure 5.



```
=== Summary ===

Correctly Classified Instances         884               82.1561 %
Incorrectly Classified Instances       192               17.8439 %
Kappa statistic                          0.2676
Mean absolute error                      0.2068
Root mean squared error                  0.3874
Relative absolute error                103.9214 %
Root relative squared error            125.7652 %
Total Number of Instances             1076

=== Detailed Accuracy By Class ===

               TP Rate   FP Rate   Precision   Recall  F-Measure  MCC      ROC Area  PRC Area  Class
                 0.862    0.518    0.934      0.862    0.896      0.279    0.758     0.962     N
                 0.482    0.138    0.293      0.482    0.364      0.279    0.758     0.228     Y
Weighted Avg.    0.822    0.477    0.866      0.822    0.840      0.279    0.758     0.884

=== Confusion Matrix ===

   a   b   <-- classified as
 829 133 |   a = N
  59  55 |   b = Y
```

Figure 5

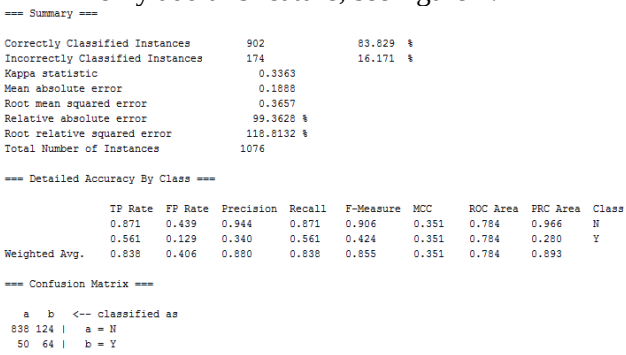
6) Combine isBody and isSymptom feature to the new isBody_Symp feature and only add this feature, see figure 6.



```
=== Summary ===

Correctly Classified Instances         886               82.342  %
Incorrectly Classified Instances       190               17.658  %
Kappa statistic                          0.2796
Mean absolute error                      0.2039
Root mean squared error                  0.3851
Relative absolute error                102.4641 %
Root relative squared error            125.0283 %
Total Number of Instances             1076

=== Detailed Accuracy By Class ===

               TP Rate  FP Rate  Precision  Recall   F-Measure  MCC      ROC Area  PRC Area  Class
               0.862    0.500    0.936      0.862    0.897      0.292    0.763     0.963     N
               0.500    0.138    0.300      0.500    0.375      0.292    0.763     0.234     Y
Weighted Avg.  0.823    0.462    0.868      0.823    0.842      0.292    0.763     0.886

=== Confusion Matrix ===

   a   b   <-- classified as
 829 133 |   a = N
  57  57 |   b = Y
```

Figure 6

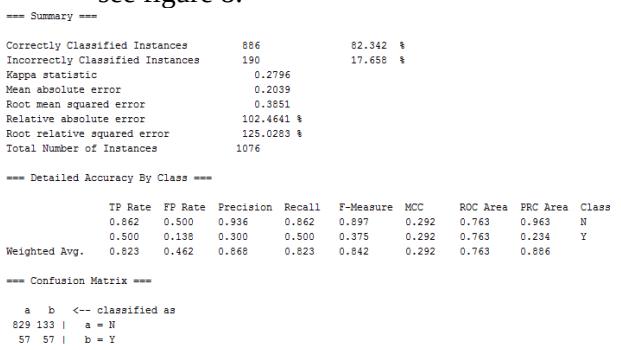
7) Combine isDrugName and isSymptom feature to the isDrug_Symp feature and only add this feature, see figure 7.



```
=== Summary ===

Correctly Classified Instances         902               83.829  %
Incorrectly Classified Instances       174               16.171  %
Kappa statistic                          0.3363
Mean absolute error                      0.1888
Root mean squared error                  0.3657
Relative absolute error                 99.3628 %
Root relative squared error            118.8132 %
Total Number of Instances             1076

=== Detailed Accuracy By Class ===

               TP Rate  FP Rate  Precision  Recall   F-Measure  MCC      ROC Area  PRC Area  Class
               0.871    0.439    0.944      0.871    0.906      0.351    0.784     0.966     N
               0.561    0.129    0.340      0.561    0.424      0.351    0.784     0.280     Y
Weighted Avg.  0.838    0.406    0.880      0.838    0.855      0.351    0.784     0.893

=== Confusion Matrix ===

   a   b   <-- classified as
 838 124 |   a = N
  50  64 |   b = Y
```

Figure 7

8) Combine all these three features to the is_All feature and only add this feature, see figure 8.



```
=== Summary ===

Correctly Classified Instances         886               82.342  %
Incorrectly Classified Instances       190               17.658  %
Kappa statistic                          0.2796
Mean absolute error                      0.2039
Root mean squared error                  0.3851
Relative absolute error                102.4641 %
Root relative squared error            125.0283 %
Total Number of Instances             1076

=== Detailed Accuracy By Class ===

               TP Rate  FP Rate  Precision  Recall   F-Measure  MCC      ROC Area  PRC Area  Class
               0.862    0.500    0.936      0.862    0.897      0.292    0.763     0.963     N
               0.500    0.138    0.300      0.500    0.375      0.292    0.763     0.234     Y
Weighted Avg.  0.823    0.462    0.868      0.823    0.842      0.292    0.763     0.886

=== Confusion Matrix ===

   a   b   <-- classified as
 829 133 |   a = N
  57  57 |   b = Y
```

Figure 8

Compared with the origin dataset with the given 94 features, the performance did not improve apparently when single feature (isBodyPart, is DrugName, is Symptom) is added. The isBodyPart feature only added one correctly classified instance and improved TP Rate, precision and recall rate to a small degree. The isDrugName feature has no influence. The isSymptom feature only improved the TP Rate, precision and recall rate for class Y for a small extend.

When single features were combined as a new one and added to the origin features, the performance is overall improved except the combination of isBodyName and isDrugName feature. The best one is the isDrug_Symp feature, which added 16 correctly classified instances and improved the TP Rate, precision and recall rate for both Class N and class Y in a larger extend.

6. Evaluation

6.1. Result Evaluation

From the summarization above, we could find three features:

- Single attributes did not improve the performance well.
- Combining two single attributes to one overall improved the performance, especially the combination of isDrugName and isSymptom.
- Combining three attributes to one improved the performance while not as good as the combination of isDrugName and isSymptom.

The reasons that might lead to this result could be listed as followed.

- Judging whether the tweet has the single feature is inaccurate because of the list for attribute judging is not full scaled. For instance, the drug name list only contains the top 100 sold medicines which is insufficient to cover all drugs. So the judge itself could be incorrect.
- The vector space contains about nighty five columns for the attributes, the value of one dimension is not able to impact on the whole result if its classification performance not good enough.
- The combination of isDrugName and is isSymptom could distinguish the classification better than other combination, because this relation is more close to the ADR. If a tweet contains at least one drug name and symptom, it is more likely to contain ADR.
- The reason why combining all three attributes did not perform so well might arise in the occurrence of the body part, which means the body part feature less related to the classification as the drug name collated with the symptom name.

6.2.Critical analysis

The tweets which contain ADR are more likely to express the bad emotion, which could be used as another feature. The sentiment analysis could be considered to be used in this case. During the implementation, the textblob lib in Python was used however the polarity for most tweets were 0

since the model has not been trained. Thus the method was not used here.

7. Conclusions

This report introduced some new features and their combination for the Weka machine learning tool to classify whether a tweet contains ADR, and researched on their influence on the system's performance with the help of Weka. The feature that whether the drug name and symptom occurred in the tweet has the best performance, which could be resulted from the close relationship between it and the ADR.

References

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