University of New Haven

TAGLIATELA COLLEGE OF ENGINEERING

ECECS Department

DSCI 6670 Artificial Intelligence
Final Project

Cancer Diagnosis using Machine Learning

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Introduction

It’s safe to say there are too many manual processes in medicine. The lab values, diagnoses, and other chart notes had to be written on paper. We always knew this was an area in which technology could help improve the workflow and hoped it would also improve patient care. Since then, advancements in electronical medical records have been remarkable, but the information they provide is not much better than the old paper charts they replaced. If technology is to improve care in the future, then the electronic information provided to doctors needs to be enhanced by the power of analytics and machine learning.

Project Motivation

The field of the medicine has developed with lots of data accumulation. Especially with the upcoming of advanced algorithms regularly, the field of AI has become a “pioneer” in achieving accuracy at “human levels”. We use some tools of Machine learning and Deep learning to try and diagnose the classes of cancer by reading **“clinical literature”** which are reviewed and tailored by researchers and scientists from the field.

Data

The data that we have gathered is from a Kaggle competition - Personalized Medicine: Redefining Cancer Treatment. The data is collectively gathered from 4 files

- training_variants - a comma separated file containing the description of the genetic mutations used for training. Fields are ID (the id of the row used to link the mutation to the clinical evidence), Gene (the gene where this genetic mutation is located), Variation (the aminoacid change for this mutations), Class (1-9 the class this genetic mutation has been classified on)
- training_text - a double pipe (||) delimited file that contains the clinical evidence (text) used to classify genetic mutations. Fields are ID(the id of the row used to link the clinical evidence to the genetic mutation), Text (the clinical evidence used to classify the genetic mutation)
- test_variants - a comma separated file containing the description of the genetic mutations used for training. Fields are ID (the id of the row used to link the mutation to the clinical evidence), Gene (the gene where this genetic mutation is located), Variation (the aminoacid change for this mutations)
- test_text - a double pipe (||) delimited file that contains the clinical evidence (text) used to classify genetic mutations. Fields are ID(the id of the row used to link the clinical evidence to the genetic mutation), Text (the clinical evidence used to classify the genetic mutation)

Data Preprocessing

Since we are going to be dealing with text data, we first need to clean it by replacing every special character with space, multiple spaces with space, converting all characters with into lower case and remove the **stopwords** from our data using **Natural Language Toolkit** package. We look for empty rows in the **text** column and fill it by concatenating the corresponding row values of **Gene** and **Variation**. Then we split the data into **70%** train data and **30%** test data.

Average Word2Vec

Term Frequency – Inverse Document Frequency is a numerical statistic that is intended to reflect how important a word is to a document in a collection or **corpus.** It is often used as a weighting factor in searches of information retrieval, text mining, and user modeling.

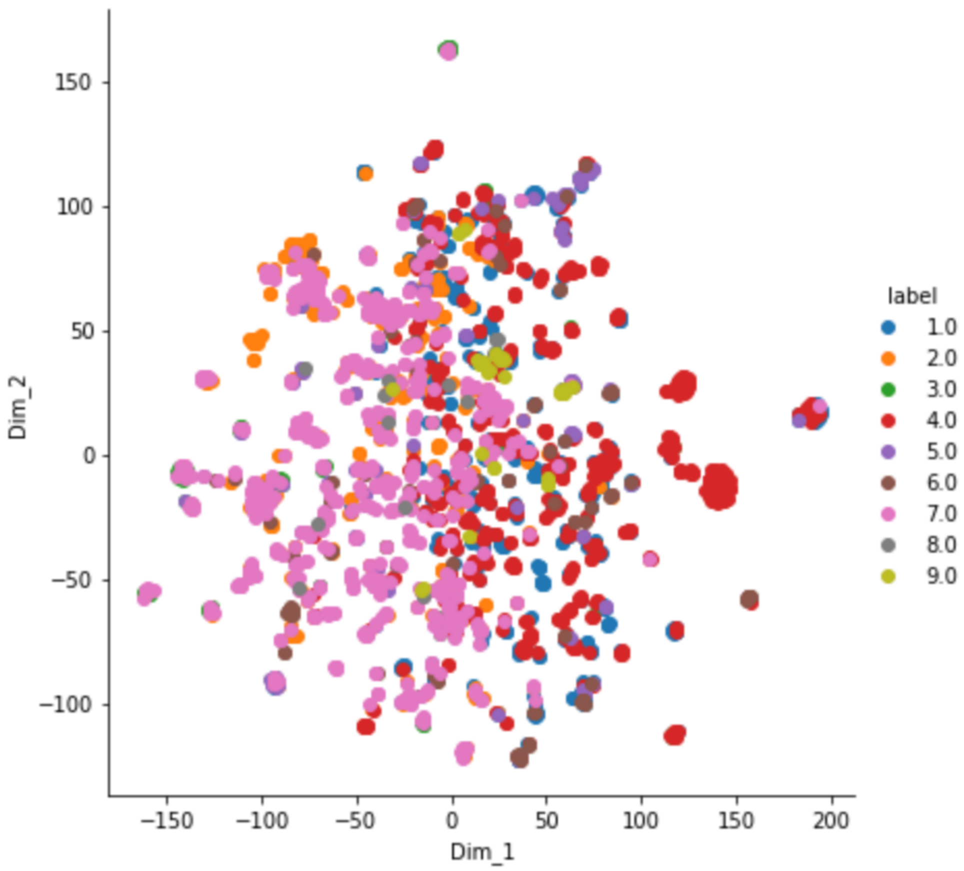
The tf-idf weighted value for word t in document d thus combines term frequency tf with idf:

$$\mathrm{tf}_{t,d} = \log_{10}(\mathrm{count}(t,d)+1)$$

$$\mathrm{idf}_t = \log_{10}\left(\frac{N}{\mathrm{df}_t}\right)$$

$$w_{t,d} = \mathrm{tf}_{t,d} \times \mathrm{idf}_t$$

t-Distributed Stochastic Neighbor Embedding (t-SNE) is a technique for dimensionality reduction that is particularly well suited for the visualization of high - dimensional datasets. We use t-SNE to plot our **y_train** and get the following plot.



Machine Learning Models

We are going to be using 3 classifying Machine learning models for our project.

1. Support Vector Machine with **Linear Kernel**
2. Support Vector Machine with **Radial Basis Function Kernel**
3. **Multinomial** Naïve Bayes Classifier

GridSearchCV

Grid Search is the process of performing hyperparameter tuning in order to determine the optimal values for a given model. As mentioned above, the performance of a model significantly depends on the value of hyperparameters. Note that there is no way to know in advance the best values for hyperparameters so ideally, we need to try all possible values to know the optimal values. Doing this manually could take a considerable amount of time and resources and thus we use GridSearchCV to automate the tuning of hyperparameters.

Support Vector Machines

A SVM is a supervised learning model that uses classification algorithms for two-group classification problems. After giving an SVM model sets of labeled training data for each category, they're able to categorize new text.

“The objective of the support vector machine algorithm is to find a hyperplane in an N-dimensional space(N — the number of features) that distinctly classifies the data points.”

SVM with Linear Kernel

Linear Kernel is used when the data is Linearly separable, that is, it can be separated using a single Line. It is one of the most common kernels to be used. It is mostly used when there are a Large number of Features in a particular Data Set.

SVM with Radial Basis Function Kernel

RBF kernel is a function whose value depends on the distance from the origin or from some point. Gaussian Kernel is of the following format;

$$K(X_1, X_2) = exponent(-\gamma\|X_1 - X_2\|^2)$$

||X1 — X2 || = Euclidean distance between X1 & X2

Naïve Bayes Methods

A Naive Bayes classifier is a probabilistic machine learning model that’s used for classification task. The crux of the classifier is based on the Bayes theorem.

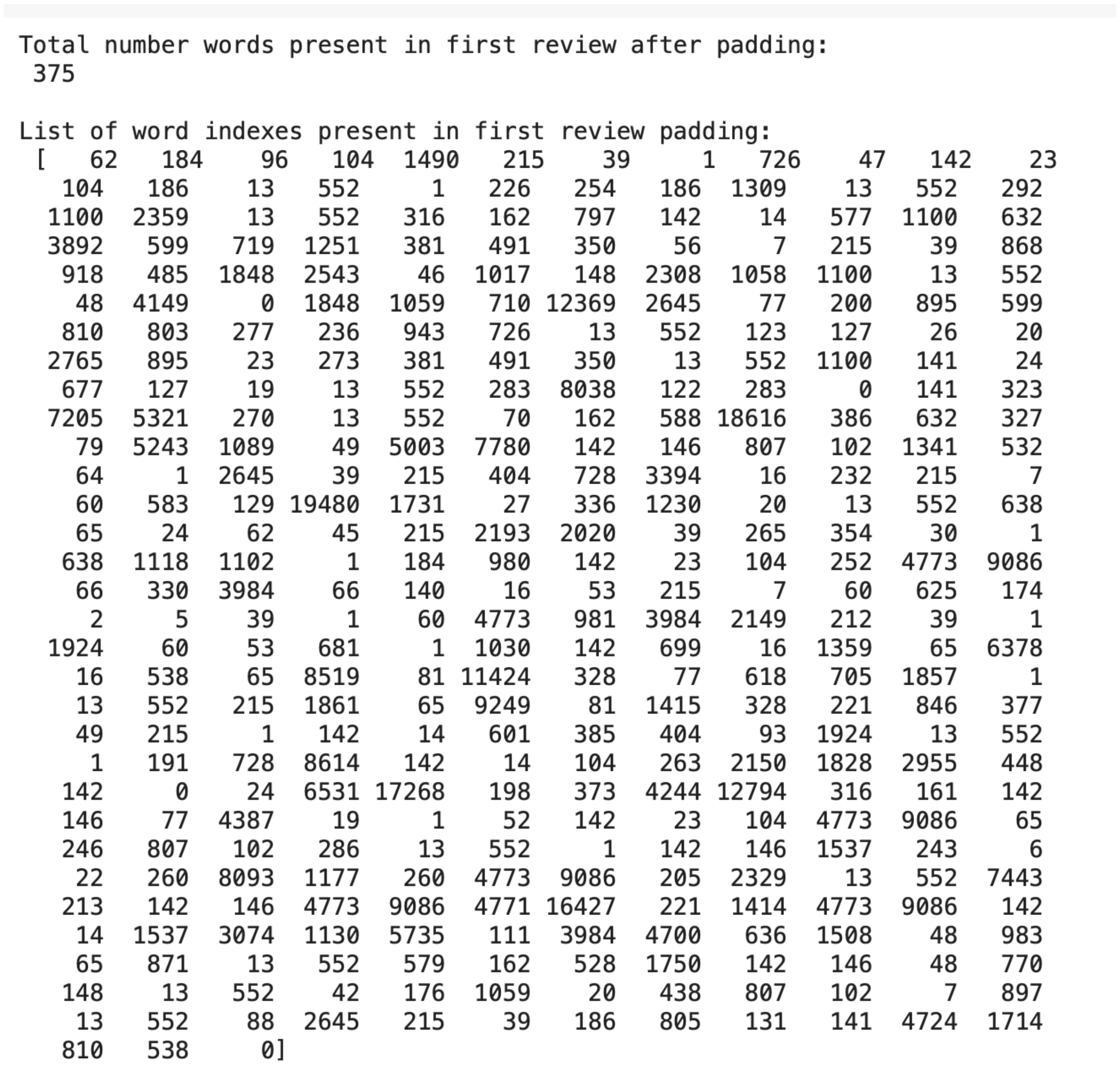
$$P(A|B) = \frac{P(B|A)P(A)}{P(B)}$$

Multinomial Naïve Bayes Classifier

Multinomial Naive Bayes is a specialized version of Naive Bayes that is designed more for text documents. Whereas simple naive Bayes would model a document as the presence and absence of particular words, multinomial naive bayes explicitly models the word counts and adjusts the underlying calculations to deal with in.

Data Preprocessing

We create a dictionary with words and their frequencies. We rank each words based on their frequency as word with highest frequency ranked 1 and lowest frequency ranked lowest. We then apply **padding** to make all the sentences of equal length. After applying ranking and padding our data would look like,



```
Total number words present in first review after padding:
 375

List of word indexes present in first review padding:
 [   62   184    96   104  1490   215    39     1   726    47   142    23
   104   186    13   552     1   226   254   186  1309    13   552   292
  1100  2359    13   552   316   162   797   142    14   577  1100   632
  3892   599   719  1251   381   491   350    56     7   215    39   868
   918   485  1848  2543    46  1017   148  2308  1058  1100    13   552
    48  4149     0  1848  1059   710 12369  2645    77   200   895   599
   810   803   277   236   943   726    13   552   123   127    26    20
  2765   895    23   273   381   491   350    13   552  1100   141    24
   677   127    19    13   552   283  8038   122   283     0   141   323
  7205  5321   270    13   552    70   162   588 18616   386   632   327
    79  5243  1089    49  5003  7780   142   146   807   102  1341   532
    64     1  2645    39   215   404   728  3394    16   232   215     7
    60   583   129 19480  1731    27   336  1230    20    13   552   638
    65    24    62    45   215  2193  2020    39   265   354    30     1
   638  1118  1102     1   184   980   142    23   104   252  4773  9086
    66   330  3984    66   140    16    53   215     7    60   625   174
     2     5    39     1    60  4773   981  3984  2149   212    39     1
  1924    60    53   681     1  1030   142   699    16  1359    65  6378
    16   538    65  8519    81 11424   328    77   618   705  1857     1
    13   552   215  1861    65  9249    81  1415   328   221   846   377
    49   215     1   142    14   601   385   404    93  1924    13   552
     1   191   728  8614   142    14   104   263  2150  1828  2955   448
   142     0    24  6531 17268   198   373  4244 12794   316   161   142
   146    77  4387    19     1    52   142    23   104  4773  9086    65
   246   807   102   286    13   552     1   142   146  1537   243     6
    22   260  8093  1177   260  4773  9086   205  2329    13   552  7443
   213   142   146  4773  9086  4771 16427   221  1414  4773  9086   142
    14  1537  3074  1130  5735   111  3984  4700   636  1508    48   983
    65   871    13   552   579   162   528  1750   142   146    48   770
   148    13   552    42   176  1059    20   438   807   102     7   897
    13   552    88  2645   215    39   186   805   131   141  4724  1714
   810   538     0]
```

The above figure is the first review with words replaced by their corresponding ranks and the **0** at last shows that we used zeroes to pad the sequence.

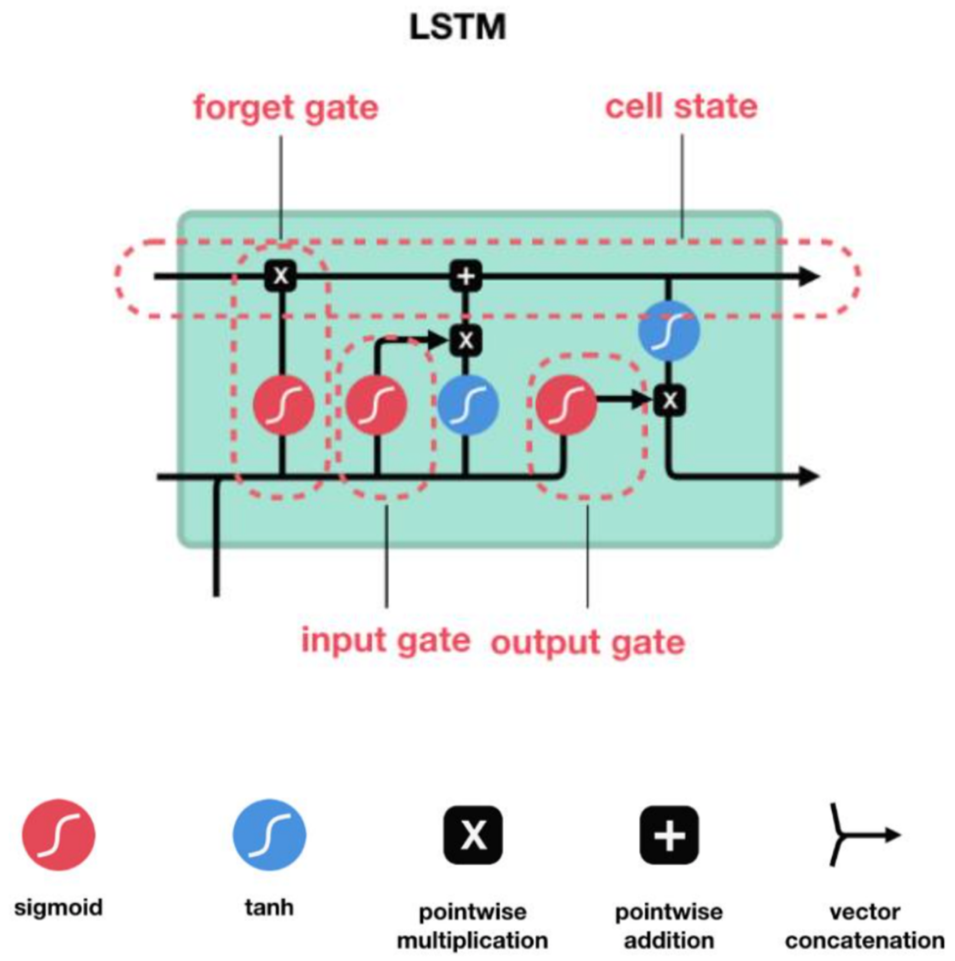
Deep Learning Models

We are going to be using 2 Deep Learning models,

1. Long Short -Term Memory
2. Bidirectional RNN with GRU

Long Short-Term Memory

The core concept of LSTM’s is the cell state, and its various gates. The cell state act as a transport highway that transfers relative information all the way down the sequence chain. You can think of it as the “memory” of the network. The cell state, in theory, can carry relevant information throughout the processing of the sequence. So even information from the earlier time steps can make its way to later time steps, reducing the effects of short-term memory. As the cell state goes on its journey, information gets added or removed to the cell state via gates. The gates are different neural networks that decide which information is allowed on the cell state. The gates can learn what information is relevant to keep or forget during training.



Bidirectional RNN with GRU

If we want to have a mechanism in RNNs that offers comparable look-ahead ability as in hidden Markov models, we need to modify the RNN design. Instead of running an RNN only in the forward mode starting from the first token, we start another one from the last token running from back to front. *Bidirectional RNNs* add a hidden layer that passes information in a backward direction to more flexibly process such information.

Bidirectional RNN are really just putting two independent RNNs together. The input sequence is fed in normal time order for one network, and in reverse time order for another. The outputs of the two networks are usually concatenated at each time step.

With a Gated Recurrent Unit (GRU), an Update gate is introduced, to decide whether to pass previous output to next cell or not. In other words, it decides what information to throw away and what new information to add.

Results

From the models' architecture and processed data, we can see that **Bidirectional RNN with GRU** has provided the best performance with log loss of 0.3762.

Models	Log-Loss
Linear SVM	1.313
SVM – RBF Kernel	0.697
Naïve Bayes	1.122
LSTM	0.541
Bidirectional RNN	0.3762

Conclusion

We have tried the simplest of models for text classification and we have achieved better performance. To improve this, we can try applying **Convolutional Markov Model, XLNet, Binary Partitioning Transformer (BPT)** etc..