

Configuration Manual

MSc Research Project Data Analytics

Ramyaa Rajasekar Student ID: x21122881

School of Computing National College of Ireland

Supervisor:

Qurrat Ul Ain

National College of Ireland Project Submission Sheet School of Computing



Student Name: Ramyaa Rajasekar				
Student ID:	x21122881			
Programme: Data Analytics				
Year: 2022-2023				
Module:	odule: MSc Research Project			
Supervisor:	upervisor: Qurrat Ul Ain			
Submission Due Date:	01/02/2023			
Project Title:	oject Title: Configuration Manual			
Word Count:	ord Count: 802			
Page Count:	9			

I hereby certify that the information contained in this (my submission) is information pertaining to research I conducted for this project. All information other than my own contribution will be fully referenced and listed in the relevant bibliography section at the rear of the project.

<u>ALL</u> internet material must be referenced in the bibliography section. Students are required to use the Referencing Standard specified in the report template. To use other author's written or electronic work is illegal (plagiarism) and may result in disciplinary action.

Signature:	Ramyaa Rajasekar
Date:	1st February 2023

PLEASE READ THE FOLLOWING INSTRUCTIONS AND CHECKLIST:

Attach a completed copy of this sheet to each project (including multiple copies).Attach a Moodle submission receipt of the online project submission, to
each project (including multiple copies).You must ensure that you retain a HARD COPY of the project, both for

your own reference and in case a project is lost or mislaid. It is not sufficient to keep a copy on computer.

Assignments that are submitted to the Programme Coordinator office must be placed into the assignment box located outside the office.

Office Use Only		
Signature:		
Date:		
Penalty Applied (if applicable):		

Configuration Manual

Ramyaa Rajasekar x21122881

1 Introduction

The motive of this paper is to outline the software requirements and provide an overview of the code artifacts implemented to achieve the objective of the research, in developing traditional machine learning, Ensemble Learning, and deep learning models with feature transformation and hyperparameter tuning to classify the gene variants using the clinical literature.

2 System Specifications

The project was implemented on a cloud platform Google Colab, which is well known for coding and executing machine learning and deep learning models by integrating tensor flow and Keras. The execution speed is increased compared to the CPU as it utilizes the GPU and TPU when required.

- Google Colab: Intel Xeon CPU @2.20 GHz
- RAM: 13 GB
- Disk Space: 78 GB
- Processor: Intel R Core (i5)
- System RAM: 16 GB
- Operating System: Windows 11 64 bit

2.1 Software Requirements

The programming language used to implement the classification approach is Python, as it is free and open source and has various integrated libraries which can be utilized for implementing NLP techniques, Word Embedding techniques, and Tenser flow and Keras versions for deep learning models.

3 Importing Python Libraries

One of the main advantages of the collab is, it is not required to install all the libraries during every session, it has multiple pre-installed libraries which can be directly imported such as numpy, panda, matplotlib, scikit-plot, gensim, nltk, and model building libraries.



Figure 1: Import Libraries

4 Loading the data

The data is categorized into different CSV files as Training and Testing Variants and Text files. As the text file is unstructured data, to reduce the time taken to load in the collab, have imported it from Google drive.



Figure 2: Loading the train and test data

4.1 Merging the Data

As the training set comprises gene variants and text files, it is required to merge it as a single data frame and proceed with the further process.

finaldf_train = df_train.merge(df_text, how="inner", left_on="ID", right_on="ID")
finaldf_train[finaldf_train["Class"]==1].head()

Figure 3: Merging the data

5 Exploratory Data Analysis

To understand Text Length distribution for each class

```
plt.figure(figsize=(15,9))
gene_count_grp = finaldf_train.groupby('Gene')["Text_Count"].sum().reset_index()
sns.violinplot(x="Class", y="Text_Count", data=finaldf_train, inner=None, color = 'blue')
sns.swarmplot(x="Class", y="Text_Count", data=finaldf_train, color="w", alpha=.5);
plt.ylabel('Text Count', fontsize=14)
plt.xlabel('Class', fontsize=14)
plt.title("Text length distribution", fontsize=18)
plt.show()
```

Analyse the class distribution

```
[] plt.figure(figsize=(12,8))
    sns.countplot(x="Class", data=finaldf_train, palette="copper")
    plt.ylabel('Frequency', fontsize=14)
    plt.xlabel('Class', fontsize=14)
    plt.title("Distribution of genetic mutation classes", fontsize=18)
    plt.show()
Analyse genes that has highest number of occurrences in each class.
```

```
[] finaldf_train=finaldf_train.reset_index()

[] fig, axs = plt.subplots(ncols=3, nrows=3, figsize=(15,15))

for i in range(3):
    for j in range(3):
        gene_count_grp = finaldf_train[finaldf_train["Class"]==((i*3+j)+1)].groupby('Gene')["ID"].count().reset_index()
        sorted_gene_group = gene_count_grp.sort_values('ID', ascending=False)
        sorted_gene_group_top_7 = sorted_gene_group[:7]
        sns.barplot(x="Gene", y="ID", data=sorted_gene_group_top_7, ax=axs[i][j])
```

Figure 4: Visualisation of data

Exploratory Data Analysis (EDA) was implemented to analyze the data and get pertinent knowledge about the gene variations and clinical text correlations.EDA is performed for the Text column to get insights about the distribution of text for every class, for the Gene column and assume which gene affects the individual and categorizes to more number cancer classes, for the class column to understand the number of samples available for each class and get insights about the data linearity.

6 Text Data Pre-processing

As the data chosen is in textual format, it is required to apply natural language processing techniques along with the handling of missing values which would upheld the modelbuilding process and performance.

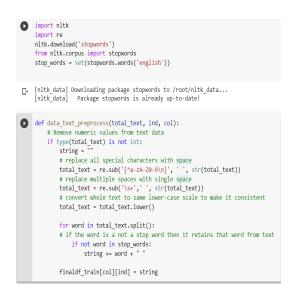
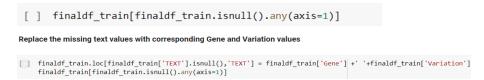


Figure 5: Pre-processing using NLP

Removal of Missing Values



7 Tranformation of Data using Embedding Technique

The word embedding technique utilized to transform the text into a numerical vector is Word2Vec by importing the genism library. This technique is applied for Gene and Variation column and visualization was performed with t-SNE and K means clustering to understand how the words are related and embedding has been performed.

To convert a document of multiple words into a single vector using our trained word2vec, we take the average or mean of the vectors of that sentence. A transformer (with a sklearn interface) is defined to convert a document into its corresponding vector.

8 Machine Learning and Deep Learning Models

Initially, The dataset was split into Train and Test split with an 80 to 20 ratio. For the purpose of model evaluation, the train set split is performed and with the best-performed model, the prediction was done on the test set provided. Following to that nine different models were built and compared before and after applying hyperparameter tuning where ever it was required. The models built are Logistic Regression, Random Forest, Support Vector Machine, K nearest neighbor, Gradient Boosting, Majority Voting Classifier, and Long Short Term memory (LSTM).

Training the word2vec model for Text column



mean_embedding_vectorizer = MeanEmbeddingVectorizer(w2vec)
mean_embedded_text = mean_embedding_vectorizer.fit_transform(finaldf_train['TEXT'])

- Logistic Regression

- [] from sklearn.linear_model import LogisticRegression
 #from sklearn.linear_model import LogisticRegression
 #log_model = LogisticRegression(solver='lbfgs', max_iter=1000)
 [] model = LogisticRegression(solver='lbfgs', max_iter=1000)
 - from sklearn.metrics import accuracy_score

from sklearn.metrics import precision_score,recall_score,f1_score

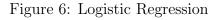
log=LogisticRegression(max_iter=1000)

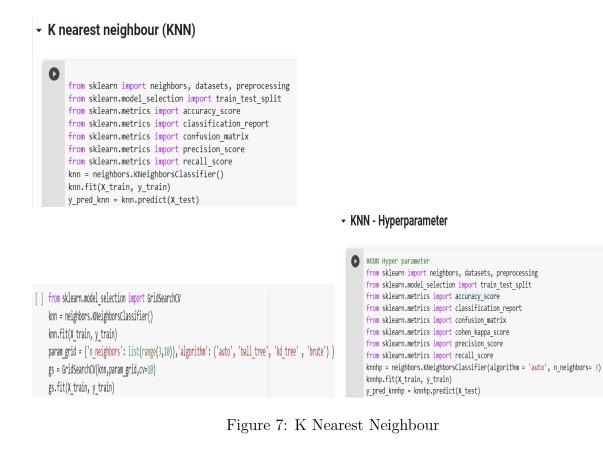
log.fit(X_train,y_train)

Y_predict_lr=log.predict(X_test)

Logistic Regression Hyperparameter







[]	<pre>[] #Hyperparameter tuning for SVM #Hypermater tuning for oversampled dATA from sklearn.swn import SVC from sklearn.swn import SVC rs = RandomizedSearchCV(SVC(gamma='auto'), {</pre>			
		•	SVM-Hyperparameter	
			<pre>[] from sklearn import svm SVM_modelhp = svm.SVC(kernel = 'rbf', C = 20, probability = True) SVM_modelhp.fit(X_train, y_train) y_predicted_SVMhp = SVM_modelhp.predict(X_test) accsvmh = round(accuracy_score(y_test,y_predicted_SVMhp),3)</pre>	

Figure 8: Support Vector Machine



<pre># build a RandomForestClassifier</pre>	
from scipy.stats import randint as sp_randint	
RF_CLF = RandomForestClassifier(n_estimators=20)	
<pre>param_dist = {"max_depth": [3, None],</pre>	
<pre>"max_features": sp_randint(1, 11),</pre>	
<pre>"min_samples_split": sp_randint(2, 11),</pre>	
<pre>"min_samples_leaf": sp_randint(1, 11),</pre>	
# "bootstrap": [True, False],	
"criterion": ["gini", "entropy"]}	
<pre>samples = 8 # number of random samples</pre>	
randomCV = RandomizedSearchCV(RF_CLF, param_distributions=param_dist, n_iter=sam	ples,cv=3)
randomCV.fit(X_train, y_train)	
<pre>print(randomCV.best_params_)</pre>	

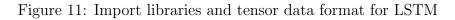
Majority Voting Classifier - Ensemble Approach (GB,RF,SVM)

[] from sklearn.ensemble import VotingClassifier

clf1 = GradientBoostingClassifier()
clf2 = RandomForestClassifier(bootstrap = False, criterion = 'entropy', max_depth = None, max_features = 5, min_samples_leaf = 4, min_samples_split = 6)
clf3 = svm.SVC(c=20, probability=True)
eclf1 = VotingClassifier(estimators=[('gbc', clf1), ('rf', clf2), ('svc', clf3)], voting='soft')
eclf1 = VotingClassifier(estimators=[('gbc', clf1), ('rf', clf2), ('svc', clf3)], voting='soft')
eclf1 = rotingClassifier(estimators=[('gbc', clf1), ('rf', clf2), ('svc', clf3)], voting='soft')
eclf1 = votingClassifier(estimators=[('gbc', clf1), ('rf', clf2), ('svc', clf3)], voting='soft')
eclf1 = votingClassifier(estimators=[('gbc', clf1), ('rf', clf2), ('svc', clf3)], voting='soft')
eclf1 = votingClassifier(estimators=[('gbc', clf1), ('rf', clf2), ('svc', clf3)], voting='soft')
eclf1 = votingClassifier(estimators=[('gbc', clf1), ('rf', clf2), ('svc', clf3)], voting='soft')
eclf1 = votingClassifier(estimators=[('gbc', clf1), axis=-1)
predictions = eclf1.predict(X_test)

Figure 10: Ensemble Classifier





[]	<pre>model = Sequential() model.add(Embedding(WAX_NB_WORDS, EMBEDDING_DIM, input_length=X.shape[1])) model.add(SpatialDropout1D(0.2)) #To avoid overfitting model.add(Longout=0.2, recurrent_dropout=0.2)) model.add(Dense(9, activation='softmax')) model.compile(loss='categorical_crossentropy', optimizer='adam', metrics=['accuracy']) epochs = 10</pre>
	batch_size = 64
	<pre>lstmmodel = model.fit(X_trainl, Y_trainl, epochs=epochs, batch_size=batch_size,validation_split=0.2) print(model.summary())</pre>

Figure 12: LSTM Model

9 Model Evaluation

The models which are implemented are evaluated using classification metrics such as Confusion Matrix, Accuracy, Precision, Recall, F1 Score and Log loss. As shown in figure 13 and 14, it was observed that the Voting Ensemble classifier and Random Forest gave the highest accuracy but the Ensemble has the minimal log loss and proves as best performed model.Whereas KNN and LSTM attained the least accuracy and KNN with the highest logloss, hence it is considered as a least performed model.

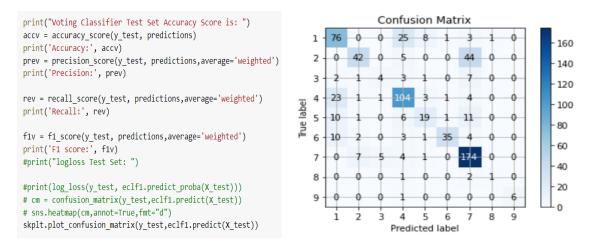
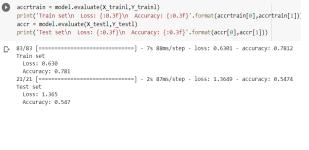
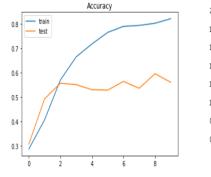


Figure 13: Evaluation of Ensemble Classifier





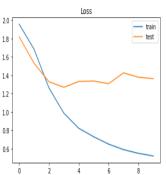


Figure 14: Evaluation of LSTM

10 Resuts

By comparing the model performance as shown in the figure 15, it is evident Ensemble classifier attained better accuracy with least mispredicted classes.

- Model Comparison Plot



