CPC251_Project_Part1_Anuran_3

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Anuran is any of the vertebrates of the order Anura, characterized by the absence of a tail and very long hind legs specialized for hopping: class Amphibia (amphibians), which is commonly known as the frogs and toads. Recently, recognition of anuran species through their calls has received a lot of attention because of its potential applicability in ecological studies.

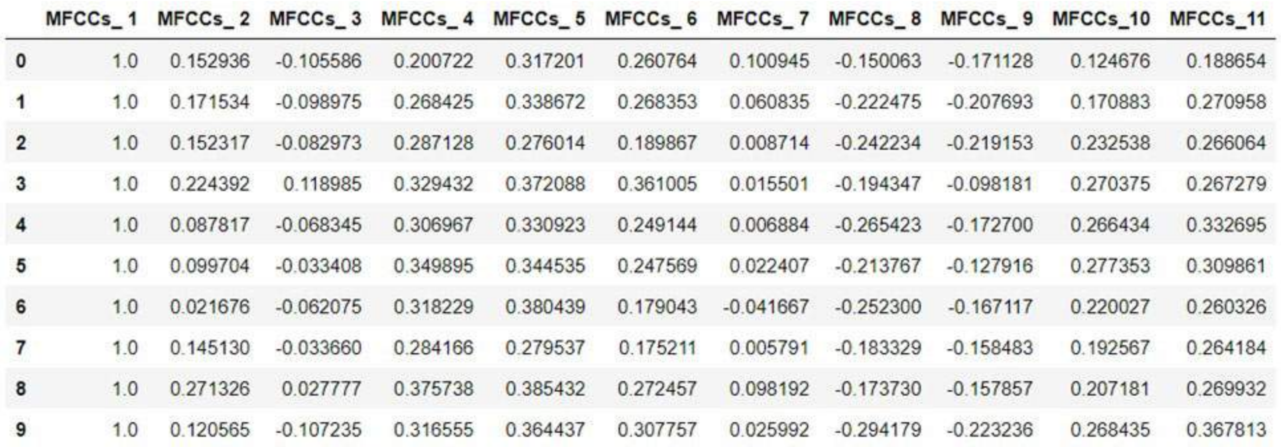
However, most of the recorded anuran species are considered to be monotypic based on various research presented. Hence, the classification of numerous anuran species would be a challenge for researchers.

Aim: To develop an interpretable and trustworthy predictive model that can classify various anuran species accurately and effectively.

In this project, we are using the given dataset about the Anuran species, to create two predictive models, to test and predict based on the dataset.

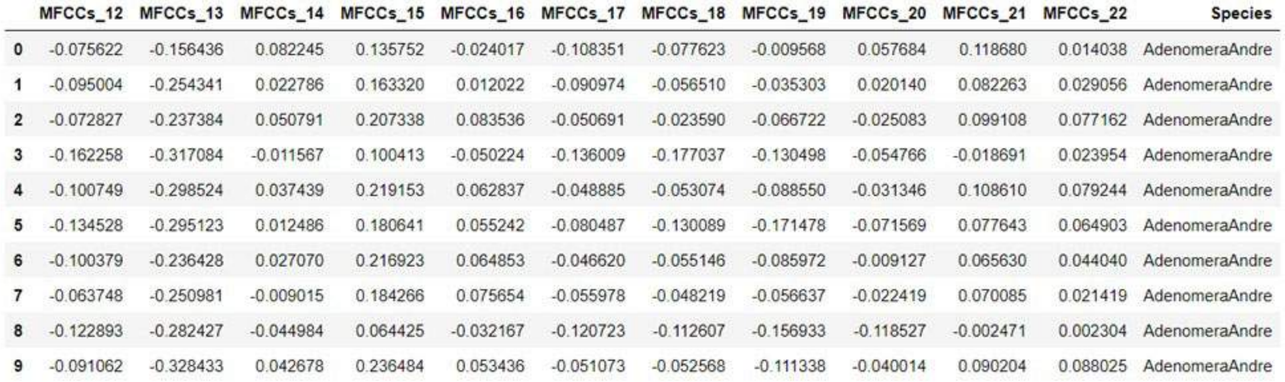
Data Description

The Anuran Species dataset is the dataset assigned to our group for project part 1. Based on the two tables below, we can notice that the dataset contains 22 columns of features and a single column of the target. There is not a very unique name for all the features, they only differ in terms of the numbering, which represents different animals without clarifying what the actual animal is. The target is the 'Species', in which we are expected to get the outcome of different types of Anuran species (10 different species).



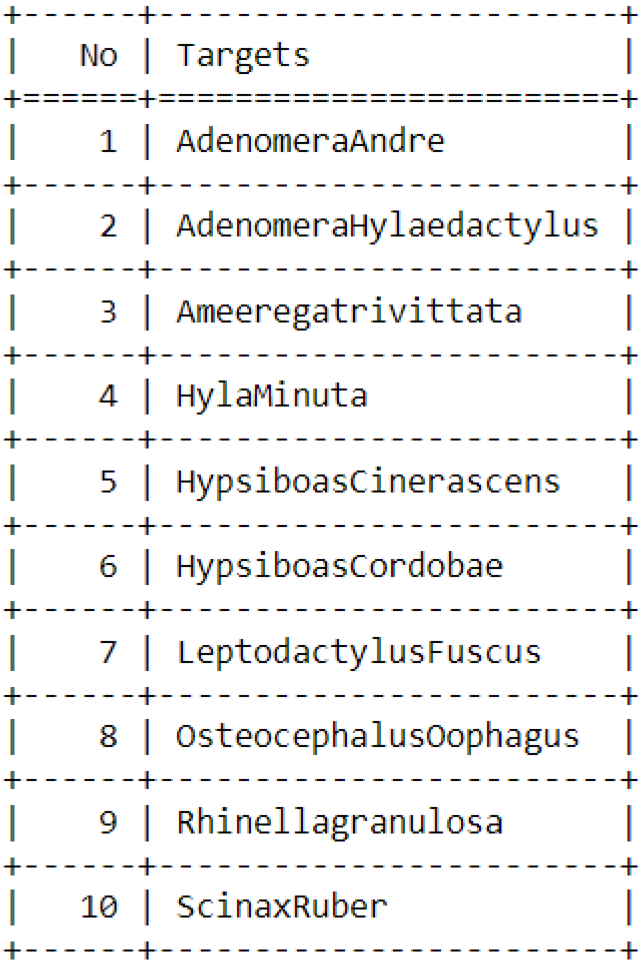
	MFCCs_ 1	MFCCs_ 2	MFCCs_ 3	MFCCs_ 4	MFCCs_ 5	MFCCs_ 6	MFCCs_ 7	MFCCs_ 8	MFCCs_ 9	MFCCs_10	MFCCs_11
0	1.0	0.152936	-0.105586	0.200722	0.317201	0.260764	0.100945	-0.150063	-0.171128	0.124676	0.188654
1	1.0	0.171534	-0.098975	0.268425	0.338672	0.268353	0.060835	-0.222475	-0.207693	0.170883	0.270958
2	1.0	0.152317	-0.082973	0.287128	0.276014	0.189867	0.008714	-0.242234	-0.219153	0.232538	0.266064
3	1.0	0.224392	0.118985	0.329432	0.372088	0.361005	0.015501	-0.194347	-0.098181	0.270375	0.267279
4	1.0	0.087817	-0.068345	0.306967	0.330923	0.249144	0.006884	-0.265423	-0.172700	0.266434	0.332695
5	1.0	0.099704	-0.033408	0.349895	0.344535	0.247569	0.022407	-0.213767	-0.127916	0.277353	0.309861
6	1.0	0.021676	-0.062075	0.318229	0.380439	0.179043	-0.041667	-0.252300	-0.167117	0.220027	0.260326
7	1.0	0.145130	-0.033660	0.284166	0.279537	0.175211	0.005791	-0.183329	-0.158483	0.192567	0.264184
8	1.0	0.271326	0.027777	0.375738	0.385432	0.272457	0.098192	-0.173730	-0.157857	0.207181	0.269932
9	1.0	0.120565	-0.107235	0.316555	0.364437	0.307757	0.025992	-0.294179	-0.223236	0.268435	0.367813

Table 1: Dataset sample 1



	MFCCs_12	MFCCs_13	MFCCs_14	MFCCs_15	MFCCs_16	MFCCs_17	MFCCs_18	MFCCs_19	MFCCs_20	MFCCs_21	MFCCs_22	Species
0	-0.075622	-0.156436	0.082245	0.135752	-0.024017	-0.108351	-0.077623	-0.009568	0.057684	0.118680	0.014038	AdenomeraAndre
1	-0.095004	-0.254341	0.022786	0.163320	0.012022	-0.090974	-0.056510	-0.035303	0.020140	0.082263	0.029056	AdenomeraAndre
2	-0.072827	-0.237384	0.050791	0.207338	0.083536	-0.050691	-0.023590	-0.066722	-0.025083	0.099108	0.077162	AdenomeraAndre
3	-0.162258	-0.317084	-0.011567	0.100413	-0.050224	-0.136009	-0.177037	-0.130498	-0.054766	-0.018691	0.023954	AdenomeraAndre
4	-0.100749	-0.298524	0.037439	0.219153	0.062837	-0.048885	-0.053074	-0.088550	-0.031346	0.108610	0.079244	AdenomeraAndre
5	-0.134528	-0.295123	0.012486	0.180641	0.055242	-0.080487	-0.130089	-0.171478	-0.071569	0.077643	0.064903	AdenomeraAndre
6	-0.100379	-0.236428	0.027070	0.216923	0.064853	-0.046620	-0.055146	-0.085972	-0.009127	0.065630	0.044040	AdenomeraAndre
7	-0.063748	-0.250981	-0.009015	0.184266	0.075654	-0.055978	-0.048219	-0.056637	-0.022419	0.070085	0.021419	AdenomeraAndre
8	-0.122893	-0.282427	-0.044984	0.064425	-0.032167	-0.120723	-0.112607	-0.156933	-0.118527	-0.002471	0.002304	AdenomeraAndre
9	-0.091062	-0.328433	0.042678	0.236484	0.053436	-0.051073	-0.052568	-0.111338	-0.040014	0.090204	0.088025	AdenomeraAndre

Table 2: Dataset sample 2



```
+------+------------------------+
|   No | Targets                |
+======+========================+
|    1 | AdenomeraAndre         |
+------+------------------------+
|    2 | AdenomeraHylaedactylus |
+------+------------------------+
|    3 | Ameeregatrivittata     |
+------+------------------------+
|    4 | HylaMinuta             |
+------+------------------------+
|    5 | HypsiboasCinerascens   |
+------+------------------------+
|    6 | HypsiboasCordobae      |
+------+------------------------+
|    7 | LeptodactylusFuscus    |
+------+------------------------+
|    8 | OsteocephalusOophagus  |
+------+------------------------+
|    9 | Rhinellagranulosa      |
+------+------------------------+
|   10 | ScinaxRuber            |
+------+------------------------+
```

Table 3: List of targets

Data analysis

Feature selection is the process of minimising the number of independent variables when building predictive models. In this project, the filter feature selection method is applied using a statistical measure in this Anuran Calls (MFCCs) dataset. Since this is a classification predictive modelling problem which contains numerical input variables and categorical output variables, the most relevant statistical measure of the filter method would be ANOVA. From the scikit-learn library, f_classif() (ANOVA F-test) is implemented to compute the ANOVA F-value and SelectKBest is used to select the top k variables. Also, data visualization technique such as the bar chart is applied to represent the relationship between MCFFs and the ANOVA f-value with vertical bars. Examples of the plotting are provided in Figure 1.

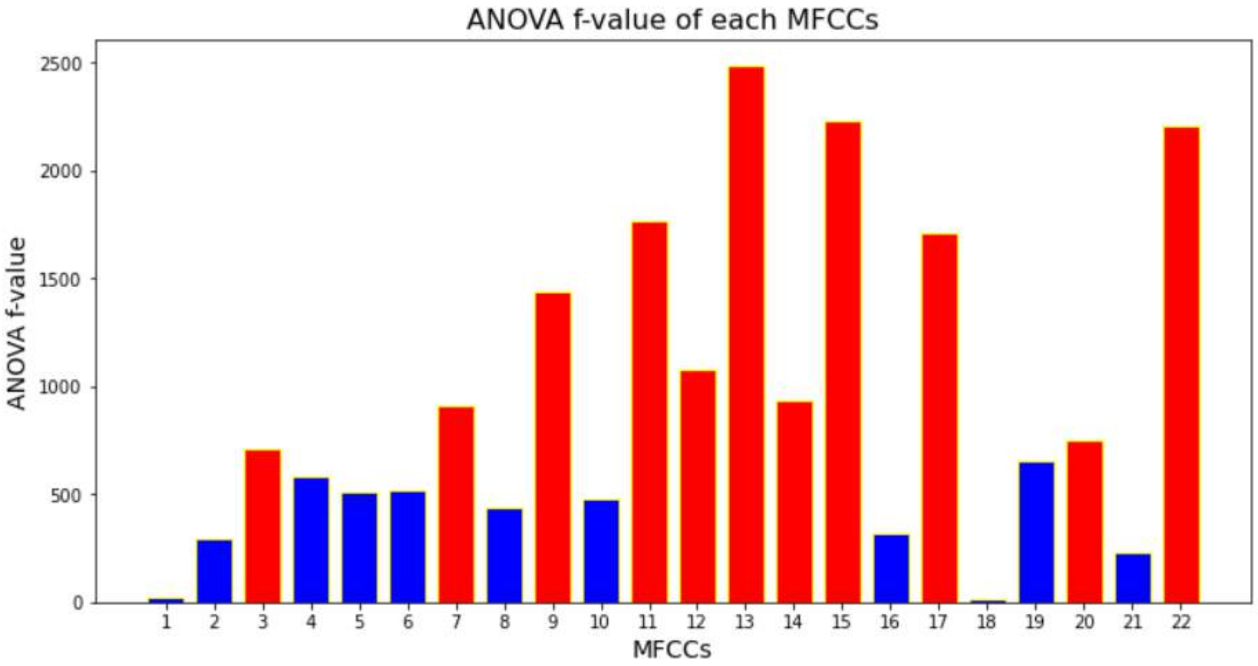


Figure 1: ANVOA f-value against MFCCs

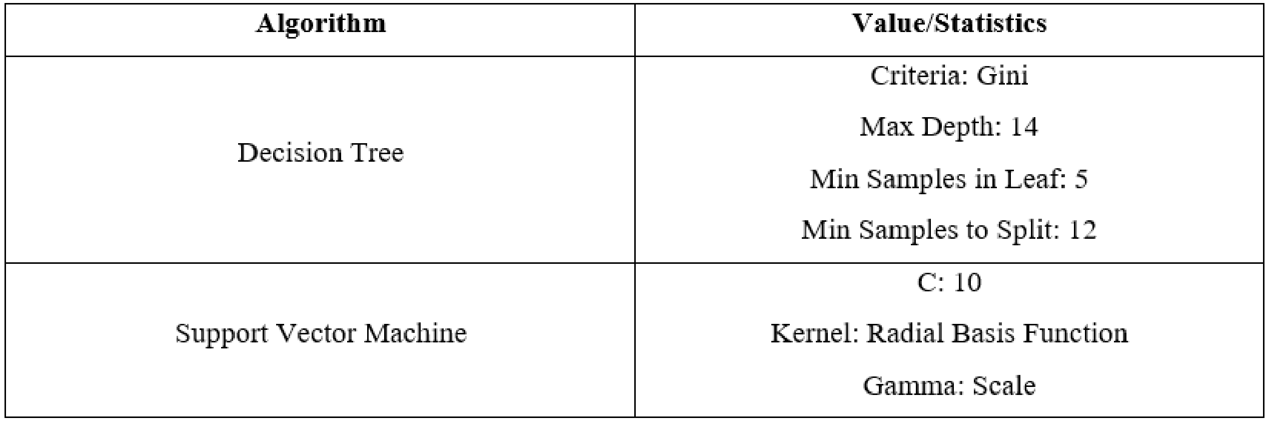
The high ANOVA f-value shows the high variation between sample means relative to the variation within the samples in order to reject the null hypothesis. Therefore, the top 11 features with the highest ANOVA f-value among the 22 features will be chosen. The reason for selecting 11 features out of 22 features is to reduce the computational cost and time of modelling as much as possible to produce a highly efficient implementation of the predictive model. Also, the probability of the overfitting problem is reduced to avoid misleading data. Hence, it can improve the performance of the predictive model by training the model faster using only the 11 significant features.

Feature	Type	Value/Statistics
MFCCs_3	Continuous numerical	Range: -0.436028 – 1.0 Mean: 0.311224 Std: 0.263527
MFCCs_7	Continuous numerical	Range: -0.538982 – 1.0 Mean: -0.001397 Std: 0.171404
MFCCs_9	Continuous numerical	Range: -0.587313 – 0.738033 Mean: 0.128213 Std: 0.179008
MFCCs_11	Continuous numerical	Range: -0.901989 – 0.523033 Mean: -0.115682 Std: 0.186792
MFCCs_12	Continuous numerical	Range: -0.799441 – 0.690889 Mean: 0.043371 Std: 0.155983
MFCCs_13	Continuous numerical	Range: -0.644116 – 0.94571 Mean: 0.150945 Std: 0.206880
MFCCs_14	Continuous numerical	Range: -0.59038 – 0.575749 Mean: -0.039244 Std: 0.152515
MFCCs_15	Continuous numerical	Range: -0.717156 – 0.668924 Mean: -0.101748 Std: 0.187618
MFCCs_17	Continuous numerical	Range: -0.42148 – 0.681157 Mean: 0.088680 Std: 0.138055
MFCCs_20	Continuous numerical	Range: -0.361649 – 0.467831 Mean: -0.053244 Std: 0.094181
MFCCs_22	Continuous numerical	Range: -0.379304 – 0.432207 Mean: 0.087567 Std: 0.123442

Table 4: The selected features

Data modeling

Two predictive models are built to predict the target variable of the Anuran Calls (MFCCs) dataset using Decision Tree and Support Vector Machine algorithms. The models are analysed using the hold-out approach, which separates the dataset into the training set and test set. The dataset splitting ratio is 80% training set and 20% test set. The parameters of the predictive models are provided in Table 5.



Algorithm	**Value/Statistics**
Decision Tree	Criteria: Gini Max Depth: 14 Min Samples in Leaf: 5 Min Samples to Split: 12
Support Vector Machine	C: 10 Kernel: Radial Basis Function Gamma: Scale

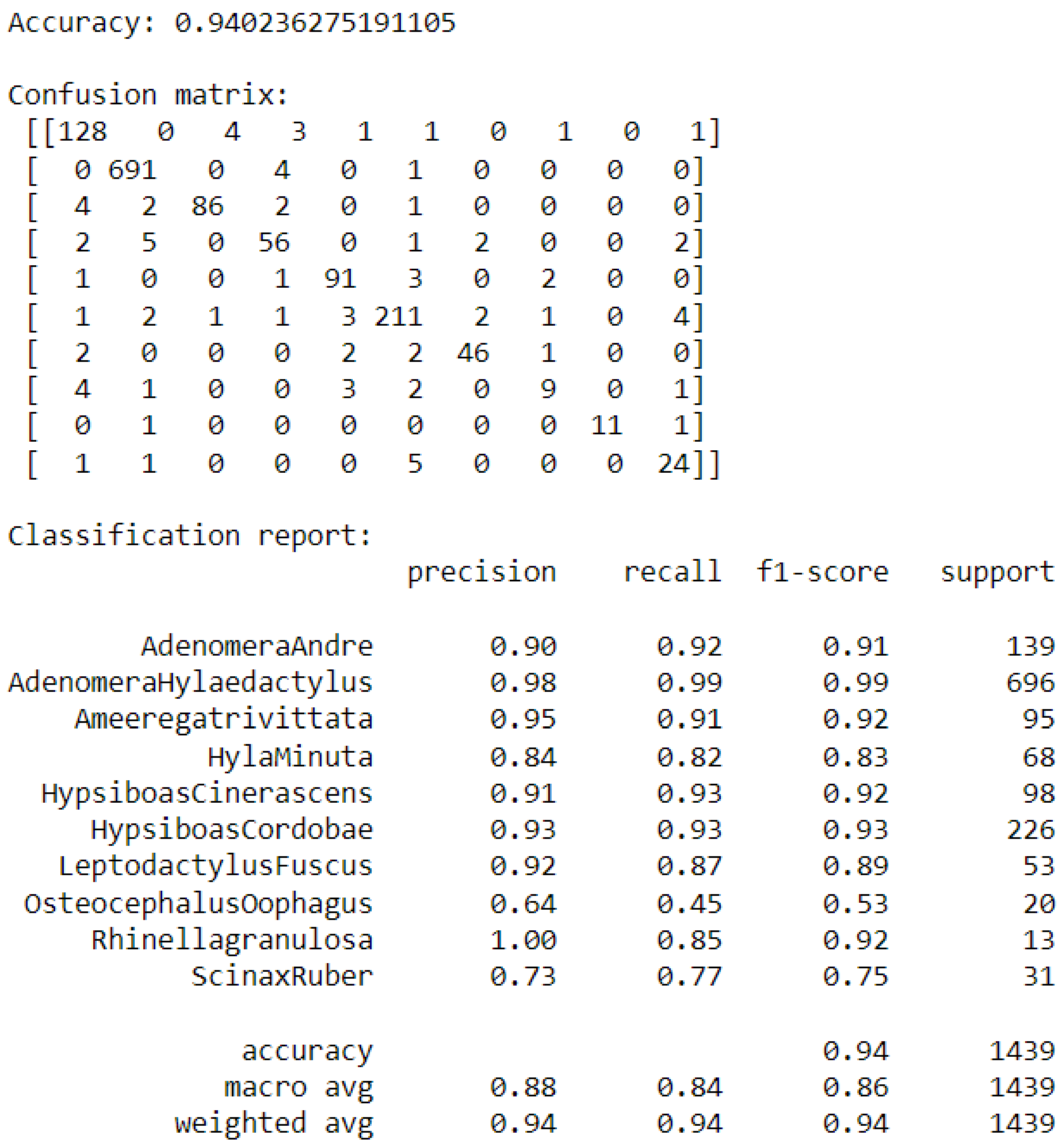
Table 5: Parameters of the predictive models

The parameter to tune in decision tree is max_depth, which means the maximum depth of the tree. Initially, the decision tree model is fit with depths ranging from 6 to 17. Then, the accuracy score of the training set is evaluated with different maximum depths of the tree. The accuracy score with the highest value is determined and the corresponding maximum depth of the tree is selected as the optimal parameter of the decision tree model.

On the other hand, the parameters to tune in support vector machine are the kernel function and the regularization (C). The support vector machine model is fitted with two different kernel functions which are radial basis function and sigmoid function. Also, the model is trained with different values of regularization. After that, GridSearchCV is implemented to find the best parameter values from the given set of the grid of the parameters. The best parameter results obtained will be used to train the support vector machine model.

Furthermore, the performance metrics are selected including accuracy, recall, precision, F1-score measures and the confusion matrix to evaluate the decision tree as well as support vector machine model so that the results can be clearly compared and the best suited predictive model can be identified accurately. The results of classification of anuran species using these 2 models are provided below.

Results of classification:



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Accuracy: 0.940236275191105

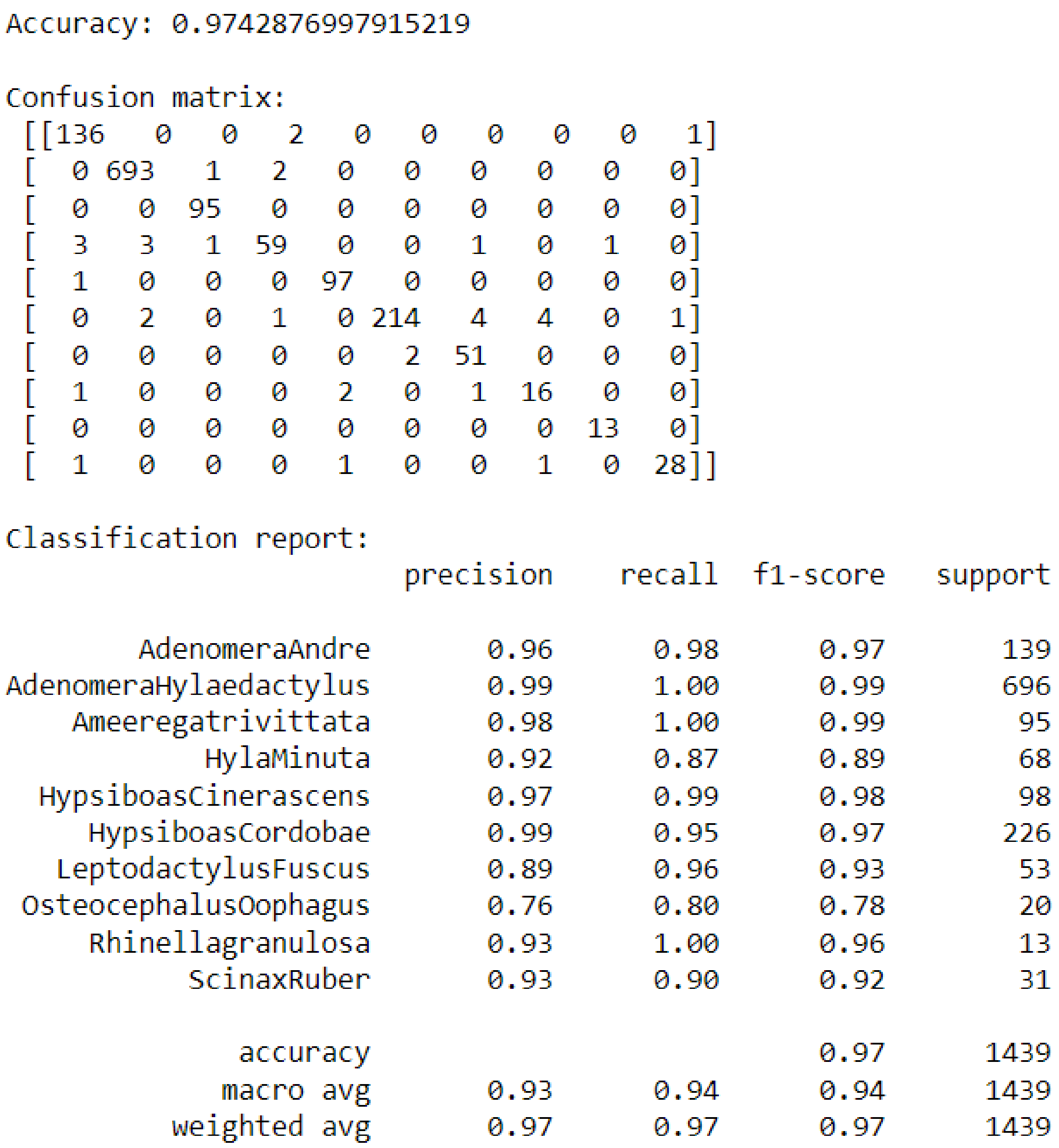
Confusion matrix:
 [[128   0   4   3   1   1   0   1   0   1]
 [  0 691   0   4   0   1   0   0   0   0]
 [  4   2  86   2   0   1   0   0   0   0]
 [  2   5   0  56   0   1   2   0   0   2]
 [  1   0   0   1  91   3   0   2   0   0]
 [  1   2   1   1   3 211   2   1   0   4]
 [  2   0   0   0   2   2  46   1   0   0]
 [  4   1   0   0   3   2   0   9   0   1]
 [  0   1   0   0   0   0   0   0  11   1]
 [  1   1   0   0   0   5   0   0   0  24]]

Classification report:
                        precision    recall  f1-score   support

        AdenomeraAndre       0.90      0.92      0.91       139
AdenomeraHylaedactylus       0.98      0.99      0.99       696
    Ameeregatrivittata       0.95      0.91      0.92        95
            HylaMinuta       0.84      0.82      0.83        68
  HypsiboasCinerascens       0.91      0.93      0.92        98
     HypsiboasCordobae       0.93      0.93      0.93       226
   LeptodactylusFuscus       0.92      0.87      0.89        53
 OsteocephalusOophagus       0.64      0.45      0.53        20
     Rhinellagranulosa       1.00      0.85      0.92        13
           ScinaxRuber       0.73      0.77      0.75        31

              accuracy                           0.94      1439
             macro avg       0.88      0.84      0.86      1439
          weighted avg       0.94      0.94      0.94      1439
```

Figure 2: Results of classification of anuran species using Decision Tree



```
Accuracy: 0.9742876997915219

Confusion matrix:
 [[136   0   0   2   0   0   0   0   0   1]
 [  0 693   1   2   0   0   0   0   0   0]
 [  0   0  95   0   0   0   0   0   0   0]
 [  3   3   1  59   0   0   1   0   1   0]
 [  1   0   0   0  97   0   0   0   0   0]
 [  0   2   0   1   0 214   4   4   0   1]
 [  0   0   0   0   0   2  51   0   0   0]
 [  1   0   0   0   2   0   1  16   0   0]
 [  0   0   0   0   0   0   0   0  13   0]
 [  1   0   0   0   1   0   0   1   0  28]]

Classification report:
                         precision    recall  f1-score   support

         AdenomeraAndre       0.96      0.98      0.97       139
 AdenomeraHylaedactylus       0.99      1.00      0.99       696
     Ameeregatrivittata       0.98      1.00      0.99        95
             HylaMinuta       0.92      0.87      0.89        68
   HypsiboasCinerascens       0.97      0.99      0.98        98
      HypsiboasCordobae       0.99      0.95      0.97       226
    LeptodactylusFuscus       0.89      0.96      0.93        53
  OsteocephalusOophagus       0.76      0.80      0.78        20
      Rhinellagranulosa       0.93      1.00      0.96        13
            ScinaxRuber       0.93      0.90      0.92        31

               accuracy                           0.97      1439
              macro avg       0.93      0.94      0.94      1439
           weighted avg       0.97      0.97      0.97      1439
```

Figure 3: Results of classification of anuran species using Support Vector Machine

According to the results above, the correct predictions that fall on the diagonal line of the confusion matrix in support vector machine algorithm are more than in decision tree algorithm. The performance metrics such as accuracy, precision, recall as well as f1-score are calculated based on the confusion matrix.

First, the accuracy score in support vector machine algorithm (97.43%) is higher than in decision tree algorithm (94.02%), which indicates that the number of correct predictions made in support vector machine algorithm is greater than in decision tree algorithm by 3.41 %.

Moreover, the precisions for each class in support vector machine algorithm are higher than in decision tree algorithm, which means that the support vector machine algorithm returns more relevant results than the decision tree algorithm. For instance, when the model predicts that an anuran belongs to HysiboasCinerascens species, it is correct around 99% of the time in support vector machine algorithm. Conversely, it is correct around 93% of the time in decision tree algorithm, which has decreased by 6%.

Furthermore, the recalls for each class in support vector machine algorithm are greater than in decision tree algorithm, which proves that the support vector machine algorithm returns most of the relevant results than the decision tree algorithm. For example, for all anurans that actually belong to AdenomeraAndre species, it is correctly identified around 98% as belonging to the AdenomeraAndre species in support vector machine algorithm. However, it is correctly identified around 92% as belonging to the AdenomeraAndre species in decision tree algorithm, which has decreased by 6%.

Last but not least, the majority of f1-scores for each class in support vector machine algorithm are higher than in decision tree algorithm. This indicates that the precision and recall evaluated in support vector machine algorithm are greater than in decision tree algorithm.

In conclusion, Support Vector Machine is the best suited predictive model for the multiclass classification of the anuran species as it has higher accuracy, precision, recall as well as f1-score when compared to Decision Tree model. Therefore, support vector machine algorithm is more suitable to correctly identify the classification of anuran species if there are more new datasets gathered in the future.

Credits:

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