

# Frog Call Acoustic Analysis

A Clustering Approach





# Introduction

- **Background:** Anurans, commonly known as frogs and toads, are known for their distinct vocalizations, often used for communication and mating. These vocalizations, or calls, have specific acoustic features that can potentially distinguish between different species or families.
- **Importance:** Understanding these calls can not only aid in the identification of different anuran species but could also contribute to the studies of behavioral patterns, mating rituals, and potentially, the impact of environmental changes on these species.

# Problem Statement



- **Objective:** Our goal is to leverage the power of machine learning, specifically unsupervised clustering algorithms, to analyze and classify these acoustic features, thereby distinguishing different anuran families based on their calls.
- **Approach:** I intend to use different clustering algorithms, including K-Means, DBSCAN, Affinity Propagation, OPTICS, Mean-shift, and Agglomerative Clustering. These algorithms will enable us to analyze the anuran call data and uncover any intrinsic groupings.
- **Evaluation:** In order to compare the performance of the different clustering algorithms, we will use the Adjusted Rand Index (ARI). The ARI is a measure that quantifies the similarity between the true labels and the labels predicted by the clustering algorithm.
- **Why ARI?:** Unlike other metrics, the ARI accounts for the fact that random label assignments will result in some amount of "agreement" and corrects for this, providing a more accurate measure of how well the clustering algorithm performs relative to a random assignment.



# Dataset

- Available on the UC Irvine Machine Learning Repository
- Name: default of credit card clients
- Creator: I-Cheng Yeh
- DOI: [10.24432/C55S3H](https://doi.org/10.24432/C55S3H)
- Link: <https://archive.ics.uci.edu/dataset/350/default+of+credit+card+clients>

# Data Overview

df.head(10)

	MFCCs_1	MFCCs_2	MFCCs_3	MFCCs_4	MFCCs_5	MFCCs_6	MFCCs_7	MFCCs_8	MFCCs_9	MFCCs_10	...	MFCCs_17	MFCCs_18	MFCCs_19	MFCCs_20	MFCCs_21	MFCCs_22	Family	Genus	Species	RecordID
0	1.0	0.152936	-0.105586	0.200722	0.317201	0.260764	0.100945	-0.150063	-0.171128	0.124676	...	-0.108351	-0.077623	-0.009568	0.057684	0.118680	0.014038	Leptodactylidae	Adenomera	AdenomeraAndre	1
1	1.0	0.171534	-0.098975	0.268425	0.338672	0.268353	0.060835	-0.222475	-0.207693	0.170883	...	-0.090974	-0.056510	-0.035303	0.020140	0.082263	0.029056	Leptodactylidae	Adenomera	AdenomeraAndre	1
2	1.0	0.152317	-0.082973	0.287128	0.276014	0.189867	0.008714	-0.242234	-0.219153	0.232538	...	-0.050691	-0.023590	-0.066722	-0.025083	0.099108	0.077162	Leptodactylidae	Adenomera	AdenomeraAndre	1
3	1.0	0.224392	0.118985	0.329432	0.372088	0.361005	0.015501	-0.194347	-0.098181	0.270375	...	-0.136009	-0.177037	-0.130498	-0.054766	-0.018691	0.023954	Leptodactylidae	Adenomera	AdenomeraAndre	1
4	1.0	0.087817	-0.068345	0.306967	0.330923	0.249144	0.006884	-0.265423	-0.172700	0.266434	...	-0.048885	-0.053074	-0.088550	-0.031346	0.108610	0.079244	Leptodactylidae	Adenomera	AdenomeraAndre	1
5	1.0	0.099704	-0.033408	0.349895	0.344535	0.247569	0.022407	-0.213767	-0.127916	0.277353	...	-0.080487	-0.130089	-0.171478	-0.071569	0.077643	0.064903	Leptodactylidae	Adenomera	AdenomeraAndre	1
6	1.0	0.021676	-0.062075	0.318229	0.380439	0.179043	-0.041667	-0.252300	-0.167117	0.220027	...	-0.046620	-0.055146	-0.085972	-0.009127	0.065630	0.044040	Leptodactylidae	Adenomera	AdenomeraAndre	1
7	1.0	0.145130	-0.033660	0.284166	0.279537	0.175211	0.005791	-0.183329	-0.158483	0.192567	...	-0.055978	-0.048219	-0.056637	-0.022419	0.070085	0.021419	Leptodactylidae	Adenomera	AdenomeraAndre	1
8	1.0	0.271326	0.027777	0.375738	0.385432	0.272457	0.098192	-0.173730	-0.157857	0.207181	...	-0.120723	-0.112607	-0.156933	-0.118527	-0.002471	0.002304	Leptodactylidae	Adenomera	AdenomeraAndre	1
9	1.0	0.120565	-0.107235	0.316555	0.364437	0.307757	0.025992	-0.294179	-0.223236	0.268435	...	-0.051073	-0.052568	-0.111338	-0.040014	0.090204	0.088025	Leptodactylidae	Adenomera	AdenomeraAndre	1

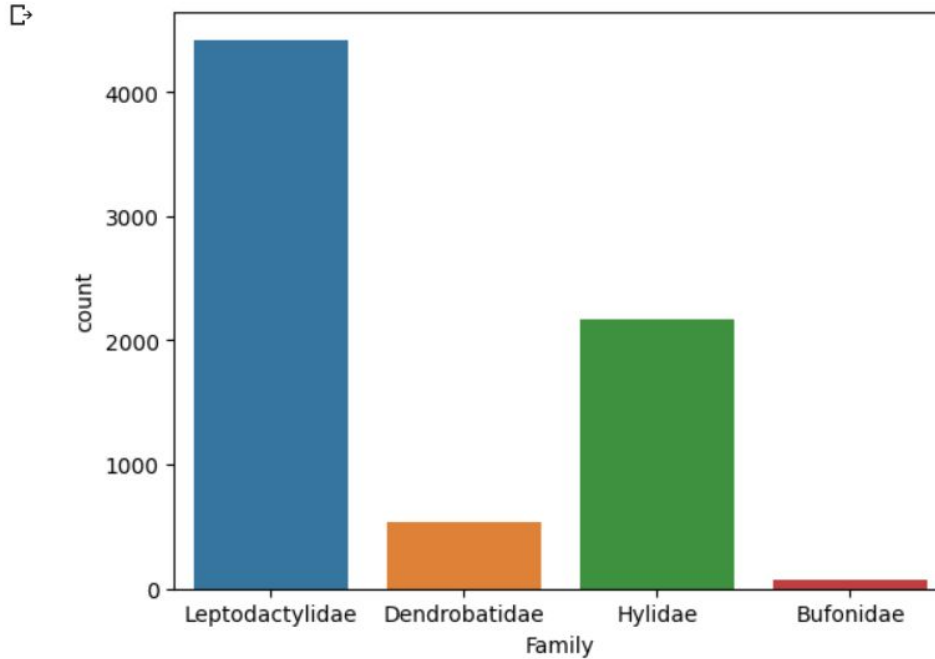
10 rows x 26 columns

Features

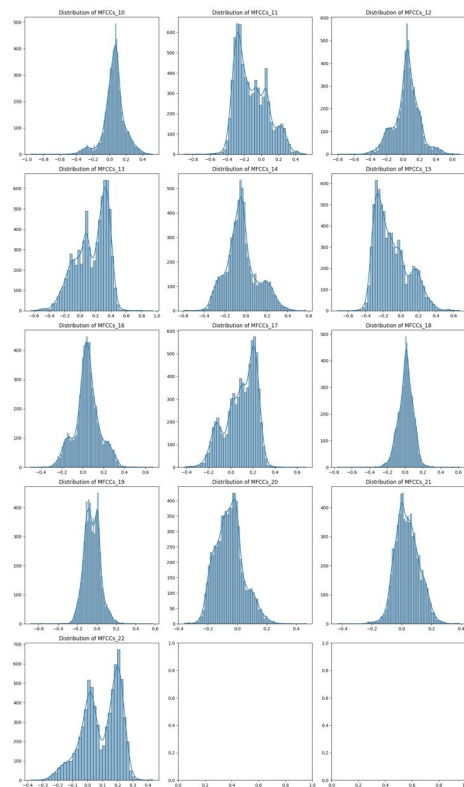
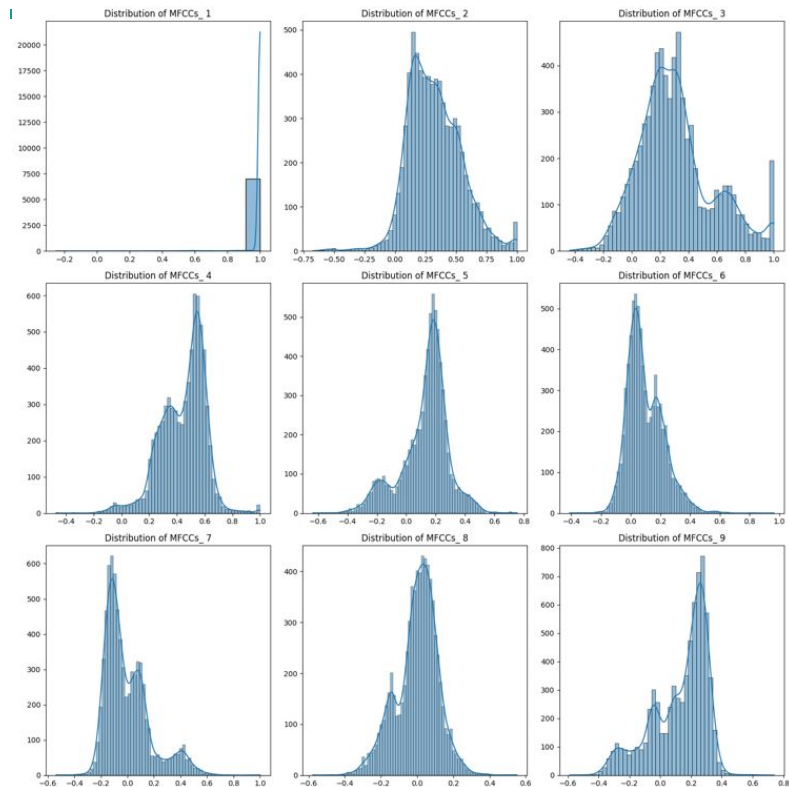
Labels

# Data Visualization

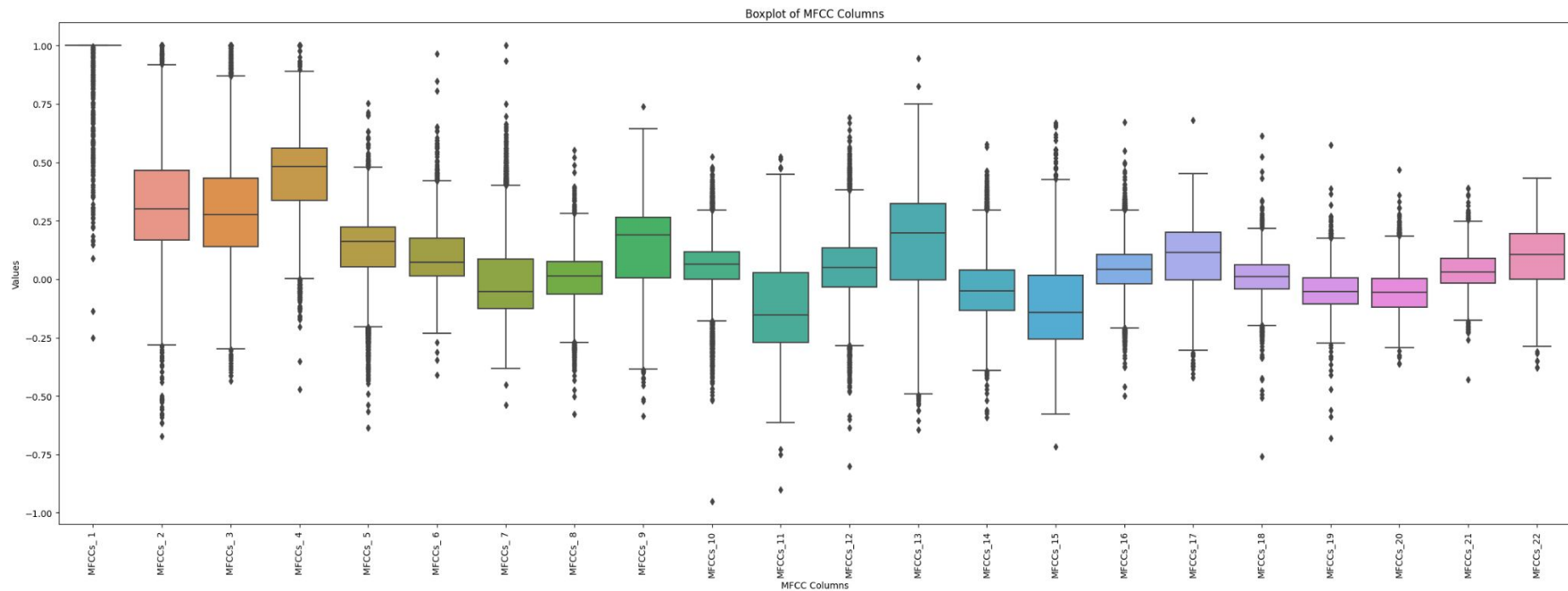
```
▶ sns.countplot(data=df, x="Family")  
plt.show()
```



# Data Visualization



# Data Visualization





# Data Transformation

```
from sklearn.preprocessing import StandardScaler

# Perform data normalization
scaler = StandardScaler()
df_normalized = scaler.fit_transform(df[mfcc_columns])

# Create a new DataFrame with the normalized values and 'Family' column
df_normalized = pd.DataFrame(df_normalized, columns=mfcc_columns)
df_final = pd.concat([df_normalized, df['Family']], axis=1)

# Print the final DataFrame
df_final.head(10)
```

MFCCs_1	MFCCs_2	MFCCs_3	MFCCs_4	MFCCs_5	MFCCs_6	MFCCs_7	MFCCs_8	MFCCs_9	MFCCs_10	...	MFCCs_14	MFCCs_15	MFCCs_16	MFCCs_17	MFCCs_18	MFCCs_19	MFCCs_20	MFCCs_21	MFCCs_22	Family
0.146578	-0.780502	-1.581769	-1.529944	1.168666	1.352327	0.597119	-1.287190	-1.672333	0.540390	...	0.796627	1.265956	-0.551081	-1.427291	-1.007678	0.483477	1.177905	1.023939	-0.595699	Leptodactylidae
0.146578	-0.695439	-1.556680	-1.107634	1.300622	1.415359	0.363097	-1.909853	-1.876612	0.903961	...	0.406743	1.412903	-0.250524	-1.301412	-0.758490	0.171681	0.779239	0.565657	-0.474036	Leptodactylidae
0.146578	-0.783334	-1.495953	-0.990973	0.915536	0.763498	0.058992	-2.079764	-1.940639	1.389091	...	0.590374	1.647536	0.345883	-1.009606	-0.369957	-0.208962	0.299030	0.777644	-0.084297	Leptodactylidae
0.146578	-0.453678	-0.729537	-0.727096	1.505993	2.184868	0.098592	-1.667990	-1.264799	1.686808	...	0.181478	1.077586	-0.769643	-1.627648	-2.181026	-0.981638	-0.016165	-0.704780	-0.515365	Leptodactylidae
0.146578	-1.078343	-1.440441	-0.867225	1.252998	1.255819	0.048313	-2.279164	-1.681117	1.655798	...	0.502823	1.710511	0.173262	-0.996517	-0.717936	-0.473426	0.232532	0.897212	-0.067430	Leptodactylidae
0.146578	-1.023975	-1.307857	-0.599452	1.336658	1.242737	0.138885	-1.834978	-1.430922	1.741708	...	0.339202	1.505230	0.109918	-1.225448	-1.626921	-1.478120	-0.194590	0.507517	-0.183621	Leptodactylidae
0.146578	-1.380858	-1.416648	-0.796972	1.557318	0.673601	-0.234957	-2.166317	-1.649927	1.290648	...	0.434832	1.698626	0.190075	-0.980114	-0.742398	-0.442185	0.468465	0.356347	-0.352636	Leptodactylidae
0.146578	-0.816205	-1.308815	-1.009448	0.937189	0.641773	0.041941	-1.573246	-1.601692	1.074581	...	0.198214	1.524554	0.280153	-1.047901	-0.660640	-0.086779	0.327323	0.412400	-0.535902	Leptodactylidae
0.146578	-0.239014	-1.075665	-0.438251	1.588005	1.449444	0.581058	-1.490700	-1.598194	1.189566	...	-0.037644	0.885759	-0.619054	-1.516910	-1.420591	-1.301907	-0.693218	-0.500659	-0.690764	Leptodactylidae
0.146578	-0.928559	-1.588027	-0.807416	1.458970	1.742628	0.159803	-2.526431	-1.963449	1.671537	...	0.537179	1.802895	0.094860	-1.012373	-0.711965	-0.749508	0.140486	0.665592	0.003707	Leptodactylidae

Features

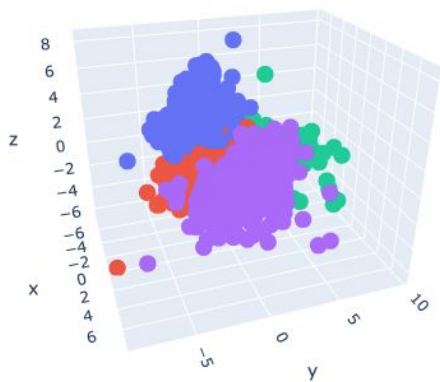
Label



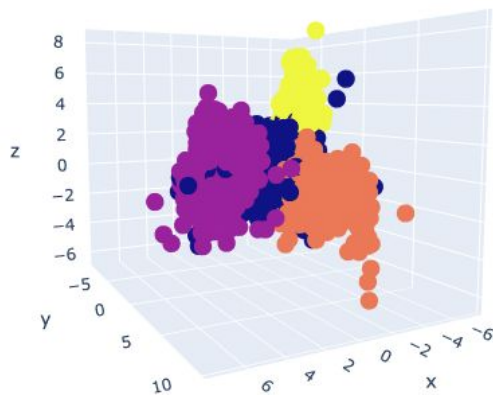
## Proposed Procedures

1. GridSearchCV for hyperparameters tuning (using the best Silhouette Score)
2. Perform the proposed clustering model
3. Perform PCA for dimensionality reduction to  $n\_components = 3$  and visualize the clusters.
4. Calculate the Adjusted Rand Index based on the assigned clusters and the ground truth classes “Family”
5. Models comparison using the Adjusted Rand Index

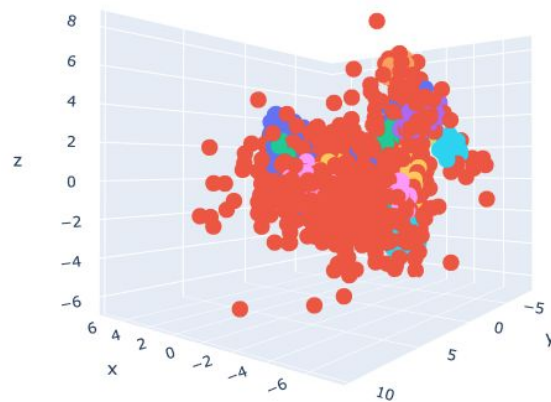
# Some Cluster Visualizations



K-Means



Agglomerative Clustering



DBSCAN

# Adjusted Rand Index

To compute the Rand index, you'd measure:

- $a$  = Number of pairs that have the same class label and same cluster assignment
- $b$  = Number of pairs that have different class labels and different cluster assignments

The raw Rand index is:

$$RI = \frac{a + b}{\binom{n}{2}}$$

where  $\binom{n}{2}$  is the number of possible pairs of points.  $RI$  ranges from 0 to 1, with 1 indicating total agreement.

- **The Adjusted Rand Index** also accounts for chance, thus ensured to have a value close to 0.0 for random labeling independently of the number of clusters and samples and exactly 1.0 when the clusterings are identical.
- The adjusted Rand index is bounded below by -0.5 for especially discordant clusterings.

**Reference:** [https://scikit-learn.org/stable/modules/generated/sklearn.metrics.adjusted\\_rand\\_score.html](https://scikit-learn.org/stable/modules/generated/sklearn.metrics.adjusted_rand_score.html)

# Results



Model	ARI
K-Means	0.3129
Mean-shift	-0.0104
Affinity Propagation	0.0268
Agglomerative Clustering	0.4774
DBSCAN	0.4669
OPTICS	0.1233

- All results are below 0.50 which shows poor coordination between the assigned clusters and the ground truth labels.
- Two models show potential for further improvement: Agglomerative Clustering (0.4774) and DBSCAN (0.4669)
- Consider supervised algorithms for this project