MAESTRA
LEARNING FROM MASSIVE, INCOMPLETELY ANNOTATED, AND STRUCTURED DATA

Anuran species recognition using a hierarchical classification approach

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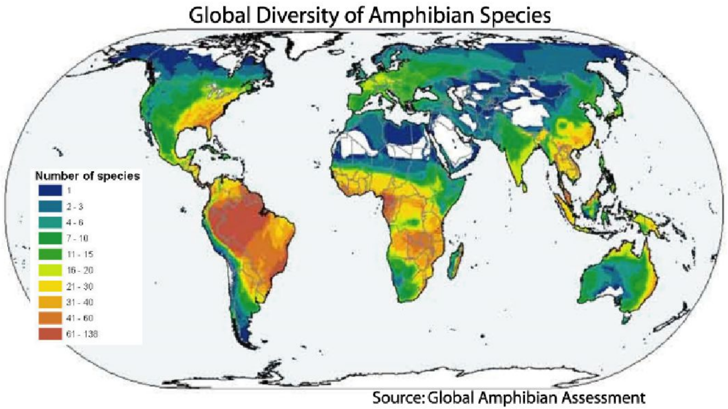
Getting more from family, genus and species of frogs

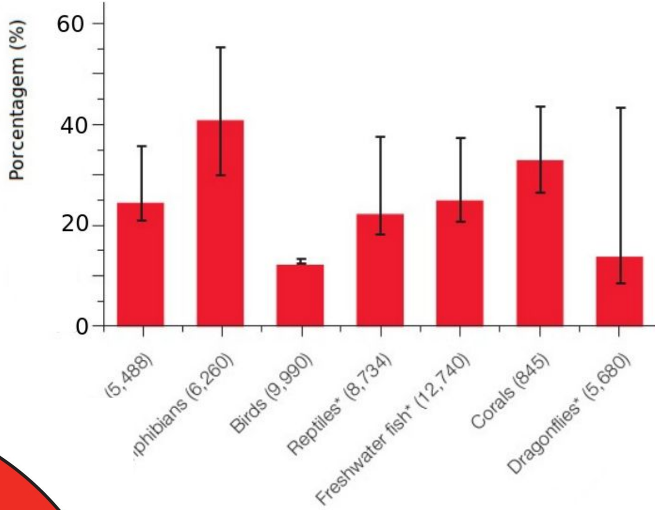
Introduction - Why frogs?

- **Anura** is the name of an order of animals in the **Amphibian** class which lack a tail, this includes **frogs** and **toads**.

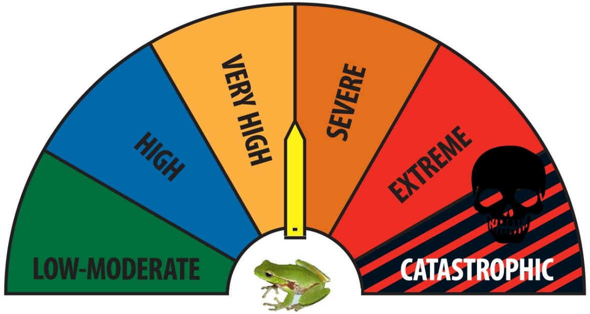


Global Diversity of Amphibian Species

Source: Global Amphibian Assessment



- **Frogs are very sensitive to environmental changes**



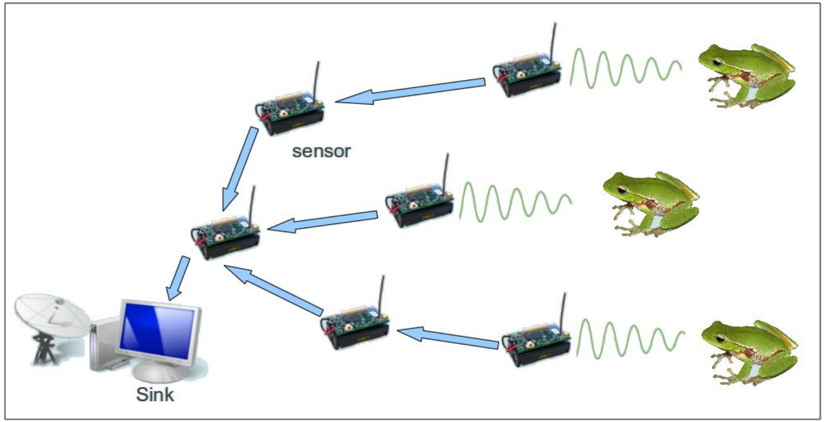
Why monitor populations of frogs?

Hypothesis: Tracking the changes in the anuran populations can help us to determine ecological problems in early stages.

It involves several manual tasks!

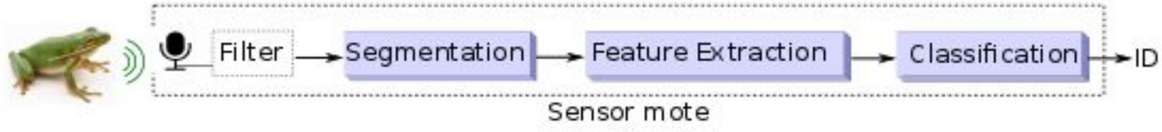
Proposal

Signal processing (SP) + Wireless Sensor Networks (WSN) + Machine Learning (ML)



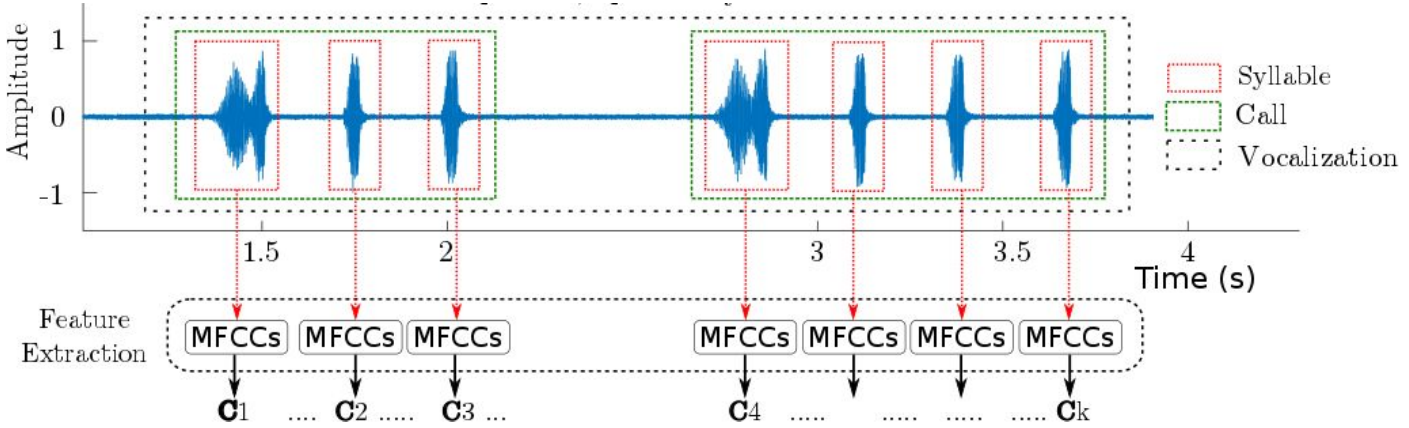
Advantages: It is Automatic, less intrusive and allows long term monitoring.

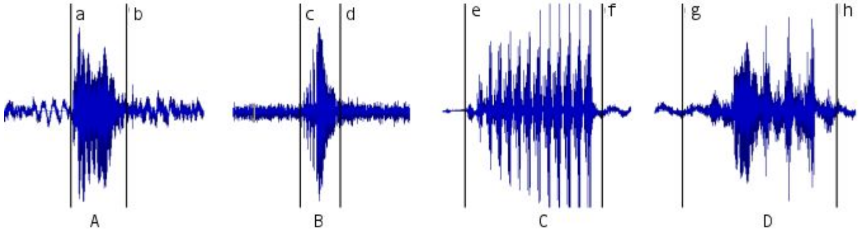
How to do that?

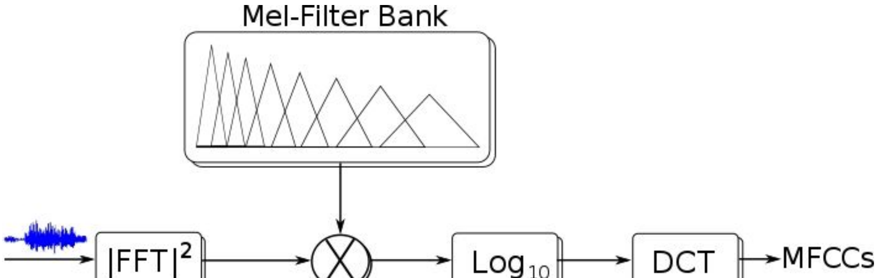


1) Pre-processing:
    a) Filter: band-pass filter, wavelet decomposition, etc.
    b) Segmentation: **syllable-based approach** (x_k)
2) Feature Extraction: that maps $x_k \rightarrow c_k$
    a) Mel-frequency cepstral coefficients (MFCCs)
    b) Spectral centroid, Spectral bandwidth, Pitch, etc.
3) Recognition: ML technique to classify $c_k \rightarrow ID$ (species ID)
    a) Support Vector Machine, kNN, Tree, etc.

Segmentation and feature extraction





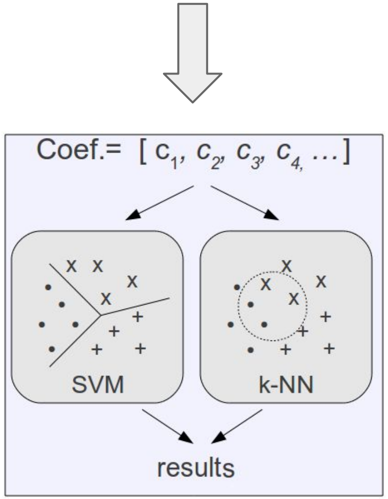


Traditional Classification Approach

Dataset with:

- *k* samples (or syllables)
- *l* coefficients
- one label (s_j={j species})

$$\text{dataset} = \begin{bmatrix} \mathbf{c}_1 = [c_1, c_2, \dots, c_l], & s \\ \mathbf{c}_2 = [c_1, c_2, \dots, c_l], & s \\ \vdots & \vdots \\ \mathbf{c}_k = [c_1, c_2, \dots, c_l], & s_j \end{bmatrix}$$

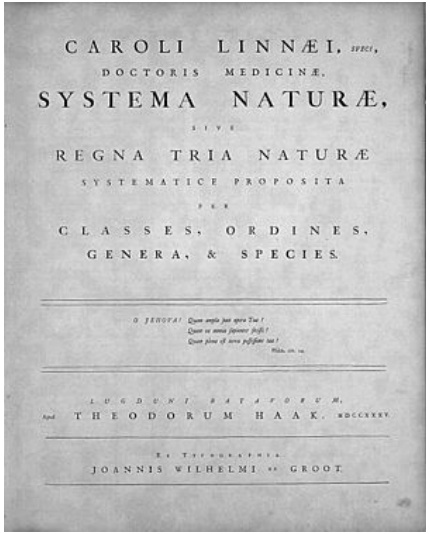


Then, apply a **“flat”** classifier (kNN, SVM, etc.)

Problem: the number of classes grows together with the number of species who wish to recognize increasing the complexity of the model.

Knowledge organization

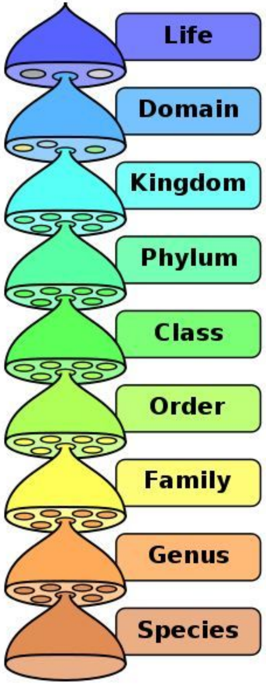
Carl Linnaeus has defined a particular form of biological organization called *taxonomy* in his work *Systema Naturae* (1735).



CAROLI LINNÆI, SVECI,
DOCTORIS MEDICINÆ,
SYSTEMA NATURÆ,
SIVE
REGNA TRIA NATURÆ
SYSTEMATICE PROPOSITA
PER
CLASSES, ORDINES,
GENERA, & SPECIES.

LUGDUNI BATAVORUM,
Apud THEODORUM HAAK. MDCCXXXV.

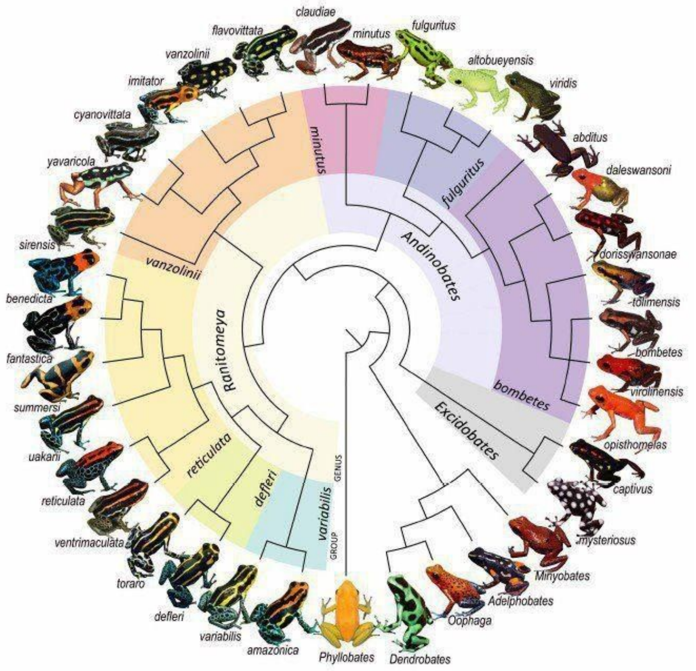
Ex Typographia
JOANNIS WILHELMI de GROOT.



How to improve the classification using the taxonomy?

- The anura Order has 31 Families (approximately)
- These Families are divided into several genus
- And finally, these genus are divided in almost 6000 species

Hypothesis: the phylogenetic taxonomy may describe similar calls among species that belong to the same genus and family[2].



Illustrative figure.

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[2] B. Gingras and W. T. Fitch.
A three-parameter model for classifying anurans into four genera based on advertisement calls.
The Journal of the Acoustical Society of America, 133(1):547–559, 2013.

A Multi-output approach (multi-class and multi-label)

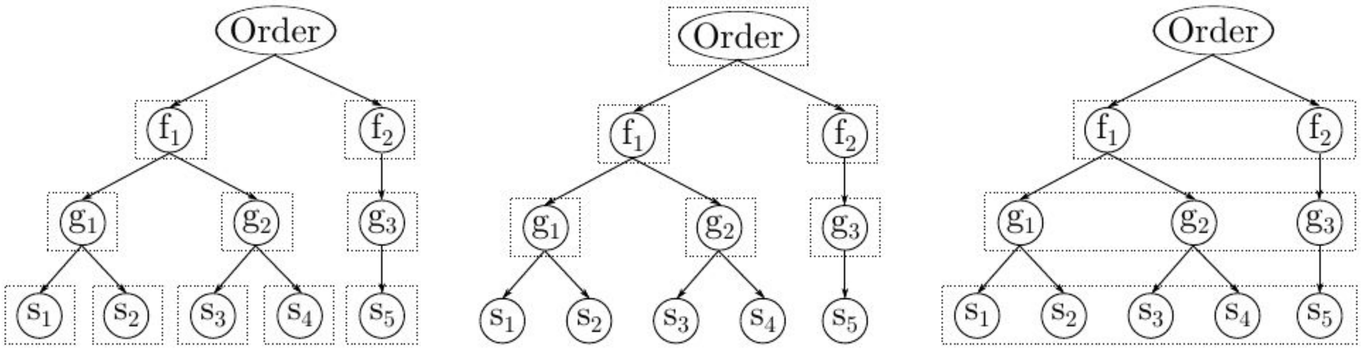
Extend the dataset incorporating the new labels:

- Label s_j = {j different species}
- Label g_i = {i different genus}
- Label f_m = {m different families}

$$\text{Multi-label dataset} = \begin{bmatrix} \mathbf{c}_1 = [c_1, c_2, \ldots, c_l], & s, & g, & f \\ \mathbf{c}_2 = [c_1, c_2, \ldots, c_l], & s, & g, & f \\ \vdots & \vdots & \vdots & \vdots \\ \mathbf{c}_k = [c_1, c_2, \ldots, c_l], & s_j, & g_i, & f_m \end{bmatrix}$$

Hierarchical problem decomposition

- Use the taxonomy relation of the labels to build a tree.



(a)

One classifier per node

(b)

One classifier per parent node

(c)

One classifier per level

Our dataset

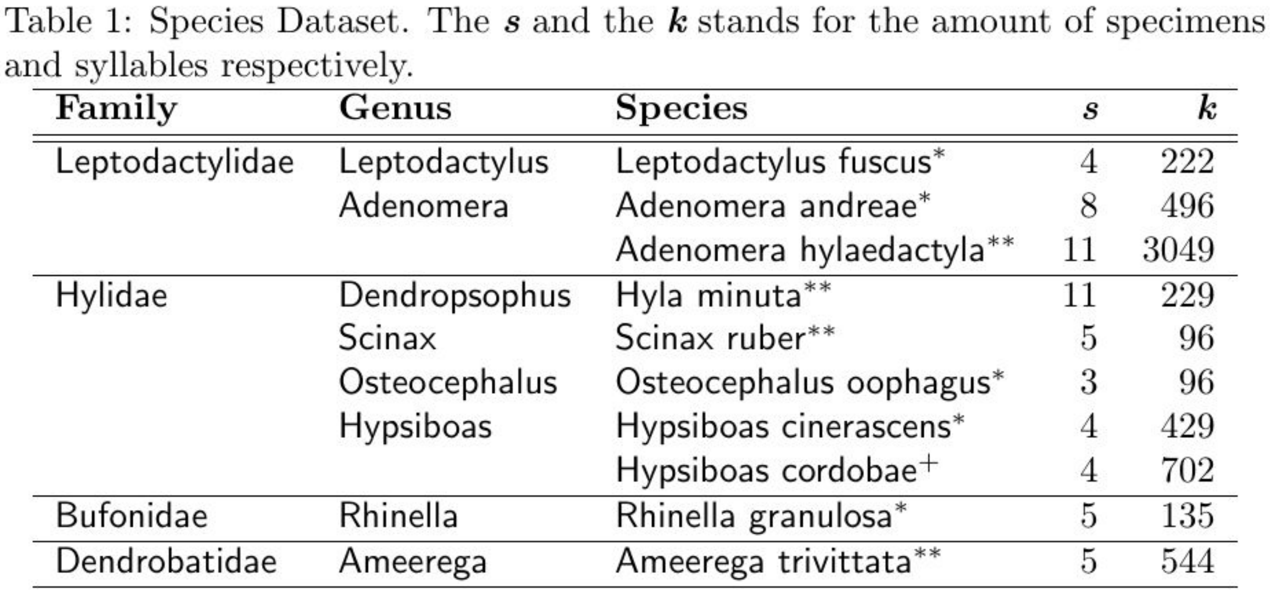
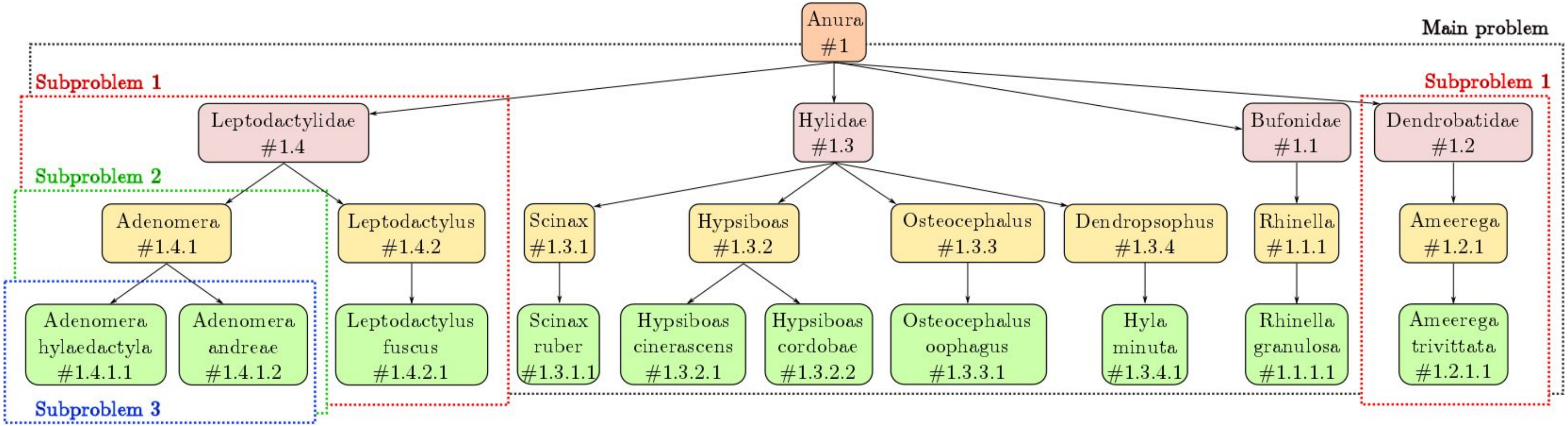


Table 1: Species Dataset. The s and the k stands for the amount of specimens and syllables respectively.

Family	**Genus**	**Species**	s	k
Leptodactylidae	Leptodactylus	Leptodactylus fuscus*	4	222
	Adenomera	Adenomera andreae*	8	496
		Adenomera hylaedactyla**	11	3049
Hylidae	Dendropsophus	Hyla minuta**	11	229
	Scinax	Scinax ruber**	5	96
	Osteocephalus	Osteocephalus oophagus*	3	96
	Hypsiboas	Hypsiboas cinerascens*	4	429
		Hypsiboas cordobae^{+}	4	702
Bufonidae	Rhinella	Rhinella granulosa*	5	135
Dendrobatidae	Ameerega	Ameerega trivittata**	5	544

- Indeed this is not a big-data dataset, but it is enough to prove our point.

Building our hierarchical classifier from our dataset

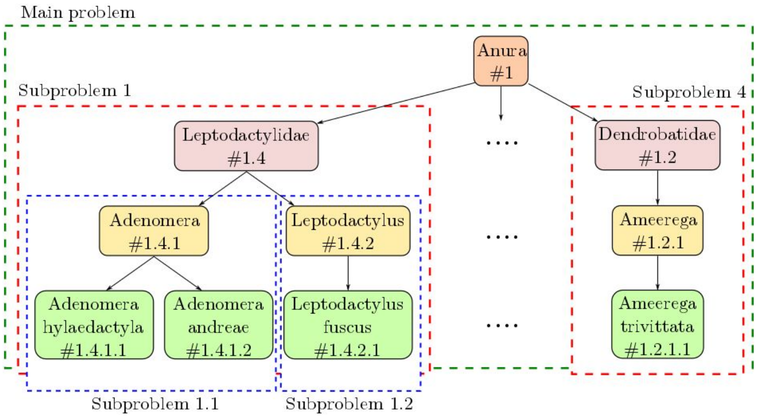


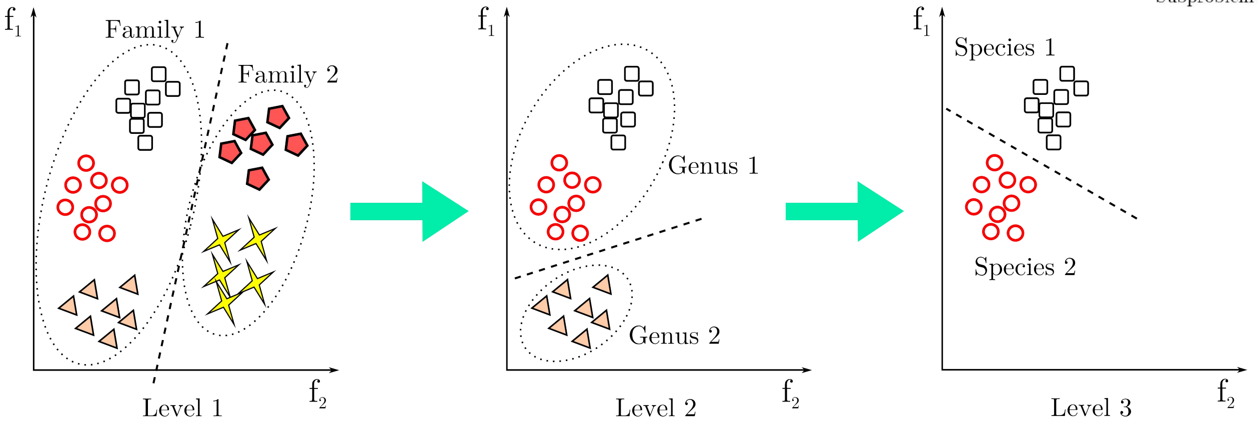
Benefit: One Classifier per Parent Node allows us to simplify the problem

Example: suppose that the first level decides in favor of the family *Bufonidae*. In this case there are no more splits in the tree, consequently it is not necessary to perform extra classifications to determine the species.

Hierarchical problem decomposition

- Subproblem decomposition and simplification:





Experiment configuration

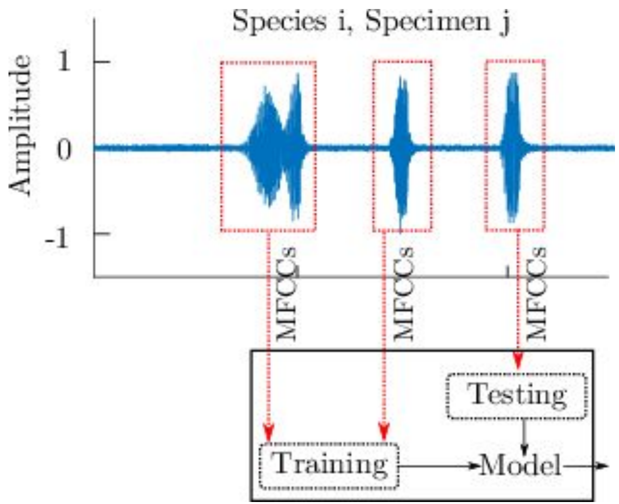
- A kNN was chosen as base classifier in each node (k=3).
- We adapted the cross-validation procedure to group syllables by individuals to test how well our method generalize.
- The Average-accuracy was used in evaluations to avoid an artificially increment of the Micro-accuracy due to unbalanced number samples in each class.

$$\text{Average-Acc} = \frac{1}{m}\sum_{i=1}^{m} \text{Acc}_i = \frac{1}{m}\sum_{i=1}^{m} \frac{tp_i}{k_i}$$

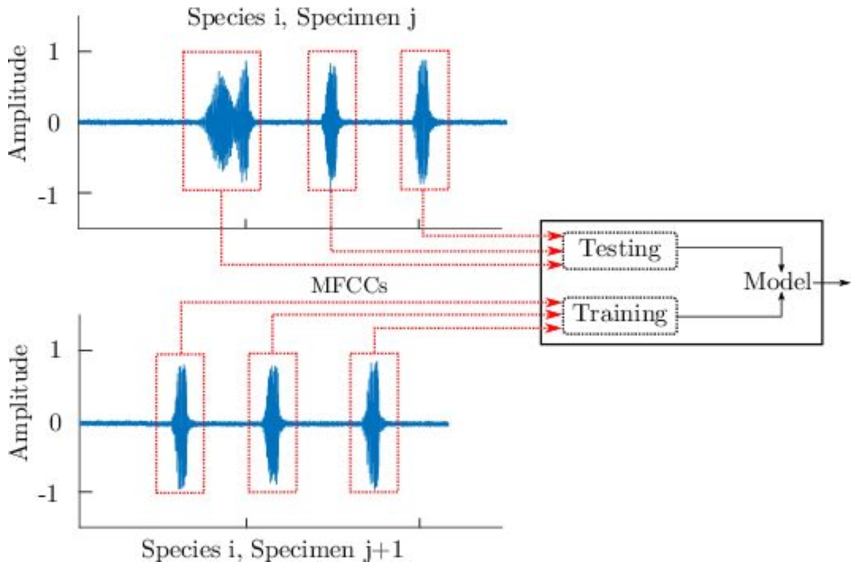
where Acc_i is the accuracy per row i of confusion matrix, m the total number of rows, tp_i are the true positives, and k_i the total number of syllables per row.

- **Random Baseline:**
  - Micro-accuracy = 0.50 (dummy classifier)
  - Average-accuracy = 0.10 (dummy classifier)

k-CV by Specimens (or individuals)



Common procedure found in the related works when syllable-based methodology is adopted.



Our Cross-Validation procedure by grouping syllables of the same individuals to test how well the model generalize.

Results per level

- Family Level (Acc = 76%)

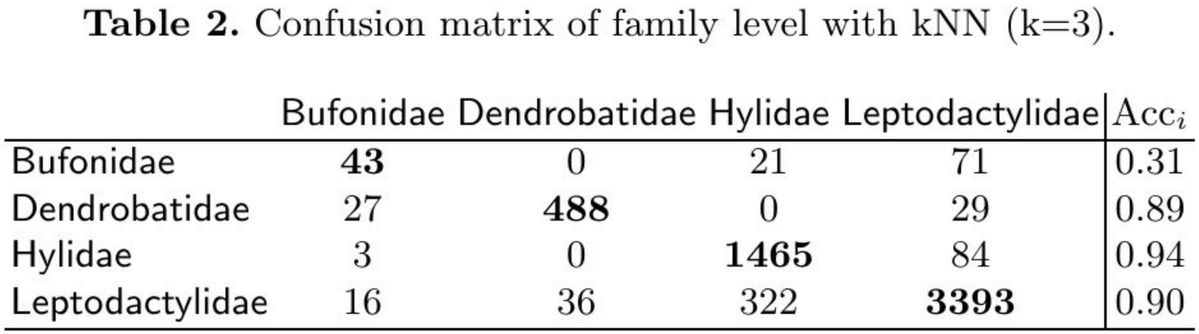


Table 2. Confusion matrix of family level with kNN (k=3).

	Bufonidae	Dendrobatidae	Hylidae	Leptodactylidae	Acc_i
Bufonidae	**43**	0	21	71	0.31
Dendrobatidae	27	**488**	0	29	0.89
Hylidae	3	0	**1465**	84	0.94
Leptodactylidae	16	36	322	**3393**	0.90

Results per level

- Family Level (Acc = 76%)
- Genus Level (Acc = 61%)

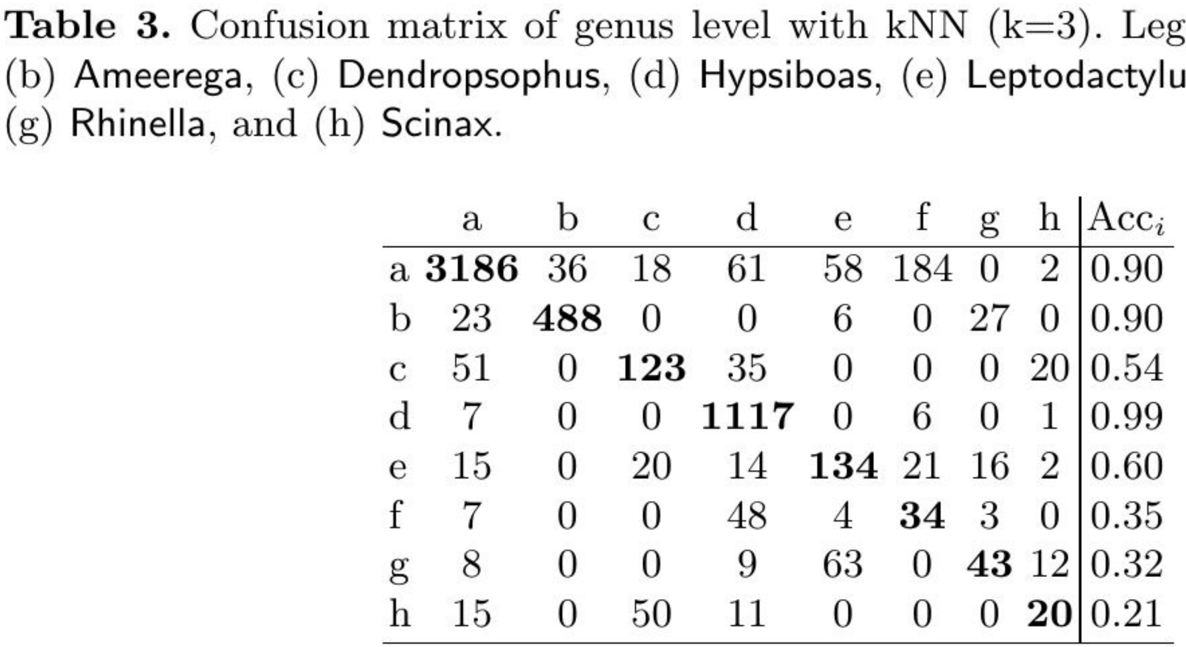


Table 3. Confusion matrix of genus level with kNN (k=3). Legend: (a) Adenomera, (b) Ameerega, (c) Dendropsophus, (d) Hypsiboas, (e) Leptodactylus, (f) Osteocephalus, (g) Rhinella, and (h) Scinax.

	a	b	c	d	e	f	g	h	Acc_i
a	**3186**	36	18	61	58	184	0	2	0.90
b	23	**488**	0	0	6	0	27	0	0.90
c	51	0	**123**	35	0	0	0	20	0.54
d	7	0	0	**1117**	0	6	0	1	0.99
e	15	0	20	14	**134**	21	16	2	0.60
f	7	0	0	48	4	**34**	3	0	0.35
g	8	0	0	9	63	0	**43**	12	0.32
h	15	0	50	11	0	0	0	**20**	0.21

Results per level

- Family Level (Acc = 76%)
- Genus Level (Acc = 61%)
- Species Level (Acc = 61%)

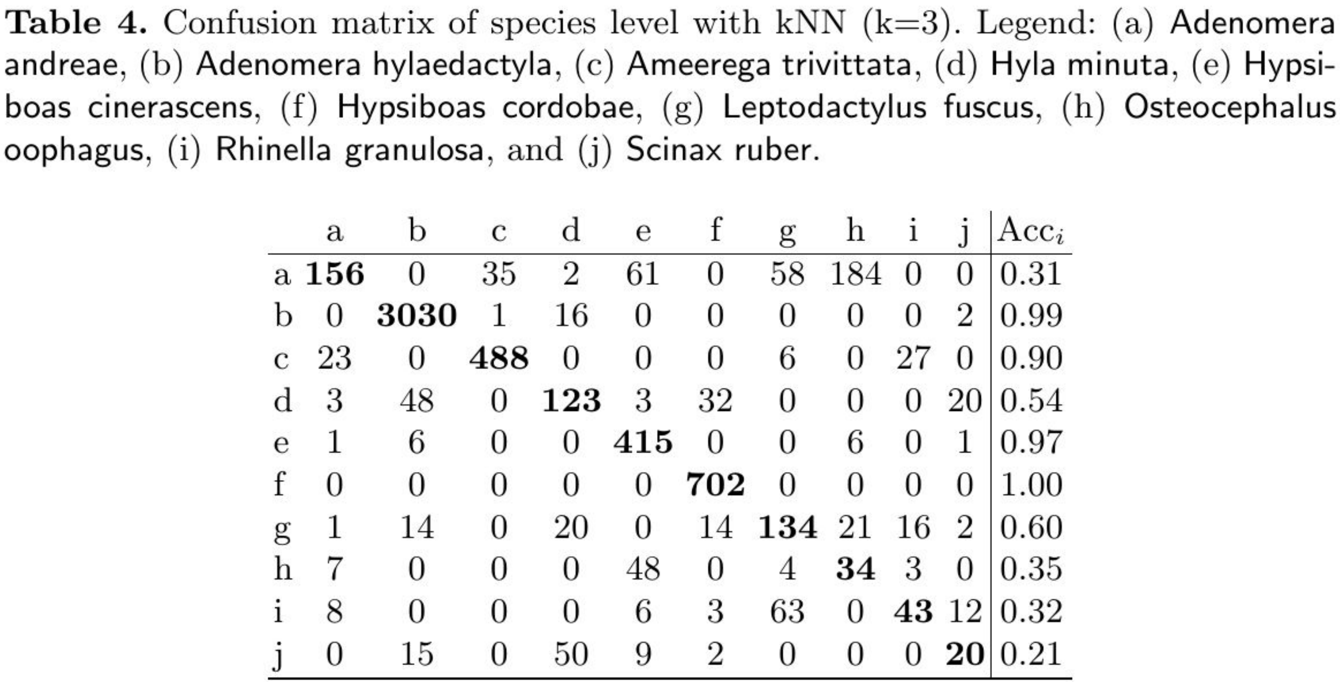


Table 4. Confusion matrix of species level with kNN (k=3). Legend: (a) Adenomera andreae, (b) Adenomera hylaedactyla, (c) Ameerega trivittata, (d) Hyla minuta, (e) Hypsiboas cinerascens, (f) Hypsiboas cordobae, (g) Leptodactylus fuscus, (h) Osteocephalus oophagus, (i) Rhinella granulosa, and (j) Scinax ruber.

	a	b	c	d	e	f	g	h	i	j	Acc_i
a	**156**	0	35	2	61	0	58	184	0	0	0.31
b	0	**3030**	1	16	0	0	0	0	0	2	0.99
c	23	0	**488**	0	0	0	6	0	27	0	0.90
d	3	48	0	**123**	3	32	0	0	0	20	0.54
e	1	6	0	0	**415**	0	0	6	0	1	0.97
f	0	0	0	0	0	**702**	0	0	0	0	1.00
g	1	14	0	20	0	14	**134**	21	16	2	0.60
h	7	0	0	0	48	0	4	**34**	3	0	0.35
i	8	0	0	0	6	3	63	0	**43**	12	0.32
j	0	15	0	50	9	2	0	0	0	**20**	0.21

Summary and conclusions

- **The hierarchical approach effectively reduces the complexity** of problems maintaining an acceptable accuracy.
- From a classification point of view the families Bufo, Hyla and Lepto were the most similar in the feature space, and also the species Adenomera andreae and Osteocephalus oophagus.
- The Scinax species was the most difficult to recognize.
- The ***k*****CV by individuals** (specimens) has an important impact in the model performance.
- Baseline comparison against a dummy random classifier:
  - Micro gain = +35% and Average gain = +50%

Future work: Implement soft decision rules in the tree to be able to correct the error propagation from the highest levels.

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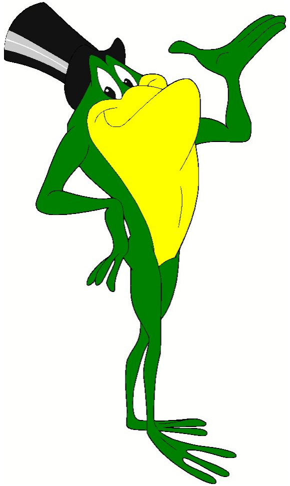

Thanks – Obrigado – Gracias

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