

Anuran species recognition using a hierarchical classification approach

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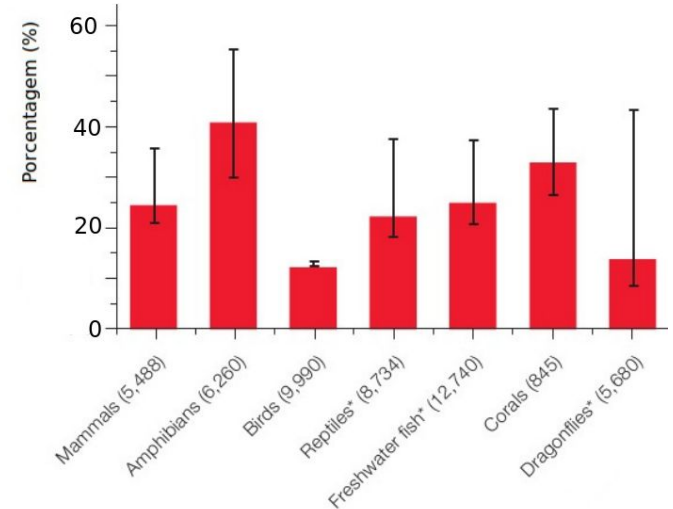
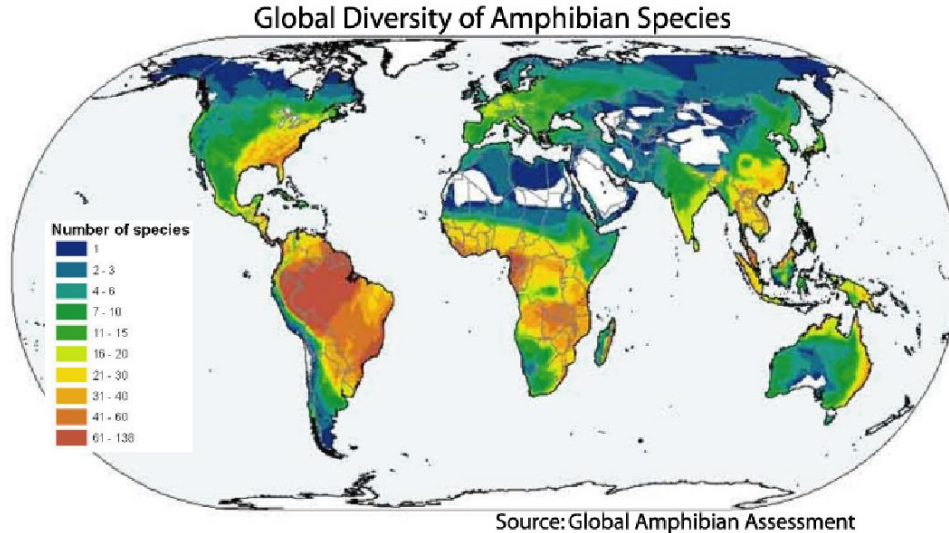
²Laboratory of Artificial Intelligence and Decision Support (LIAAD), INESC Tec



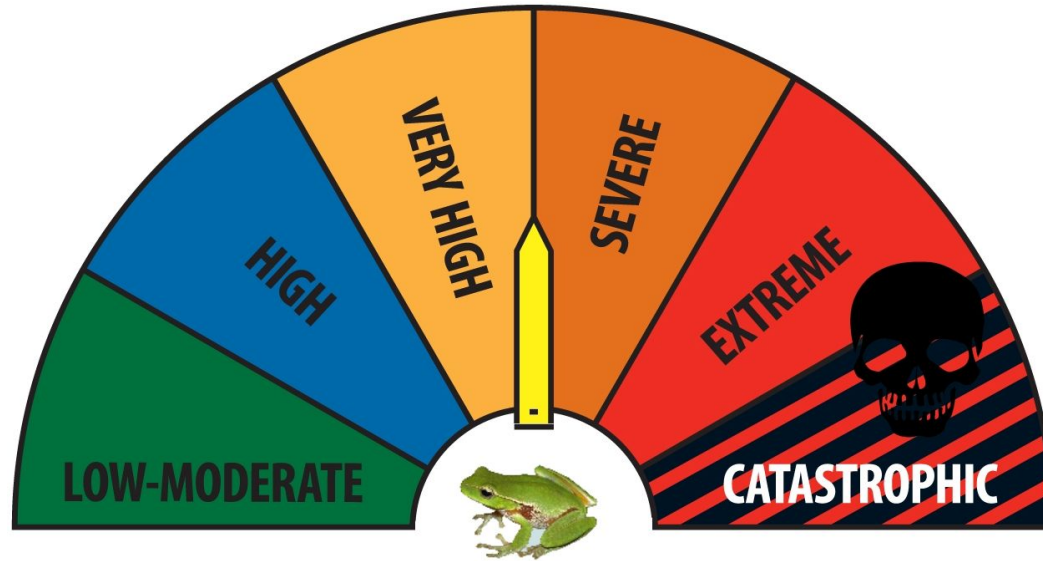
Getting more from family, genus and species of frogs

Introduction

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



Why monitor populations of frogs?



- Frogs have a semipermeable skin → It makes them sensitive to environmental changes

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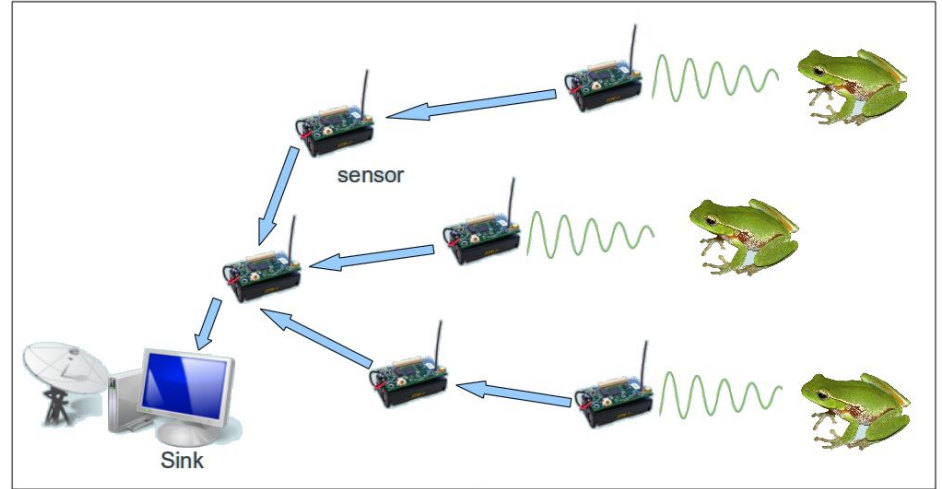
Hypothesis: Tracking the changes in the anuran populations can help us to determine ecological problems in early stages.



It involves several manual tasks!

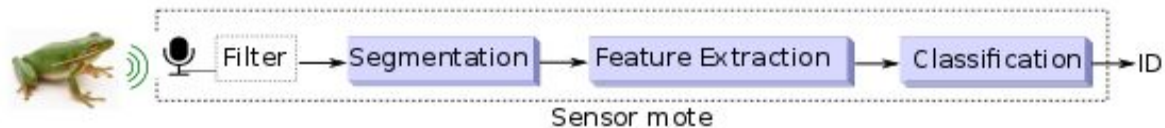
Proposal

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



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

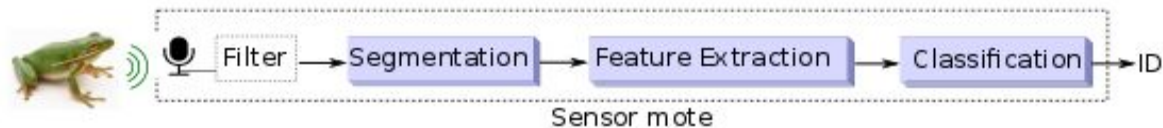
How to do that?



1) Pre-processing:

- a) Filter: band-pass filter, wavelet decomposition, etc.
- b) Segmentation: syllable-based approach (x_k)

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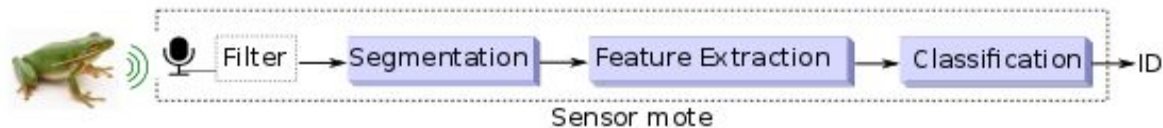
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2) Feature Extraction: that maps $x_k \rightarrow c_k$

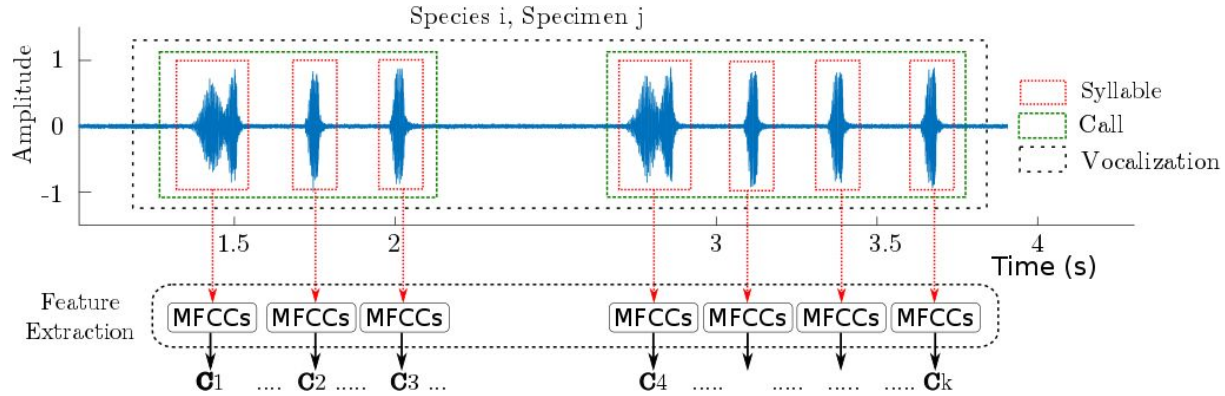
- a) Mel-frequency cepstral coefficients (MFCCs)
- b) Spectral centroid, Spectral bandwidth, Pitch, etc.

How to do that?

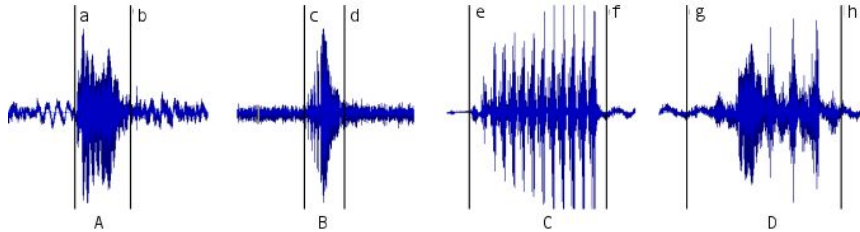
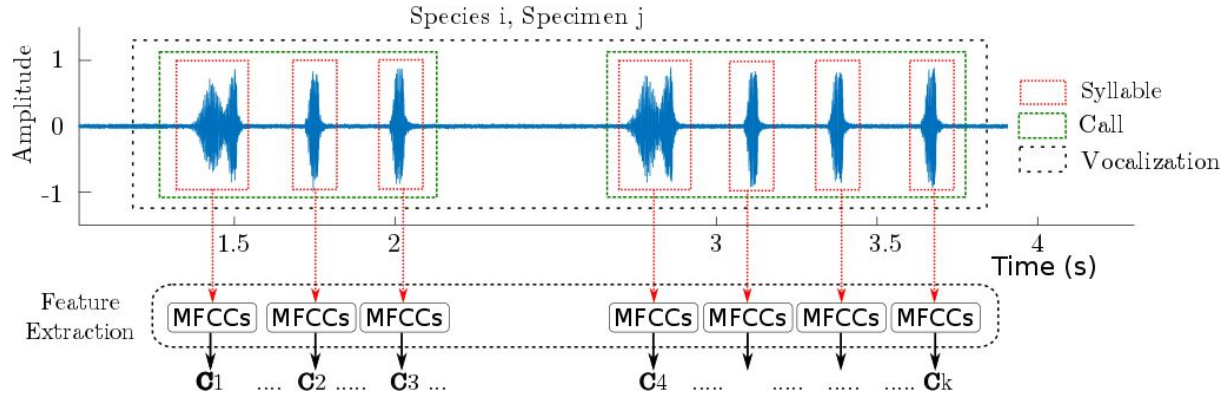


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- 2) Feature Extraction: that maps $x_k \rightarrow c_k$
 - a) Mel-frequency cepstral coefficients (MFCCs)
 - b) Spectral centroid, Spectral bandwidth, Pitch, etc.
- 3) Recognition: ML technique to classify $c_k \rightarrow \text{ID}$ (species ID)
 - a) Support Vector Machine
 - b) kNN
 - c) Tree, etc.

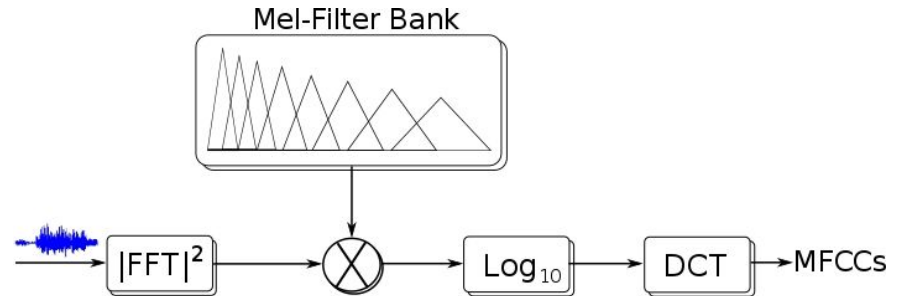
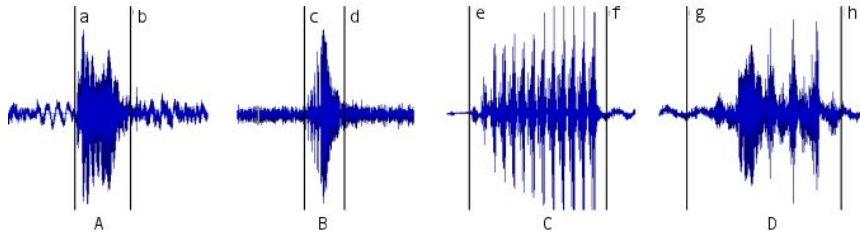
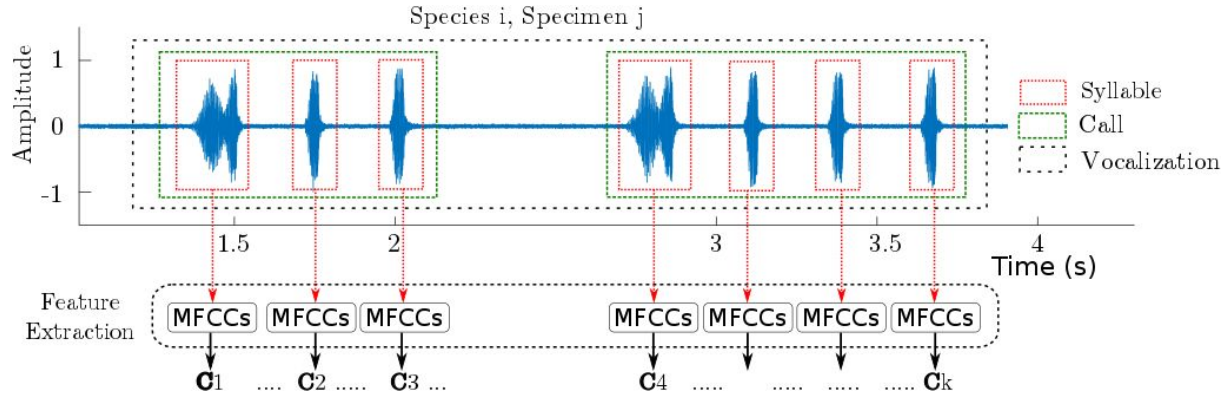
Segmentation and feature extraction



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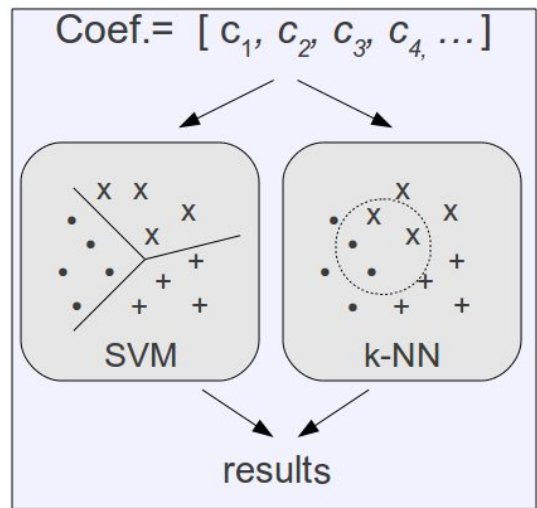
segmentation and feature extraction



Classification

Dataset with k samples (or syllables) composed of l coefficients and one label (s).

$$\text{dataset} = \begin{array}{c} \text{Coefficients} \\ \mathbf{c}_1 = [c_1, c_2, \dots, c_l], \\ \mathbf{c}_2 = [c_1, c_2, \dots, c_l], \\ \vdots \\ \mathbf{c}_k = [c_1, c_2, \dots, c_l], \end{array} \begin{array}{c} \text{Species} \\ s \\ s \\ \vdots \\ s_j \end{array} \quad \longrightarrow$$



where j is the number of different species

Problem of this approach?

- The order Anura has the most extant species, with 6.500 members worldwide¹.
- Is it possible to train a flat classifier with 6.500 different labels?

1- <http://research.amnh.org/herpetology/amphibia/index.html>. American Museum of Natural History, New York, USA.

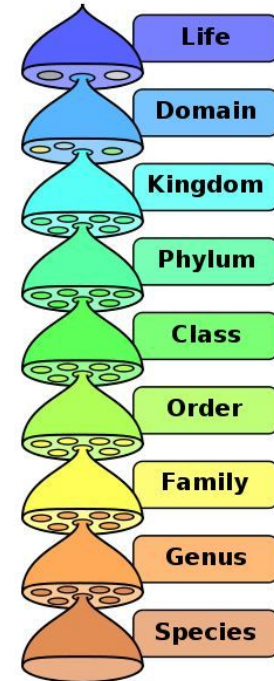
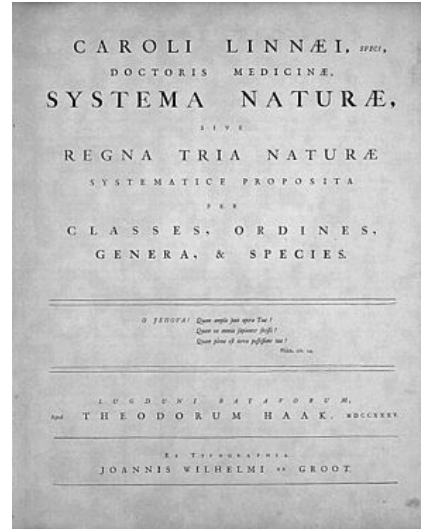
Problem of this approach?

- The order Anura has the most extant species, with 6.500 members worldwide¹.
- It is possible to training a flat classifier with 6.500 different labels?
- In order to monitor a small region a subset of species should be sufficient. However, there could be many species, mainly in tropical regions.

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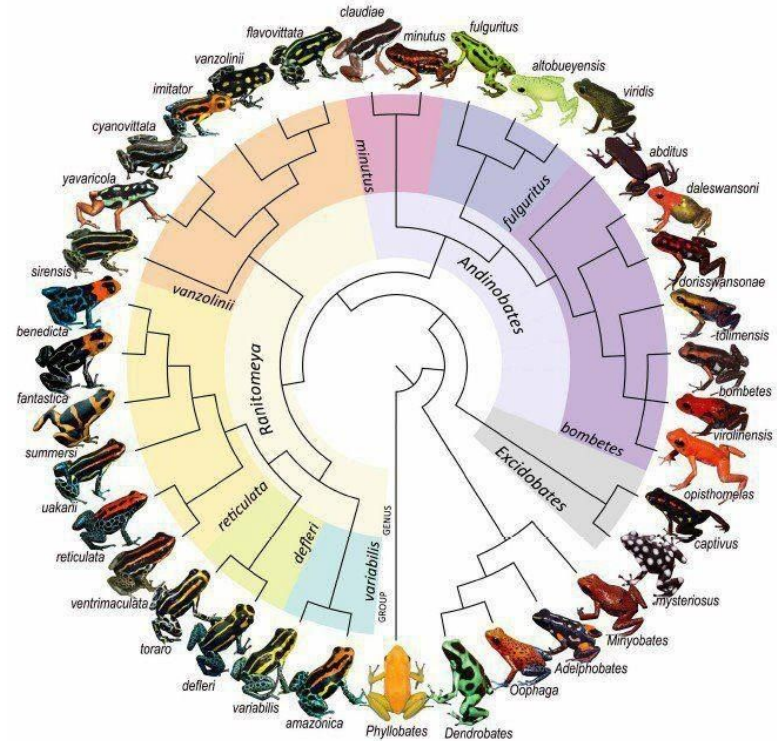
Knowledge organization

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



How to improve the classification using the taxonomy?

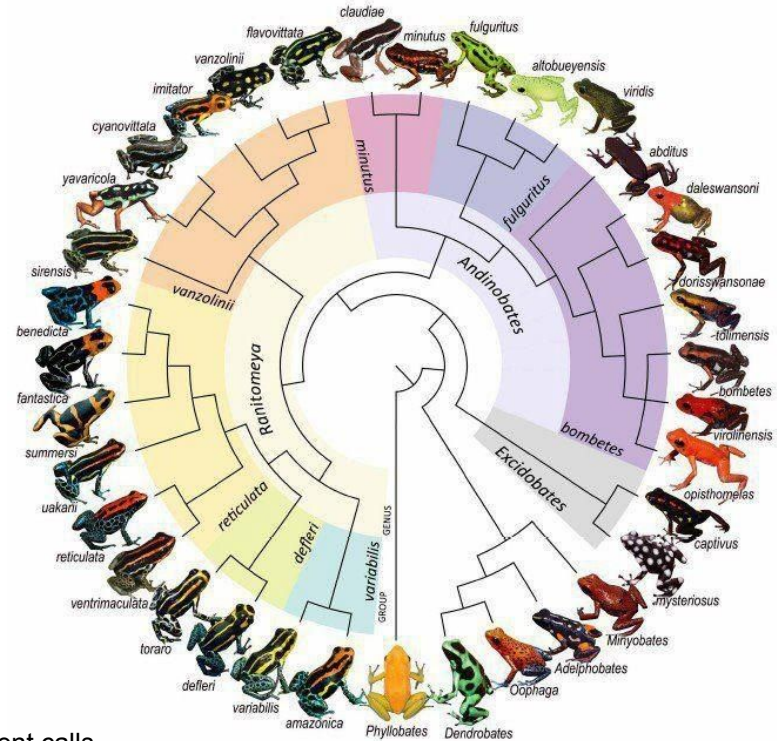
- The anura Order has 31 Families (approximately)
- These Families are divided into several genus
- And finally, these genus are divided in almost 6K species



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- These Families are divided into several genus
- And finally, these genus are divided in almost 6K species

Hypothesis: the phylogenetic taxonomy may describe similar calls among species that belong to the same genus and family².



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-label approach

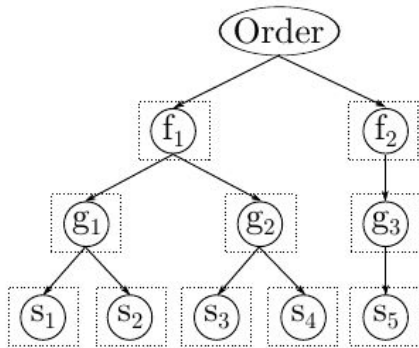
- Building a new dataset incorporating the new labels:

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

where s , g and f are the labels of species, genus, and family respectively.

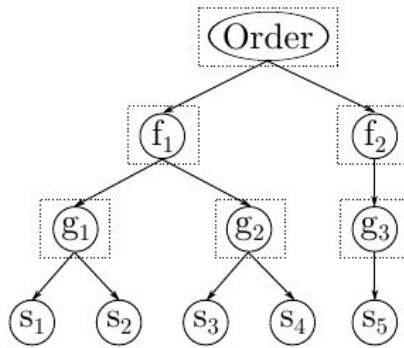
Hierarchical problem decomposition

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



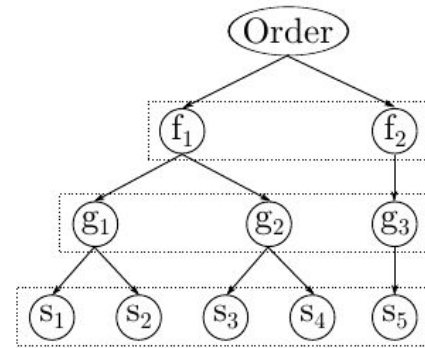
(a)

One
classifier
per node



(b)

One classifier
per parent node

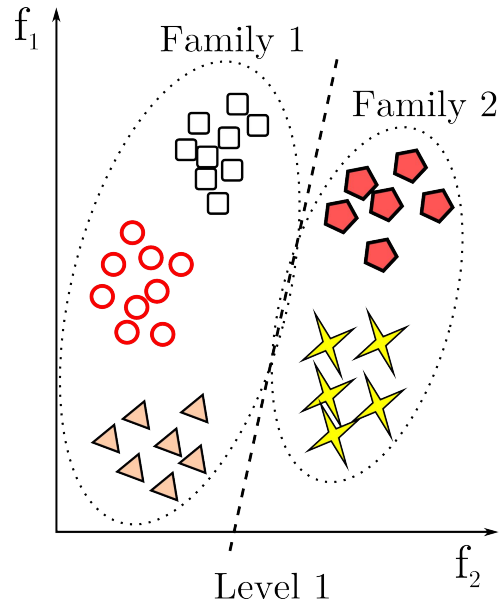


(c)

One
classifier
per level

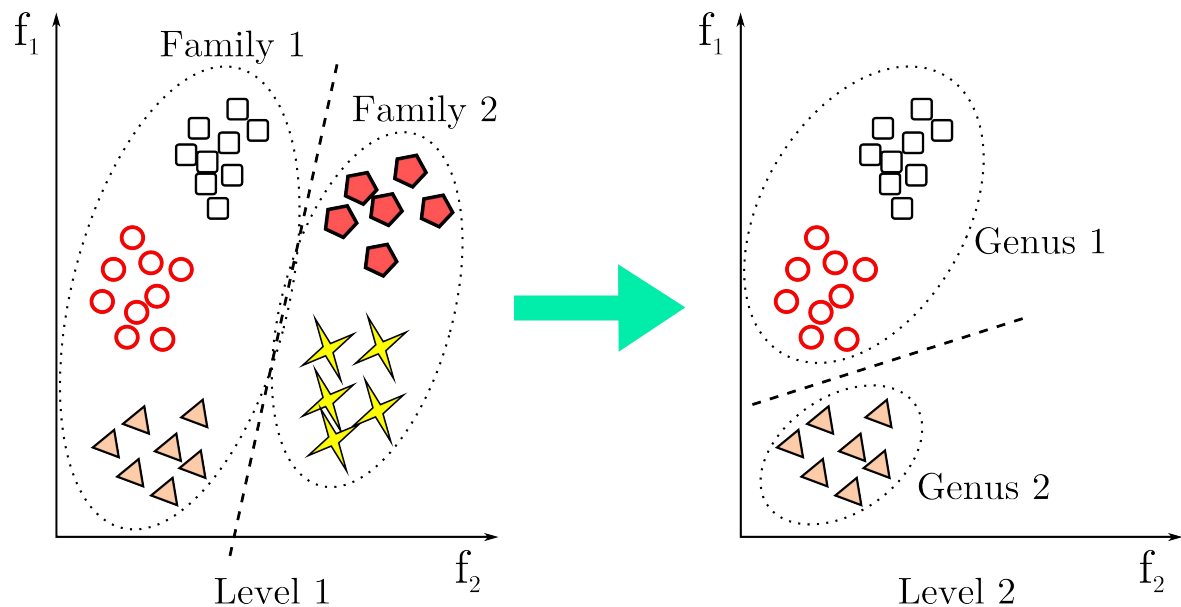
Hierarchical problem decomposition

- Problem simplification:



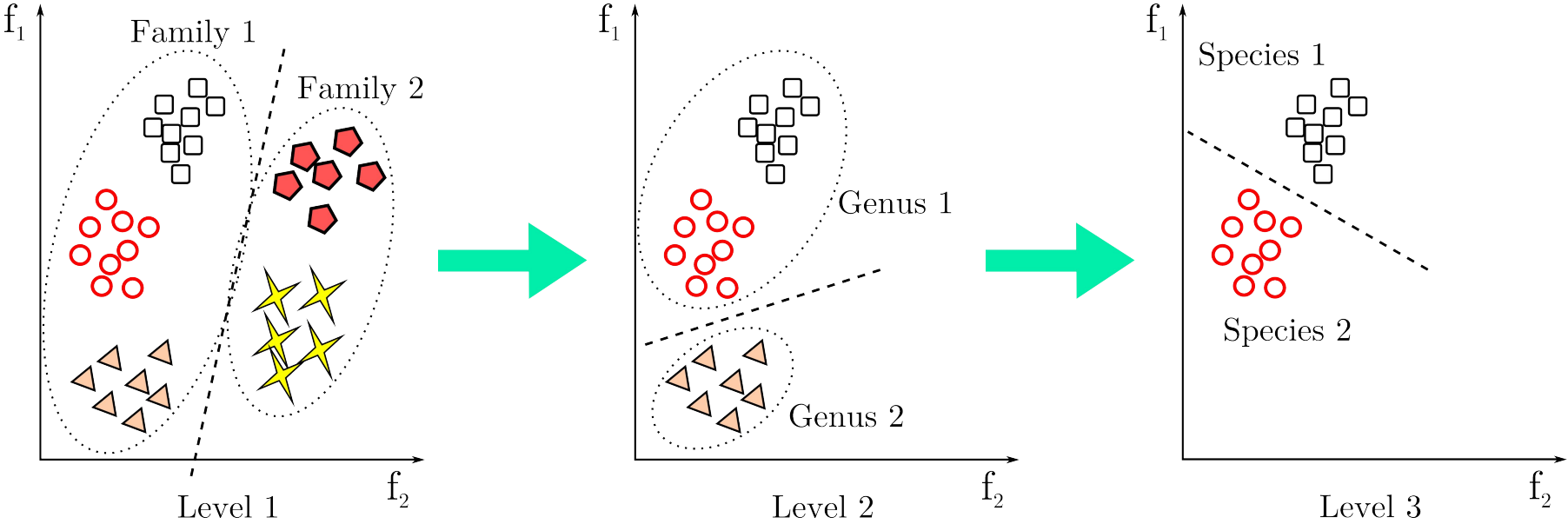
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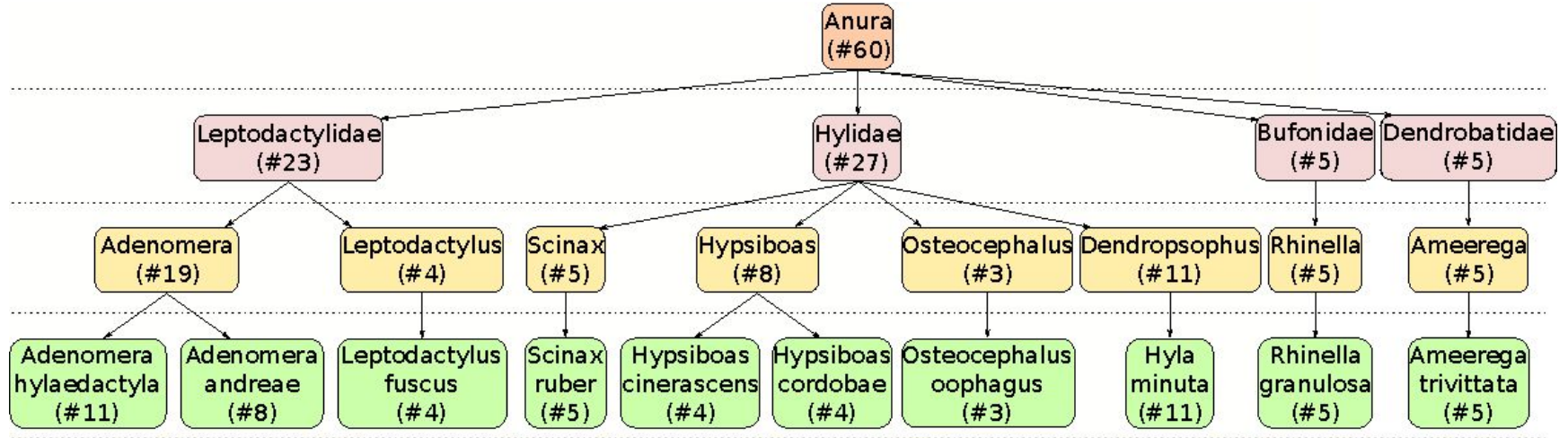


Our dataset

Family	Gender	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



This configuration allows us to simplify the problem, for instance: 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.

Experiment configuration

- A **kNN** was chosen as base classifier in each node ($k=3$).

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- A **Macro-accuracy** was used in evaluations to avoid an artificially increment of the Micro-accuracy due to unbalanced number samples in each class.
- **Baseline** comparison (dummy classifier):
 - Micro-accuracy = 0.5083
 - Macro-accuracy = 0.10

Results of family level

- Macro-accuracy is the average of the accuracies in each class, $M\text{-acc}=(0.31+0.89+0.94+0.90)/4=0.76$
- Micro=0.89

Table 2: Confusion matrix of family level with kNN (k=3). Last row (Acc) is the accuracy of each column.

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

Results of genus level

Macro-acc=0.60 and Micro=0.85

Table 3: Confusion matrix of gender level with kNN (k=3). Legend: (a) Adenomera, (b) Ameerega, (c) Dendropsophus, (d) Hypsiboas, (e) Leptodactylus, (f) Osteocephalus, (g) Rhinella, and (h) Scinax. Last row (Acc) is the accuracy of each column.

	a	b	c	d	e	f	g	h
a	3186	36	18	61	58	184	0	2
b	23	488	0	0	6	0	27	0
c	51	0	123	35	0	0	0	20
d	7	0	0	1117	0	6	0	1
e	15	0	20	14	134	21	16	2
f	7	0	0	48	4	34	3	0
g	8	0	0	9	63	0	43	12
h	15	0	50	11	0	0	0	20
Acc	0.89	0.89	0.53	0.98	0.60	0.35	0.31	0.20

Results of species level

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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*. Last row (Acc) is the accuracy of each column.

	a	b	c	d	e	f	g	h	i	j
a	156	0	35	2	61	0	58	184	0	0
b	0	3030	1	16	0	0	0	0	0	2
c	23	0	488	0	0	0	6	0	27	0
d	3	48	0	123	3	32	0	0	0	20
e	1	6	0	0	415	0	0	6	0	1
f	0	0	0	0	0	702	0	0	0	0
g	1	14	0	20	0	14	134	21	16	2
h	7	0	0	0	48	0	4	34	3	0
i	8	0	0	0	6	3	63	0	43	12
j	0	15	0	50	9	2	0	0	0	20
Acc	0.31	0.99	0.89	0.53	0.96	1.00	0.60	0.35	0.31	0.20

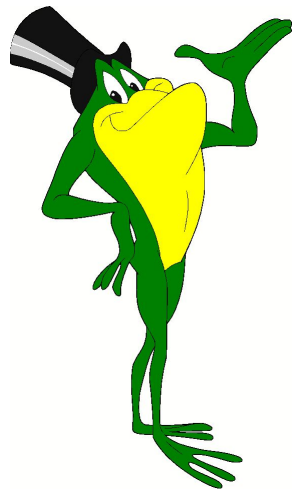
Summary and conclusions

- Baseline comparison against a dummy classifier:
 - **Micro gain** = +35%
 - **Macro gain** = +50%
- From a classification point of view the families **Bufo**, **Hyla** and **Lepto** were the most similar in the feature space.
- The **Scinax** species was the most difficult to recognize.
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Future work: Implement soft decision rules in the tree.



Thanks - Obrigado - Gracias