



# General introduction to barcoding and metabarcoding

Agnès Bouchez

The INRAE logo is positioned at the bottom left of the slide. It consists of the letters "INRAE" in a bold, teal, sans-serif font. The letter "E" is stylized with a circular element at its top right corner. The logo is partially overlaid by a large, abstract graphic on the left side of the slide, which is composed of several overlapping rounded hexagonal shapes in various shades of green and teal.

**INRAE**

The CARRTEL logo is located at the bottom right of the slide. It features the word "CARRTEL" in a bold, sans-serif font, with "CARR" in blue and "TEL" in green. To the right of the text is a circular emblem containing a stylized mountain range and a blue sky. Below the emblem, the text "CENTRE ALPAIN DE RECHERCHE SUR LES RÉSEAUX TROPHIQUES ET ÉCOSYSTÈMES LIMNIQUES" is written in a smaller, blue, sans-serif font.

**CARRTEL**  
CENTRE ALPAIN DE RECHERCHE  
SUR LES RÉSEAUX TROPHIQUES  
ET ÉCOSYSTÈMES LIMNIQUES



## Summary

- **DNA - some basics**
- DNA and barcoding
- DNA and metabarcoding

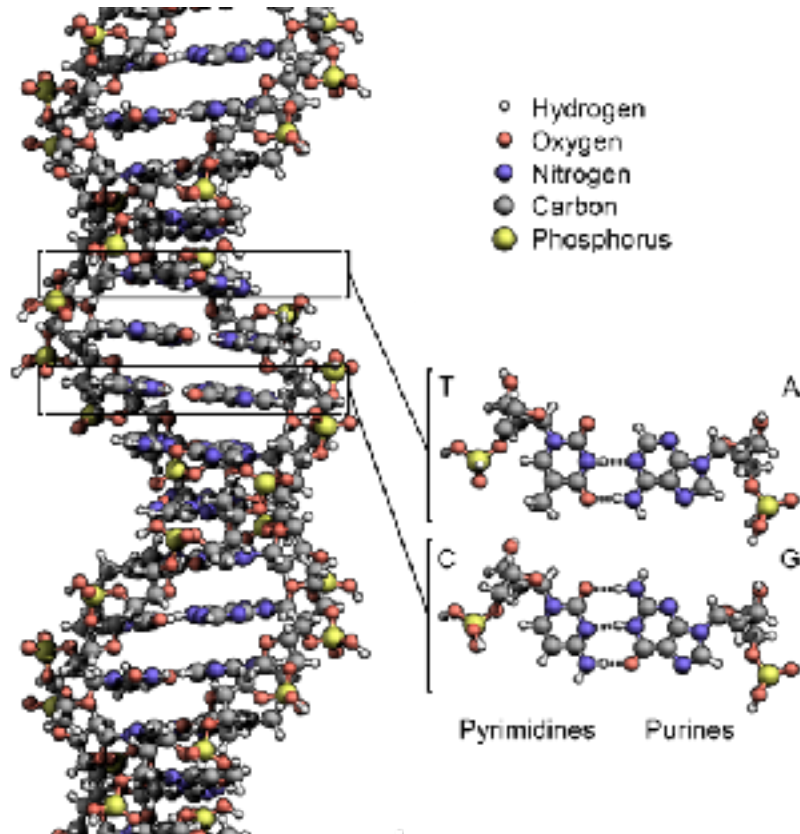




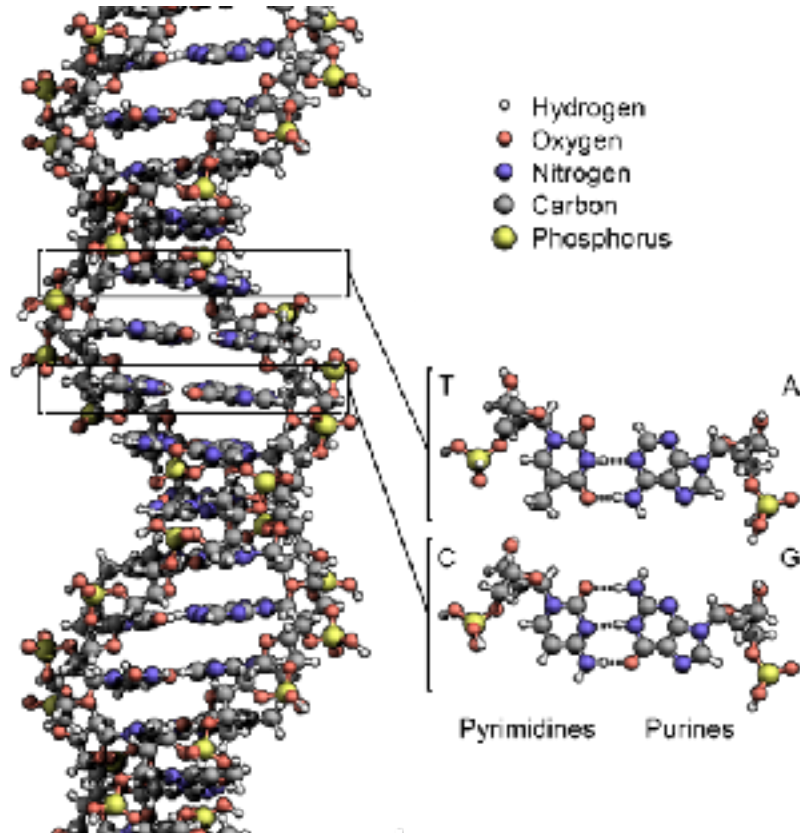
DNA = DesoxyriboNucleic Acid

Watson and Crick 1953

DNA molecule → a 3-dimensional  
double helix



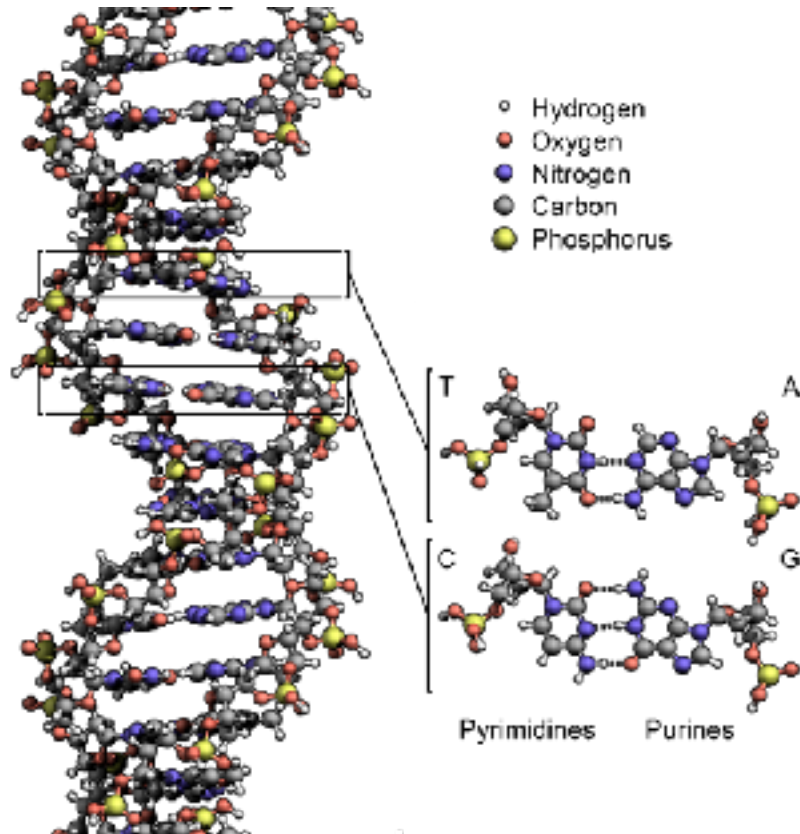
# DNA in all living organisms



DNA = DesoxyriboNucleic Acid

- All living organisms store genetic information using DNA

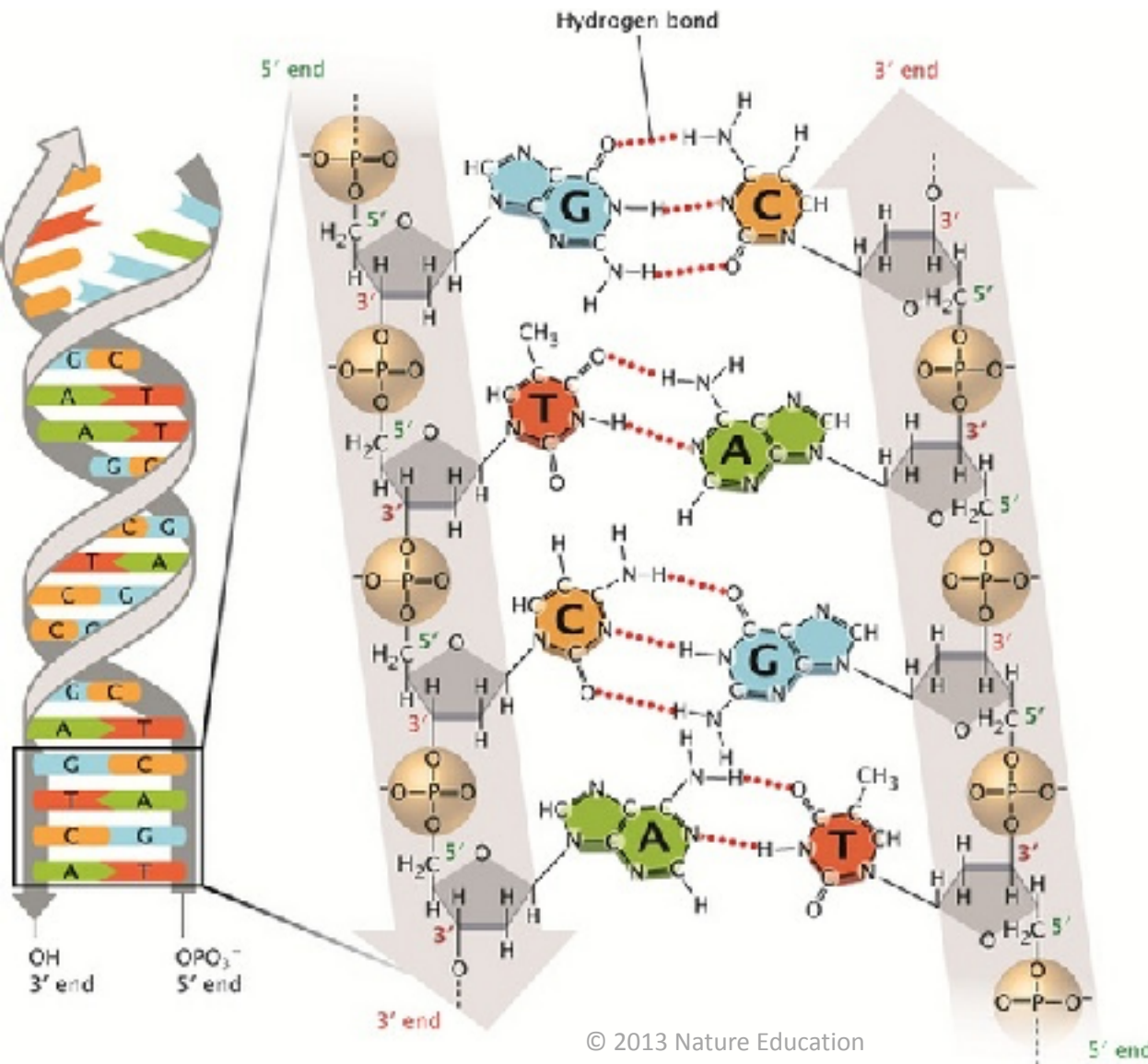
# DNA in all living organisms



## DNA = DesoxyriboNucleic Acid

- All living organisms store genetic information using DNA
- The genetic code is based on an assembly of 4 nucleic bases:
  - ✓ A = Adenine    ✓ T = Thymine
  - ✓ G = Guanine   ✓ C = Cytosine
- Bases go by pair A-T G-C linked by hydrogen bonds

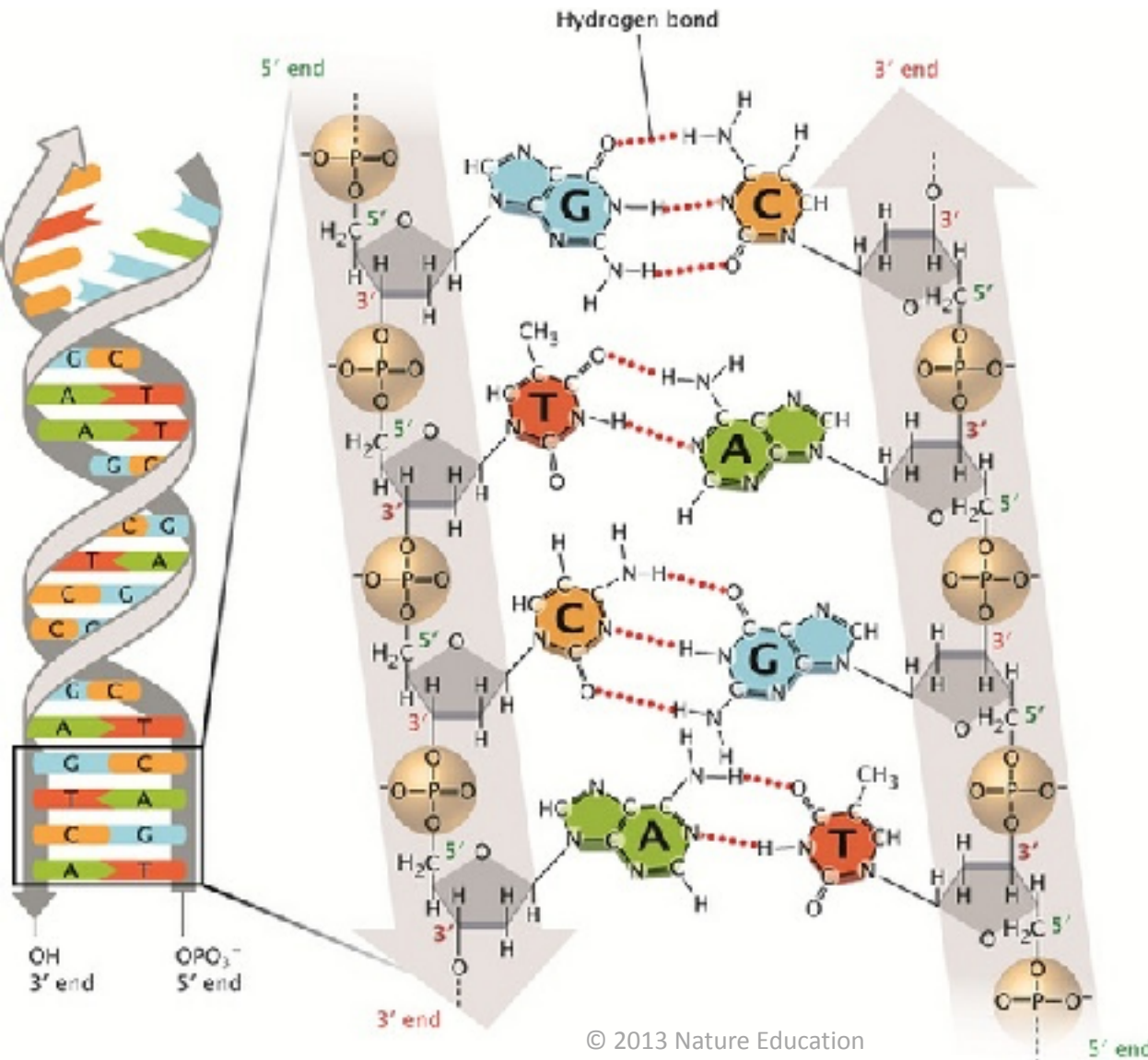
# DNA in all living organisms



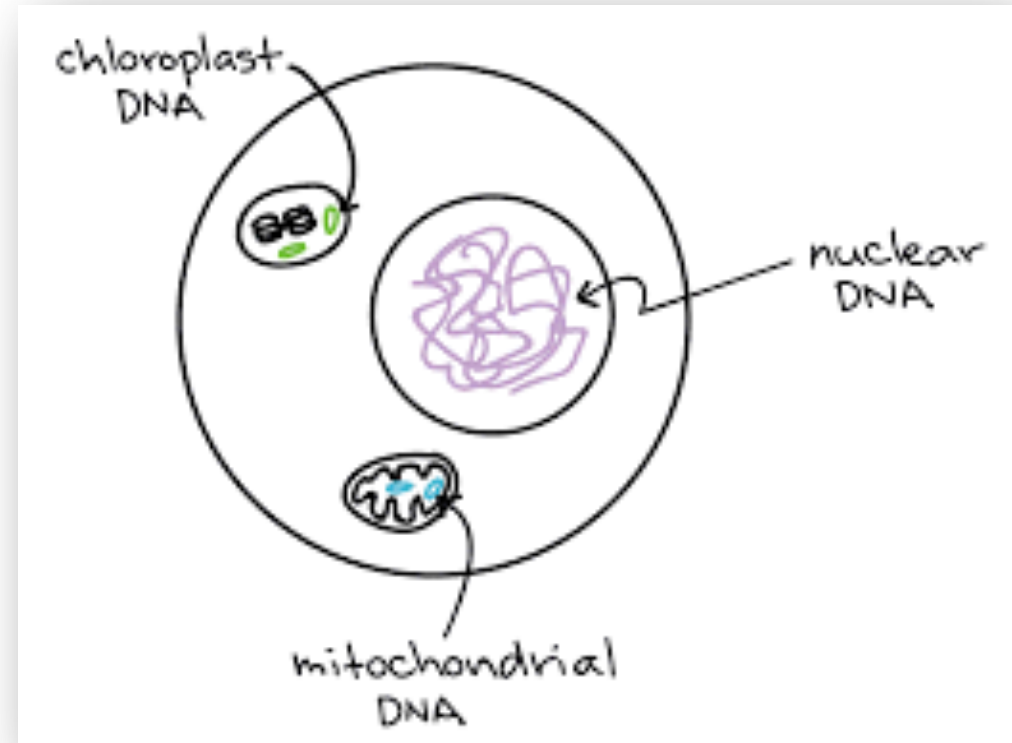
## DNA = DesoxyriboNucleic Acid

- All living organisms store genetic information using DNA
- The genetic code is based on an assembly of 4 nucleic bases:
  - ✓ A = Adénine
  - ✓ T = Thymin
  - ✓ G = Guanine
  - ✓ C = Cytosine
- Bases go by pair A-T & G-C linked by 2 or 3 hydrogen bonds, respectively
- Base/sugar/phosphate: Nucleotide
- Nucleotides assemble in a double helix

# DNA in all living organisms



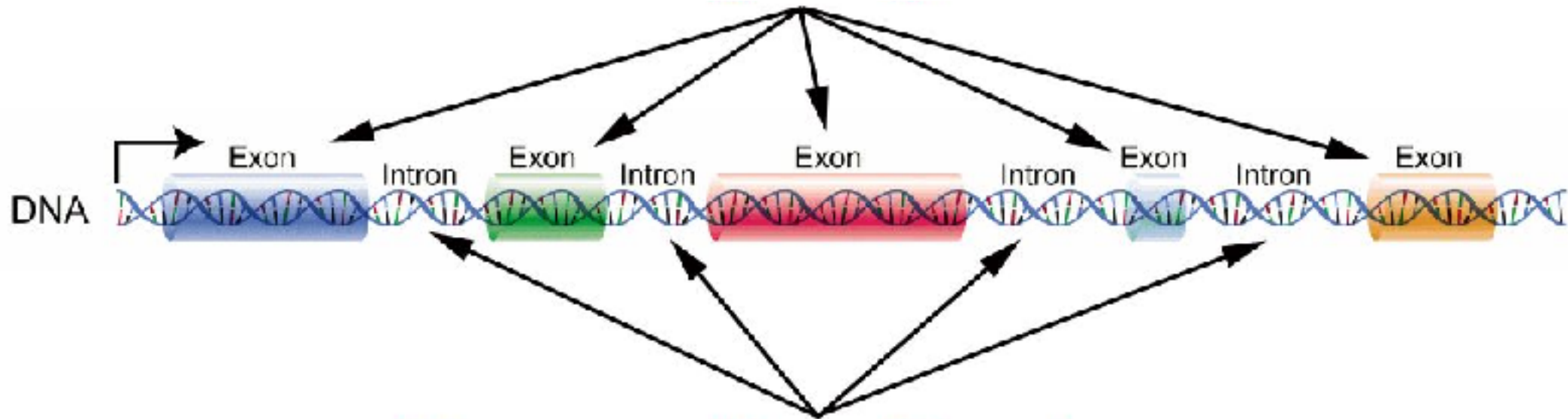
## DNA In the nucleus and organelles



# DNA in all living organisms



**Coding Regions (2%)**



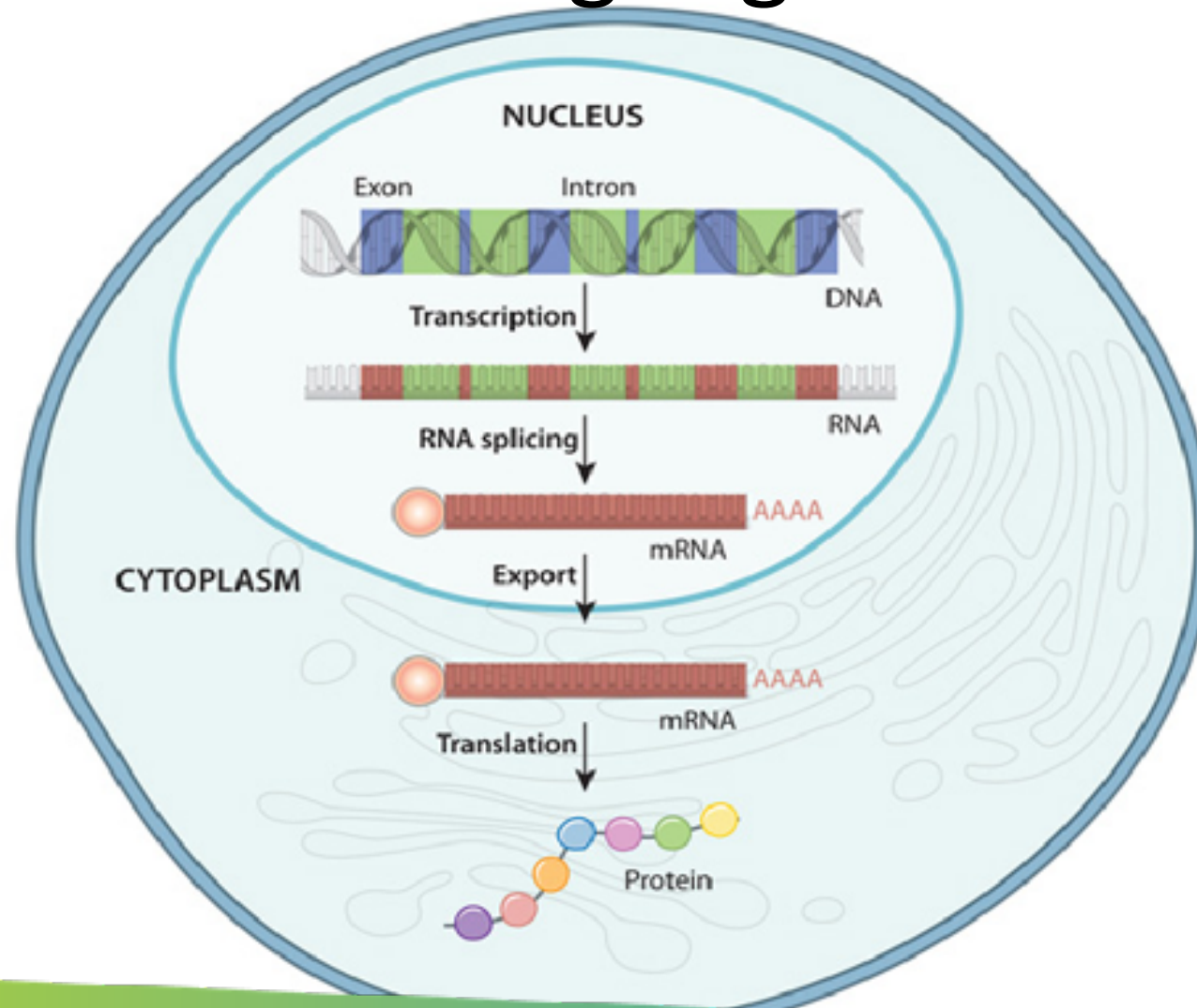
**Non-coding Regions (98%)**





# DNA in all living organisms

From DNA  
to proteins

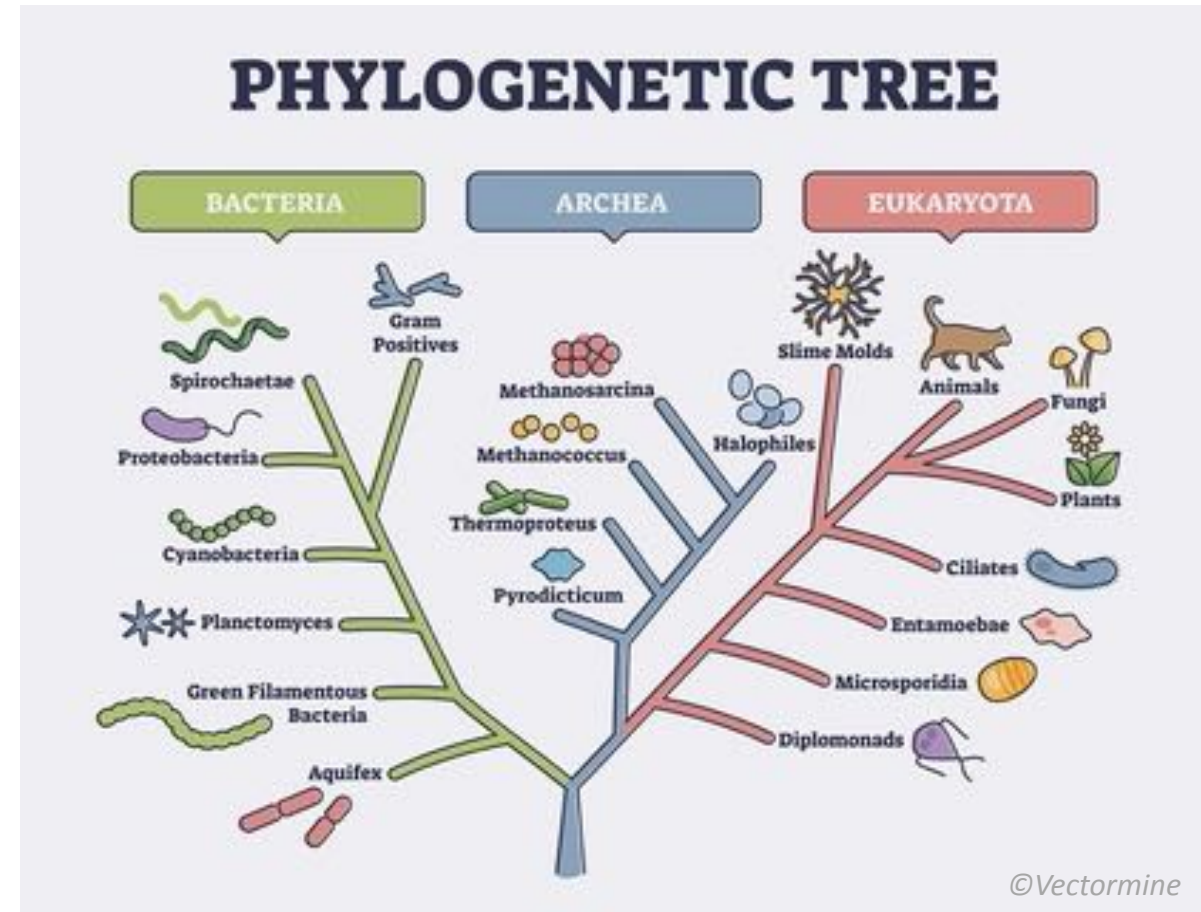




# DNA in all living organisms



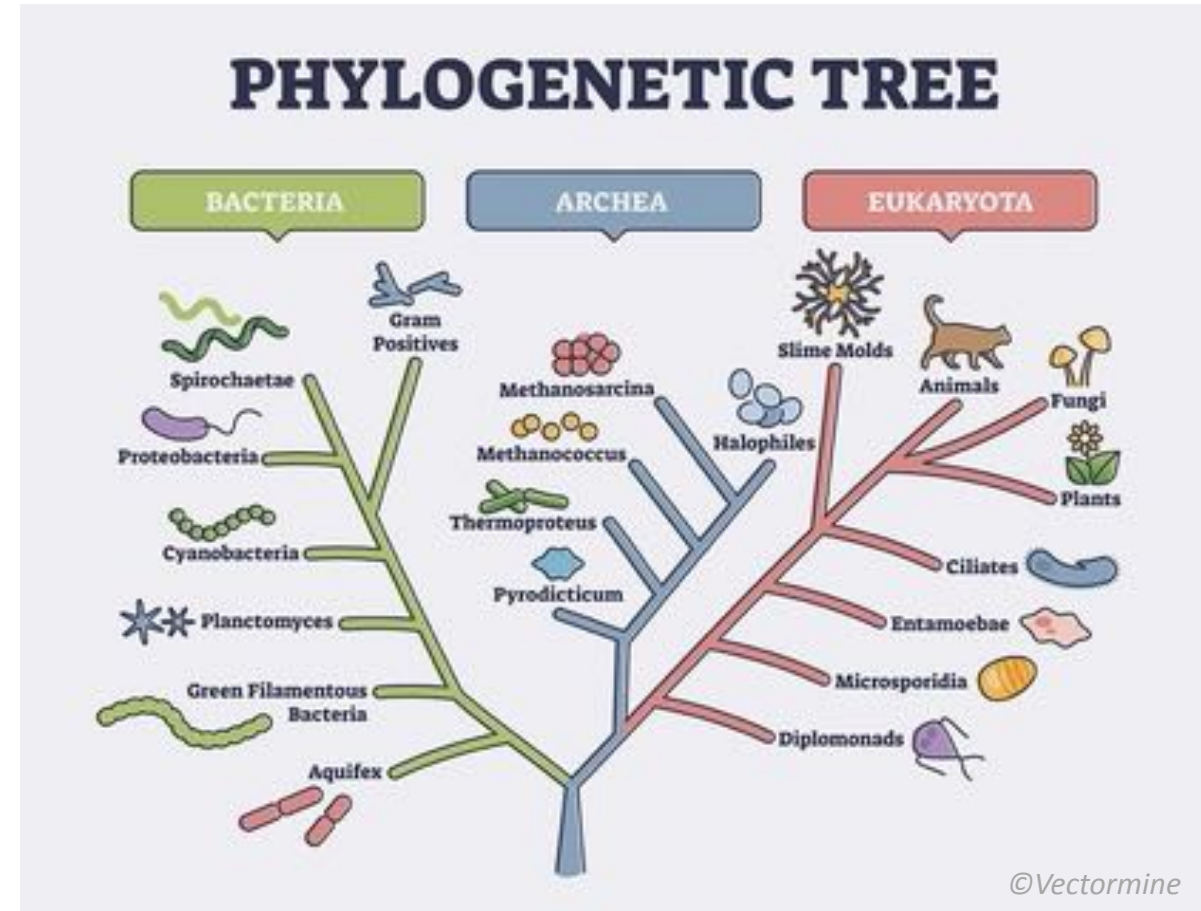
- Similar genes ... inherited from a common ancestor



# DNA in all living organisms



- Similar genes ... inherited from a common ancestor
- But each living organism has a different genetic code





## Summary

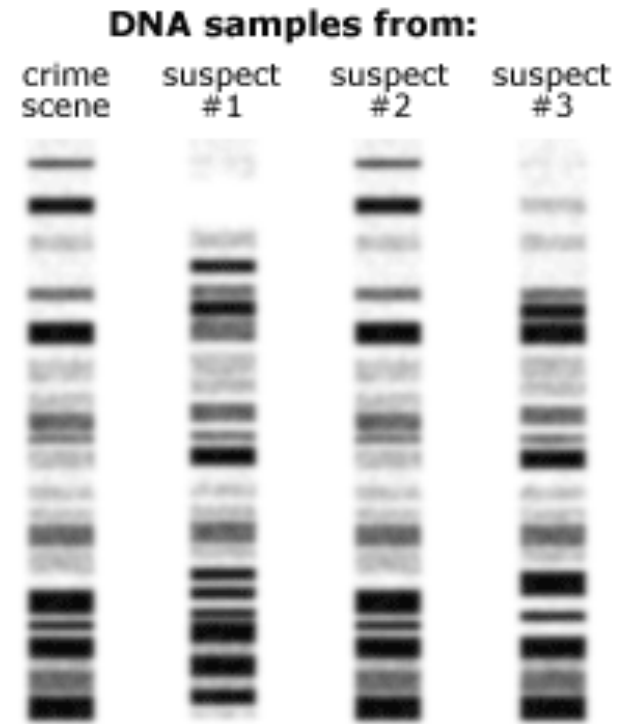
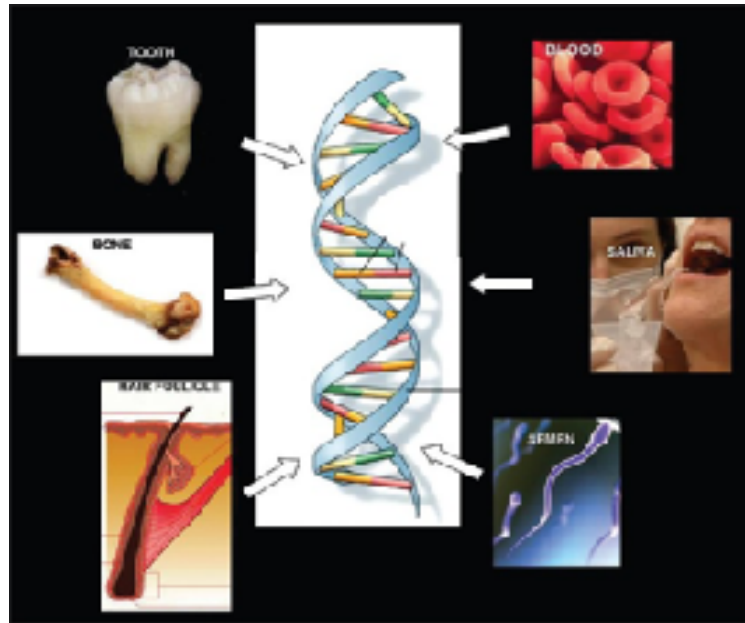
- DNA - some basics
- **DNA and barcoding**
- DNA and metabarcoding



# DNA: an identification tool

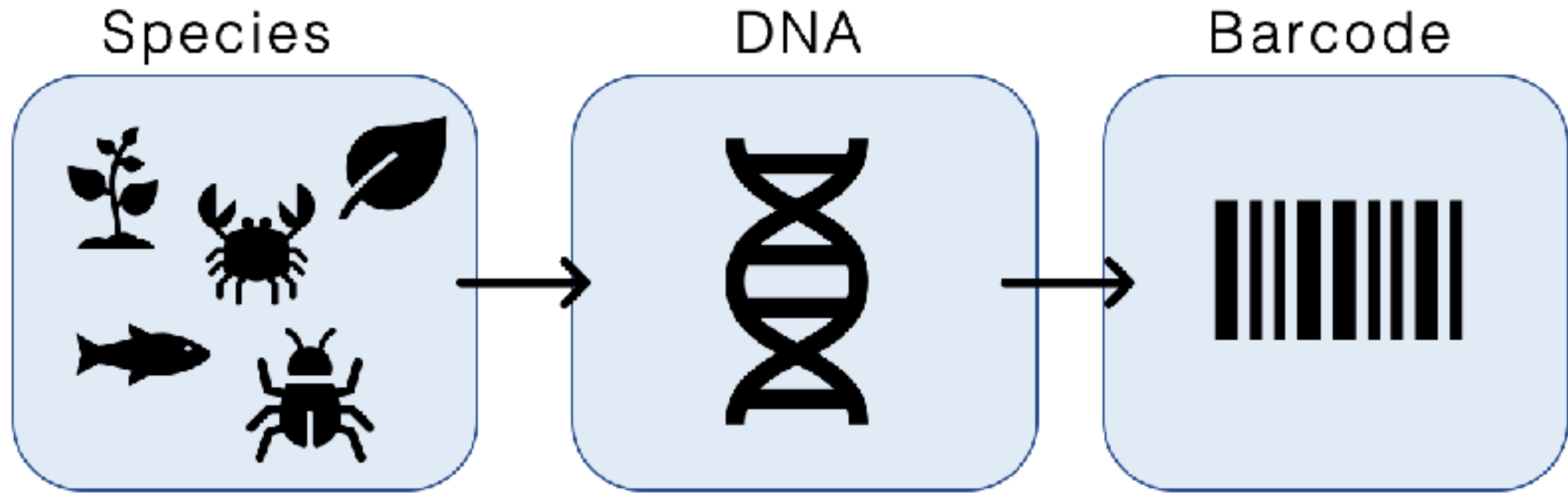


- In all living organisms
- In all their cells... and cell-remains





# ID tool à DNA Barcoding





# ID tool à DNA Barcoding

 THE ROYAL SOCIETY

Received 29 July 2002  
Accepted 30 September 2002  
Published online 8 January 2003

## Biological identifications through DNA barcodes

Paul D. N. Hebert\*, Alina Cywinska, Shelley L. Ball  
and Jeremy R. deWaard

*Department of Zoology, University of Guelph, Guelph, Ontario N1G 2W1, Canada*



*Hebert et al. 2003*





# DNA Barcoding



- Mitochondrial gene: cytochrome c oxidase subunit 1
- Barcode: a 658 pb region of the gene COX1 (or COI)

« *can serve as the core of a global bioidentification system for animals* »

# DNA Barcoding

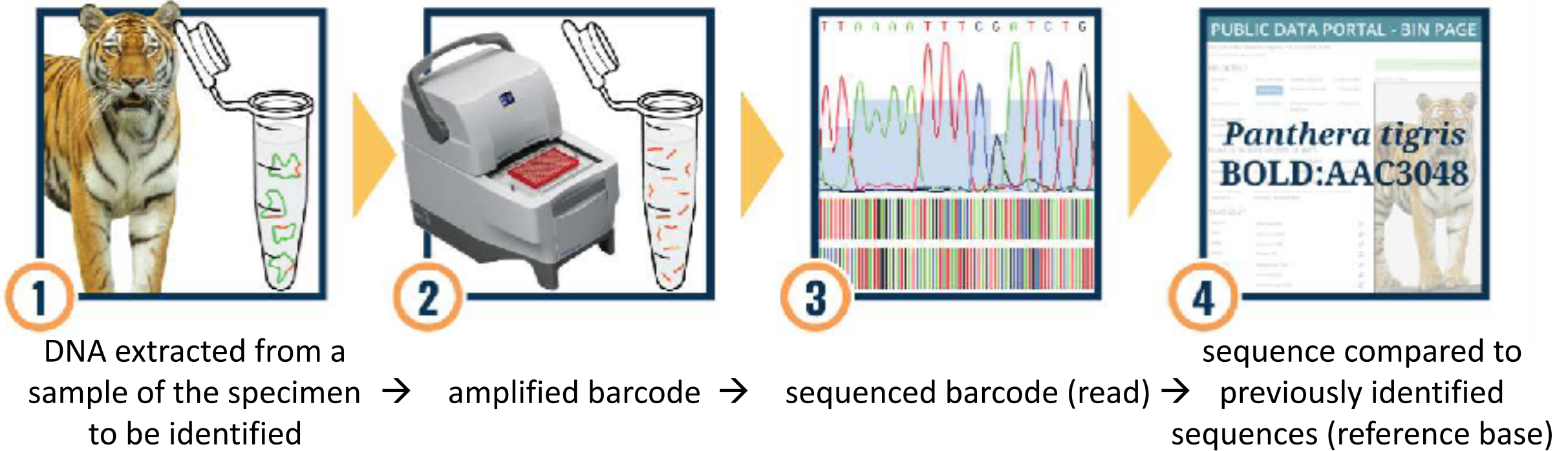


- Mitochondrial gene: cytochrome c oxidase subunit 1
- Barcode: a 658 pb region of the gene COX1 (or COI)

« *can serve as the core of a global bioidentification system for animals* »

- ❑ A DNA-based taxonomic ID tool for species
- ❑ A tool for sharing taxonomic expertise, overcoming the lack of experts
- ❑ A standardised method using specific information present:
  - in all species
  - at all their life stages (including early life stages)
  - In all their tissues

# DNA Barcoding



↓  
ID

# DNA Barcoding

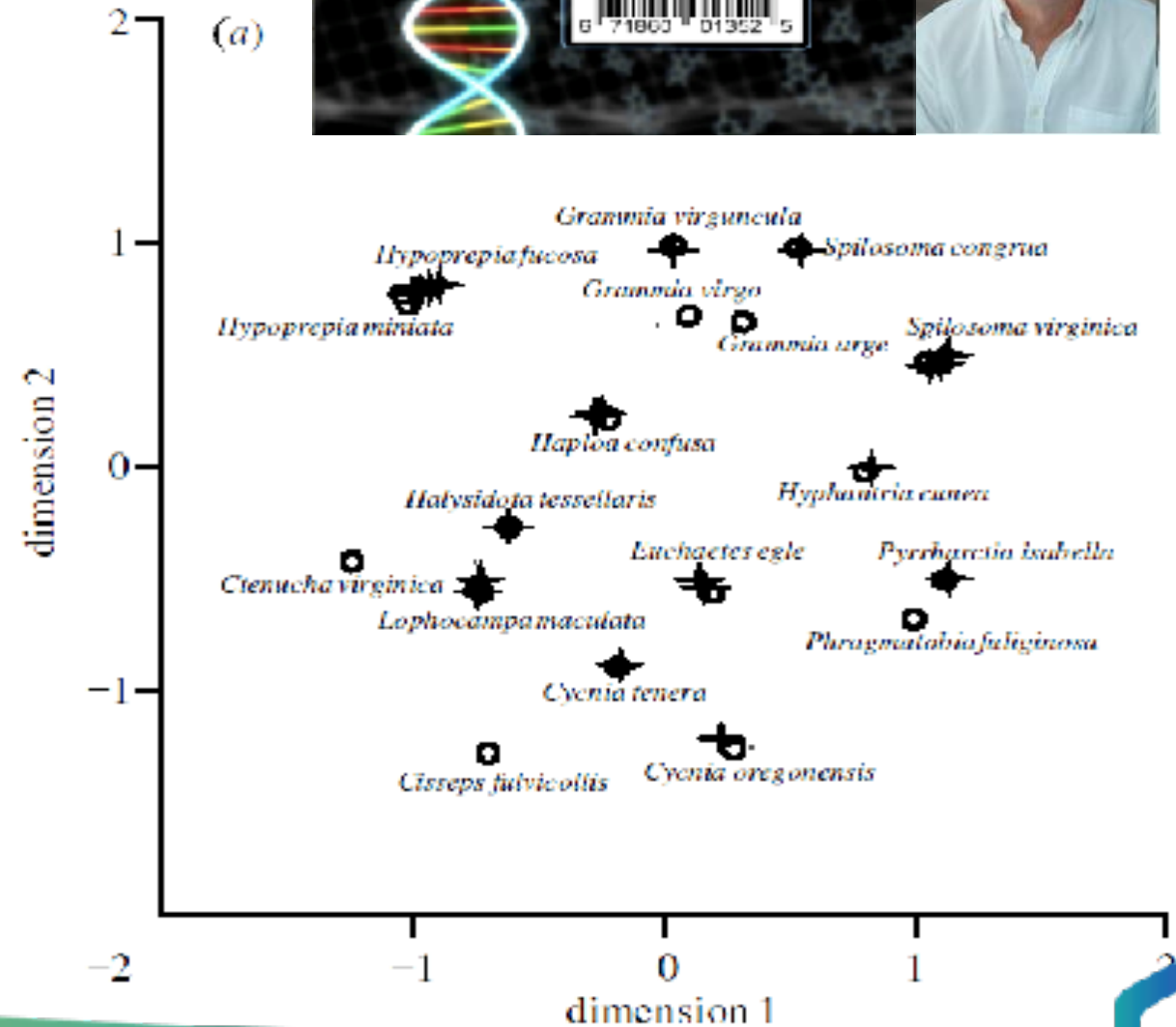


- ✓ Insects : 100 families from 8 orders
- ✓ **1 specimen per family (previously identified – morpho-taxonomy)**
- ✓ Sequencing of the COX1 barcode
  - Reference DNA/taxonomy
  - Taxonomic classification is consistent: morpho / DNA
- ✓ **50 specimens to identify**
- ✓ Sequencing of the COX1 barcode and comparison to references
  - 100% correctly identified at the order level

# DNA Barcoding

Test on **Lepidoptera**: a challenging group as there is little polymorphism in the COI barcode

- ✓ 200 species with ref DNA/taxonomy
- ✓ **Test on 150 specimens to identify**
- ✓ 100% correct ID at species level by comparing sequenced barcodes to reference barcodes
- ✓ ex: 18 sp articideae (+ tests; 0 refs)

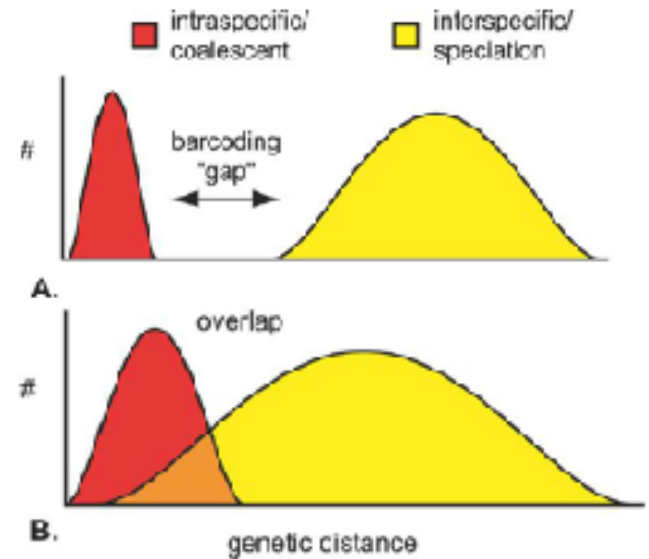
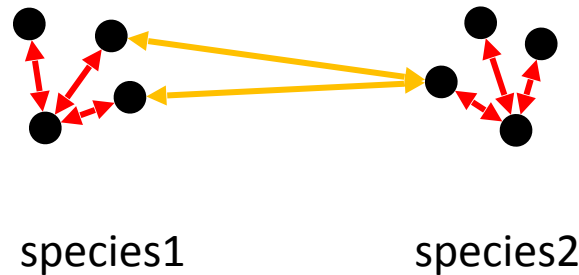
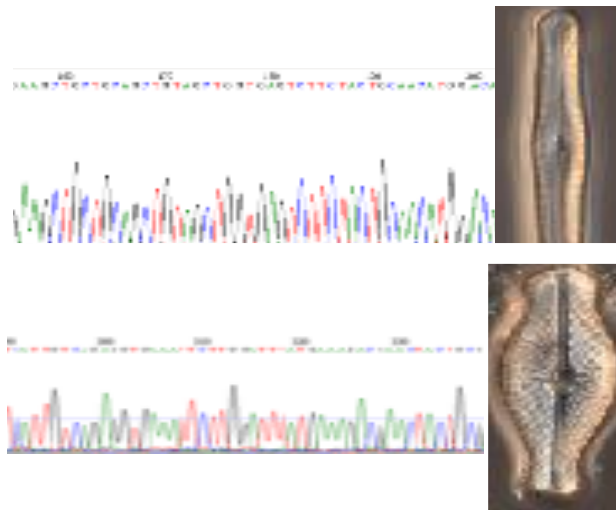


# DNA Barcoding

Hebert et al. 2003

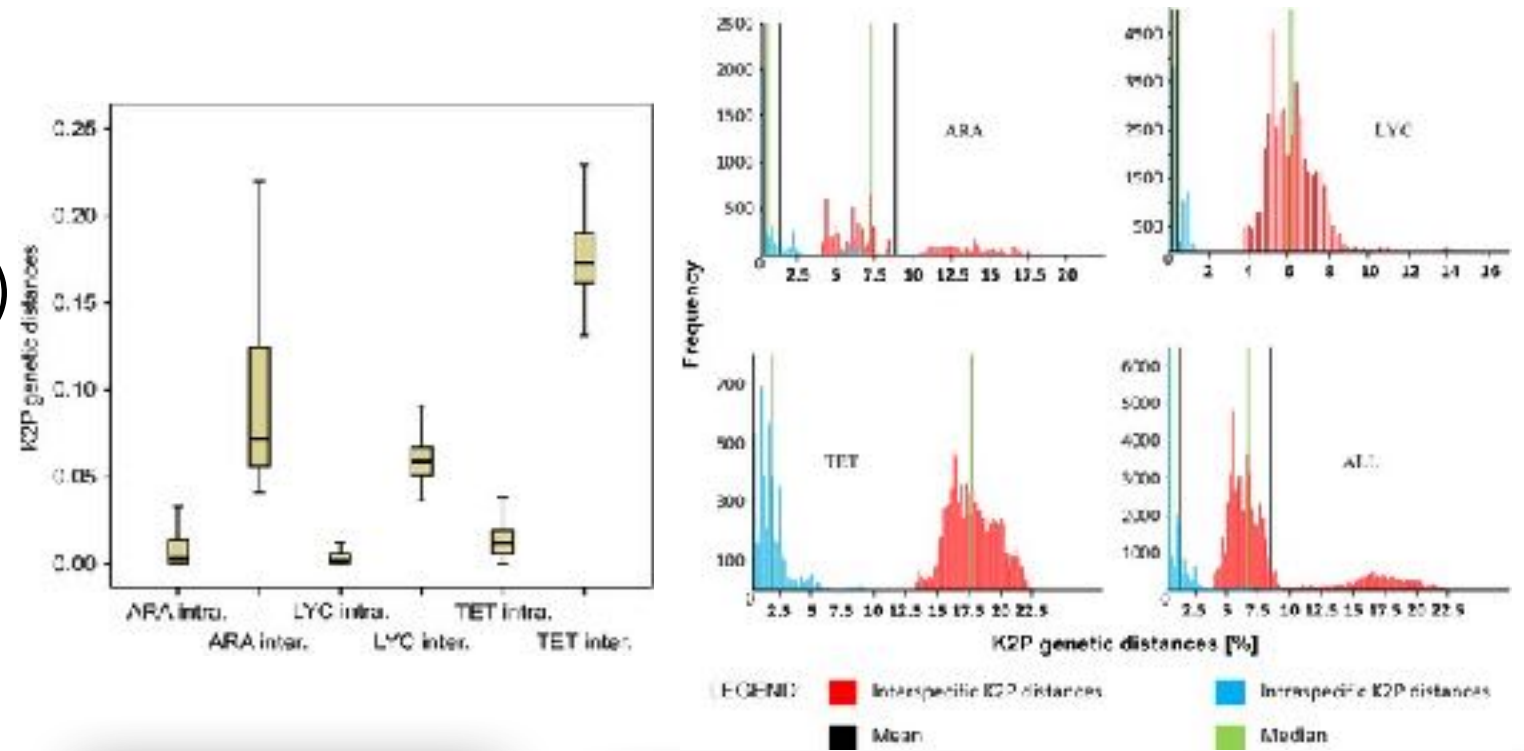


- Standardised approach to taxonomic ID
- Barcode: small DNA fragment specific to a taxa
- Identification is based on the existence of a “barcoding gap”



# DNA Barcoding: example

- ✓ 1203 individual spider barcodes
- ✓ 162 sp of 3 families
- ✓ (*Araneidae*, *Tetragnathidae*, *Lycosidae*)
- Good efficiency of the DNA barcode for the identification of spider species.
- The size of the barcoding-gap depends on the taxonomic group.



Candek and Kuntner 2015

# DNA Barcoding

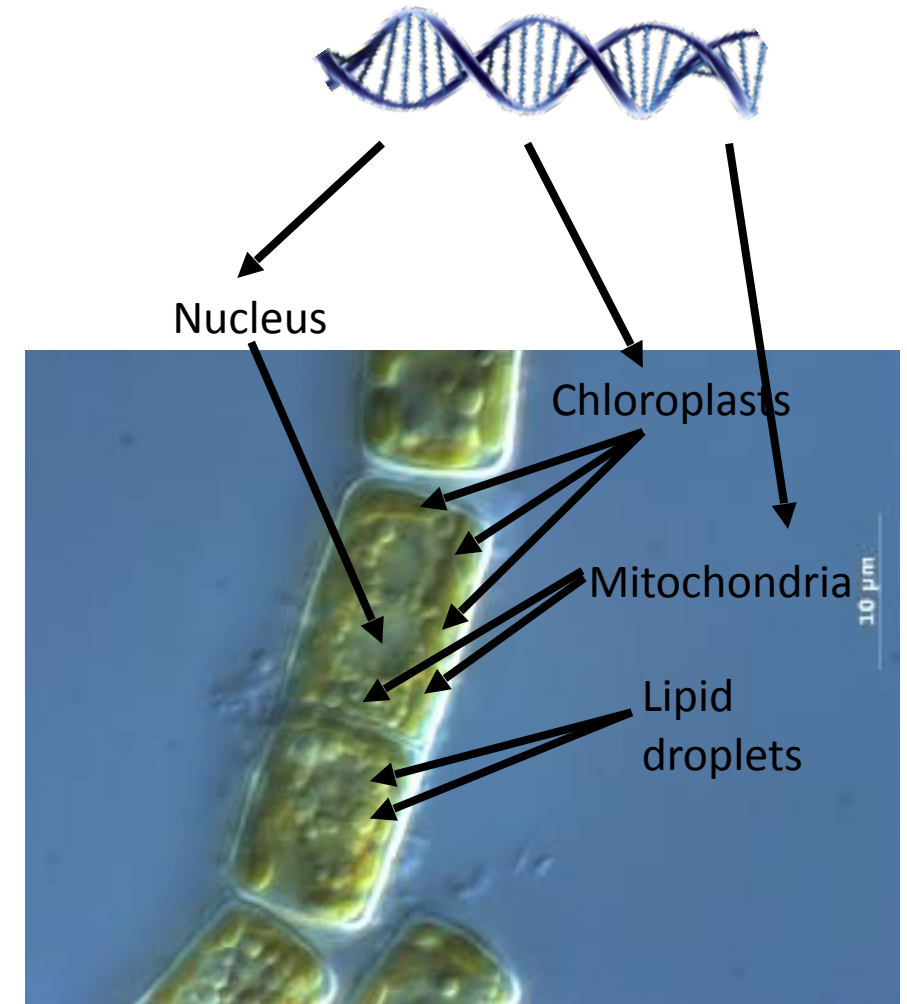
- Identification to species level using a single "universal" molecular marker s barcode... Not an achievable goal!
  
- Group-specific barcodes
  - Metazoans: COI
    - Fish: 12S
  - Fungi: ITS
  - Plants : *rbcL* et *MATK*
    - Diatoms : *rbcL* (18S)



# DNA Barcoding: diatoms

## Barcodes

- ***rbcL*** chloroplastic gene coding for the large sub-unit of the RuBisCo (photosynthesis)
- ***CO1*** mitochondrial gene coding for the cytochrome c oxydase I
- ***rDNA 18S*** nuclear gene coding for ribosomal RNA18S



# DNA Barcoding: diatoms

*Gomphonema parvulum* :

25 strains from tropical streams

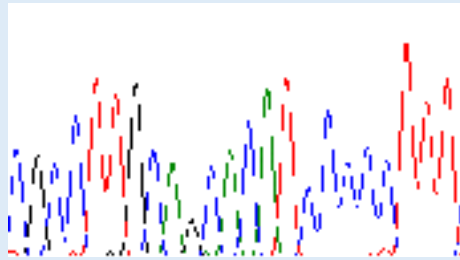
11 strains from temperate streams

+ 1 *G. exilissimum* (tropical stream)

+ 1 *G. cf. lagenula* (tropical stream)

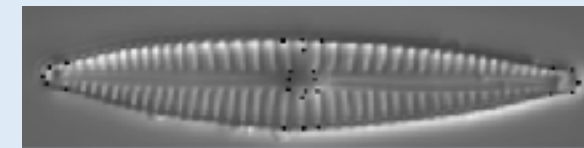
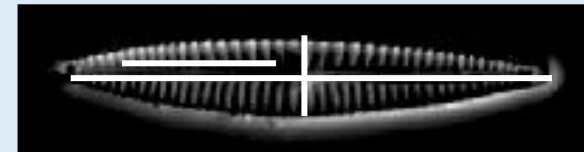


Sanger sequencing



Kermarrec et al., 2013

Morphotaxonomy



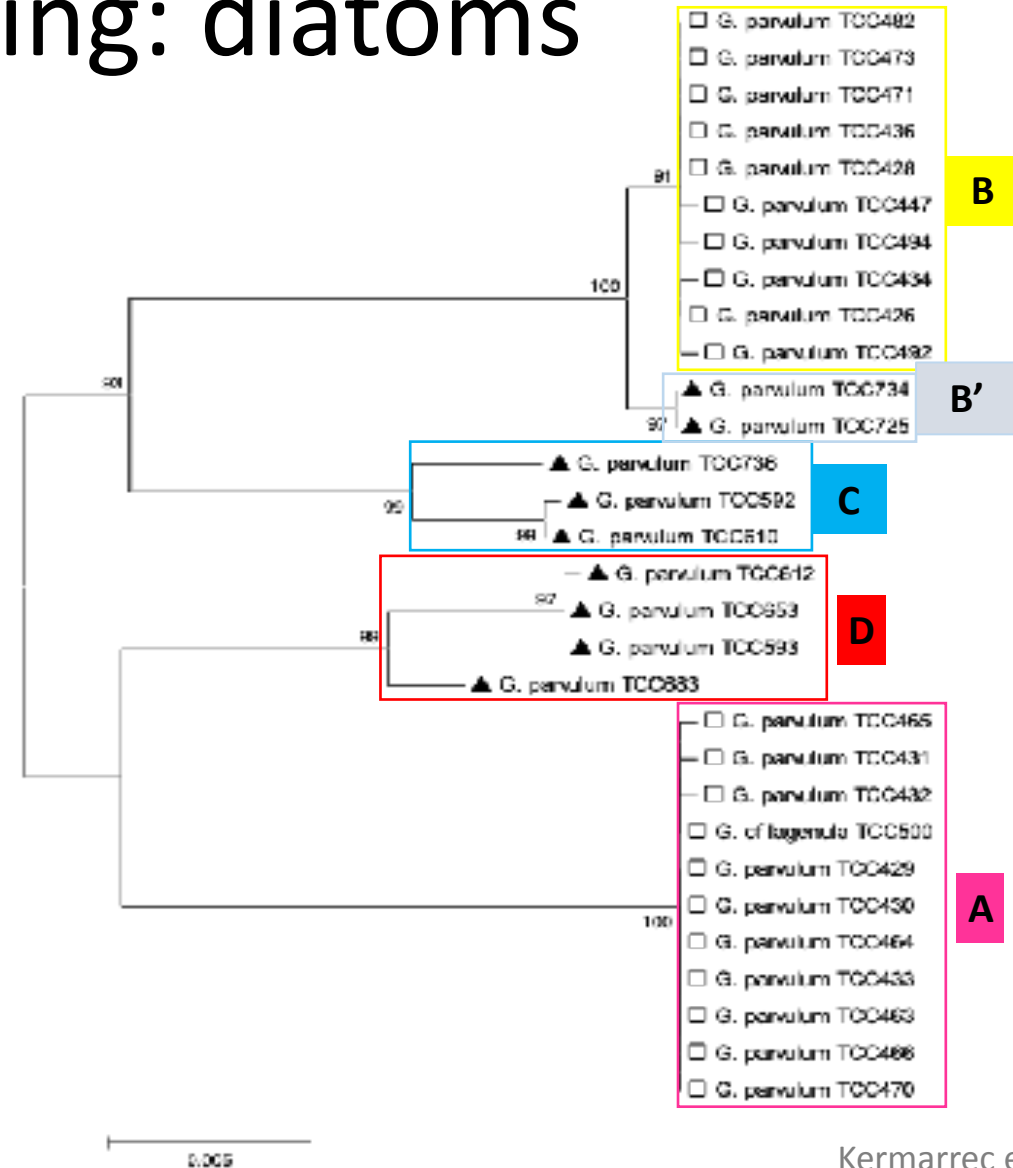
# DNA Barcoding: diatoms

**18S:** allows defining the group of *G. parvulum* in the *Gomphonema* genera

**cox1 / rbcL:**

- 4 main clades: A, B/B', C et D

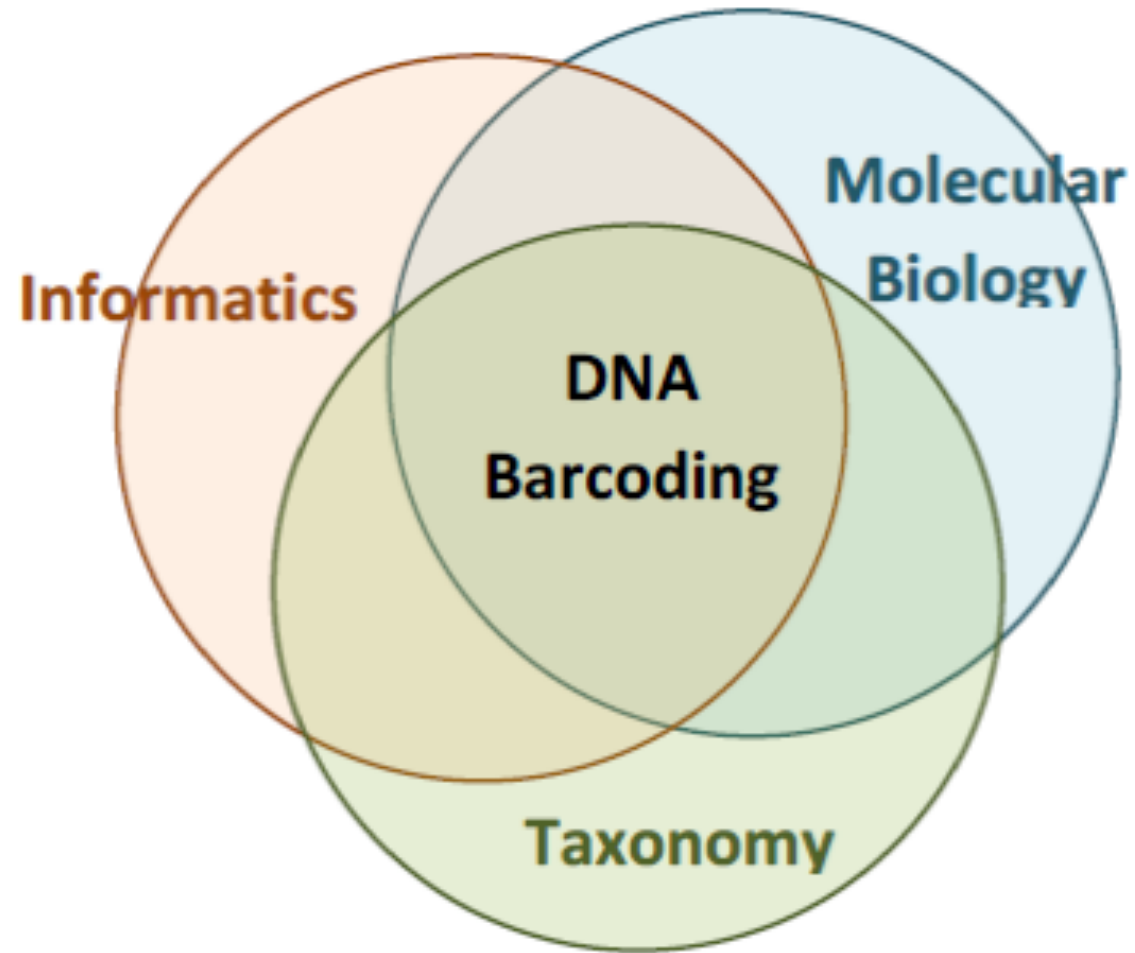
→ highlighting cryptic diversity in *G. parvulum*



Kermarrec et al., 2013

# DNA Barcoding

A tool for taxonomic ID  
at the crossroads of  
several disciplines

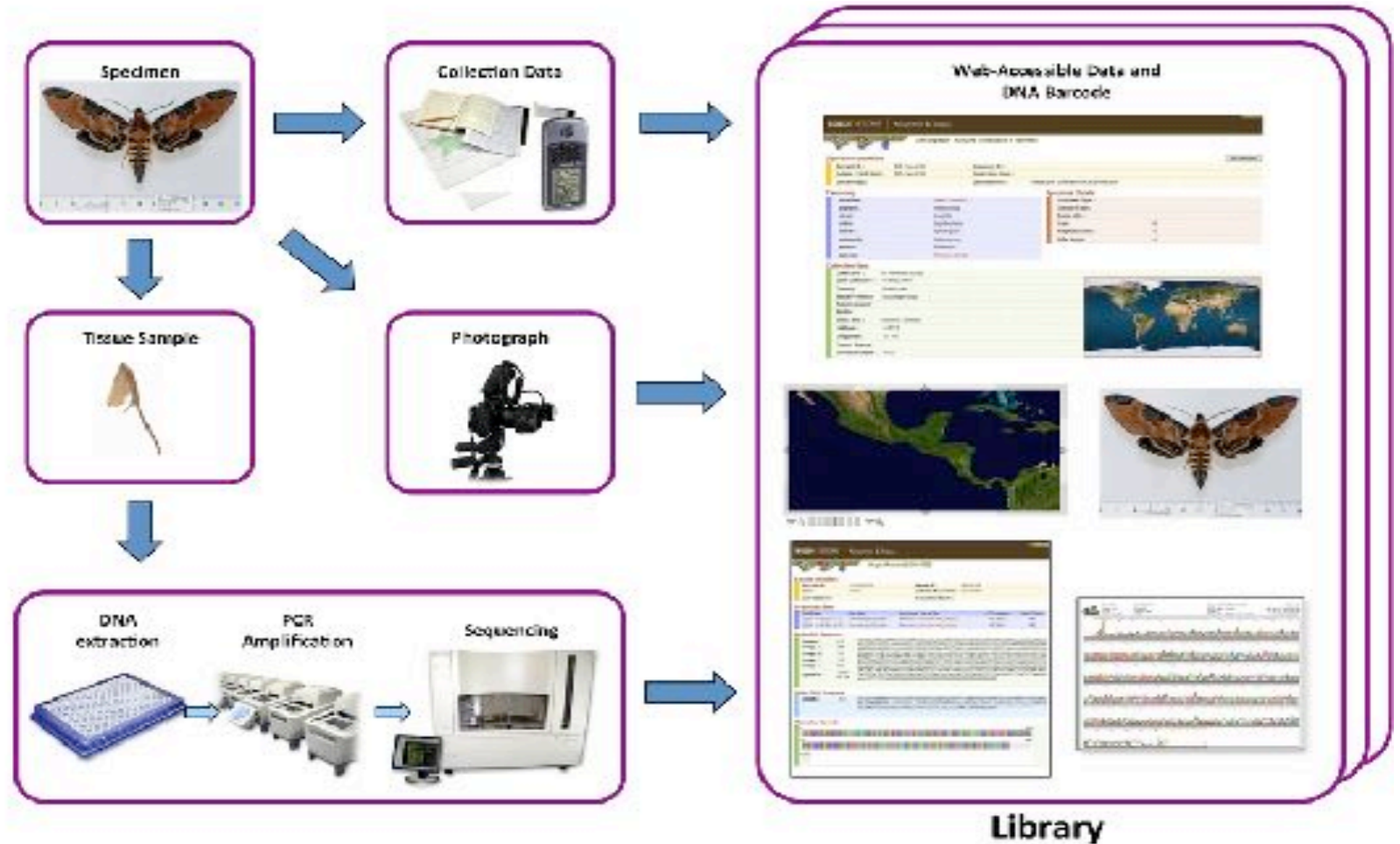


# DNA Barcoding

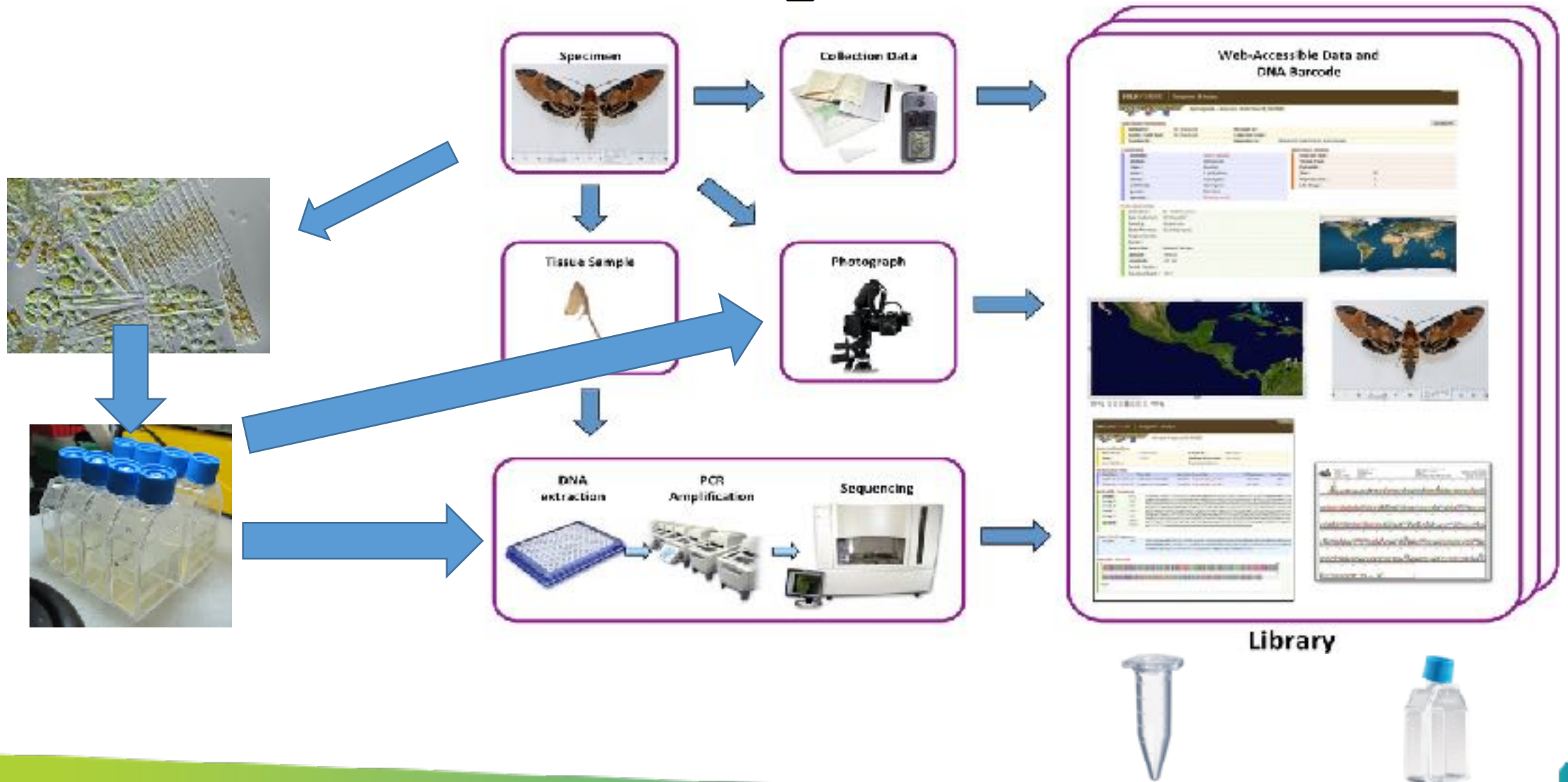


# DNA Barcoding

Key point:  
The Reference Library!



# DNA Barcoding



# DNA Barcoding: uses



Endangered species



Invasive alien species



Environmental monitoring



Food fraud



Wildlife crime



Pathogens and vectors

## Identify:

- Invasive alien species
- Endangered species
- «*sensitive*» species (*commercial, biomedical, pathogenic...*)
- Indicator species or key species

## For the purposes of:

- Quarantine inspection
- Fraud control
- Environmental assessment
- Biodiversity conservation



# DNA Barcoding: uses

## Detection of morphologically 'unidentifiable' organisms

→ early detection

- Incomplete specimens (tissue, fragment...) *e.g. paleo samples*
- Degraded specimens (feces, food...) *e.g. gut content*
- Young stages (larva) *e.g. macroinvertebrate inventories*

## But also:

- Access to undescribed diversity
- Access to cryptic diversity





## Summary

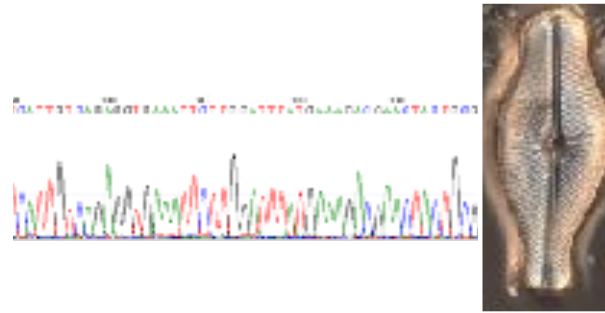
- DNA - some basics
- DNA and barcoding
- **DNA and metabarcoding**



# DNA Barcoding → DNA Metabarcoding

## ❖ 2003: DNA Barcoding (Hebert et al. 2003)

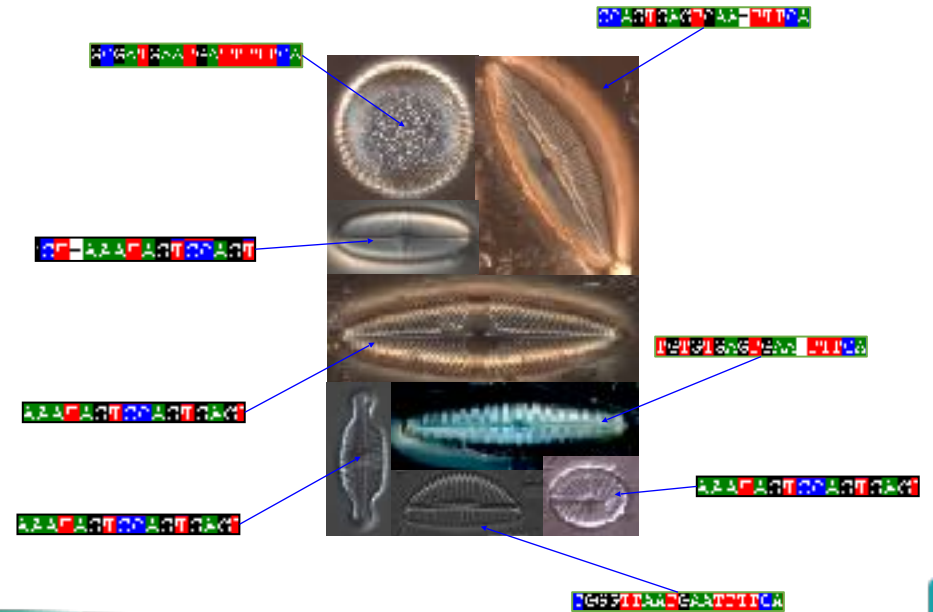
Standardised DNA-based ID tool  
Barcode: short DNA fragment  
taxa-specific  
easy to sequence



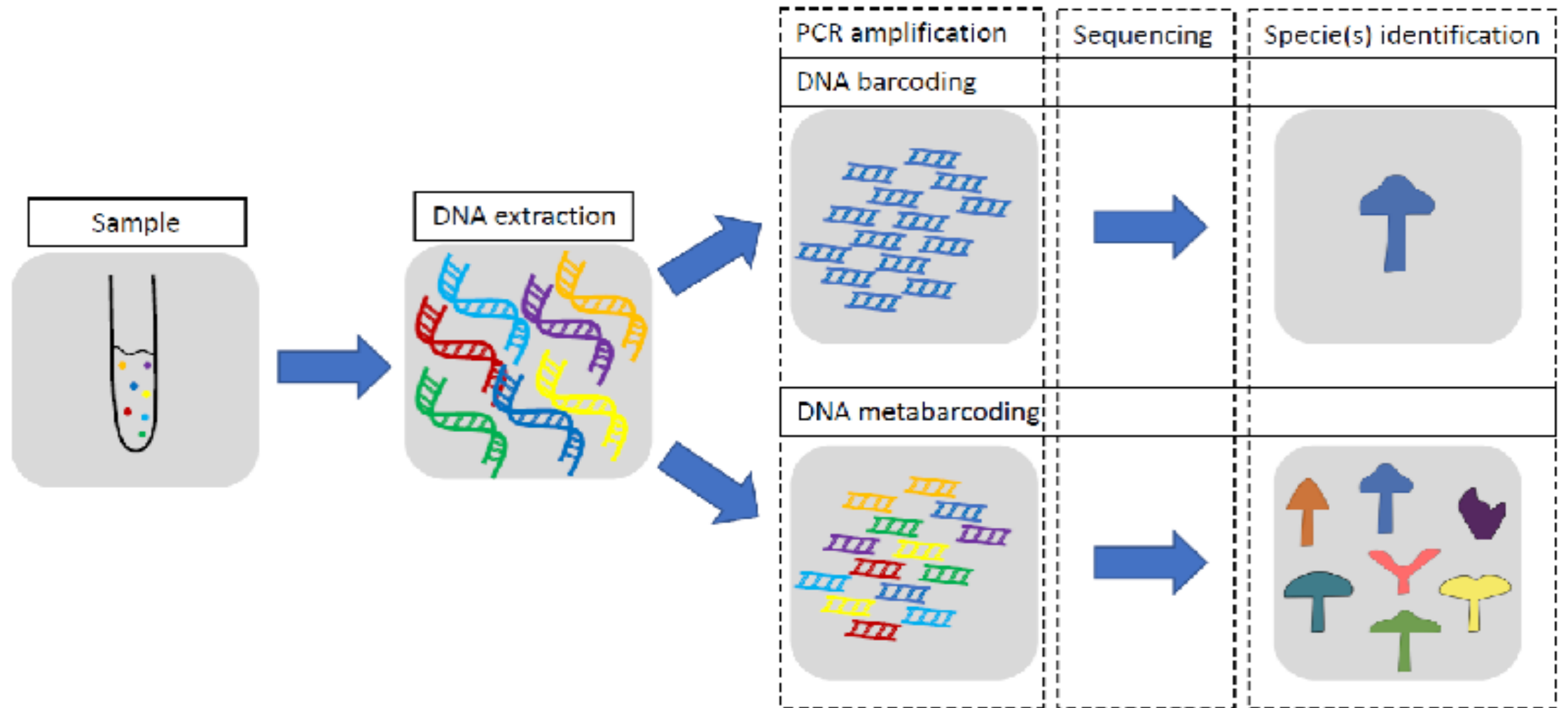
## ❖ 2012: DNA Metabarcoding (Taberlet et al. 2012)

- Extending the concept to the study of natural samples
- Identification of organisms within a community
- Use of "next-generation", "high-throughput" sequencing

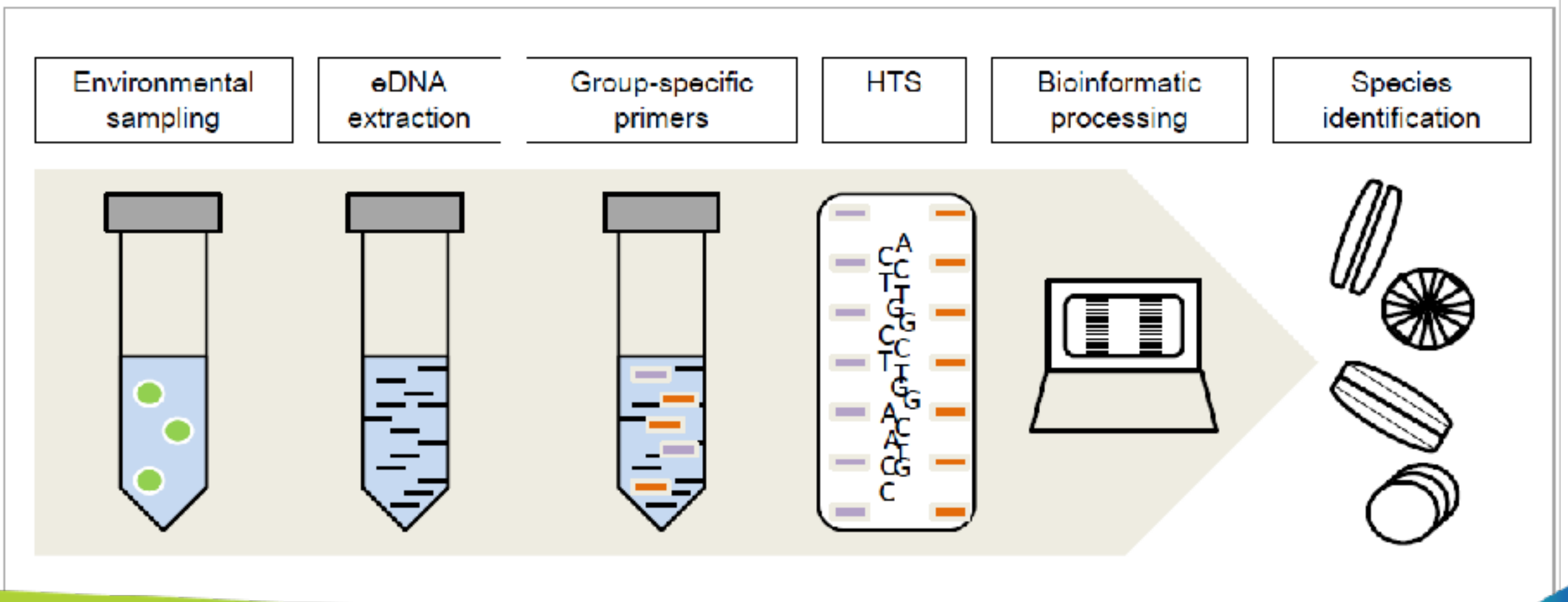
>> **Benefits: Reduce analysis time, reduce costs, facilitate intercalibration**



# Barcoding / Metabarcoding



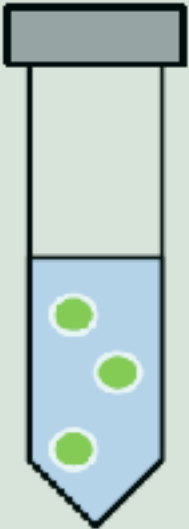
# DNA Metabarcoding



# DNA Metabarcoding

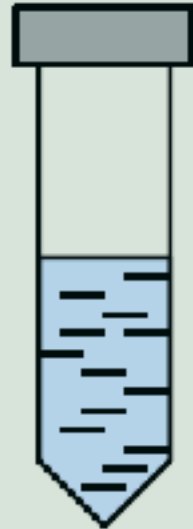
## Field sampling

Environmental  
sampling



## Molecular biology

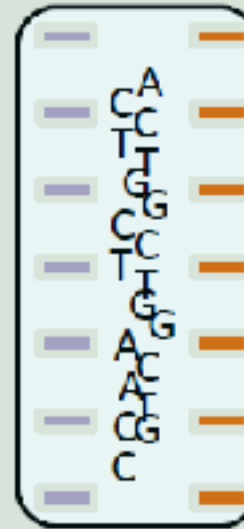
eDNA  
extraction



Group-specific  
primers



HTS



## Bioinformatics

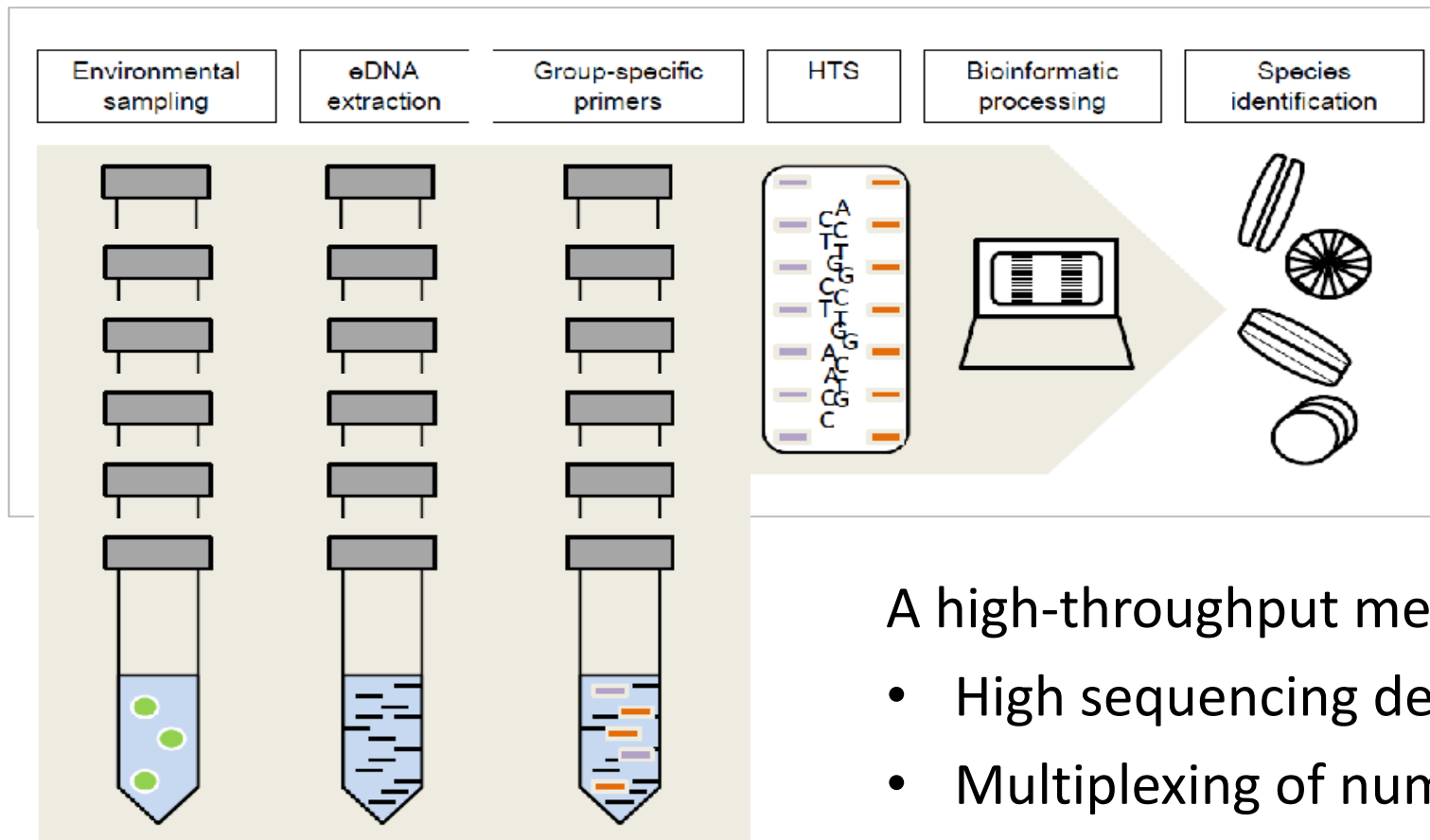
Bioinformatic  
processing



Species  
identification



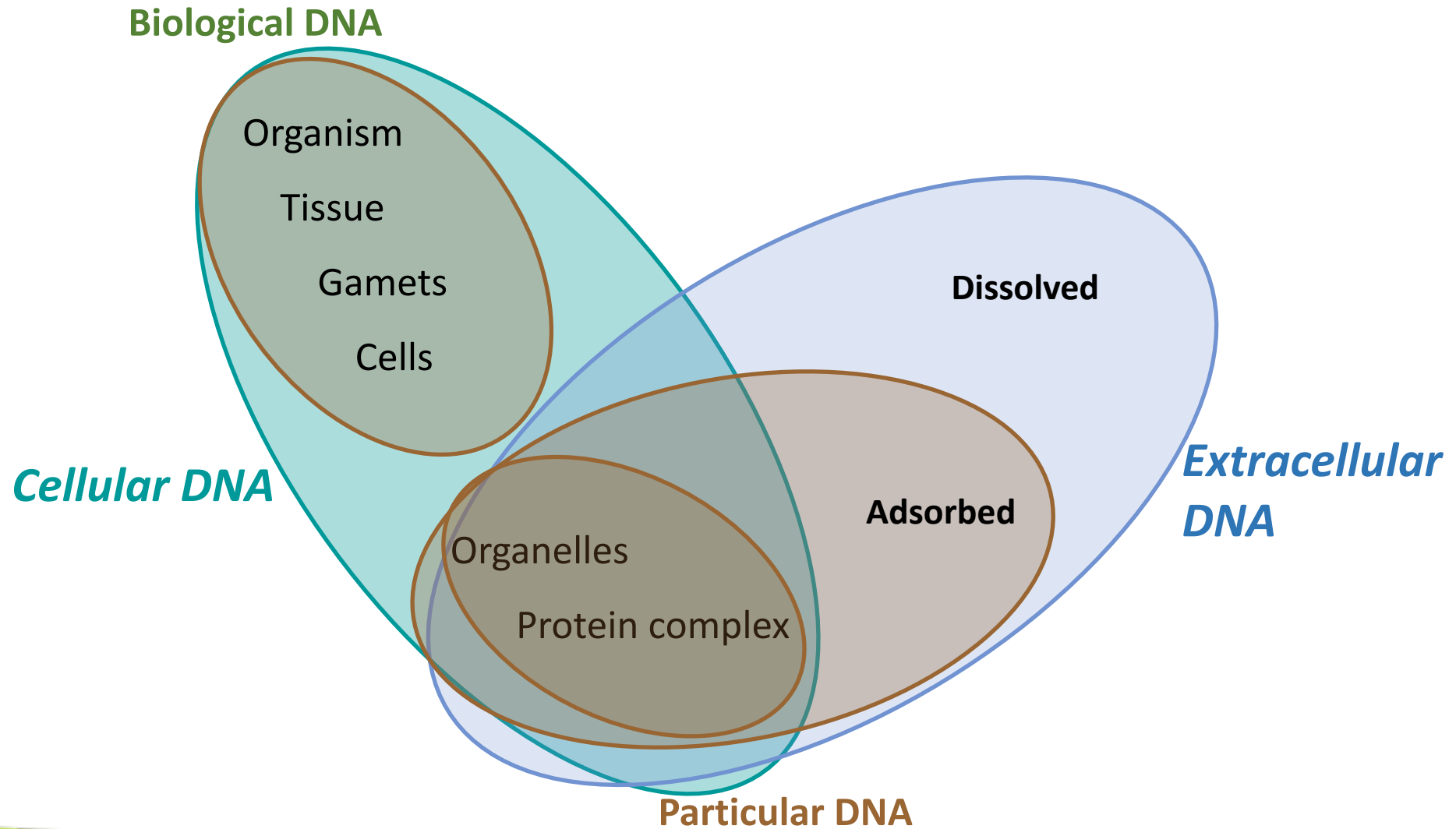
# DNA Metabarcoding



A high-throughput method

- High sequencing depth per sample
- Multiplexing of numerous samples

# Metabarcoding: DNA material

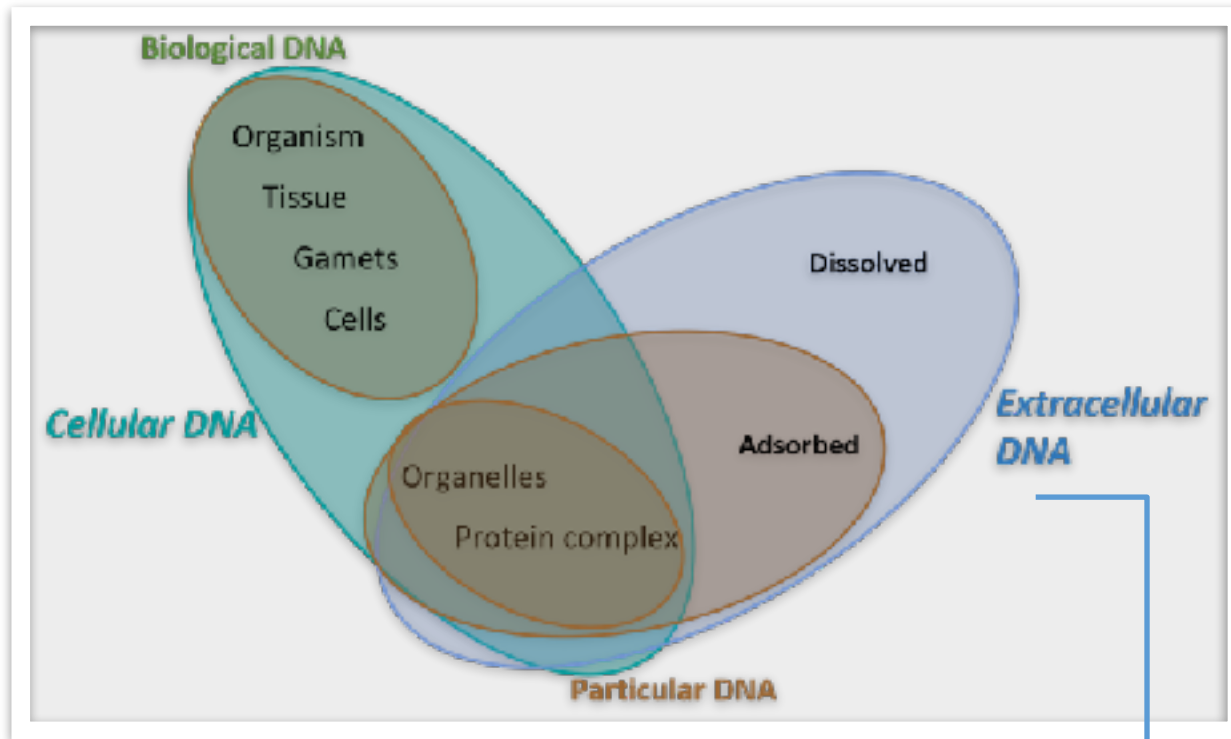


From Lefébure - LEHNA





# Metabarcoding: DNA material

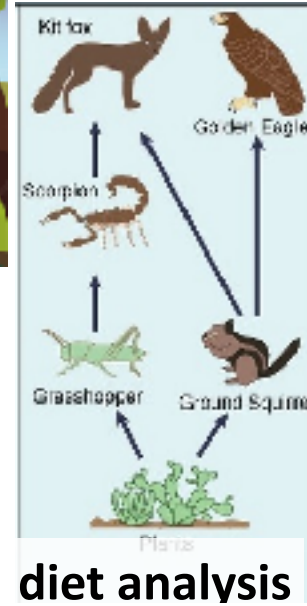
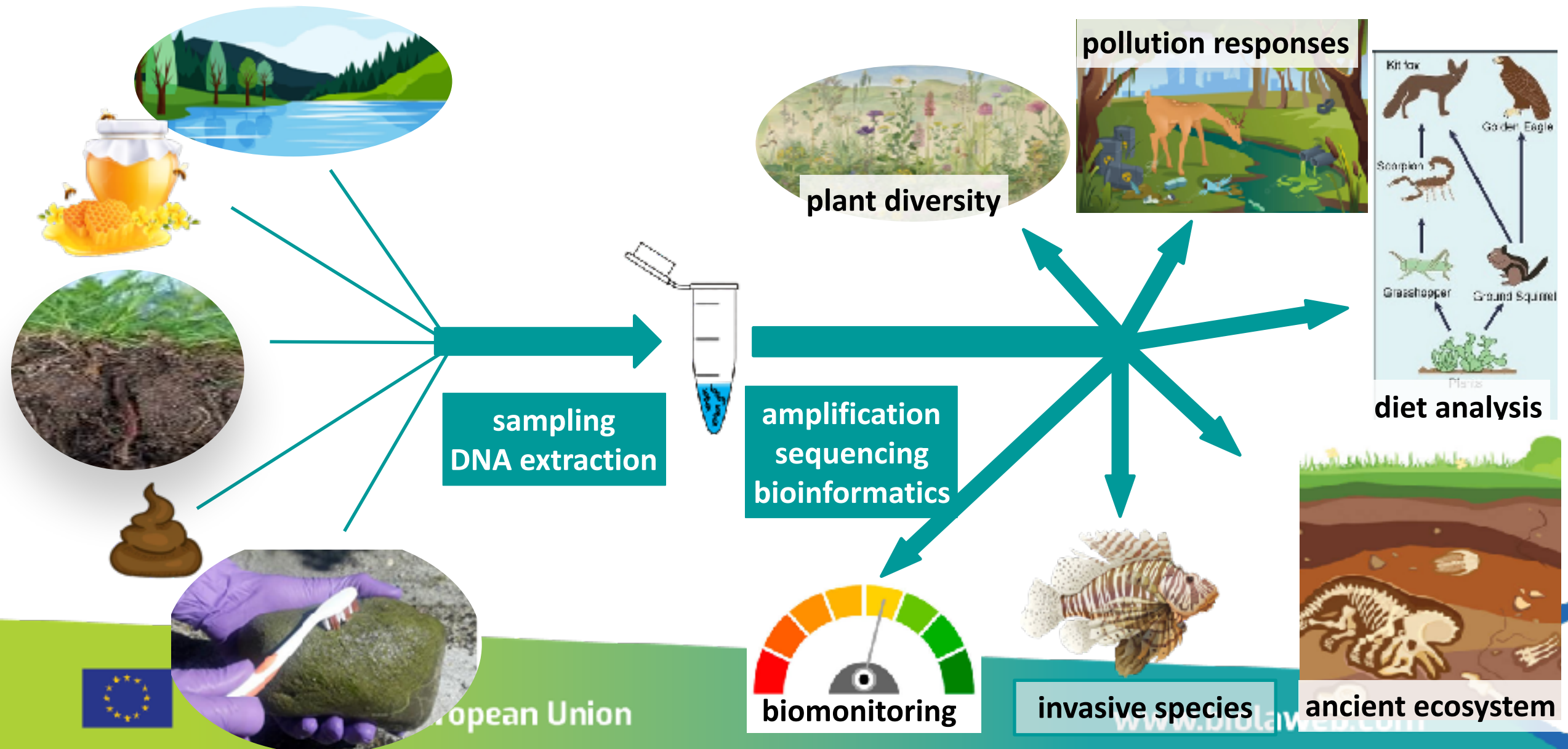


**Environmental DNA / eDNA ?**

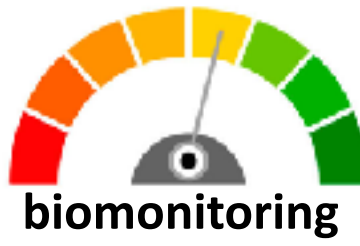
in the broad sense: all DNA in environmental samples

in the strict sense: extracellular DNA in environmental samples

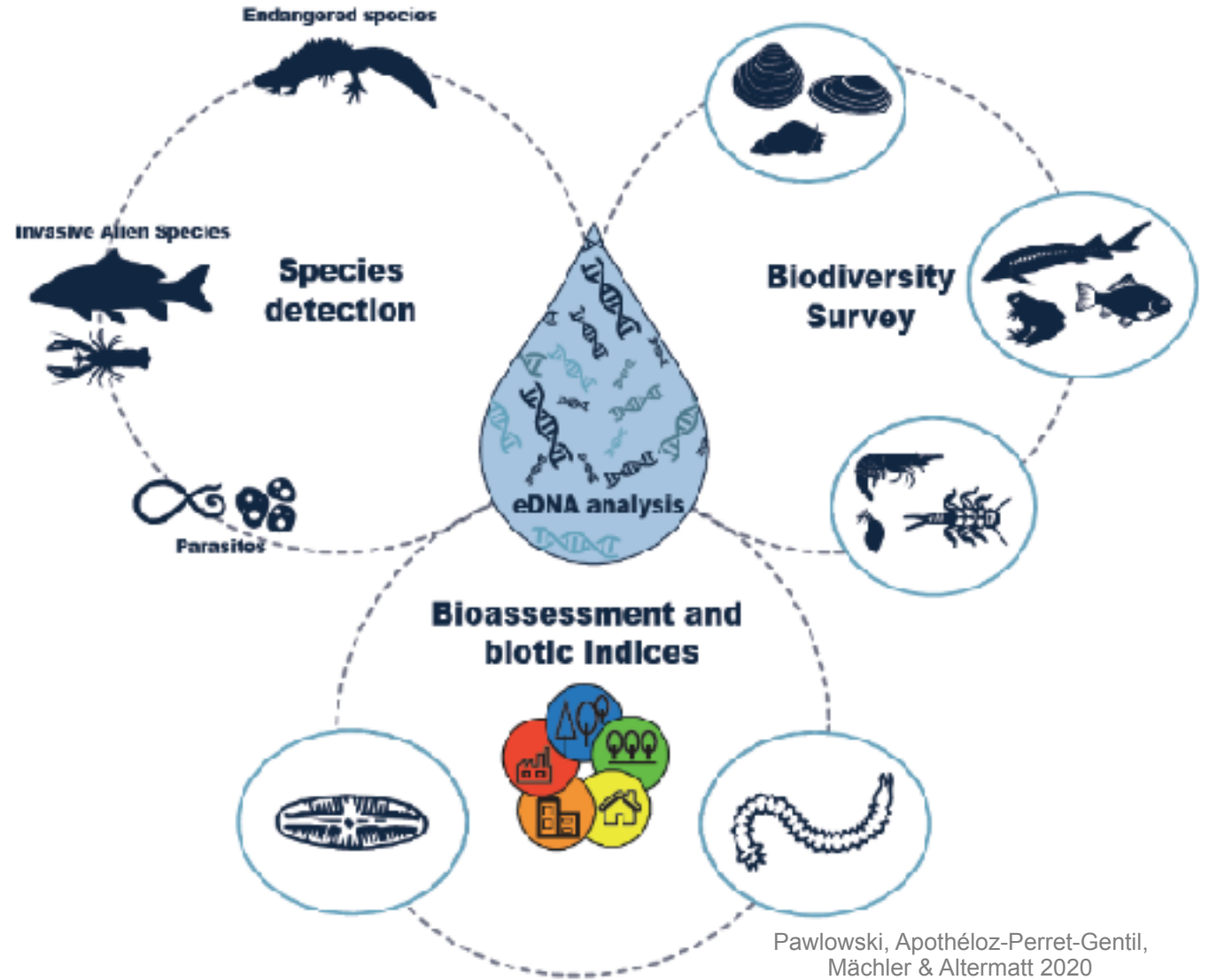
# DNA Metabarcoding: uses



amplification  
sequencing  
bioinformatics

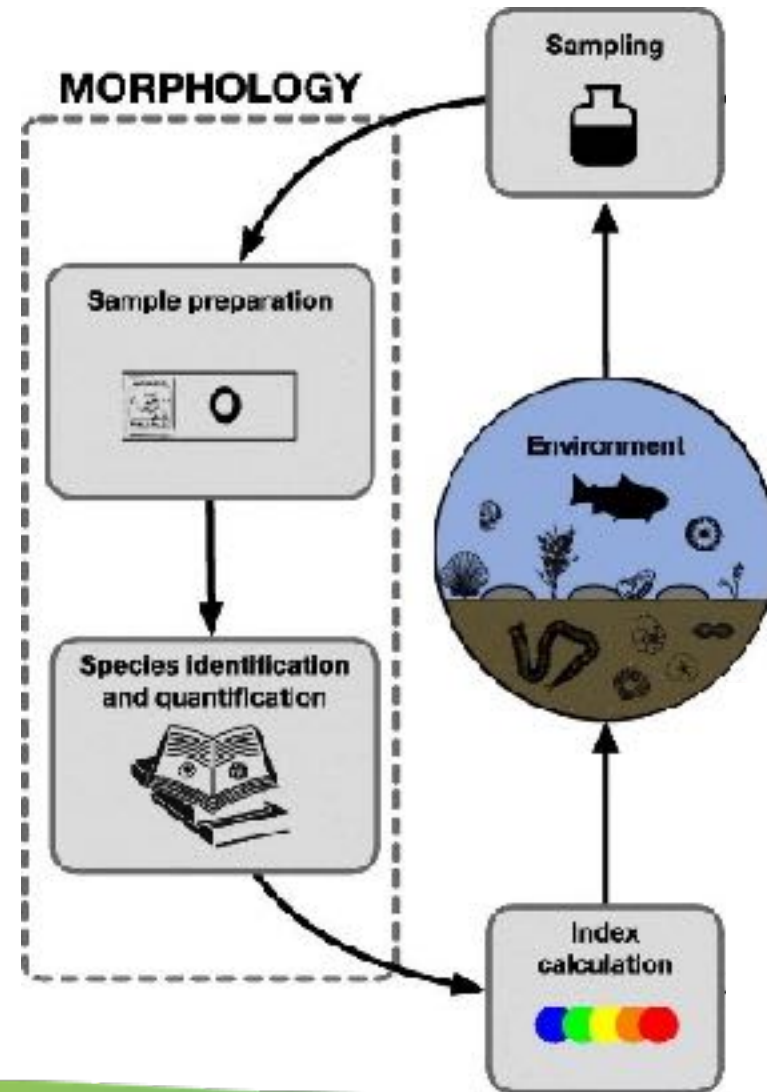


→ Many uses for eDNA in aquatic environments

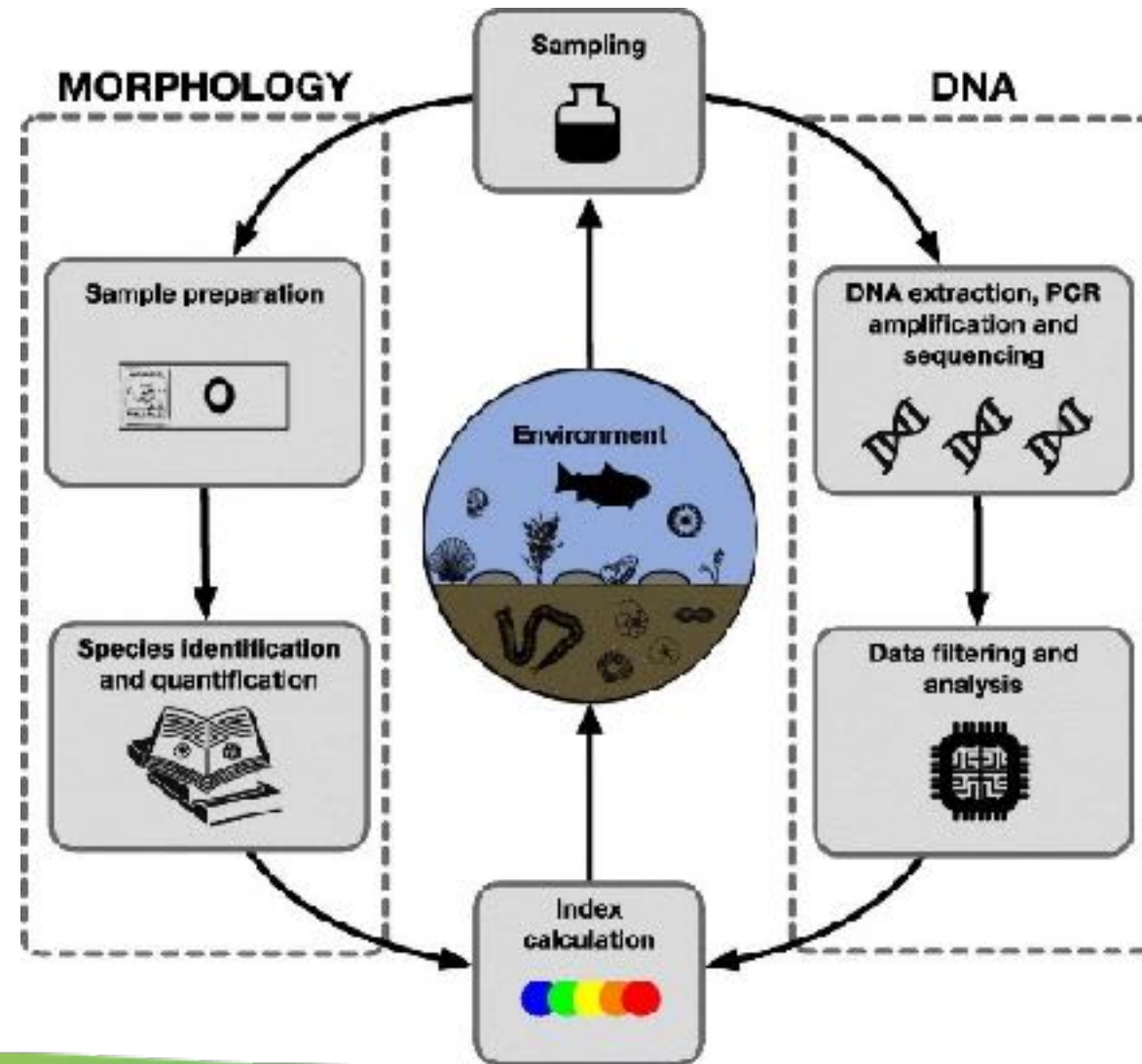


Pawlowski, Apothéloz-Perret-Gentil,  
Mächler & Altermatt 2020  
Swiss Federal Office for the Environment

# DNA Metabarcoding: uses



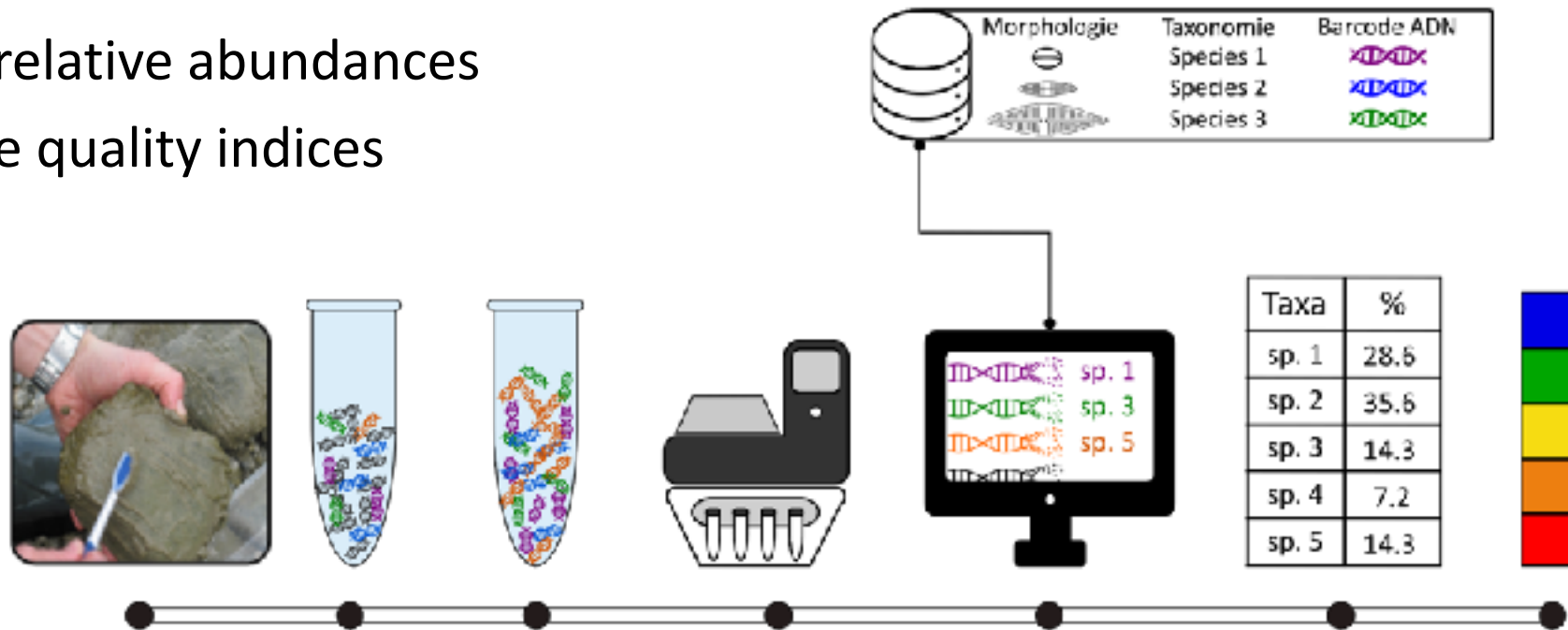
# DNA Metabarcoding: uses



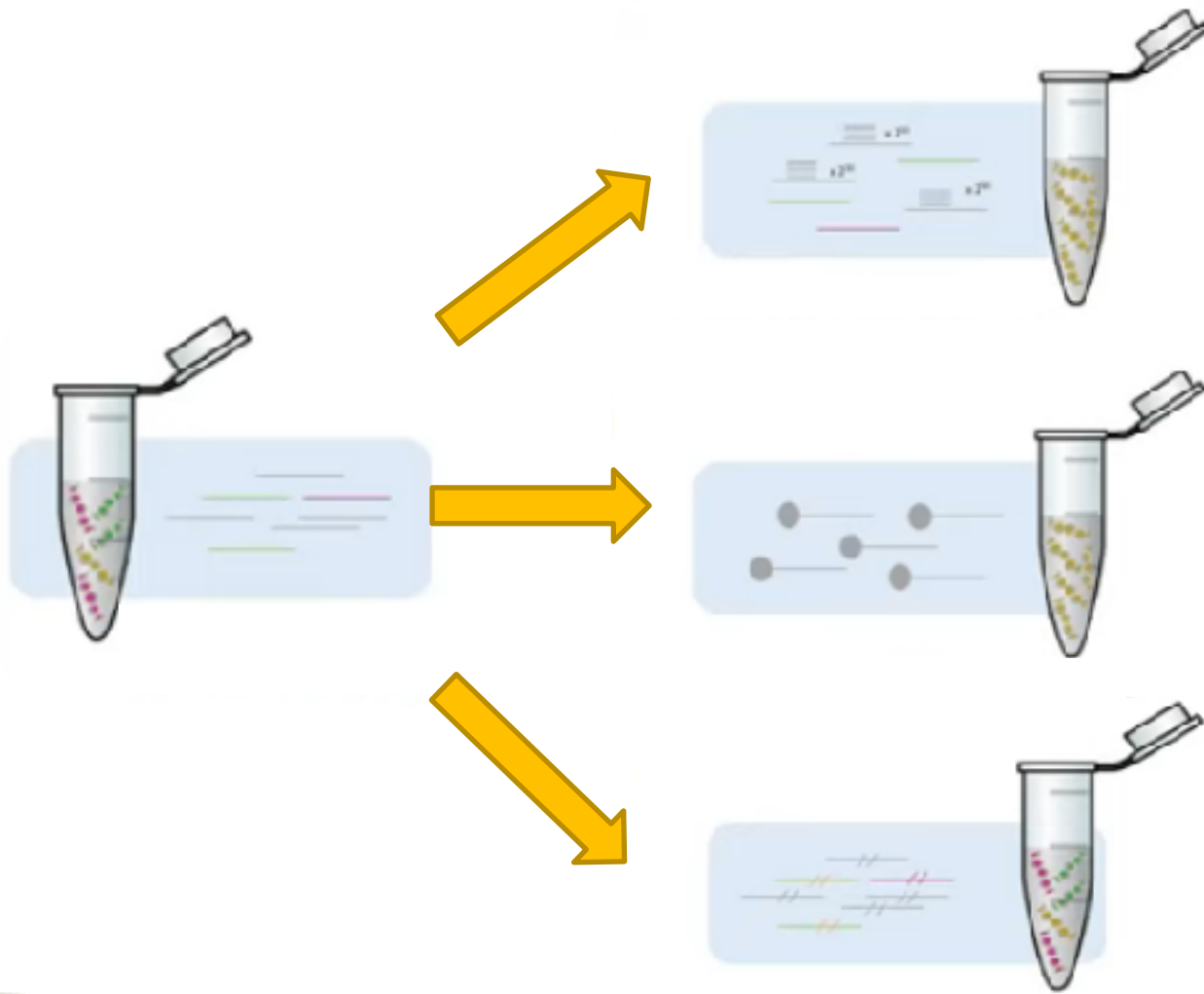
# DNA Metabarcoding: uses

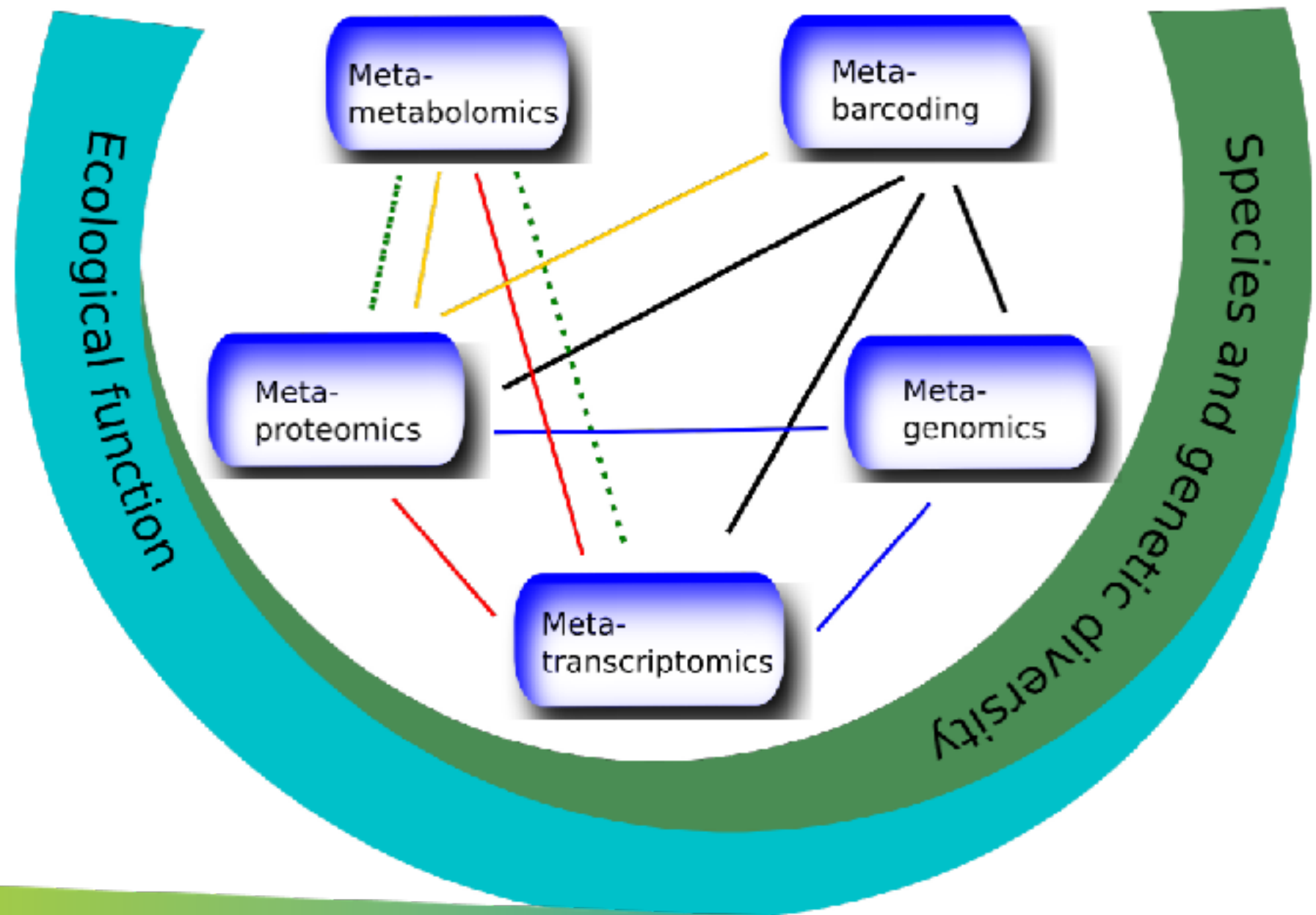
**Diatoms:** biological quality element (BQE)

- taxonomic inventories
- with relative abundances
- derive quality indices



# DNA Metabarcoding: uses







# Questions ?



INRAE



