UC Flora e Vegetação

Flora and vegetation: from field to molecular Analysis

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Outline

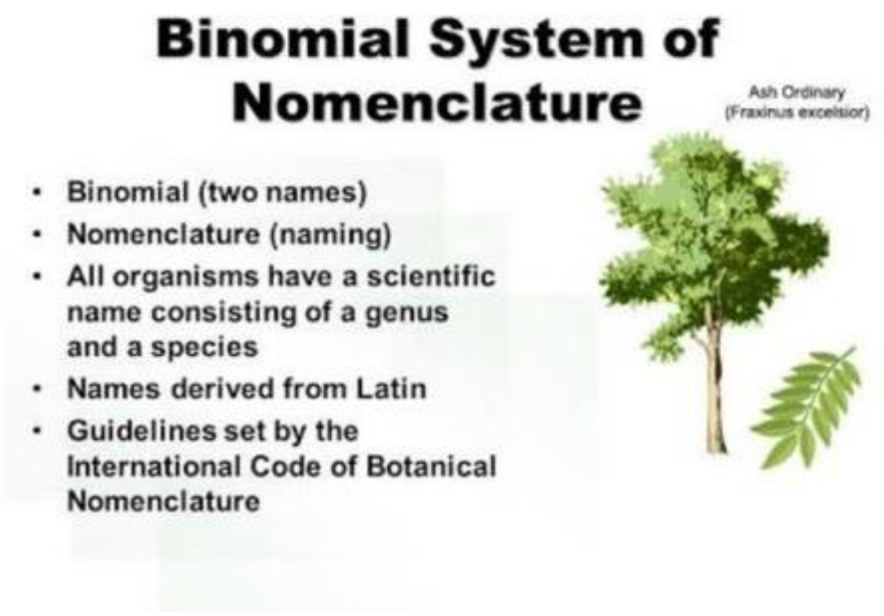
- Plant field inventory workflow
- Field sampling methods
- Species identification using molecular methods: from collection to analyses

A **Field Plant Inventory** typically focuses on how to identify, catalog, and manage data about plant species in a specific natural or agricultural area. Here's an overview of what such a course would generally include:

- Learn to identify native and invasive plant species.
- Conduct accurate field surveys and inventories.
- Use tools like GPS, plant ID guides, and data sheets or digital platforms.
- Understand ecological relationships and vegetation types.
- Apply data for land management, conservation, or research.

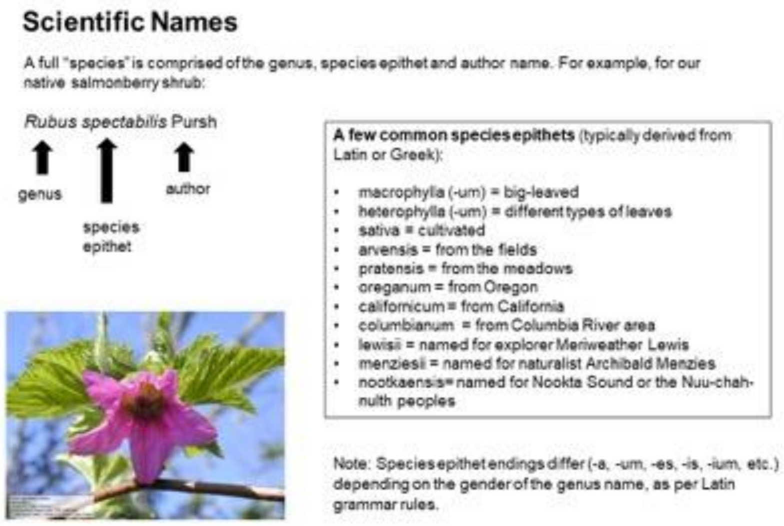
1. Introduction to Plant Taxonomy

- Scientific names & classification



Binomial System of Nomenclature

- Binomial (two names)
- Nomenclature (naming)
- All organisms have a scientific name consisting of a genus and a species
- Names derived from Latin
- Guidelines set by the International Code of Botanical Nomenclature



Scientific Names

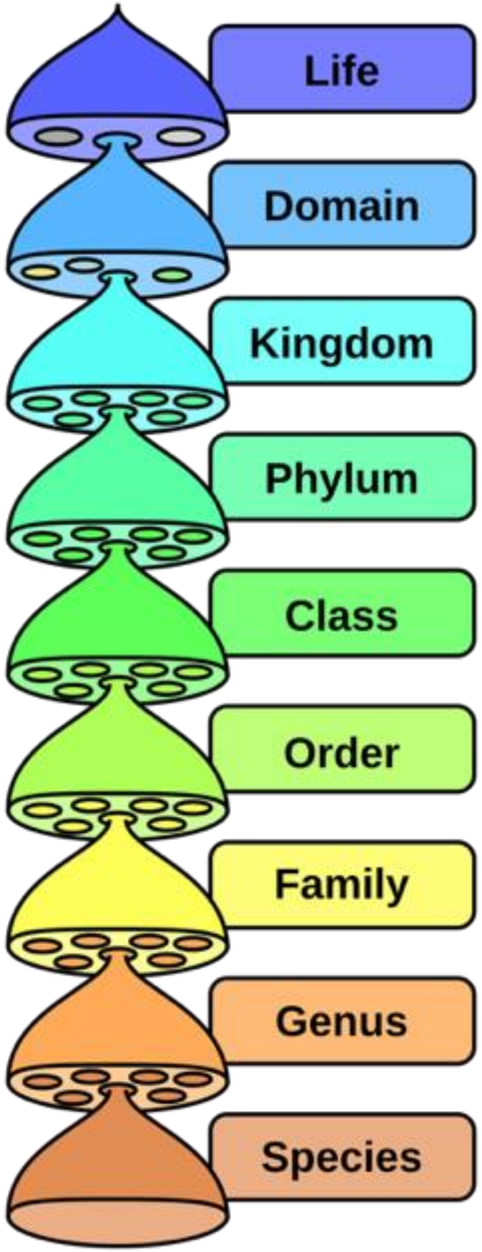
A full "species" is comprised of the genus, species epithet and author name. For example, for our native salmonberry shrub:

Rubus spectabilis Pursh

A few common species epithets (typically derived from Latin or Greek):

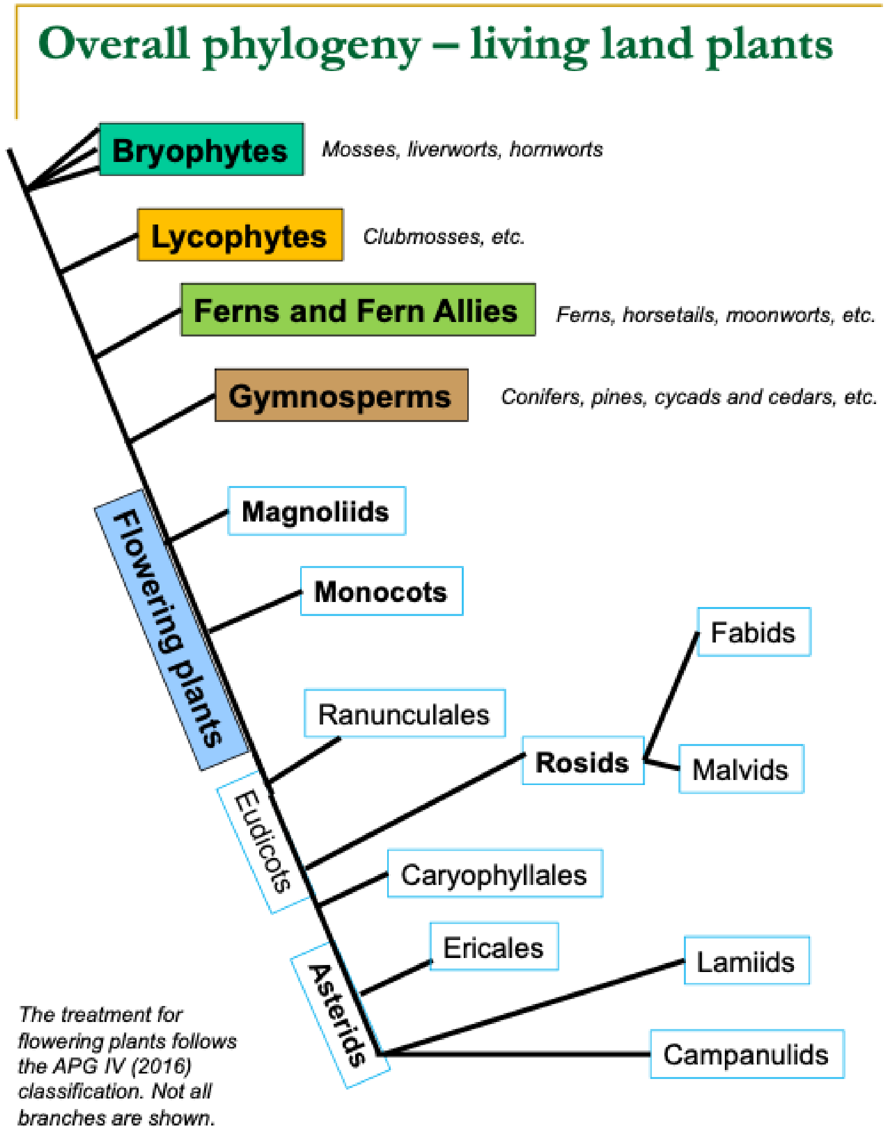
- macrophylla (-um) = big-leaved
- heterophylla (-um) = different types of leaves
- sativa = cultivated
- arvensis = from the fields
- pratensis = from the meadows
- oreganum = from Oregon
- californicum = from California
- columbianum = from Columbia River area
- lewisii = named for explorer Meriweather Lewis
- menziesii = named for naturalist Archibald Menzies
- nootkaensis = named for Nookta Sound or the Nuu-chah-nulth peoples

Note: Species epithet endings differ (-a, -um, -es, -is, -ium, etc.) depending on the gender of the genus name, as per Latin grammar rules.



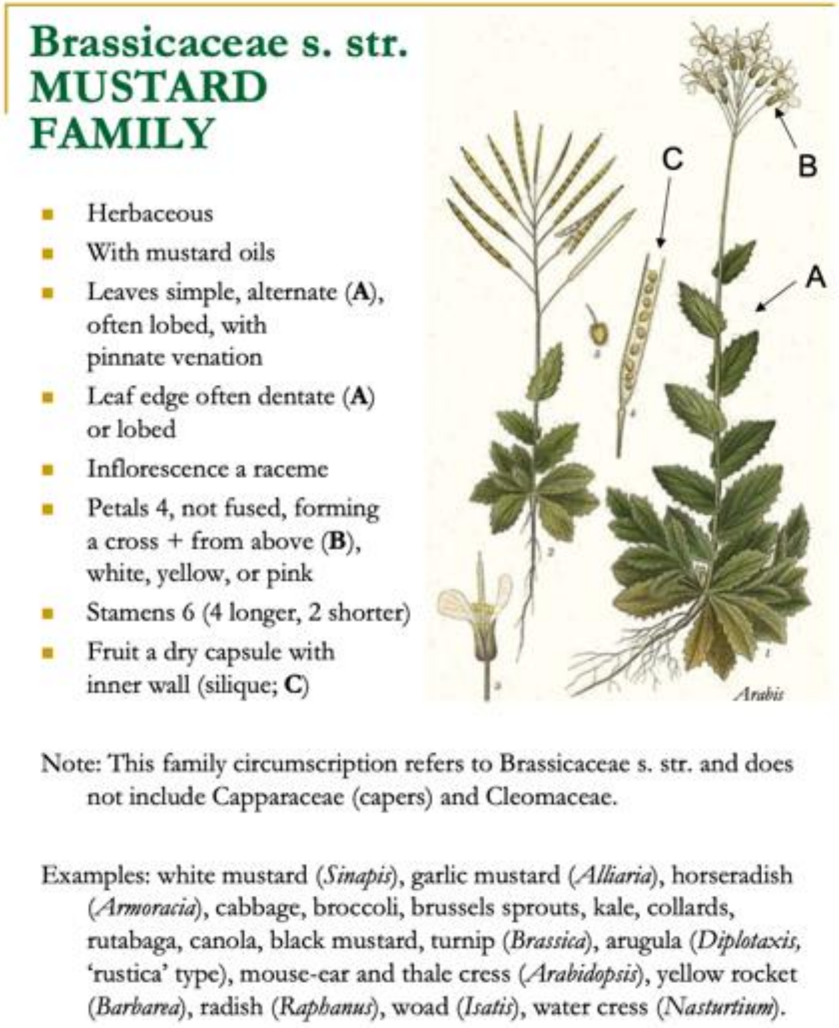
Plant family characteristics

Understanding plant family characteristics can be helpful for identifying plants, understanding their evolutionary relationships, and even for predicting their growth habits and potential pest problems.



The treatment for flowering plants follows the APG IV (2016) classification. Not all branches are shown.

- **Example**

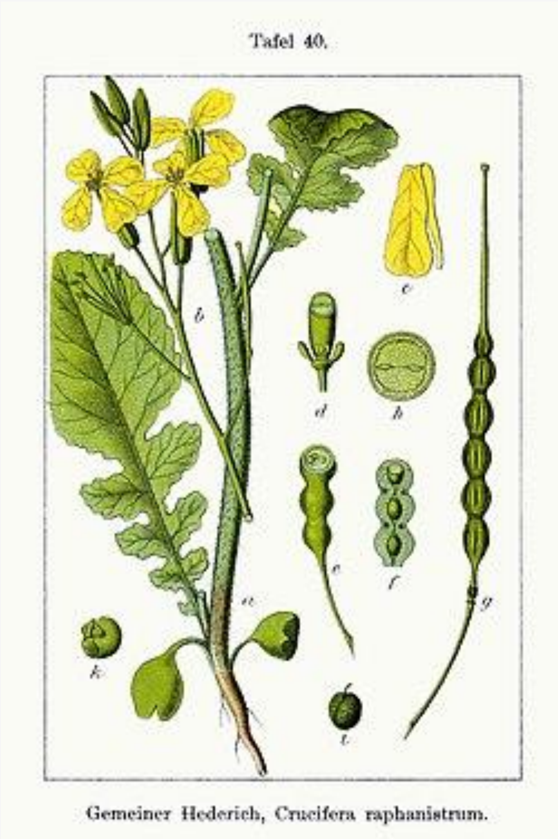


Brassicaceae s. str. MUSTARD FAMILY

- Herbaceous
- With mustard oils
- Leaves simple, alternate (**A**), often lobed, with pinnate venation
- Leaf edge often dentate (**A**) or lobed
- Inflorescence a raceme
- Petals 4, not fused, forming a cross + from above (**B**), white, yellow, or pink
- Stamens 6 (4 longer, 2 shorter)
- Fruit a dry capsule with inner wall (silique; **C**)

Note: This family circumscription refers to Brassicaceae s. str. and does not include Capparaceae (capers) and Cleomaceae.

Examples: white mustard (*Sinapis*), garlic mustard (*Alliaria*), horseradish (*Armoracia*), cabbage, broccoli, brussels sprouts, kale, collards, rutabaga, canola, black mustard, turnip (*Brassica*), arugula (*Diplotaxis*, 'rustica' type), mouse-ear and thale cress (*Arabidopsis*), yellow rocket (*Barbarea*), radish (*Raphanus*), woad (*Isatis*), water cress (*Nasturtium*).

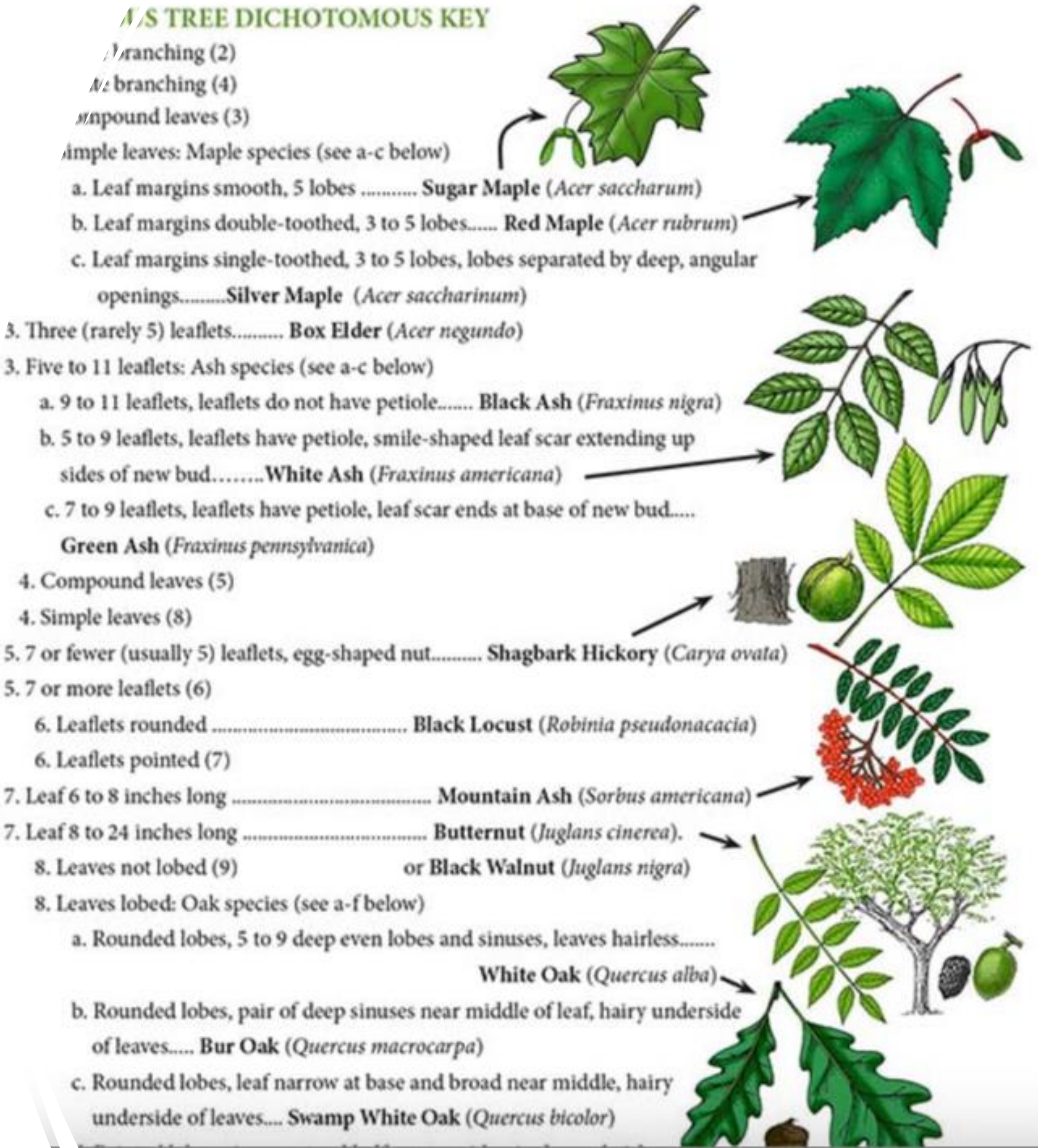


Raphanus raphanistrum

Sinapis alba

Use of dichotomous keys

- Dichotomous keys are valuable tools used to identify plants by guiding users through a series of paired choices or characteristics



S TREE DICHOTOMOUS KEY

branching (2)

branching (4)

mpound leaves (3)

imple leaves: Maple species (see a-c below)

a. Leaf margins smooth, 5 lobes .... **Sugar Maple** (*Acer saccharum*)

b. Leaf margins double-toothed, 3 to 5 lobes...... **Red Maple** (*Acer rubrum*)

c. Leaf margins single-toothed, 3 to 5 lobes, lobes separated by deep, angular openings.........**Silver Maple** (*Acer saccharinum*)

3. Three (rarely 5) leaflets.......... **Box Elder** (*Acer negundo*)

3. Five to 11 leaflets: Ash species (see a-c below)

a. 9 to 11 leaflets, leaflets do not have petiole....... **Black Ash** (*Fraxinus nigra*)

b. 5 to 9 leaflets, leaflets have petiole, smile-shaped leaf scar extending up sides of new bud........**White Ash** (*Fraxinus americana*)

c. 7 to 9 leaflets, leaflets have petiole, leaf scar ends at base of new bud..... **Green Ash** (*Fraxinus pennsylvanica*)

4. Compound leaves (5)

4. Simple leaves (8)

5. 7 or fewer (usually 5) leaflets, egg-shaped nut.......... **Shagbark Hickory** (*Carya ovata*)

5. 7 or more leaflets (6)

6. Leaflets rounded .... **Black Locust** (*Robinia pseudonacacia*)

6. Leaflets pointed (7)

7. Leaf 6 to 8 inches long .... **Mountain Ash** (*Sorbus americana*)

7. Leaf 8 to 24 inches long .... **Butternut** (*Juglans cinerea*). or **Black Walnut** (*Juglans nigra*)

8. Leaves not lobed (9)

8. Leaves lobed: Oak species (see a-f below)

a. Rounded lobes, 5 to 9 deep even lobes and sinuses, leaves hairless....... **White Oak** (*Quercus alba*)

b. Rounded lobes, pair of deep sinuses near middle of leaf, hairy underside of leaves..... **Bur Oak** (*Quercus macrocarpa*)

c. Rounded lobes, leaf narrow at base and broad near middle, hairy underside of leaves.... **Swamp White Oak** (*Quercus bicolor*)

Benefits of Dichotomous Keys

Dichotomous keys offer numerous advantages across scientific and educational domains, simplifying the process of identification and classification.

Accurate Identification

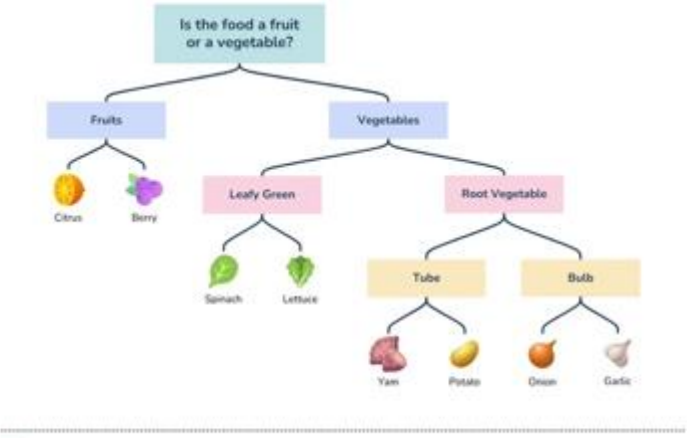
Ease of Use

Consistency: These keys adhere to a standardized format, employing specific terminology and criteria, ensuring consistent identification outcomes across different users.

Research Utility: cataloging and documenting biodiversity, contributing to the comprehension of species relationships and ecological dynamics.

Fieldwork Facilitation: Portable and adaptable for field use, dichotomous keys are invaluable for on-site surveys, ecological studies, and biodiversity assessments.

Simplicity and Accessibility: By breaking down complex identification tasks into binary choices, dichotomous keys make the process accessible to both experts and novices, streamlining identification efforts.

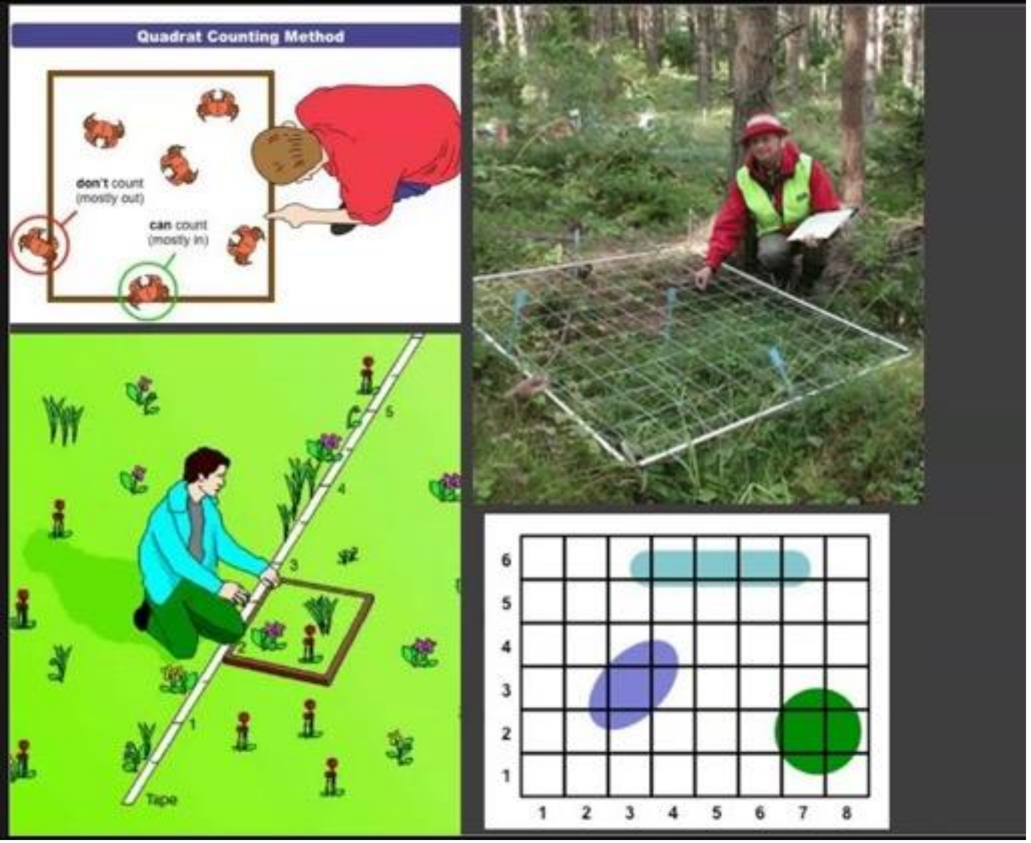


A

Flora de Portugal

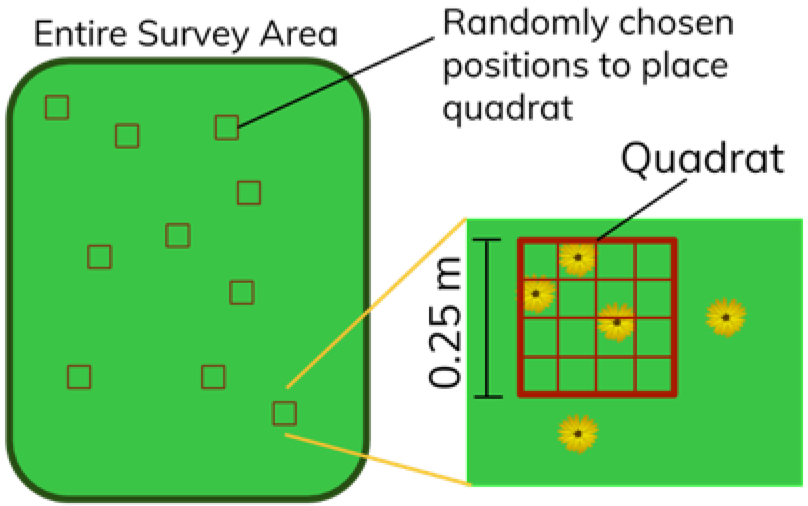
Obstacles of Dichotomous Keys

Limited distinguishing forms
Incomplete coverage of the characteristics
Differing observation conditions
Language as a Barrier
Obsolescence



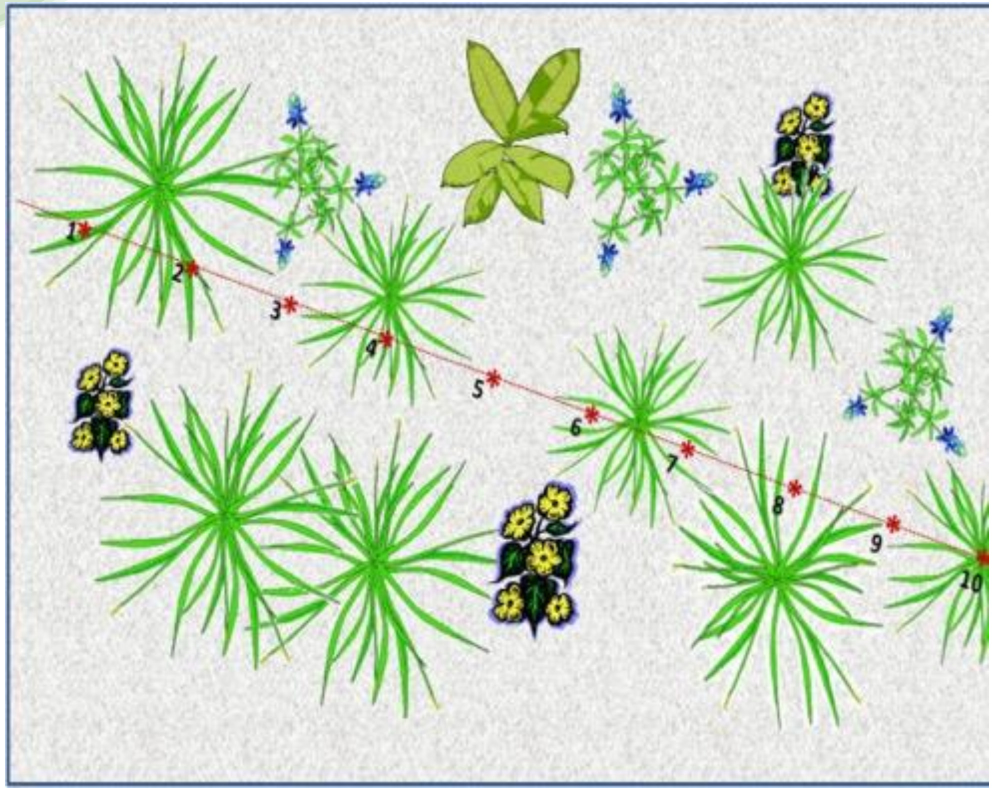
2. Methods of Sampling Plant Communities

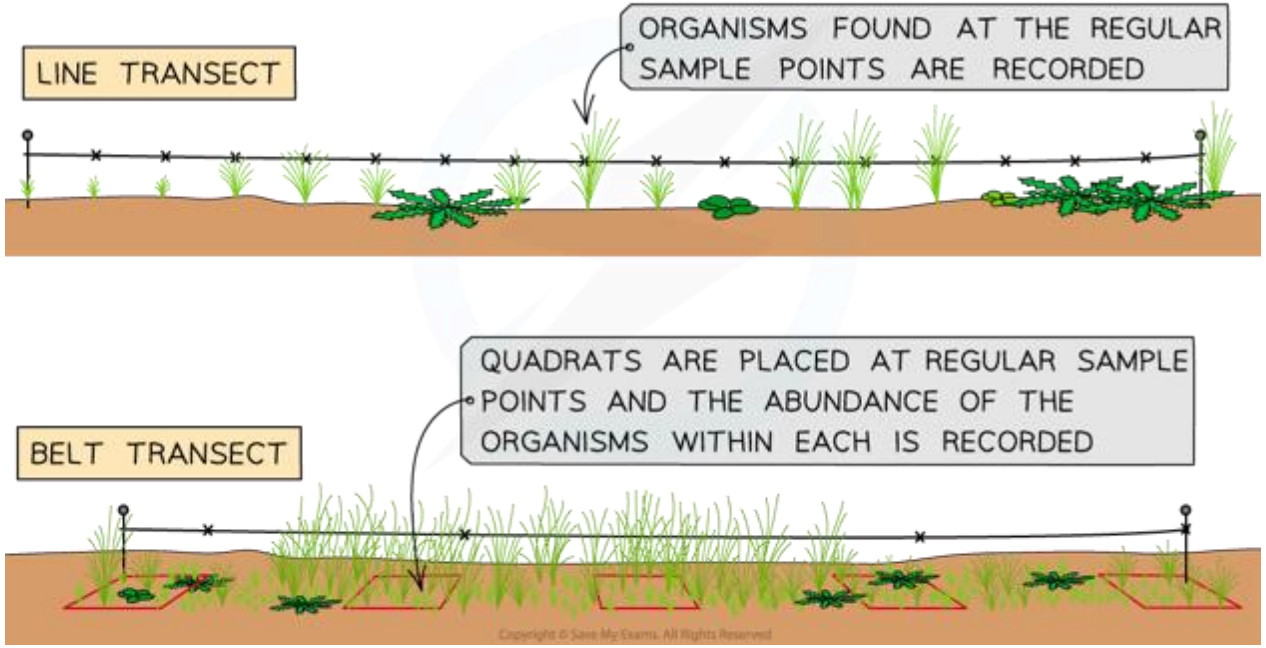
- Quadrats



Transects

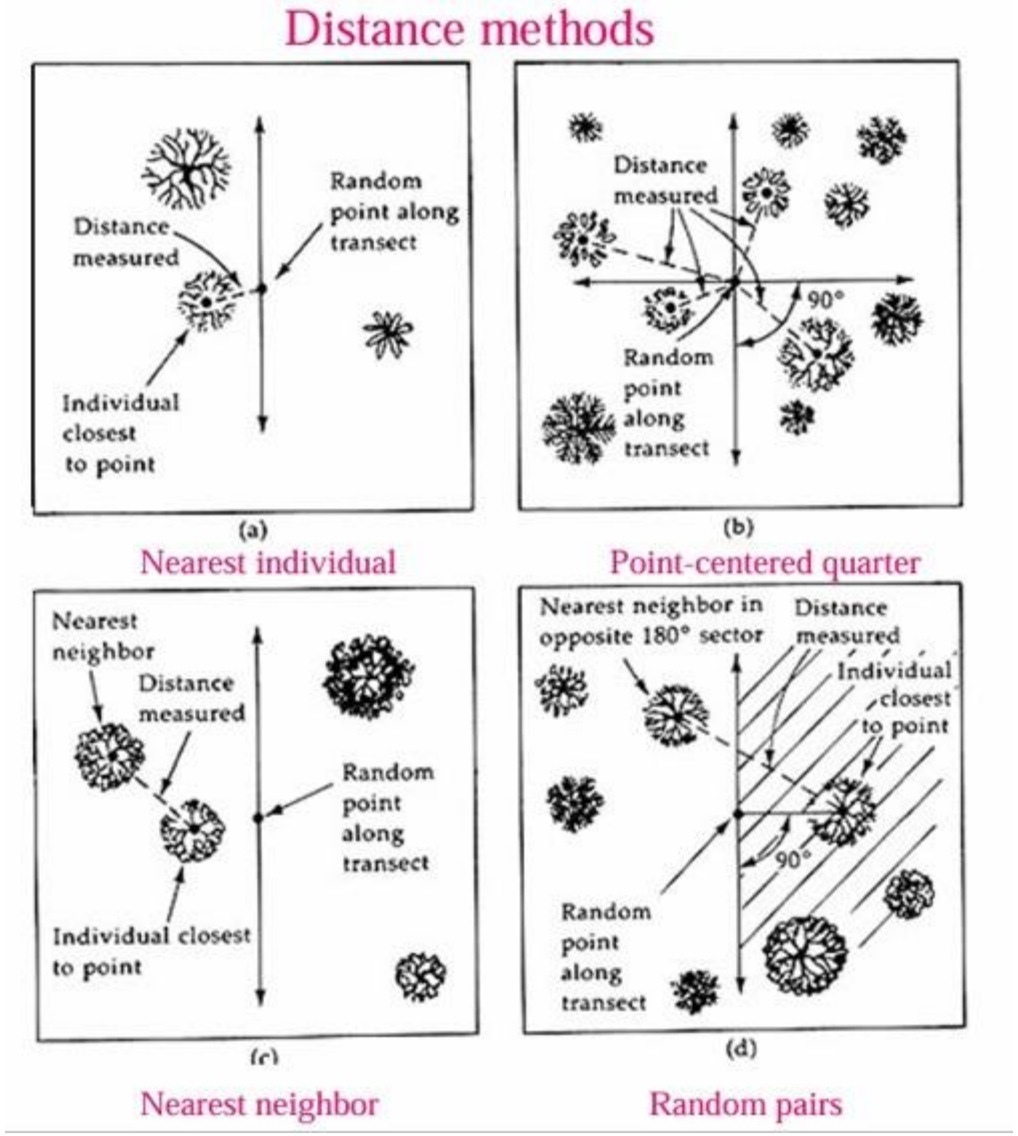
- Transects involve sampling along a straight line or a series of lines across a study area. They are particularly useful for studying gradients or changes in vegetation over space.





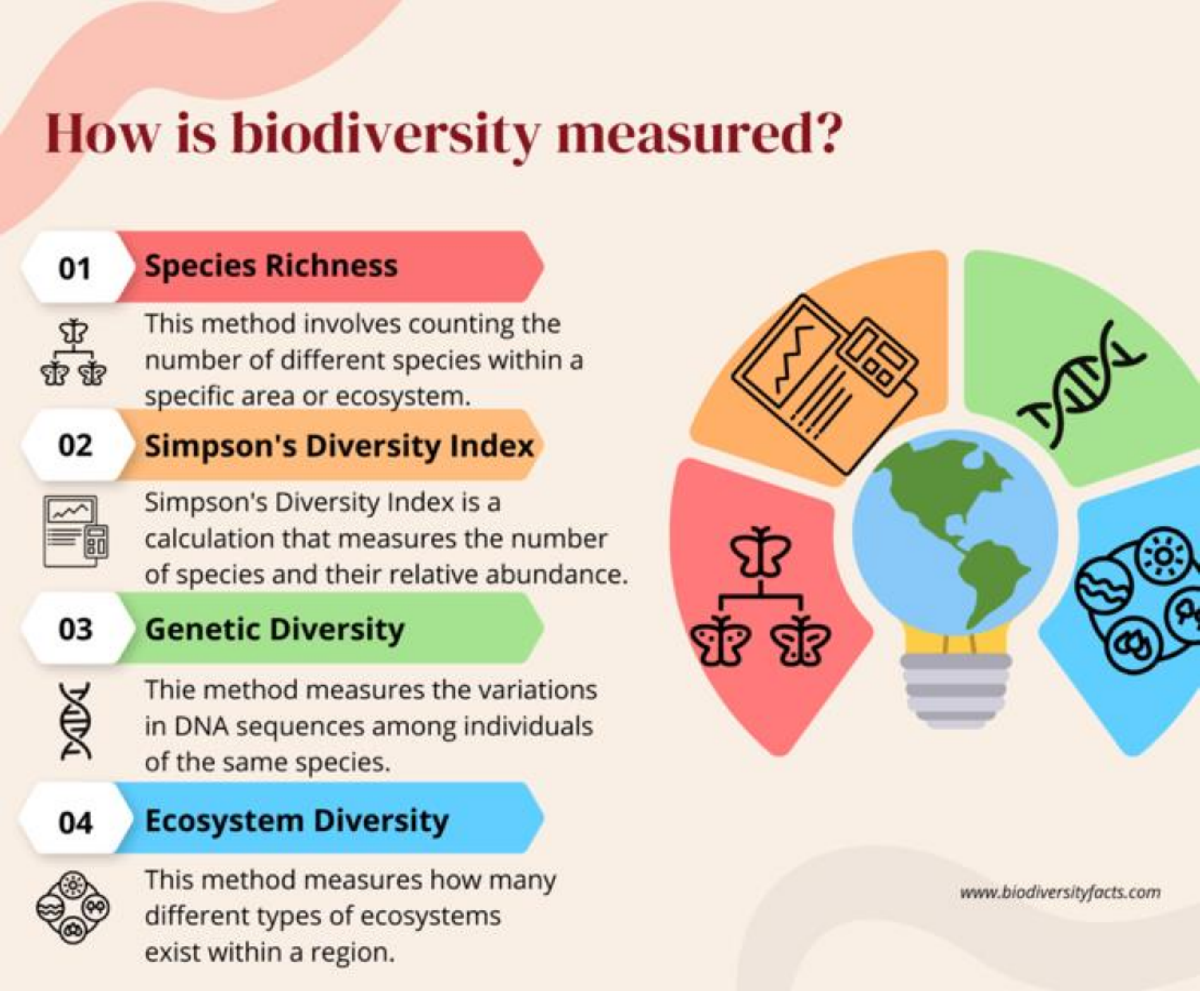
Plotless Sampling Methods

Plotless methods are used when setting up quadrats or transects is impractical. These methods rely on measuring distances between plants or random points.



- Different measures on flora and vegetation

From field data collection to diversity analyses



How is biodiversity measured?

01 Species Richness

This method involves counting the number of different species within a specific area or ecosystem.

02 Simpson's Diversity Index

Simpson's Diversity Index is a calculation that measures the number of species and their relative abundance.

03 Genetic Diversity

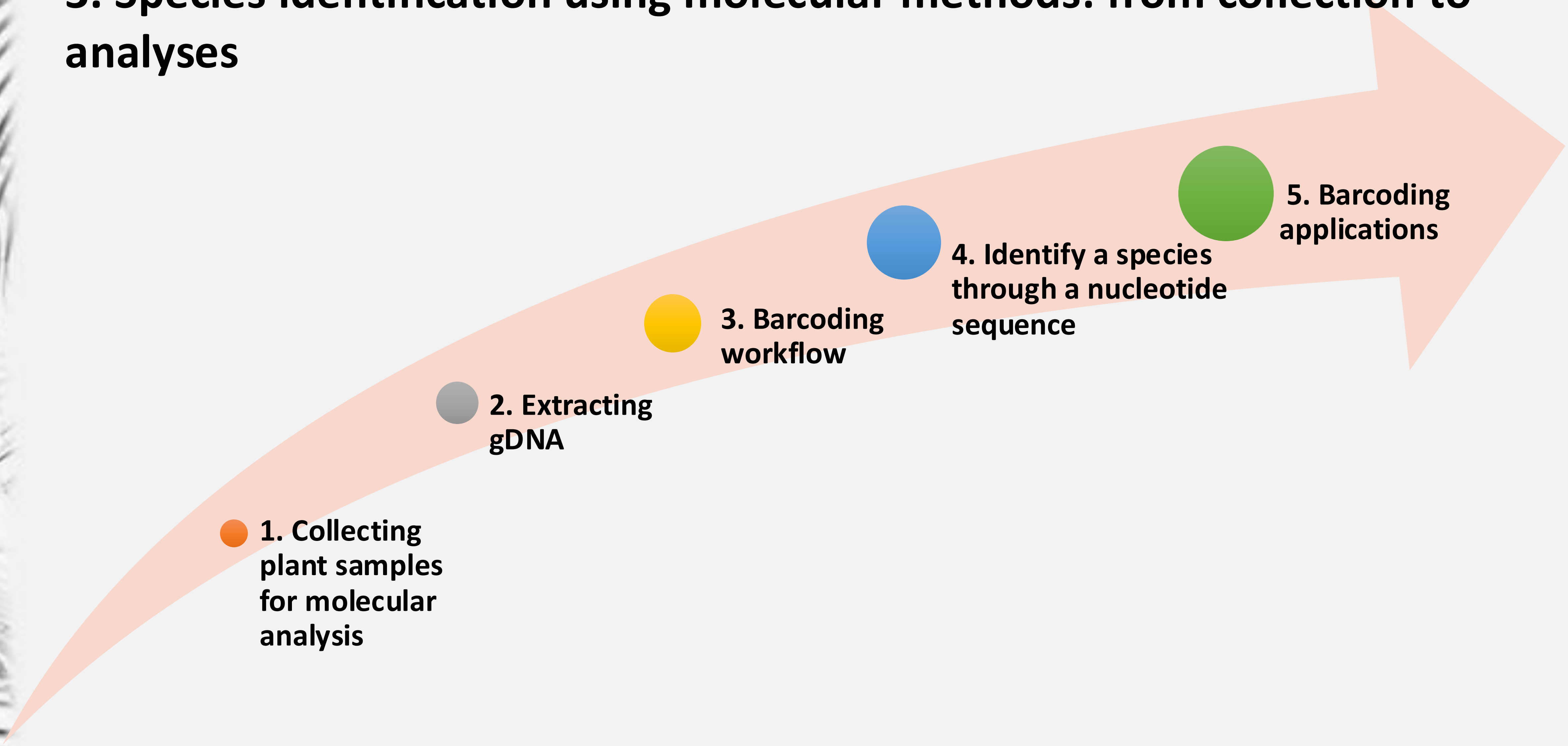
Thie method measures the variations in DNA sequences among individuals of the same species.

04 Ecosystem Diversity

This method measures how many different types of ecosystems exist within a region.

www.biodiversityfacts.com

3. Species identification using molecular methods: from collection to analyses

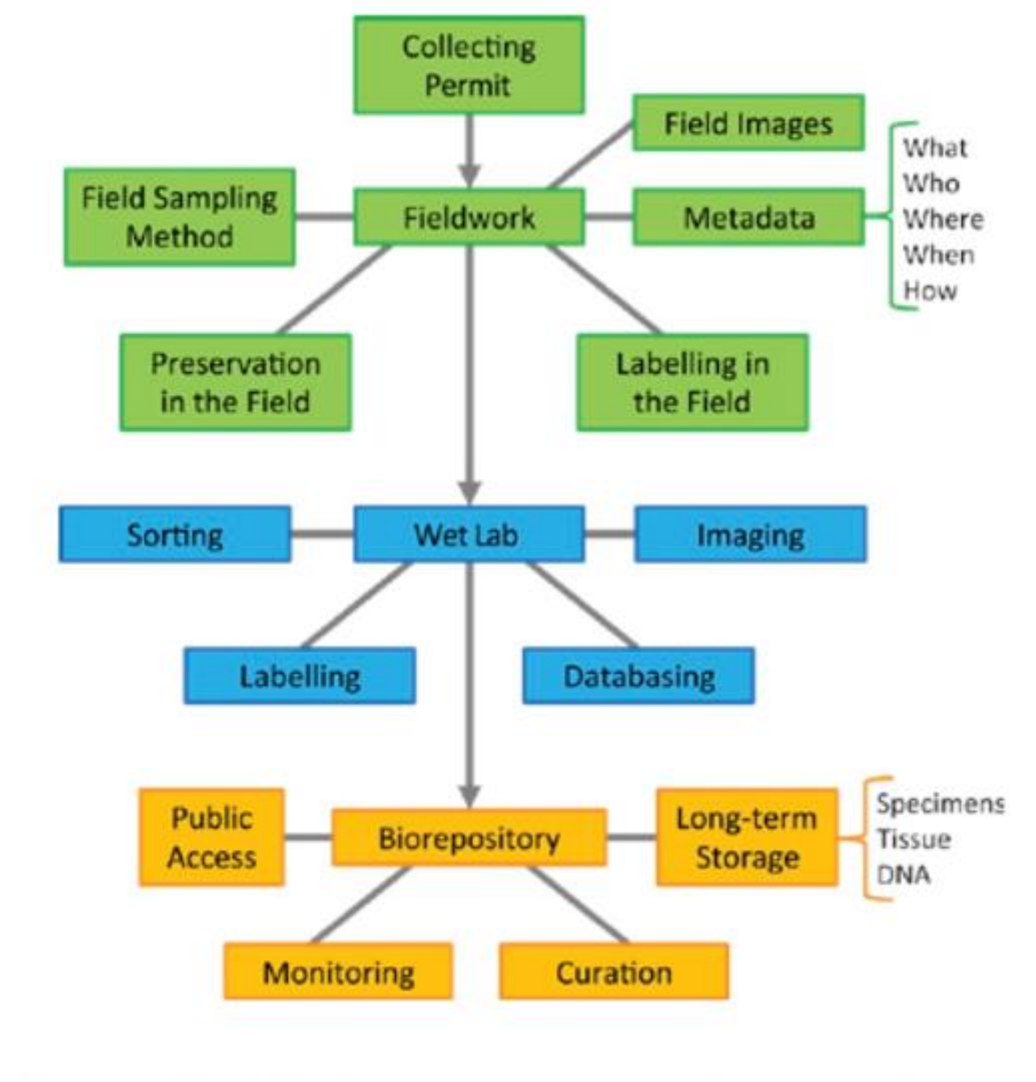


1. Collecting plant samples for molecular analysis
2. Extracting gDNA
3. Barcoding workflow
4. Identify a species through a nucleotide sequence
5. Barcoding applications

1. Collecting plant samples for molecular analysis

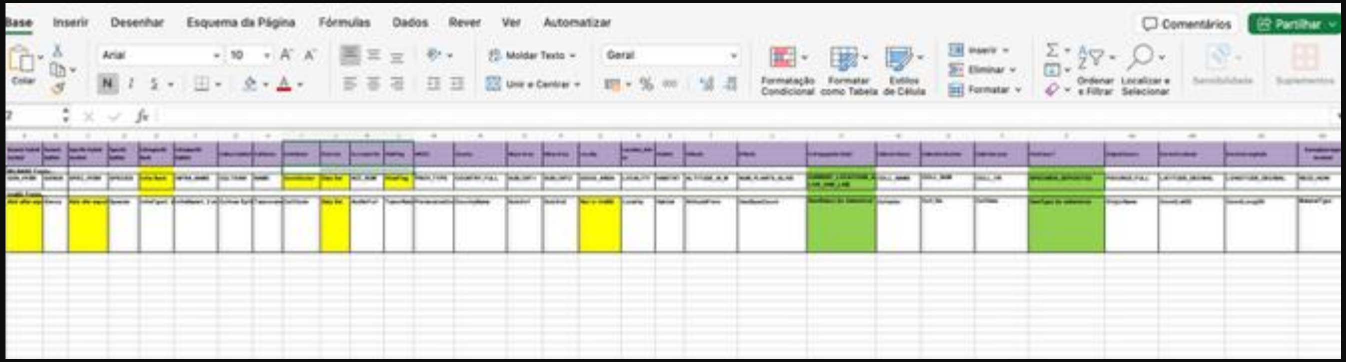
Planning the collection

Field notebook, hand lens, GPS device or smartphone, measuring tape, plant press



Registering plant collection information

- **ID**: Unique identifier for each entry.
- **Scientific Name**: Latin name of the species.
- **Common Name**: Commonly used name.
- **Family**: Botanical family (e.g., Fabaceae, Rosaceae).
- **Category**: Type of plant (Tree, Shrub, Herb, Vine, Grass, etc.).
- **Location**: Where the plant was found (GPS coordinate, plot number, or habitat type).
- **Abundance**: Rare, Occasional, Common, Abundant.
- **Health Status**: Healthy, Fair, Poor, Dead.
- **Date Observed**: Date the observation was recorded.
- **Notes**: Additional observations (e.g., flowering, pests, invasive species).



Sheet Name: Flora Inventory

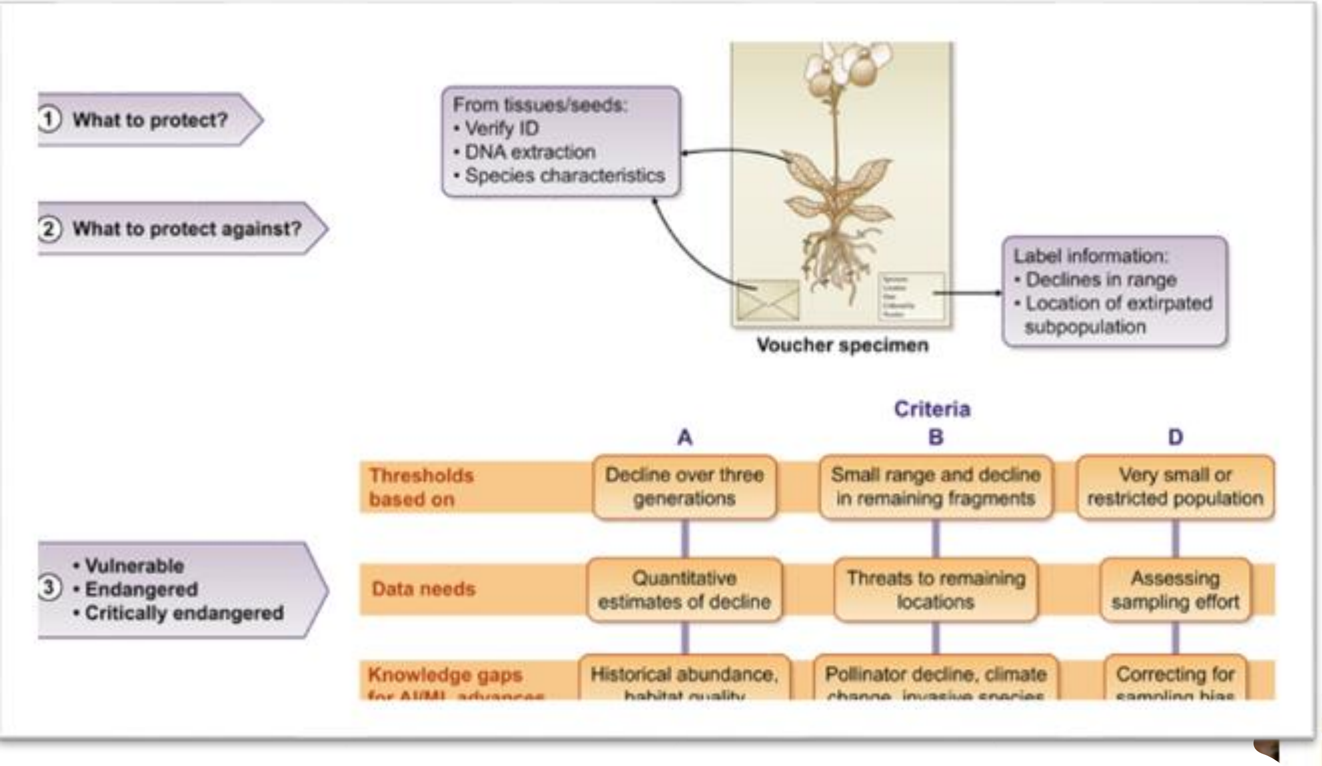
ID	Scientific Name	Common Name	Family	Category	Location	Abundance	Health Status	Date Observed	Notes
1	*Quercus alba*	White Oak	Fagaceae	Tree	Plot A	Common	Healthy	2025-05-20	Mature tree
2	*Rosa carolina*	Carolina Rose	Rosaceae	Shrub	Plot B	Rare	Fair	2025-05-20	Flowering

1. Collecting plant samples for molecular analysis

A- Preservation in the field

B- Voucher specimen

- **Importance of voucher specimen**



① What to protect?

② What to protect against?

③
- Vulnerable
- Endangered
- Critically endangered

From tissues/seeds:
- Verify ID
- DNA extraction
- Species characteristics

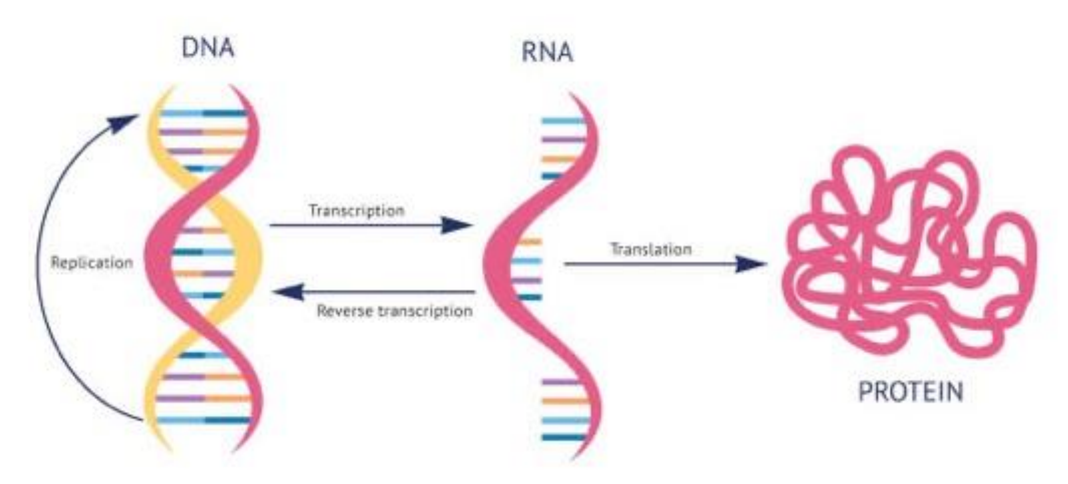
Voucher specimen

Label information:
- Declines in range
- Location of extirpated subpopulation

Criteria

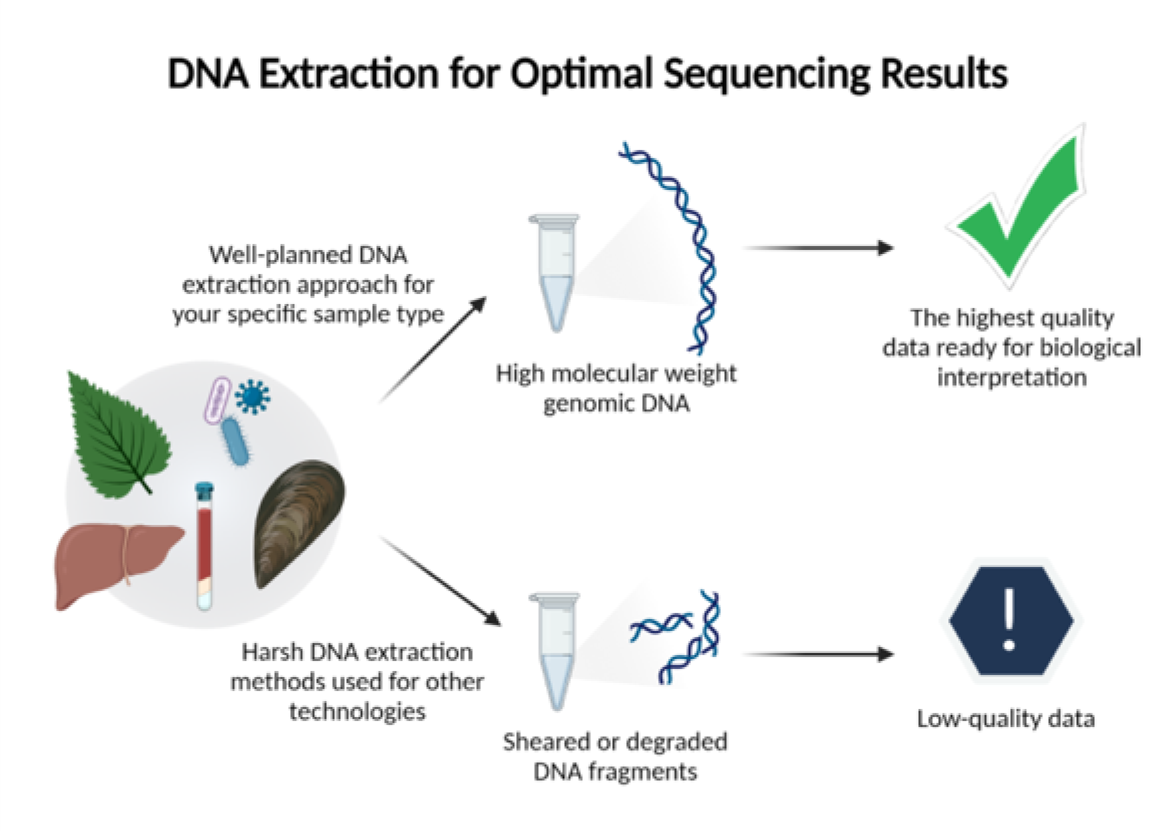
	A	B	D
Thresholds based on	Decline over three generations	Small range and decline in remaining fragments	Very small or restricted population
Data needs	Quantitative estimates of decline	Threats to remaining locations	Assessing sampling effort
Knowledge gaps for AI/ML advances	Historical abundance, habitat quality	Pollinator decline, climate change, invasive species	Correcting for sampling bias

Genomic DNA as the key molecule

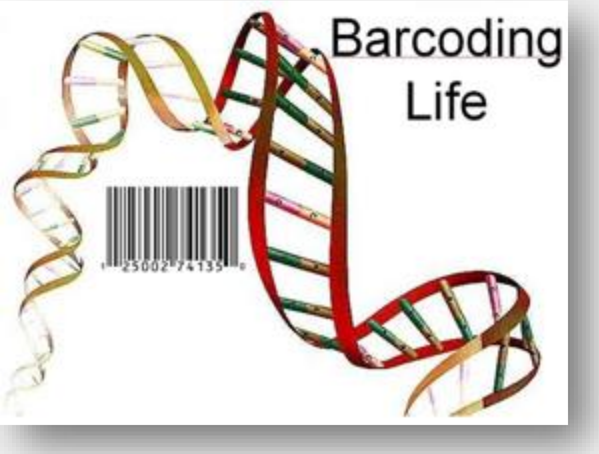


DNA e RNA são ácidos nucleicos que possuem diferentes estruturas e funções.

Enquanto o DNA é responsável por armazenar as informações genéticas dos seres vivos, o RNA atua na produção de proteínas



DNA barcoding



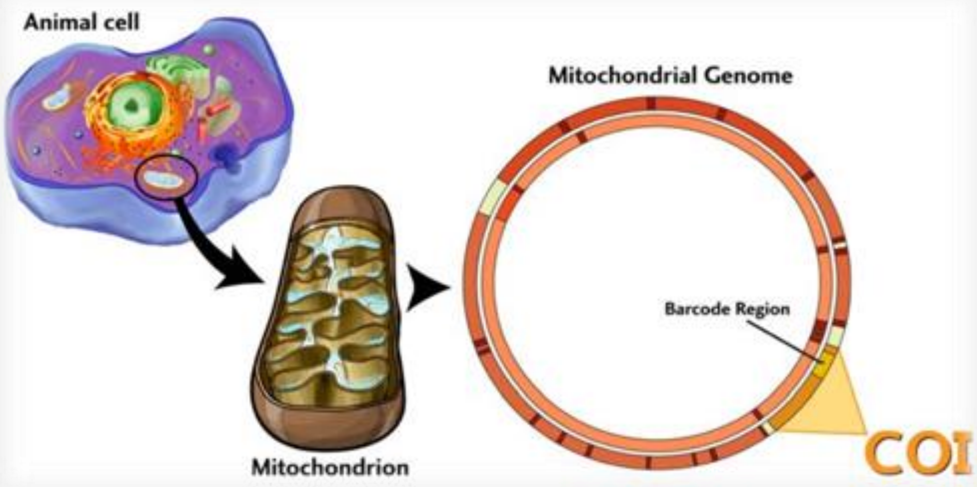
DNA barcoding is the use of short DNA sequence or sequences in a standardize locus (or loci) as a species identification tool.

Applications:

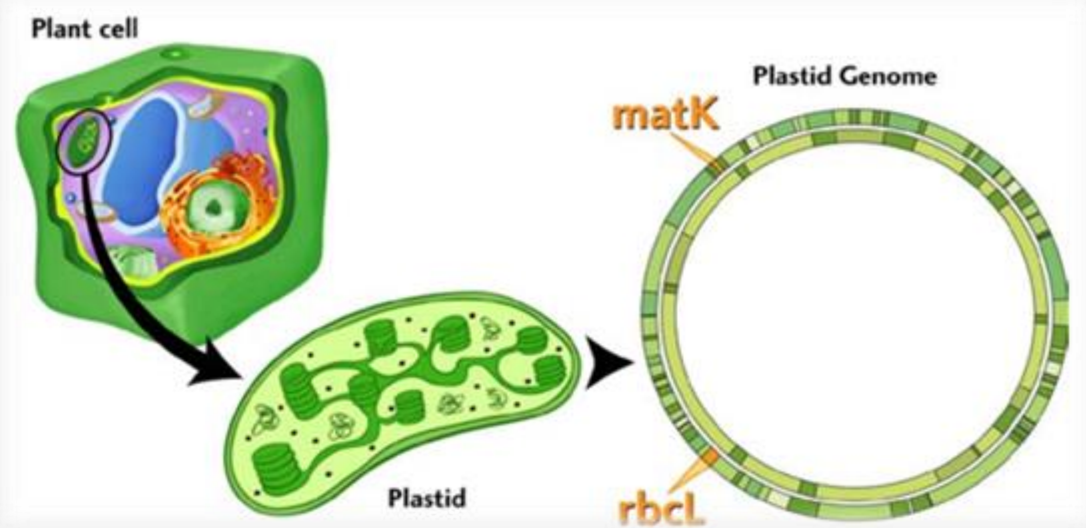
- Ecological surveys
- Identification of cryptic species (two or more distinct species classified as a single species)
- Identify and characterize species (abundant or rare, native or invasive)

Barcode regions

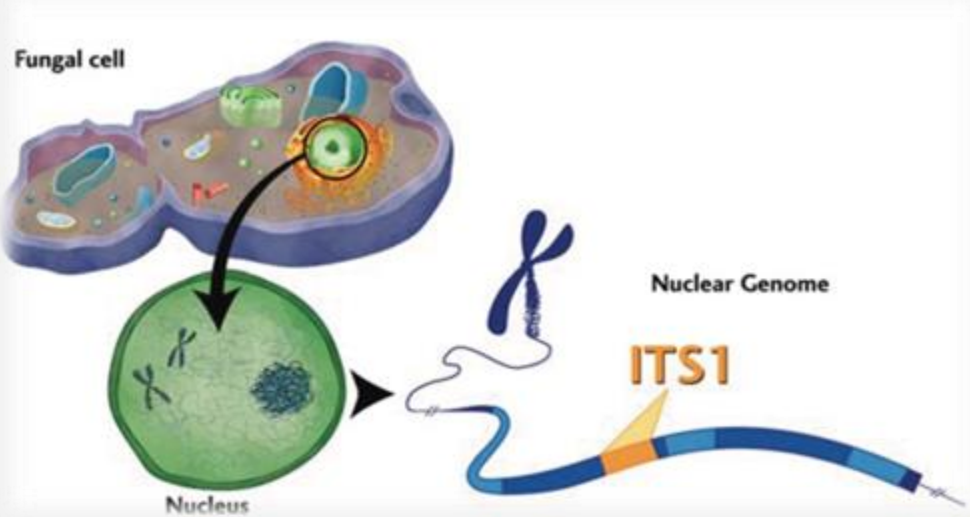
For animals



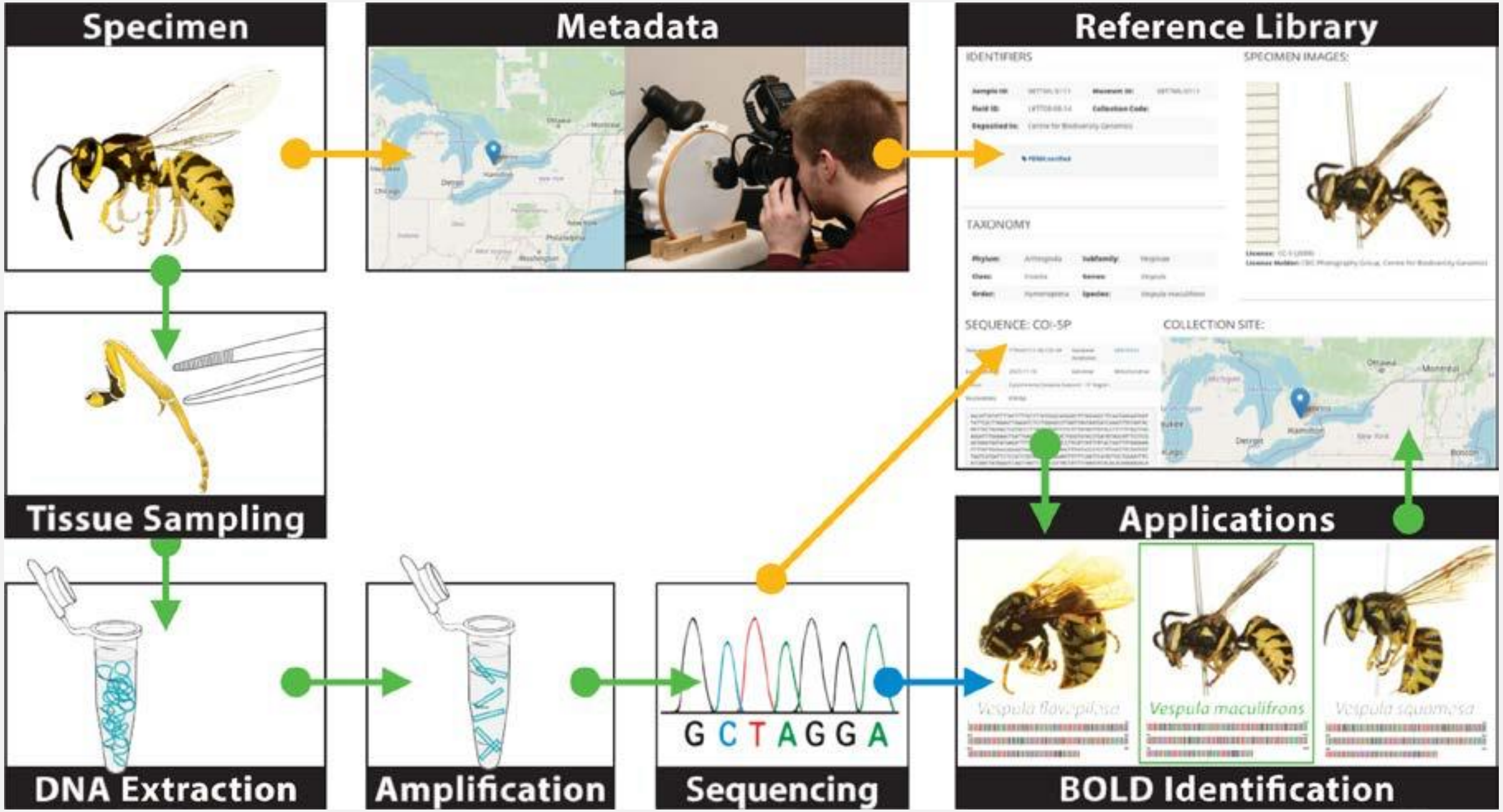
For plants



For fungi



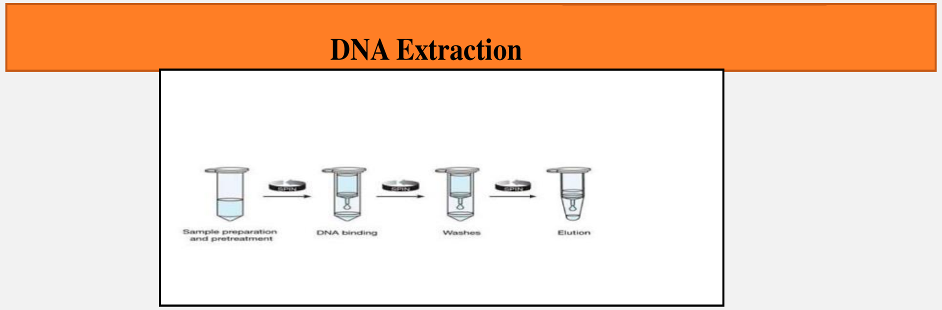
2. Barcode Pipeline

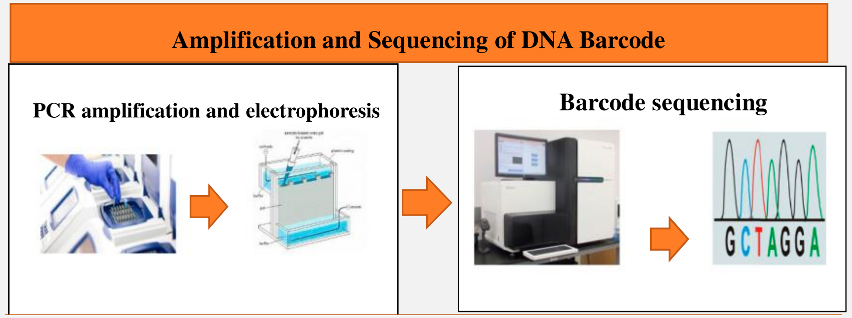


Four Barcoding components

1. Specimens: Natural history museums, herbaria, zoos, aquaria, frozen tissue collections, seed banks, type culture collections and other repositories of biological materials are treasure troves of identified specimens.

2. Laboratory Analysis: Laboratory protocols can be followed to obtain DNA barcode sequences from these specimens.


DNA Extraction


Amplification and Sequencing of DNA Barcode

PCR amplification and electrophoresis

Barcode sequencing

Plant DNA Barcode markers

- Polymorphic DNA region
- Conserved regions for easy amplification
- Sequence length suitable for sequencing

No unique barcode marker!

Consortion for the Barcode of Life (CBOL) Plant Working Group," proposed two "core barcode" the plastid *rbcL* and *matK* (Hollingworth et al., 2009 PNAS), the internal transcribed spacers of nuclear ribosomal DNA (nrDNA ITS, De-Zhu Li et al., 2011 PNAS).

Nuclear genes usually evolve too rapidly to distinguish between the same species, but chloroplast genes evolve at a slower rate, allowing differences to occur in the DNA code between species.

Barcode markers

Plastidial markers

rbcL

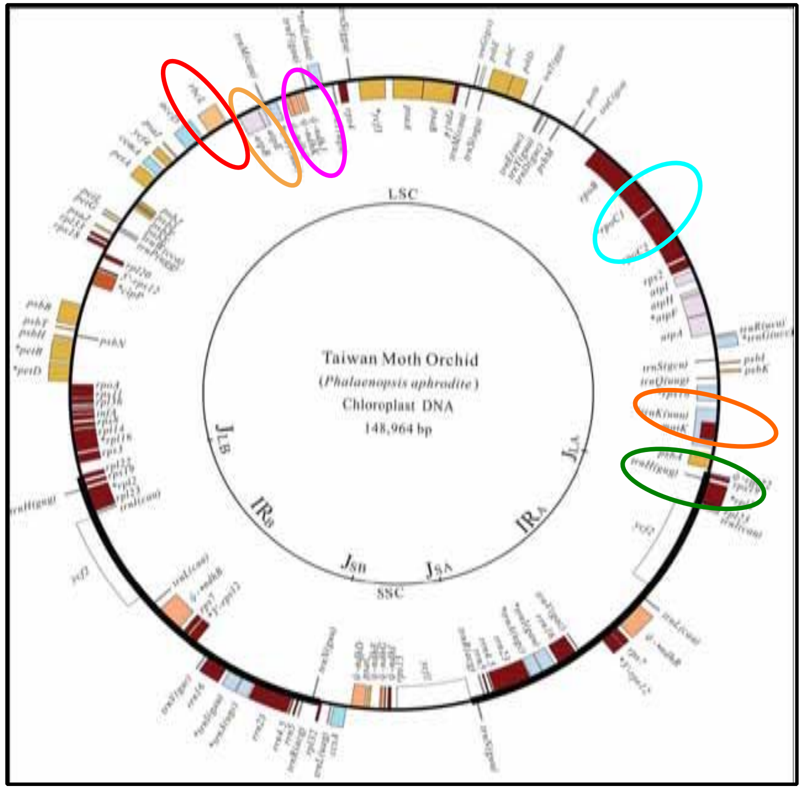
atpB

rpoC1

ndhJ

trnH-psbA

matK



Nuclear markers

Internal transcribed spacers of nuclear ribosomal DNA (nrDNA ITS) yields a good resolving power

Three major problems

1- Fungal contamination

2- Paralogous gene copies

3- Difficult to amplify/sequence

Plant barcode markers: *matk+rbcl*, nrDNA ITS

Four Barcoding components

3. Database construction of a public reference library of species identifiers which could be used to assign unknown specimens to known species. There are currently two main barcode databases that fill this role:

1. **International Nucleotide Sequence Database Collaborative**

GenBank, the Nucleotide Sequence Database of the EMBL in Europe, and the DNA Data Bank of Japan. - CBOL's data standards for barcode records.

Basic Local Alignment Search Tool

BLAST finds regions of similarity between biological sequences. The program compares nucleotide or protein sequences to sequence databases and calculates the statistical significance.

A new feature was added to the NCBI IgBLAST webpage

IgBLAST is now able to determine Ig isotypes

Mon, 01 Nov 2021 12:00:00 EST

Web BLAST

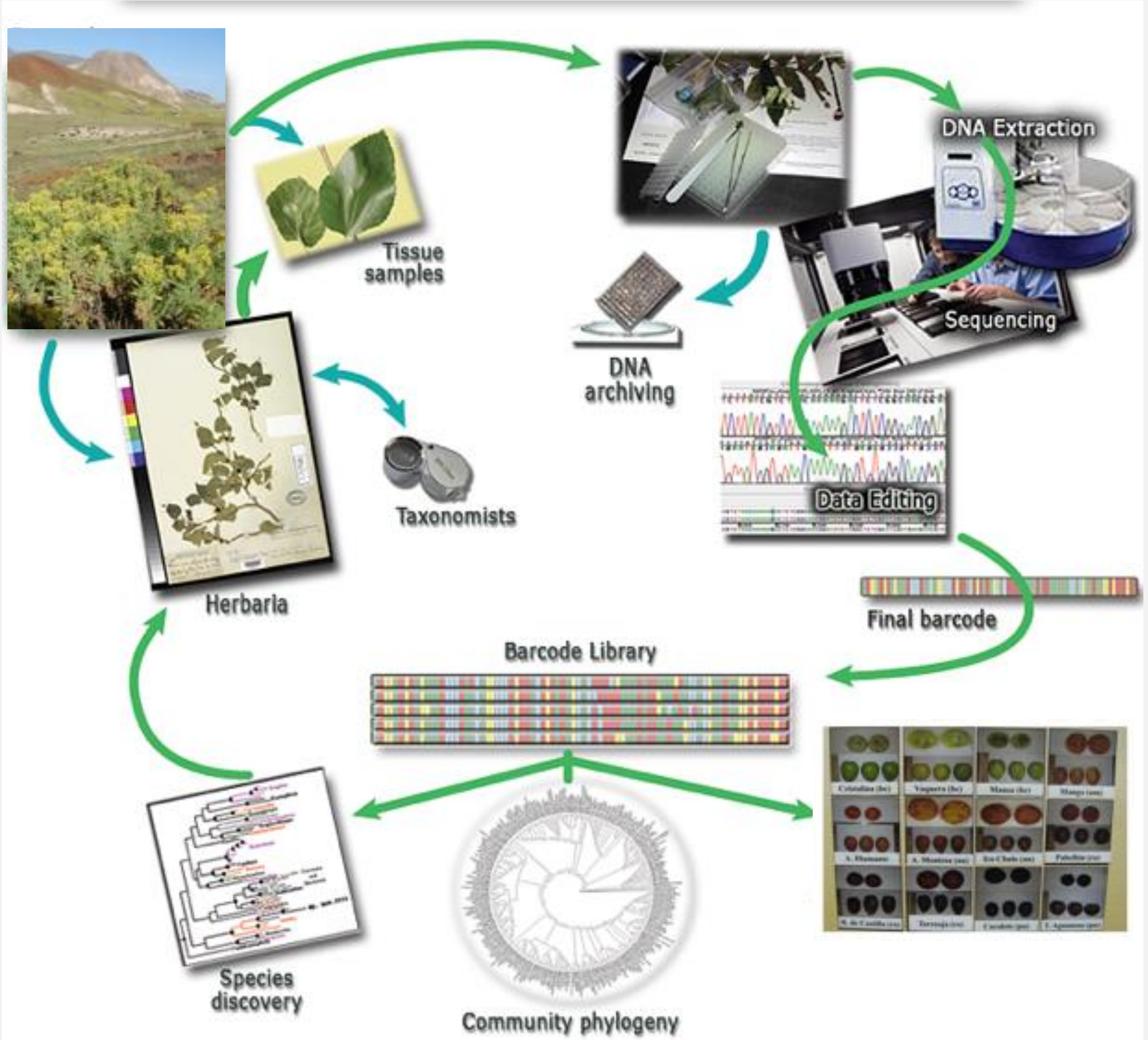
https://blast.ncbi.nlm.nih.gov/Blast.cgi

2. **Barcode of Life Database** (**BOLD**) created and is maintained by University of Guelph in Ontario.

Advancing biodiversity science through DNA-based species identification.

https://www.boldsystems.org/

Plant DNA barcode cycle



http://botany.si.edu/projects/dnabarcode/cycle.htm

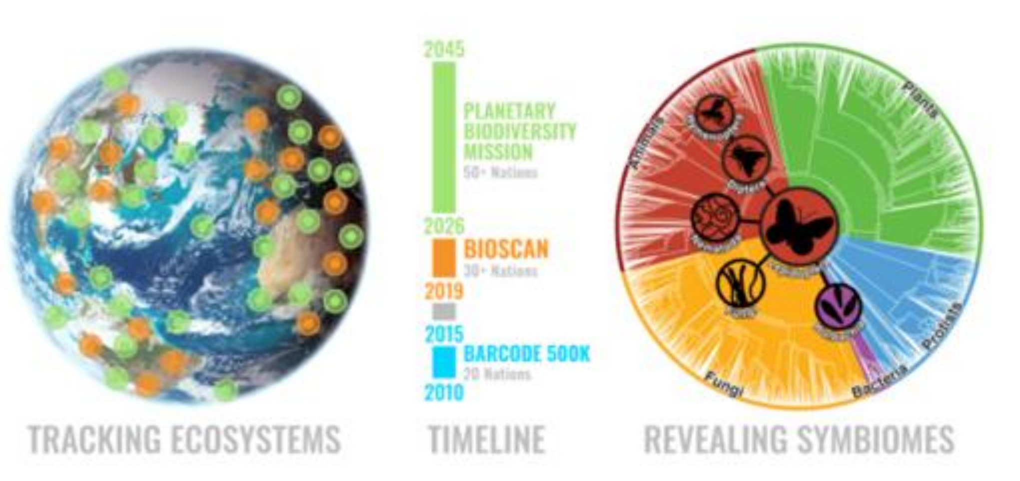

Agri-Food Canada
Agroalimentaire Canada
DNA BARCODING
0:03 / 3:35
HD

Four Barcoding components

4. Data Analysis: Specimens are identified by finding the closest matching reference record in the database. CBOL's Data Analysis Working Group

CONSORTIUM FOR THE BARCODE OF LIFE

international BARCODE OF LIFE



Consortium for the Barcode of Life (CBOL) is an international initiative devoted to developing DNA barcoding as a global standard for the identification of biological species.

Major Sequence Repositories

GenBank or NCBI (all known nucleotide and protein sequences)

www.ncbi.nlm.nih.gov/Web/Genbank/

Ensembl (all known nucleotide and protein sequences)

www.ensembl.org/index.html

TIGR Gene Indices (non-redundant, gene oriented clusters)

www.tigr.org/tdb/tdb.html

Gene Expression

BodyMap (Human and mouse gene expression data)

bodymap.ims.u-tokyo.ac.jp

Gene Identification and Structure

EID (Protein-coding, intron-containing genes)

mcb.harvard.edu/gilbert/EID/

Exint (Exon-intron structure of eukaryotic genes)

intron.bic.nus.edu.sg/exint/extint.html

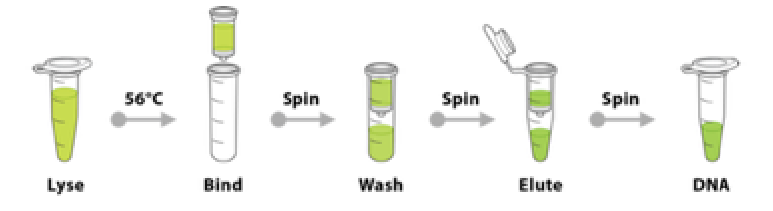
TRRD (Regulatory regions of eukaryotic genes)

www.mgs.bionet.nsc.re/mgs/dbases/trrd4/

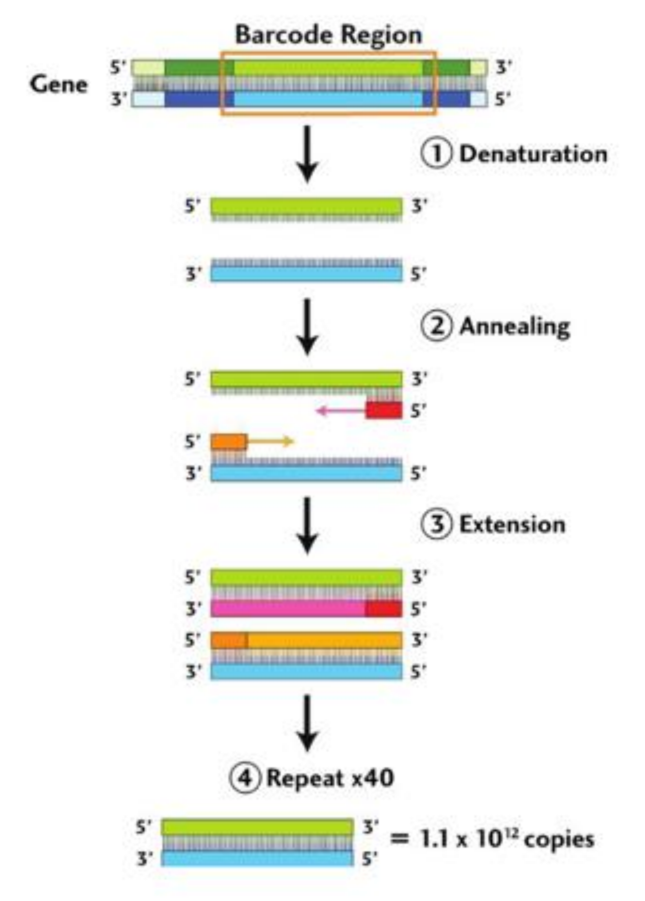
Sequence Databases

3. Acquire a DNA barcoding sequence

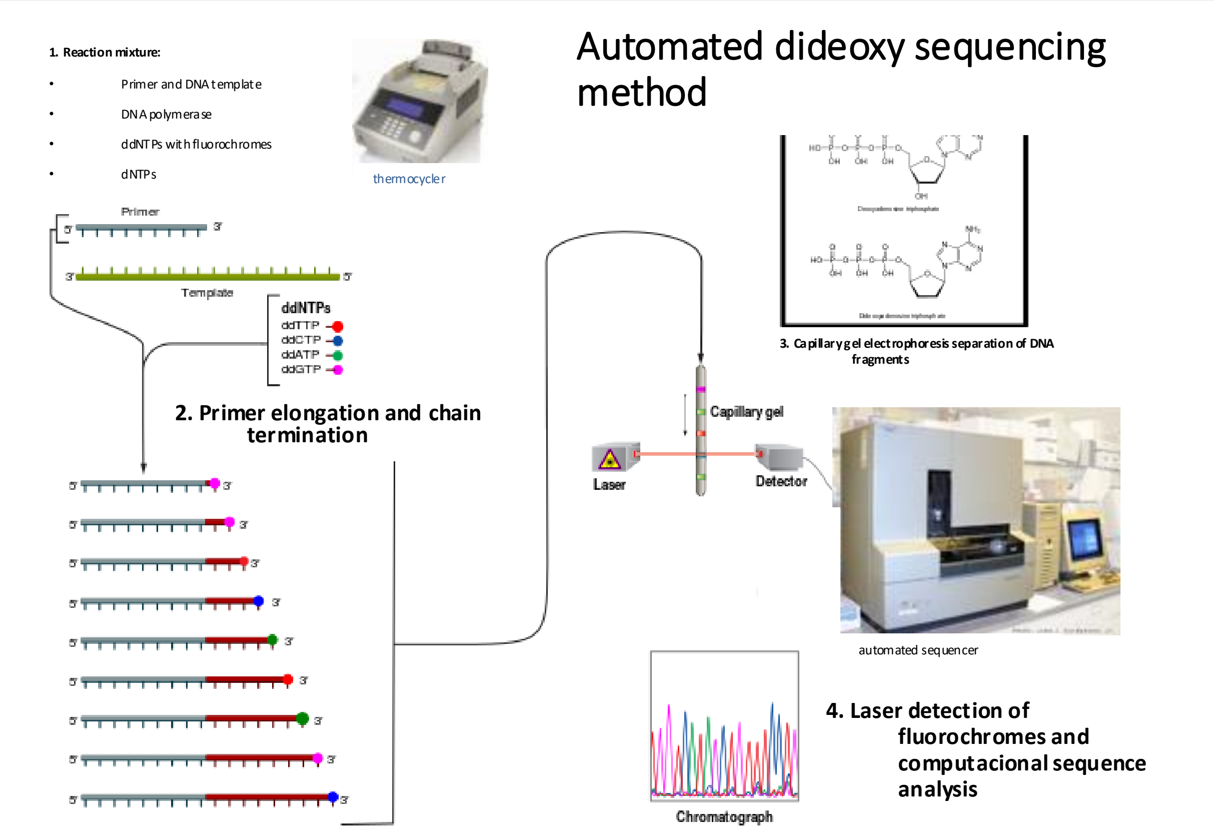
1. DNA extraction



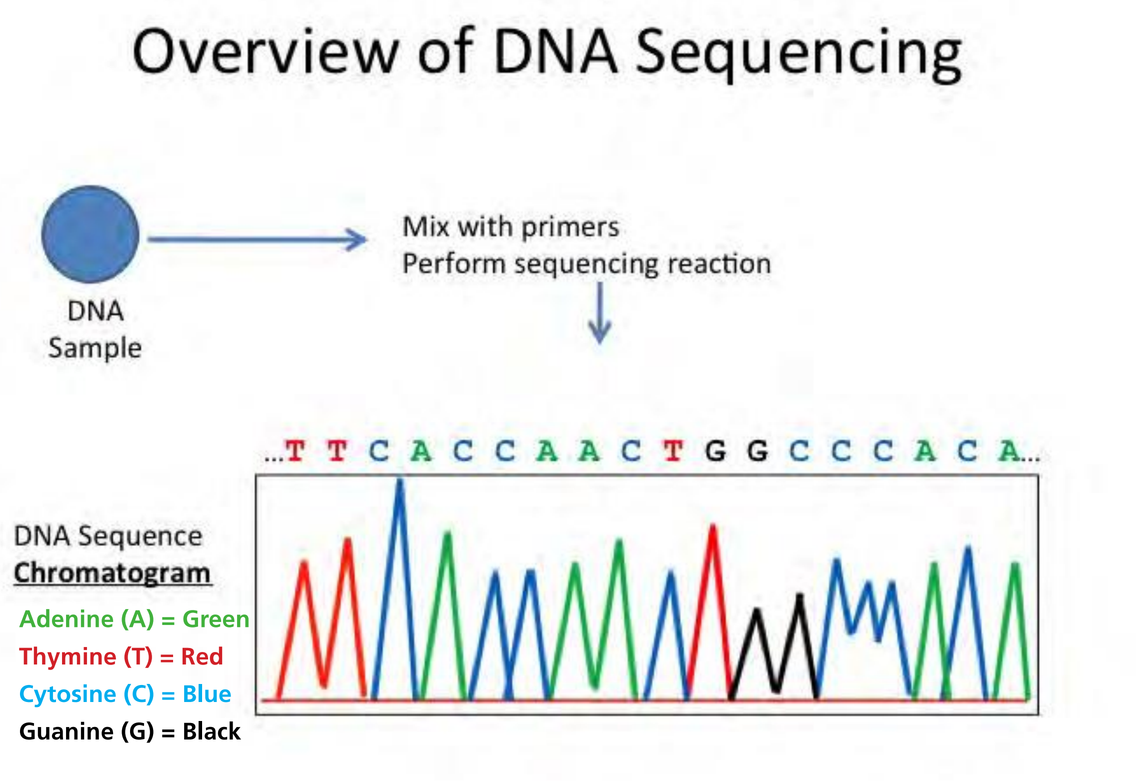
2. Barcode Region amplification by PCR

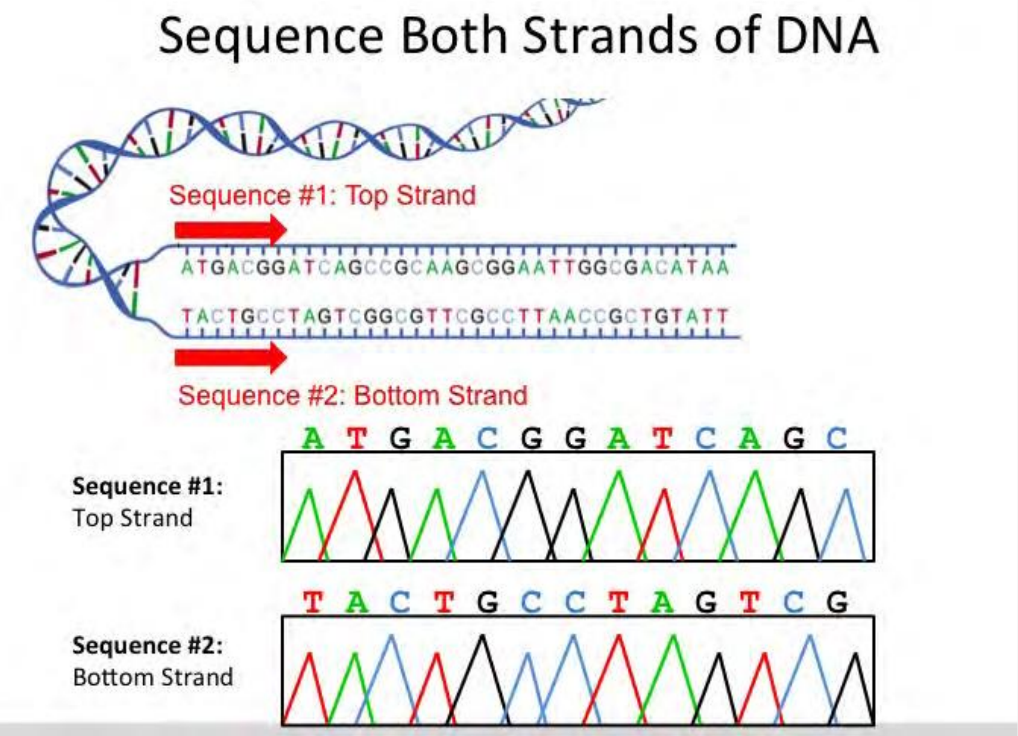


Automated dideoxy sequencing method

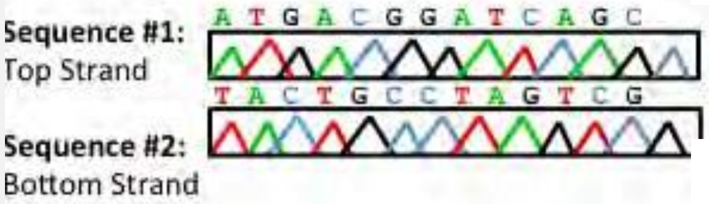


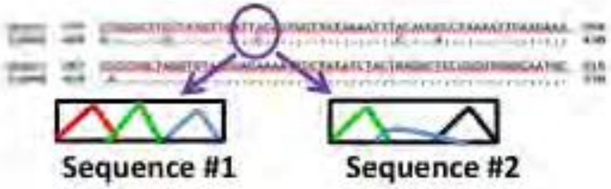
3. Acquire a Barcode sequence





Analyzing DNA Sequences





ATGCCGTAA
M P STOP

1. Obtain two chromatograms for each sample.
2. Align the sequences with BLAST.
3. Visualize the chromatograms using FinchTV. Compare BLAST alignments against base calls in chromatogram.
4. Review any differences and determine which base is most likely correct.
5. Edit and trim the DNA sequence using quality data.
6. Translate the sequence to check for stop codons.
7. Use BLAST to identify origin of sequence.
8. Use BOLD to confirm identity and make phylogenetic tree.

3. Viewing and analysing sequences

Import
- Import trace files into software

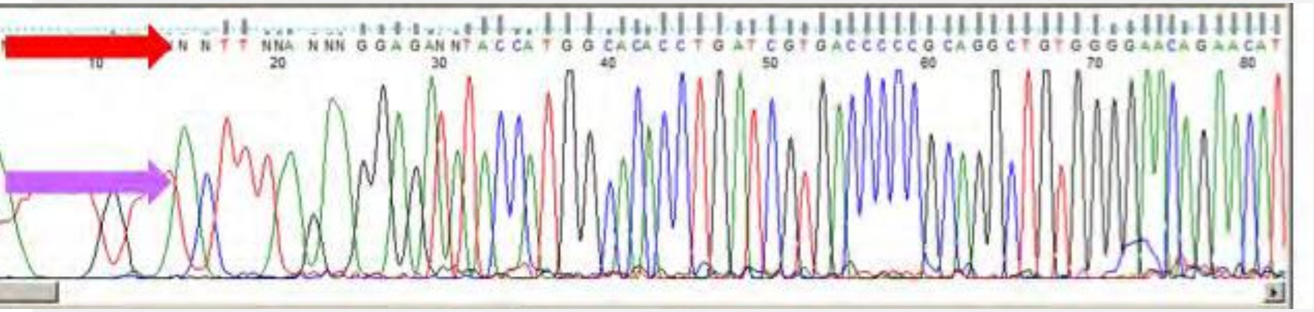
Trim Ends
- Remove low quality ends

Trim Primers
- Forward trace: look for reverse primer (reverse complement)
- Reverse trace: look for forward primer (reverse complement)

Assemble Contig
- Change orientation of reverse strand (reverse complement)*
- Assemble forward and reverse into a contig

Edit
- Inspect traces for ambiguities and solve them
- If uncertain, use IUPAC ambiguity code

Export
- Save contig
- Export contig as fasta files (.fas)



FASTA format

FASTA format is used to represent either nucleotide or peptide sequences. The first line is a comment line, beginning with “>” and describing the sequence. All the following lines are the sequence, in plain text.

Example DNA sequence in FASTA format:

```
>gi|23423|ref|NM_23542.0| Homo sapiens protein
ATGAATCGATACGATAGCTAGCTATCGATGCA
GATCAGAGAGGGGCTTTAGCTAGCTAAGCTAG
```

4. Building a consensus

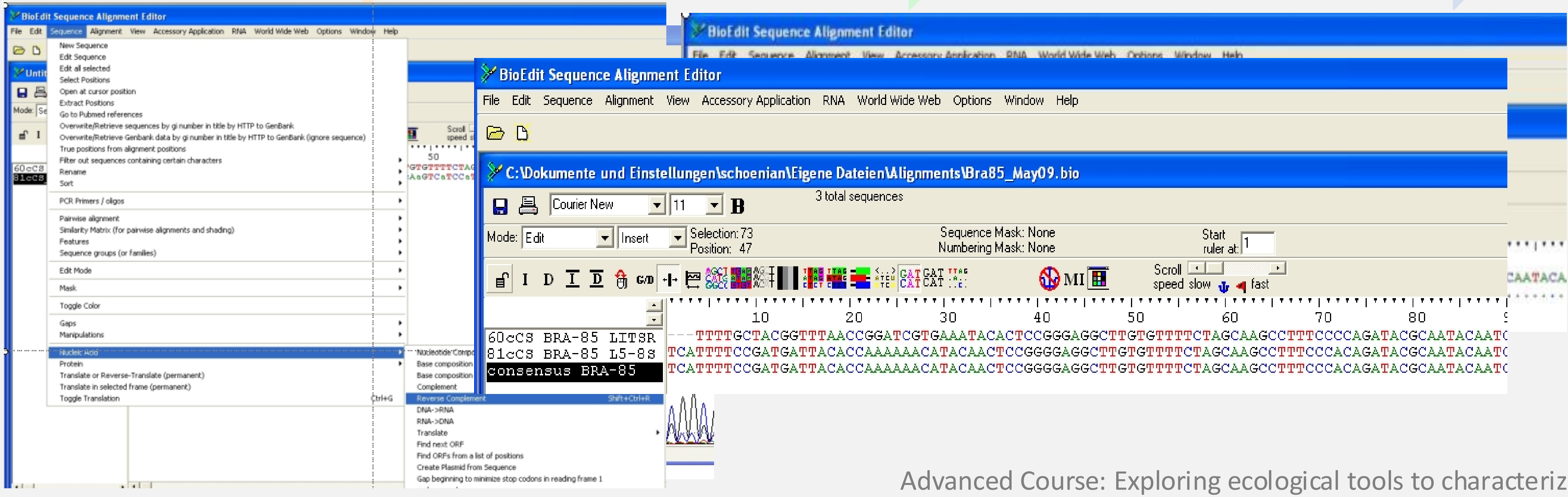
BioEdit 7.2 Free
BioEdit is a biological sequence alignment editor

1 Import forward and reverse sequences

(.abi files)

2 Reverse complement reverse strand and align both strands

3 Create consensus and analyze mismatches and chromatograms (save as .fas file)



C:\Dokumente und Einstellungen\schoenian\Eigene Dateien\Alignments\Bra85_May09.bio

Courier New 11

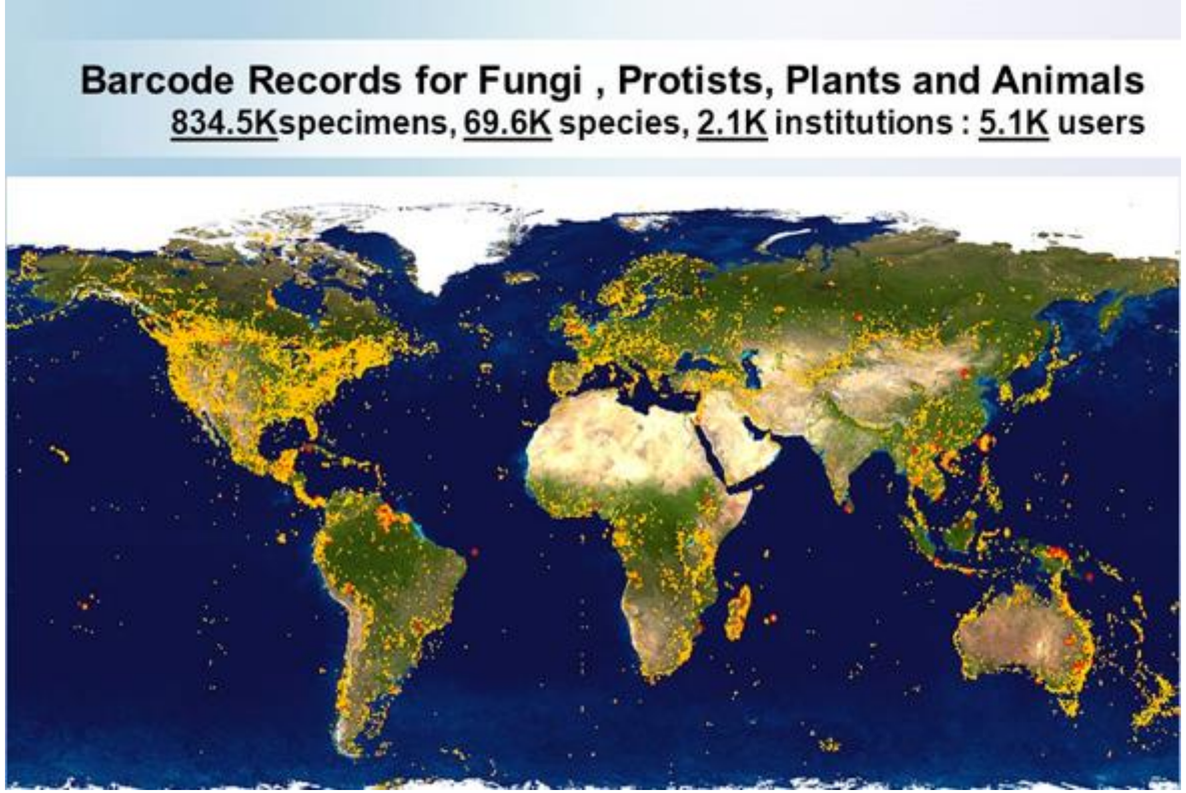
3 total sequences

Mode: Edit Insert
Selection: 73
Position: 47
Sequence Mask: None
Numbering Mask: None
Start ruler at: 1

```
60cCS BRA-85 LITSR  ---TTTTGCTACGGTTTAACCGGATCGTGAAATACACTCCGGGAGGCTTGTGTTTTCTAGCAAGCCTTTCCCCAGATACGCAATACAAT
81cCS BRA-85 L5-8S  TCATTTTCCGATGATTACACCAAAAAACATACAACTCCGGGGAGGCTTGTGTTTTCTAGCAAGCCTTTCCCACAGATACGCAATACAAT
consensus BRA-85    TCATTTTCCGATGATTACACCAAAAAACATACAACTCCGGGGAGGCTTGTGTTTTCTAGCAAGCCTTTCCCACAGATACGCAATACAAT
```

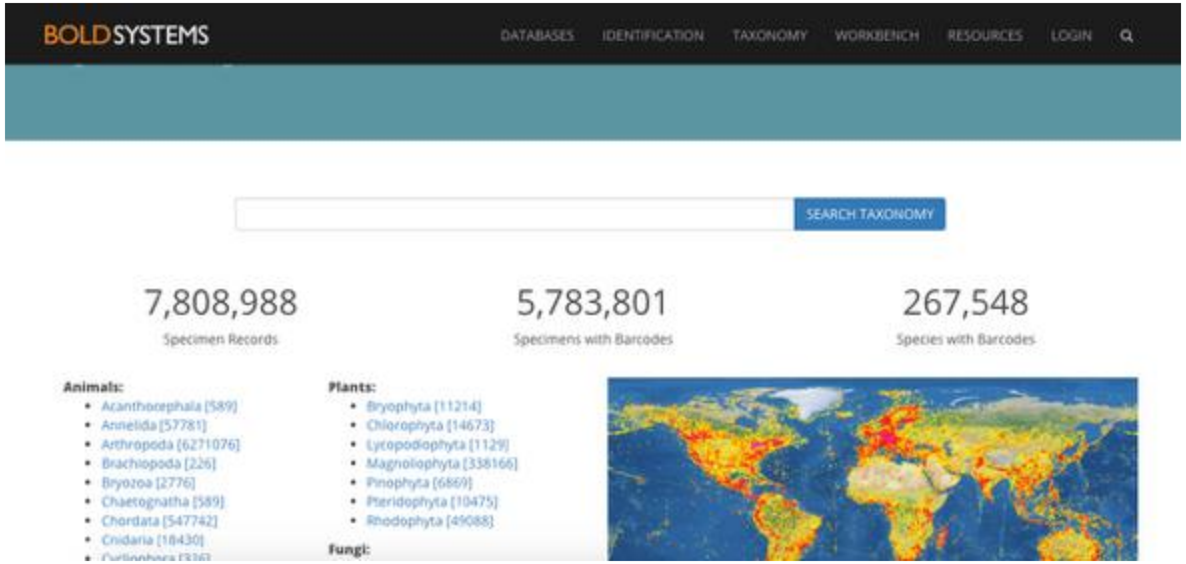
Bold database

Databases



Barcode Records for Fungi , Protists, Plants and Animals

834.5Kspecimens, 69.6K species, 2.1K institutions : 5.1K users



7,808,988 Specimen Records

5,783,801 Specimens with Barcodes

267,548 Species with Barcodes

Animals:

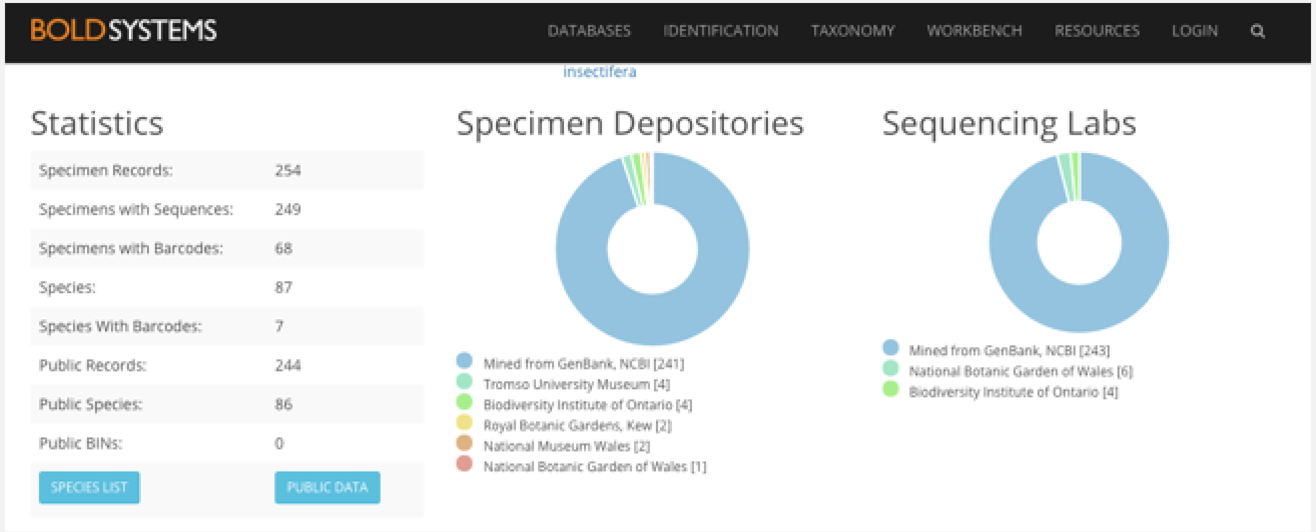
- Acanthocephala [589]
- Annelida [57781]
- Arthropoda [6271076]
- Brachiopoda [226]
- Bryozoa [2776]
- Chaetognatha [589]
- Chordata [547742]
- Cnidaria [18430]
- Cyclophora [316]

Plants:

- Bryophyta [11214]
- Chlorophyta [14673]
- Lycopodiophyta [1129]
- Magnoliophyta [338166]
- Pinophyta [6869]
- Pteridophyta [10475]
- Rhodophyta [49088]

Fungi:

Example of BOLD information



Statistics

Specimen Records:	254
Specimens with Sequences:	249
Specimens with Barcodes:	68
Species:	87
Species With Barcodes:	7
Public Records:	244
Public Species:	86
Public BINs:	0

Specimen Depositories

- Mined from GenBank, NCBI [241]
- Tromso University Museum [4]
- Biodiversity Institute of Ontario [4]
- Royal Botanic Gardens, Kew [2]
- National Museum Wales [2]
- National Botanic Garden of Wales [1]

Sequencing Labs

- Mined from GenBank, NCBI [243]
- National Botanic Garden of Wales [6]
- Biodiversity Institute of Ontario [4]

TAXONOMY BROWSER: Ophrys

Genus : Ophrys

Magnoliophyta / Liliopsida / Asparagales / Orchidaceae / Ophrys

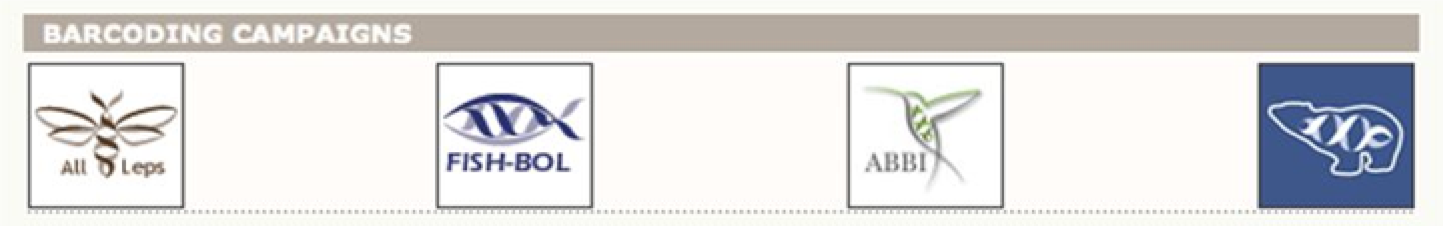
Taxon Description (Wikipedia)

The genus ***Ophrys*** is a large group of orchids from the alliance Orchis in the subtribe Orchidinae. They are widespread across much of Europe, North Africa, the Canary Islands, and the Middle East as far east as Turkmenistan. [http://apps.kew.org/wcsp/namedetail.do?name_id=140696 Kew World Checklist of Selected Plant Families] These plants are remarkable in that they successfully reproduce through pseudocopulation, that is, their flowers mimic female insects to such a degree that amorous males are fooled into mating with the flowers, thereby pollinating them. There are many natural hybrids. They are referred to as the "**bee orchids**" due to the flowers of some species resemblance to the furry bodies of bees and other insects. Their scientific... full article at Wikipedia

Organizations

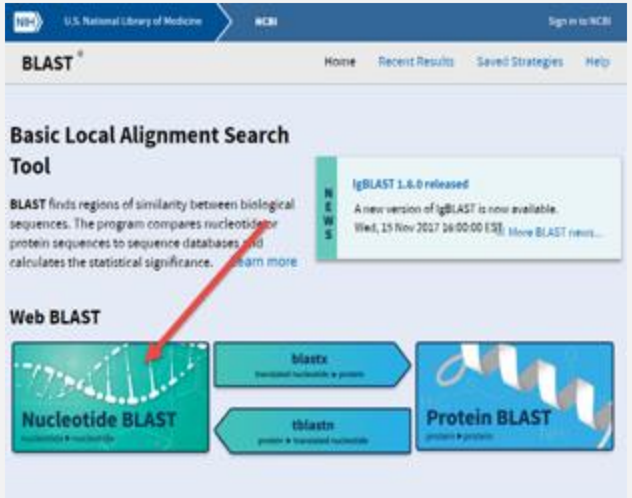
- Consortium for the Barcode of Life (CBOL)
  (www.barcoding.si.edu)
- Barcode of Life Database (BOLD)
  (www.barcodinglife.org)
- International Barcode of Life (iBOL)
  (www.ibolprojec.org)
- FishBOL, All Birds Barcoding Initiative, MarBOL, etc. etc.

iBOL
INTERNATIONAL BARCODE OF LIFE


BARCODING CAMPAIGNS

Comparing our DNA sequence with database for species identification

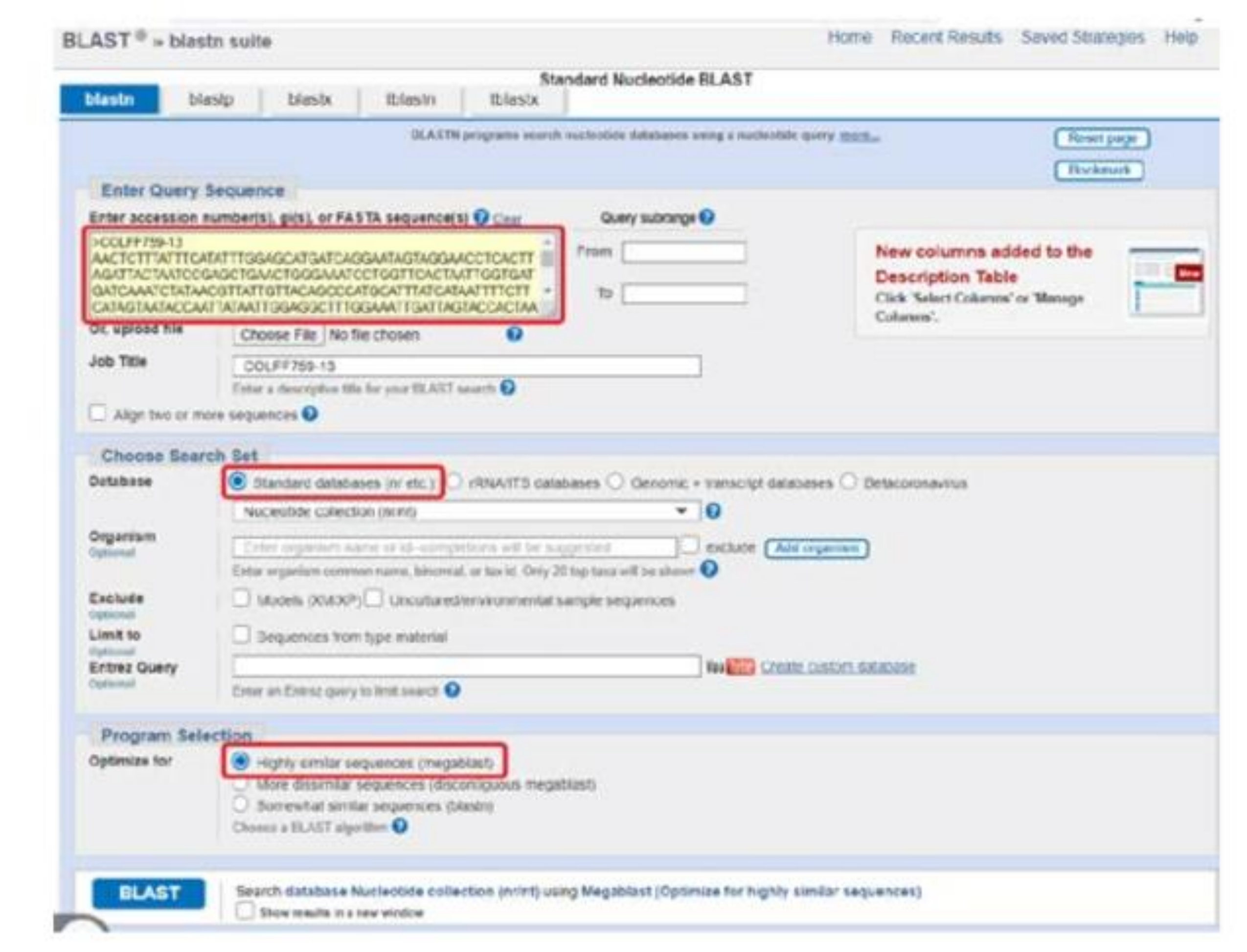
BLAST (**B**asic **L**ocal **A**lignment **S**earch **T**ool) is an online search tool provided by NCBI (National Center for Biotechnology Information). It allows you to “find regions of similarity between biological sequences” (nucleotide or protein).



Basic Local Alignment Search Tool

BLAST finds regions of similarity between biological sequences. The program compares nucleotide or protein sequences to sequence databases and calculates the statistical significance. Learn more

A new version of IgBLAST is now available.
Wed, 15 Nov 2017 16:00:00 EST



BLASTN programs search nucleotide databases using a nucleotide query. more...

Enter accession number(s), gi(s), or FASTA sequence(s) Clear

```
>COLFF759-13
AACTCTTTATTTCATATTTGGAGCATGATCAGGAATAGTAGGAACCTCACTT
AGATTACTAATCCGAGCTGAACTGGGAATCCTGGTTCACTAATTGGTGAT
GATCAAATCTATAACGTTATTGTTACAGCCCATGCATTTATCATAATTTTCTT
CATAGTAATACCAATTATAATTGGAGGCTTTGGAAATTGATTAGTACCACTAA
```

Or, upload file: No file chosen

Job Title: COLFF759-13

Enter a descriptive title for your BLAST search

☐ Align two or more sequences

New columns added to the Description Table
Click 'Select Columns' or 'Manage Columns'.

Database: ● Standard databases (nr etc.) ○ rRNA/ITS databases ○ Genomic + transcript databases ○ Betacoronavirus

Nucleotide collection (nr/nt)

Organism (Optional): Enter organism name or id--completions will be suggested ☐ exclude

Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown

Exclude (Optional): ☐ Models (XM/XP) ☐ Uncultured/environmental sample sequences

Limit to (Optional): ☐ Sequences from type material

Entrez Query (Optional):

Enter an Entrez query to limit search

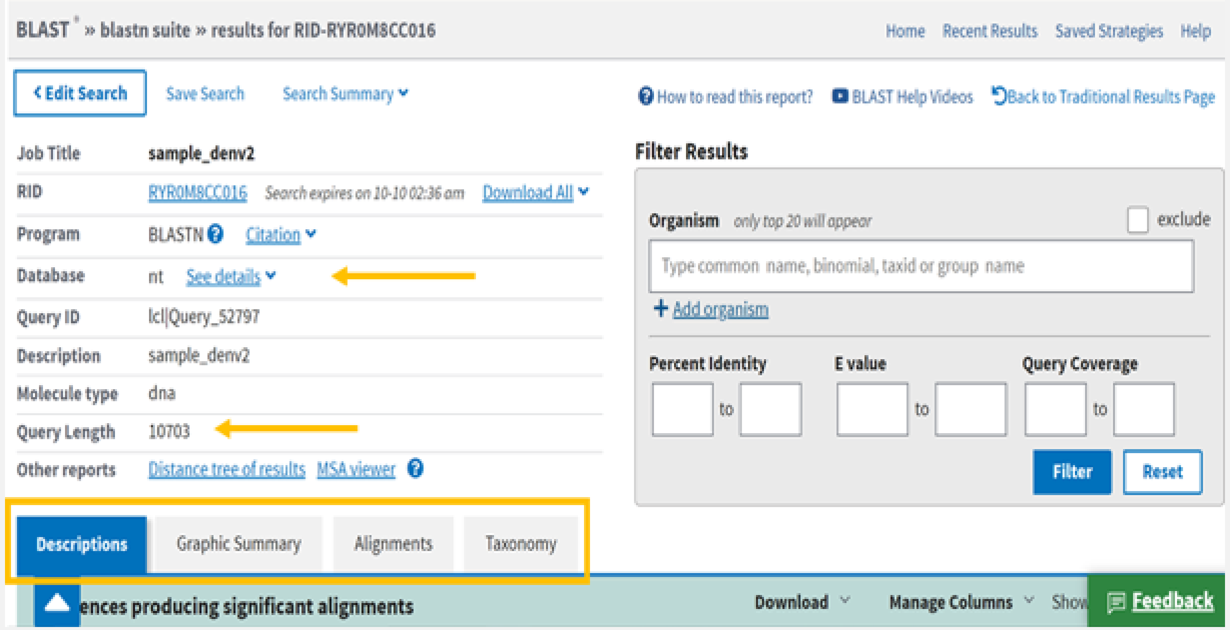
Optimize for:
● Highly similar sequences (megablast)
○ More dissimilar sequences (discontiguous megablast)
○ Somewhat similar sequences (blastn)

Choose a BLAST algorithm

Search database Nucleotide collection (nr/nt) using Megablast (Optimize for highly similar sequences)

☐ Show results in a new window

After sequence Blast



Job Title	sample_denv2
RID	RYR0M8CC016 Search expires on 10-10 02:36 am Download All
Program	BLASTN Citation
Database	nt See details
Query ID	lcl|Query_52797
Description	sample_denv2
Molecule type	dna
Query Length	10703
Other reports	Distance tree of results MSA viewer

Filter Results

Organism *only top 20 will appear* ☐ exclude

Type common name, binomial, taxid or group name

+ Add organism

Percent Identity ☐ to ☐ E value ☐ to ☐ Query Coverage ☐ to ☐

Filter Reset

ences producing significant alignments

Max score: the highest bit score that is calculated from alignment matches and mismatches.

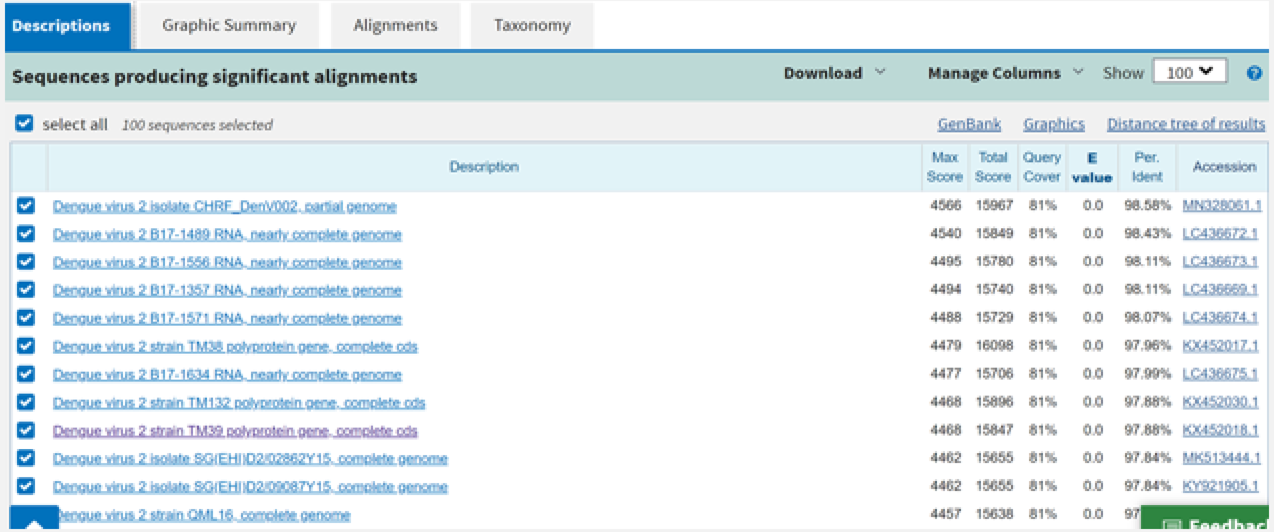
Total score: the sum of the alignment scores of all of the segments from the sequence.

Query coverage: the % of the contig length that aligns with the NCBI hit.

E value: the number of hits expected to be seen by chance. The closer to 0, the better.

Percent identity: the % of bases that are identical to the reference genome.

Accession [number]: a unique identifier assigned to records in the NCBI databases.



Sequences producing significant alignments

☑ select all *100 sequences selected*

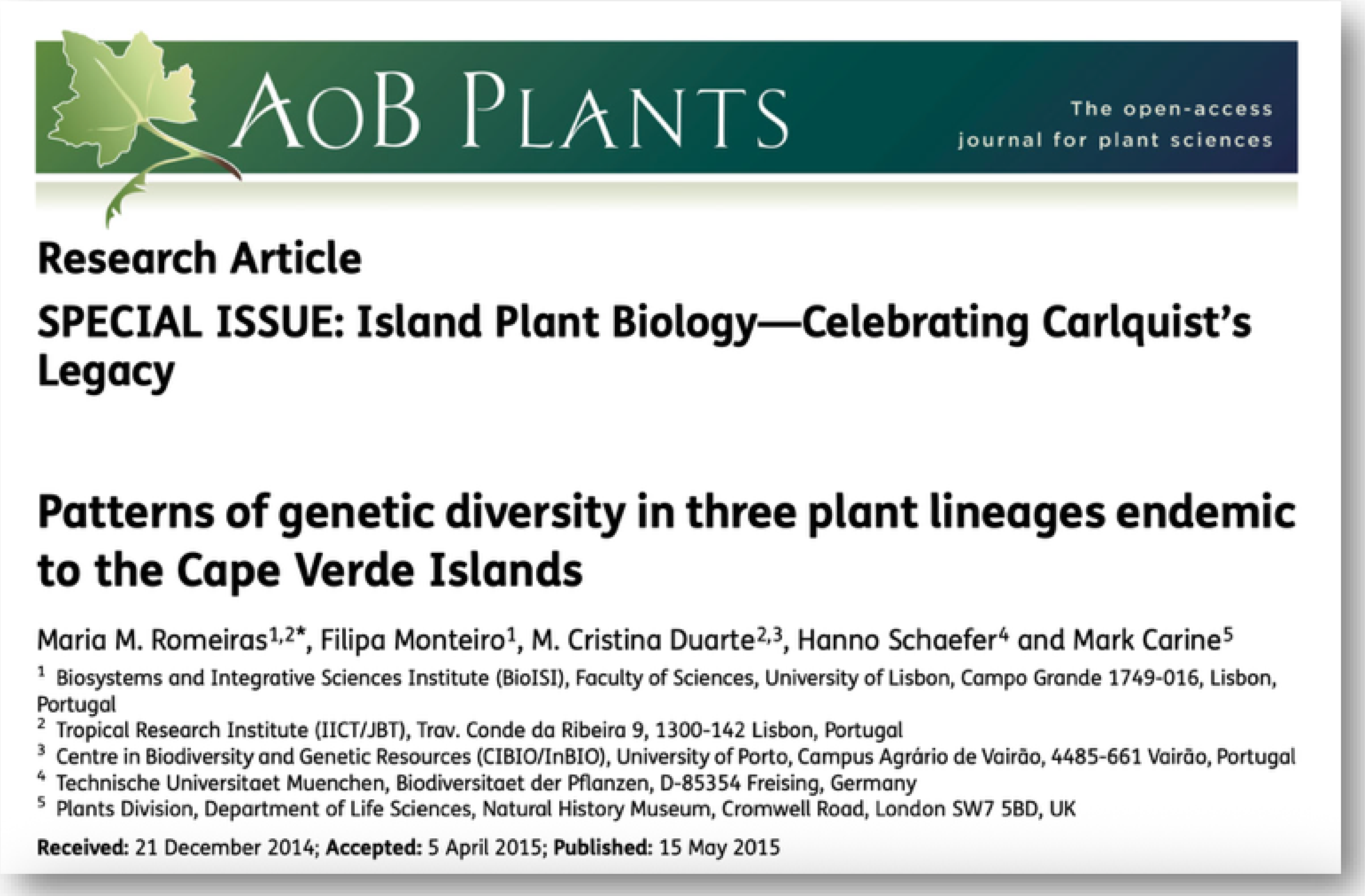
	Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
☑	Dengue virus 2 isolate CHRF_DenV002, partial genome	4566	15967	81%	0.0	98.58%	MN328061.1
☑	Dengue virus 2 B17-1489 RNA, nearly complete genome	4540	15849	81%	0.0	98.43%	LC436672.1
☑	Dengue virus 2 B17-1556 RNA, nearly complete genome	4495	15780	81%	0.0	98.11%	LC436673.1
☑	Dengue virus 2 B17-1357 RNA, nearly complete genome	4494	15740	81%	0.0	98.11%	LC436669.1
☑	Dengue virus 2 B17-1571 RNA, nearly complete genome	4488	15729	81%	0.0	98.07%	LC436674.1
☑	Dengue virus 2 strain TM38 polyprotein gene, complete cds	4479	16098	81%	0.0	97.96%	KX452017.1
☑	Dengue virus 2 B17-1634 RNA, nearly complete genome	4477	15706	81%	0.0	97.99%	LC436675.1
☑	Dengue virus 2 strain TM132 polyprotein gene, complete cds	4468	15896	81%	0.0	97.88%	KX452030.1
☑	Dengue virus 2 strain TM39 polyprotein gene, complete cds	4468	15847	81%	0.0	97.88%	KX452018.1
☑	Dengue virus 2 isolate SG(EHI)D2/02862Y15, complete genome	4462	15655	81%	0.0	97.84%	MK513444.1
☑	Dengue virus 2 isolate SG(EHI)D2/09087Y15, complete genome	4462	15655	81%	0.0	97.84%	KY921905.1
	engue virus 2 strain QML16, complete genome	4457	15638	81%	0.0	97	

Anacardium occidentale isolate 92 maturase K (matK) gene, partial cds; chloroplast

GenBank: AY594459.1

```
LOCUS       AY594459                1945 bp    DNA     linear   PLN 26-JUL-2016
DEFINITION  Anacardium occidentale isolate 92 maturase K (matK) gene, partial
            cds; chloroplast.
ACCESSION   AY594459
VERSION     AY594459.1
KEYWORDS    .
SOURCE      chloroplast Anacardium occidentale (cashew)
  ORGANISM  Anacardium occidentale
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliopsida; eudicotyledons; Gunneridae;
            Pentapetalae; rosids; malvids; Sapindales; Anacardiaceae;
            Anacardium.
REFERENCE   1  (bases 1 to 1945)
  AUTHORS   Pell,S.K.
  TITLE     Molecular Phylogeny of Anacardiaceae: Intrafamilial Classification
            and Evolutionary Relationships of Noted Genera
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1945)
  AUTHORS   Pell,S.K.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-APR-2004) Cullman Program for Molecular Systematics
            Studies, New York Botanical Garden, 200th St. and Kazimiroff Blvd.,
            Bronx, NY 10458, USA
FEATURES             Location/Qualifiers
     source          1..1945
                     /organism="Anacardium occidentale"
                     /organelle="plastid:chloroplast"
                     /mol_type="genomic DNA"
                     /isolate="92"
                     /specimen_voucher="Mori 24142"
                     /db_xref="taxon:171929"
                     /country="French Guiana"
                     /note="authority: Anacardium occidentale L."
     gene            399..>1945
```

Case study on Cabo Verde flora



AoB PLANTS

The open-access journal for plant sciences

Research Article

SPECIAL ISSUE: Island Plant Biology—Celebrating Carlquist's Legacy

Patterns of genetic diversity in three plant lineages endemic to the Cape Verde Islands

Maria M. Romeiras[1,2]*, Filipa Monteiro[1], M. Cristina Duarte[2,3], Hanno Schaefer[4] and Mark Carine[5]

[1] Biosystems and Integrative Sciences Institute (BioISI), Faculty of Sciences, University of Lisbon, Campo Grande 1749-016, Lisbon, Portugal
[2] Tropical Research Institute (IICT/JBT), Trav. Conde da Ribeira 9, 1300-142 Lisbon, Portugal
[3] Centre in Biodiversity and Genetic Resources (CIBIO/InBIO), University of Porto, Campus Agrário de Vairão, 4485-661 Vairão, Portugal
[4] Technische Universitaet Muenchen, Biodiversitaet der Pflanzen, D-85354 Freising, Germany
[5] Plants Division, Department of Life Sciences, Natural History Museum, Cromwell Road, London SW7 5BD, UK

Received: 21 December 2014; **Accepted:** 5 April 2015; **Published:** 15 May 2015

Species diversity and richness

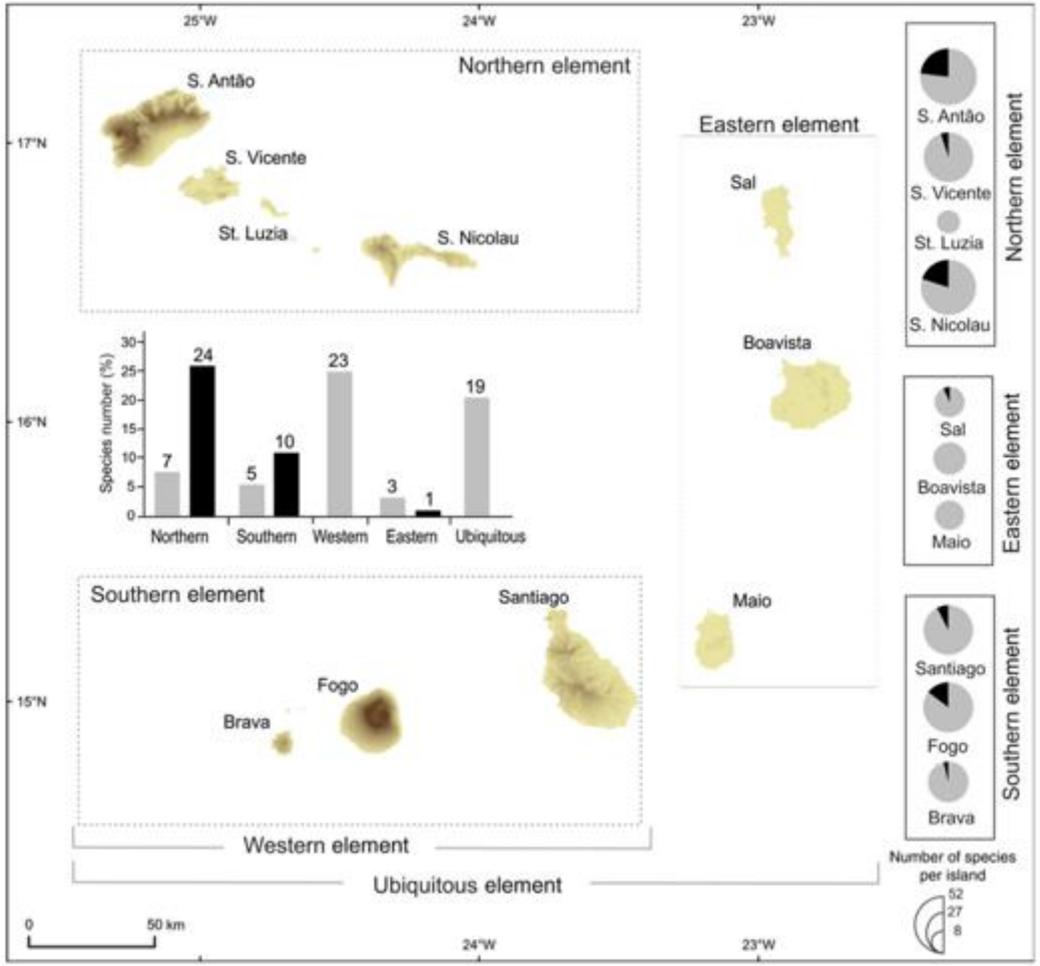
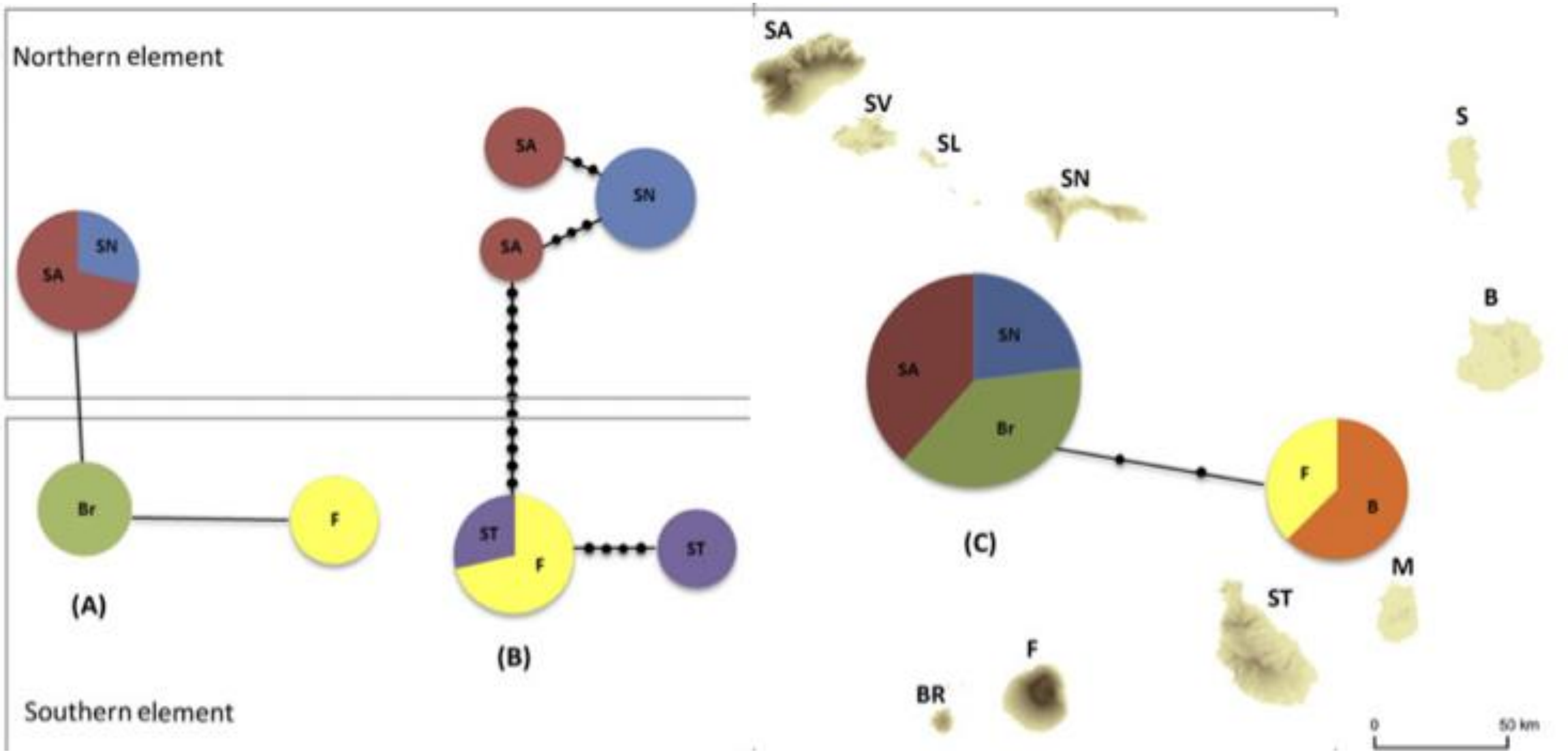
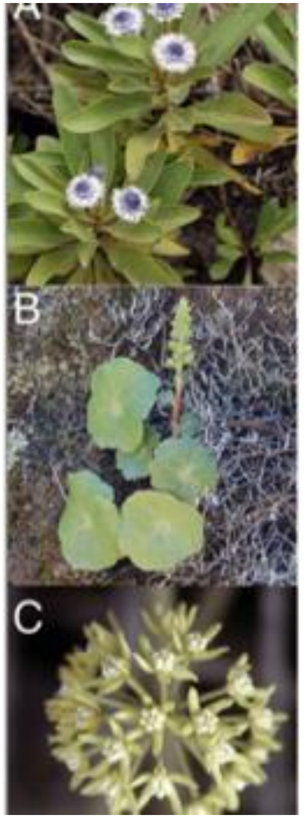


Figure 1. Relationship between the vascular endemic species of Cape Verde and their distribution within the five distributional elements: northern (i.e. Santo Antão, São Vicente, Santa Luzia and São Nicolau), southern (i.e. Santiago, Fogo and Brava), western (including species simultaneously present in northern and southern islands), eastern (i.e. Maio, Sal and Boavista) and ubiquitous (including species present in both western and eastern islands). The distribution of multi-island endemics—MIEs (grey) and single-island endemics—SIEs (black) in each island (right); and within the five distributional elements (bar graph in the centre; the number of taxa is placed above each bar).





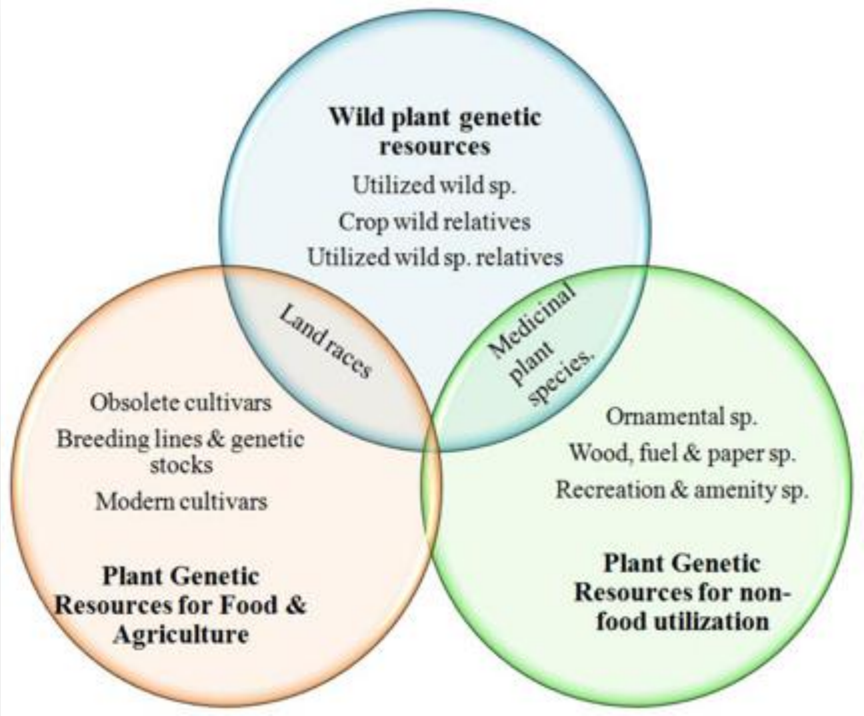
Molecular data supporting species identification and diversity

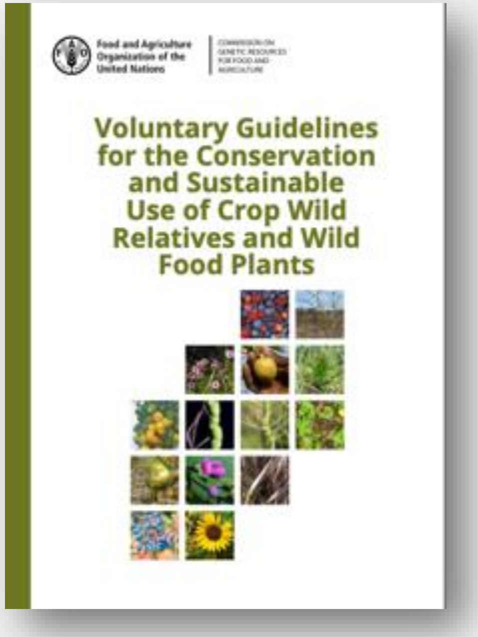
- **Potential new species disclosed by molecular data?**
- **Reverse taxonomy assessment and diversity analyses**

Application to wild useful plants

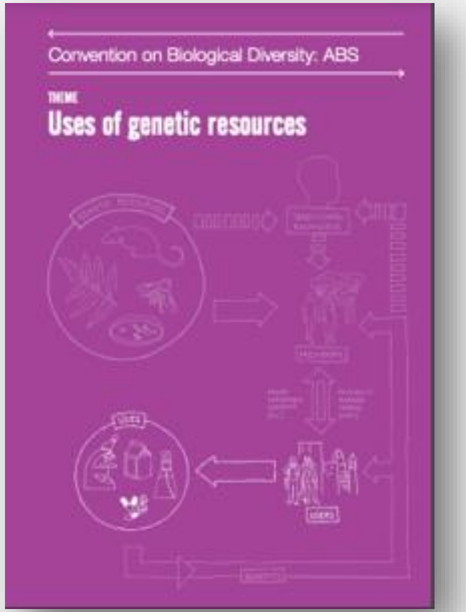
The FAO Commission developed the Genebank Standards for Plant Genetic Resources for Food and Agriculture and recently endorsed the Voluntary guidelines for national level conservation of crop wild relatives and wild food plants.

COMMISSION ON GENETIC RESOURCES FOR FOOD AND AGRICULTURE




Food and Agriculture Organization of the United Nations | Commission on Genetic Resources for Food and Agriculture

Voluntary Guidelines for the Conservation and Sustainable Use of Crop Wild Relatives and Wild Food Plants


Convention on Biological Diversity: ABS

THEME

Uses of genetic resources

Food and Agriculture Organization of the United Nations

Convention on Biological Diversity