



# Phytoplankton metabarcoding 4th part

B. Alric

- 1- Phytool reference library
- 2- Tests on environmental samples

INRAE

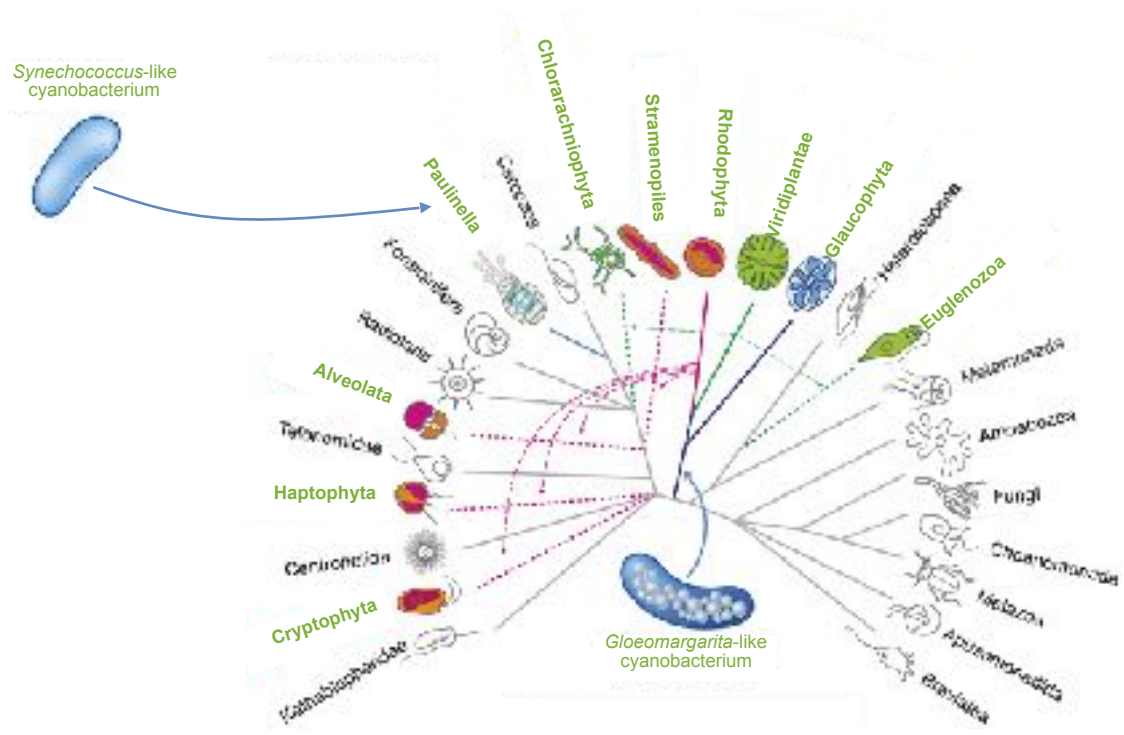




## Reminders

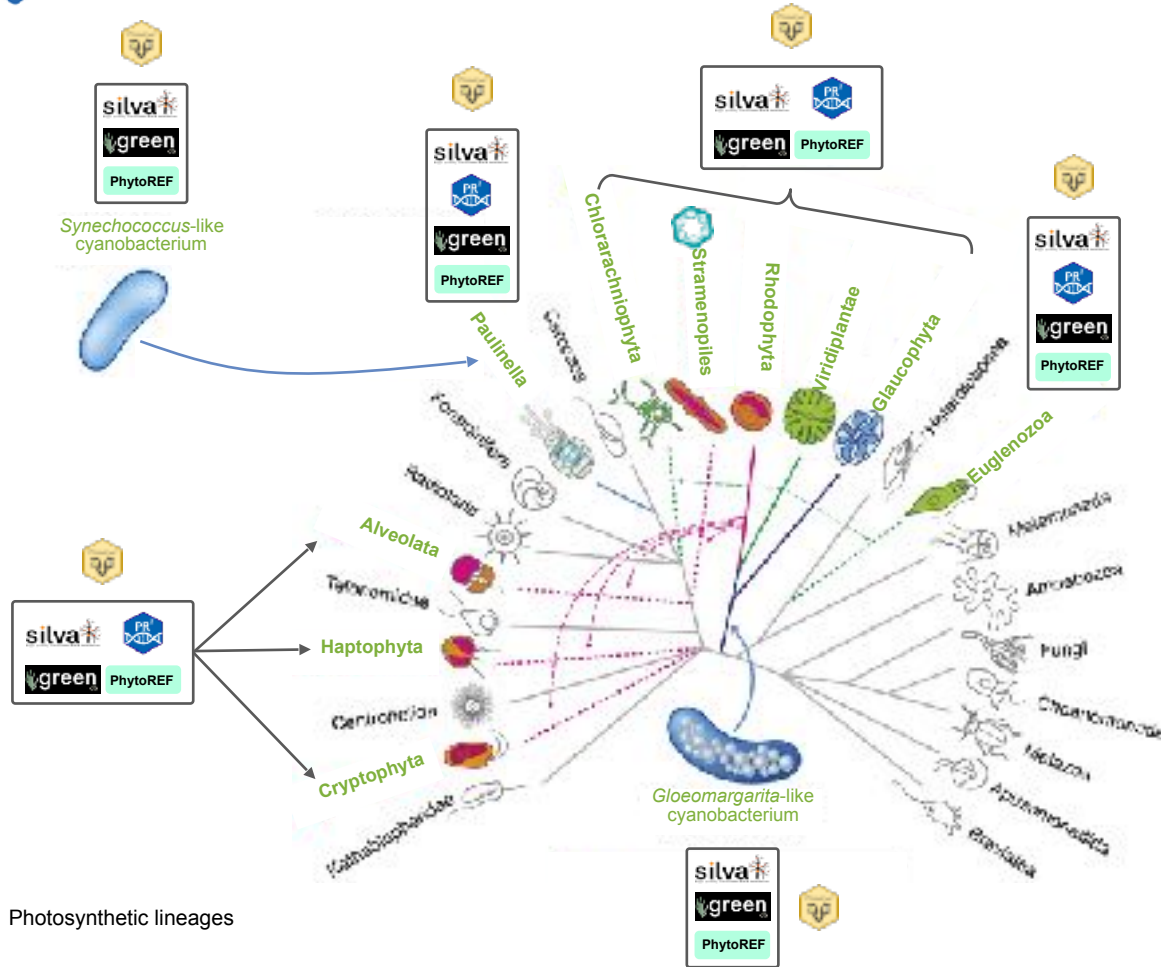
- 1- Phytool reference library ←
- 2- Tests on environmental samples





■ Photosynthetic lineages





	SSU	LSU	
	16S / 18S	23S / 28S	
	18S		
		23S	
	16S		
			rbcl
	16S / 18S	23S	rbcl

[https://github.com/Github-Carrtel/Phytool\\_V2](https://github.com/Github-Carrtel/Phytool_V2)

Quast et al. (2013) Nucl. Acids Res.  
 Guillou et al. (2013) Nucl. Acids Res.  
 Djemiel et al. (2013) Sci. Rep.  
 Decelle et al. (2015) Mol. Ecol. Res.  
 Rimet et al. (2019) Sci. Rep.

[Code](#)
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**Benjamin Ahr** Update README.md 2 weeks ago

figures	Devote image' prog	4 months ago
RENDER-v4	Update README.md	4 months ago
RENDER-mc	Update README.md	2 weeks ago

[10 commits](#)

## Phytool\_v2

### Overview

Phytool\_v2 is a web application allows, for phytoplankton, the homogenization between the taxonomic nomenclature used by molecular (eg. metabarcoding) and morphological (eg. microscopy) approaches. This application has been built with the K-javascript which allows the creation of interactive web application from the open-source R software.

This application was produced as part of the article:

Carleo A., Jochim A., Laplace-Freyre C., Domelzon I., Fimot F. 2021. Phytool, a ShinyApp to homogenise taxonomy of freshwater microalgae from DNA barcodes and microscopic observations. *Microscopy & Microanalysis*, 19: 265. <https://doi.org/10.1017/mms.2021.096>

### Utilization

We can access the web application [here](#)

**About**

ShinyApp to homogenise taxonomy of freshwater microalgae from DNA barcodes and microscopic observations

[Open in Shiny](#)


[Readme](#)  
[Issues](#)  
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[Forks](#)

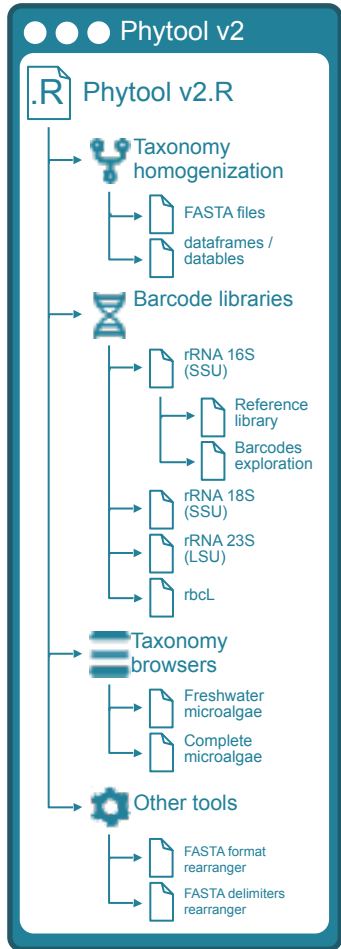
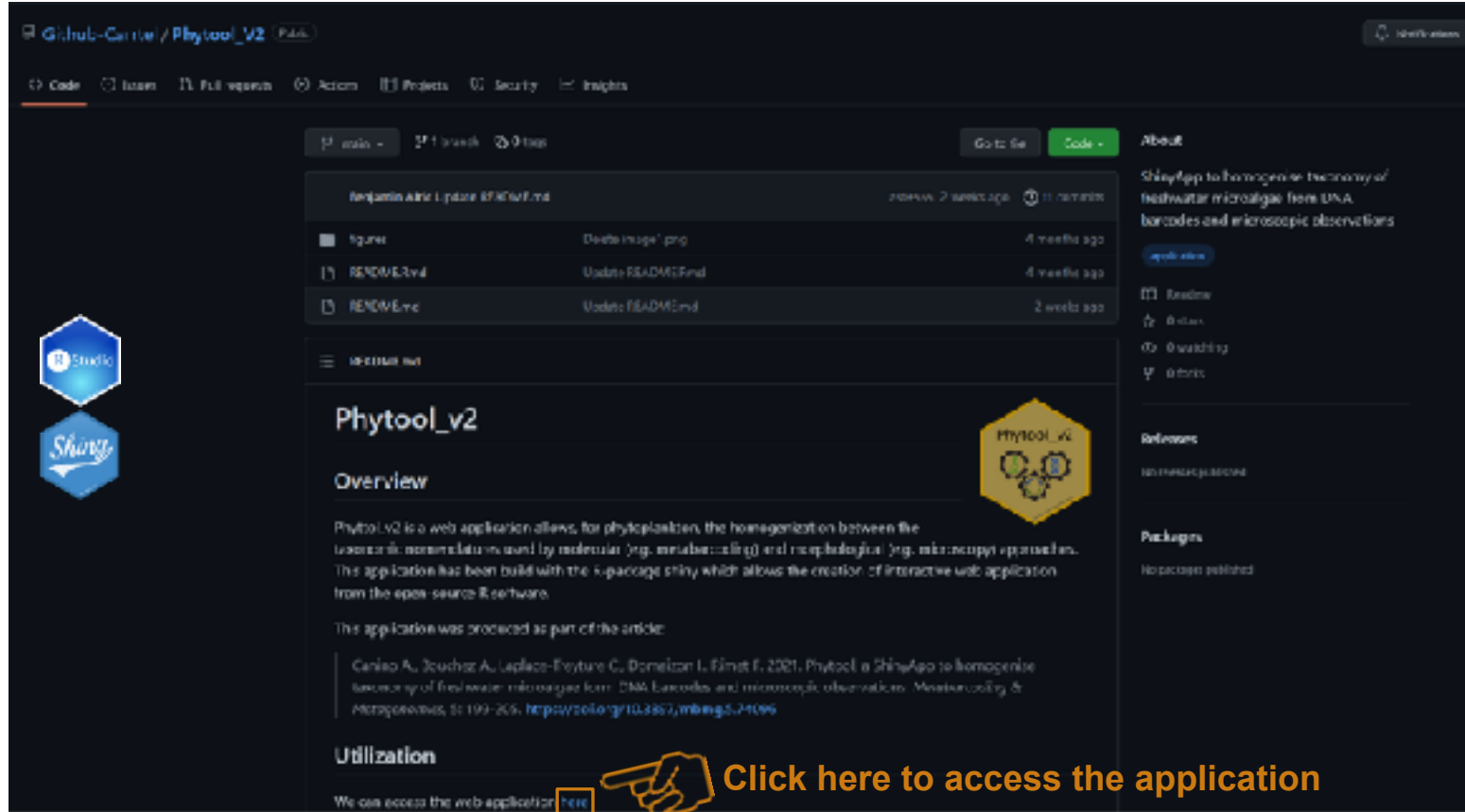
**Releases**

10 releases published

**Packages**

10 packages published



GitHub-Cartel / Phytool\_v2

Code Issues Pull requests Actions Projects Security Insights

Benjamin Ahrle Update README.md 2 months ago

figures	Devote image! prog	4 months ago
RENDER-v4	Update README.md	4 months ago
RENDER-enc	Update README.md	2 weeks ago

## Phytool\_v2

### Overview

Phytool\_V2 is a web application allows, for phytoplankton, the homogenization between the taxonomic nomenclature used by molecular (eg. metabarcoding) and morphological (eg. microscopy) approaches. This application has been build with the R-package shiny which allows the creation of interactive web application from the open-source R software.

This application was produced as part of the article:

Cartel A., Jouchot A., Laplace-Festre C., Domelzon I., Fimet F. 2021. Phytool, a ShinyApp to homogenise taxonomy of freshwater microalgae from DNA barcodes and microscopic observations. *Microscopy & Microanalysis*, 19: 265. <https://doi.org/10.1002/mima.21096>

### Utilization

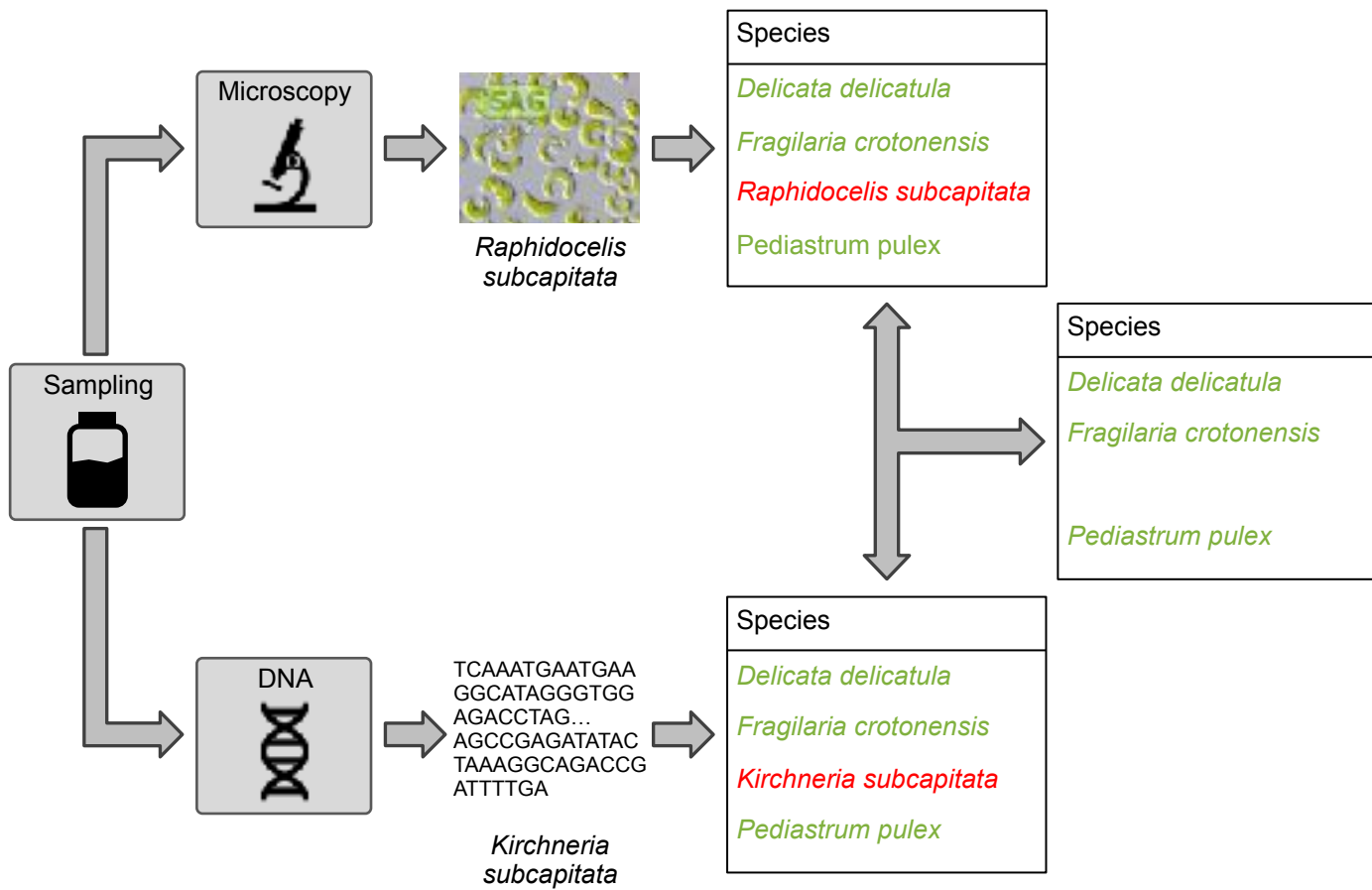
We can access the web application [here](#)

 [Click here to access the application](#)

Phytool v2

Phytool v2.R

- Taxonomy homogenization
  - FASTA files
  - dataframes / datables
- Barcode libraries
  - rRNA 16S (SSU)
  - Reference library
  - Barcodes exploration
  - rRNA 18S (SSU)
  - rRNA 23S (LSU)
  - rbcl
- Taxonomy browsers
  - Freshwater microalgae
  - Complete microalgae
- Other tools
  - FASTA format rearranger
  - FASTA delimiters rearranger





Phytool v2

Phytool v2.R

- Taxonomy homogenization
  - FASTA files
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1




FASTA files [dataframes / databbles](#)

The homogenization process uses the taxonomy from [PhyTOC3](#) and [TAXREFv25](#) which are themselves based on [AlgaeBase](#) taxonomies.

## Homogenize & Update taxonomic names from your sequences file (FASTA)

Help



Example of input file allowed  
Upload a FASTA file

Browse... [Homogenization\\_example...](#)

Submit

MAXIMUM FILE SIZE: 100MB

Back home

2



Phytool v2

Phytool v2.R

- Taxonomy homogenization
  - FASTA files
  - dataframes / datables
- Barcode libraries
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  - rRNA 18S (SSU)
  - rRNA 23S (LSU)
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  - Complete microalgae
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  - FASTA delimiters rearranger

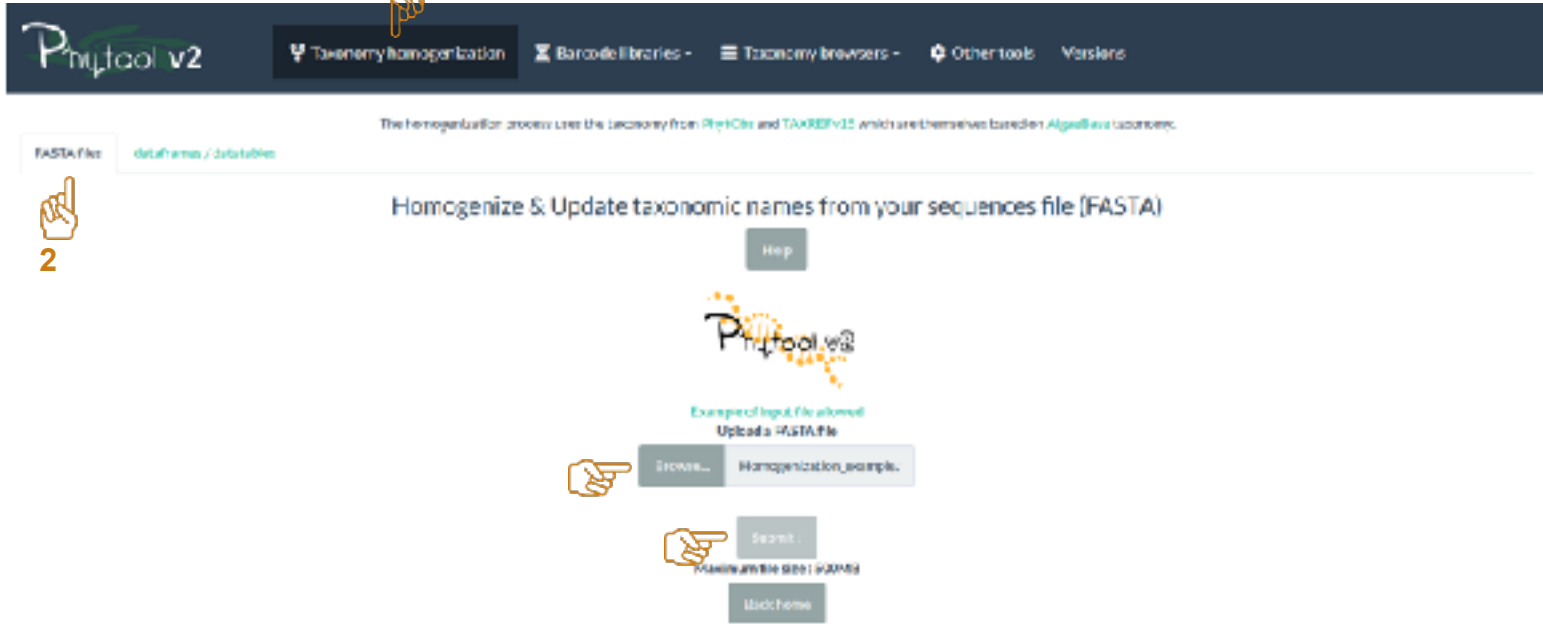
Your FASTA file should looks like:

```
>PHYTOOL.example1      Chromista;Bacillariophyta;Bacillariophyceae;Fragilariiales;>fragilariaceae;Fragilaria;Fragilaria crotonensis;
GGACAGAAAGACCTATGAACTGTGAAC TTGAAATTGAAATGGACTTTATTGTCAGTATAGG TGGAAGGCTTTGAAAGATTCCTGCGGAATTCGGAGCCATTAGTGGATACCACTCCTATATATTTA
>Phytool.example2      Plantae;Chlorophyta;Chlorophyceae;Sphaeropleales;Selenastreae;Kintneria;Kintneria subcapitata;
GGACAGAAAGACCTATGAAAGCTGTAGCTGGAATGGAAATTCGGGCTTTCTTCGCGAGCTAGG TGGAAGGCTTTGAAAGATTCCTTCGGGGAATCAGAGCCATCAGTGAGAGACCACTCTGGGAAGGCT
>PHYTOOL.example3      Chordata;Amphibia;Anura;Dendrobatidae;Dendrobatinae;Dendrobates;Dendrobates tinctorius;
ACTTGTCTTTAATTGAGGACTAGTATGAACGGCTTACGGAAGACTACACTGTCCTCTTTTCTAATCAATGAACTAATCTCCCGTGAAGAAGCGGGGATAAACCTATAGACGAGAGAAGACCTATGGAGCT
```

Phytool v2

Phytool v2.R

- Taxonomy homogenization
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    - dataframes / databases
- Barcode libraries
  - rRNA 16S (SSU)
    - Reference library
    - Barcodes exploration
  - rRNA 18S (SSU)
  - rRNA 23S (LSU)
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Phytool v2

Taxonomy homogenization

Barcode libraries

Taxonomy browsers

Other tools

FASTA files

dataframes / databases

rRNA 16S (SSU)

Reference library

Barcodes exploration

rRNA 18S (SSU)

rRNA 23S (LSU)

rbcl

Freshwater microalgae

Complete microalgae

FASTA format rearranger

FASTA delimiters rearranger

The homogenization process uses the taxonomy from PhyloCris and TAXREFv25 which are themselves based on AlgaeBase taxonomy.

FASTA files

dataframes / databases

Homogenize & Update taxonomic names from your sequences file (FASTA)

Help

Phytool v2

Example of input file allowed

Upload a FASTA file

Browse... Homogenization\_example

Submit

Maximum file size: 100MB

Back home

Reference for taxonomy homogenization process:

Phytool v2

Phytool v2.R

- Taxonomy homogenization
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Phytool v2

- Taxonomy homogenization
- Barcode libraries -
- Taxonomy browsers -
- Other tools
- Versions



The homogenization process uses the taxonomy from **PhyloC** and **TAXREF v15** which are themselves based on **AlgaeBase** taxonomies.

FASTA files: [dataframes / datables](#)

### Homogenize & Update taxonomic names from your sequences file (FASTA)

Help

Example of input file allowed  
Upload a FASTA file

Choose... Homogenization\_example.fasta

Secret

Go to file

« input file »

```
>Phytool_example2      Plantae;Chlorophyta;Chlorophyceae;Sphaeropleales;Selenastraceae;kirchneria;kirchneria_subcapitata;
GGACAGAAAGACCCATGAAGACTGTAGTCTGGAAATGGAAATTCGGGCTTTCTTGGCCAGCCTAGGTGGGAGGCGTTGAAATTTCTTCCGGGAAATCAGAGCCATCAGTGGAGAGCCACTCTGGGAAGCCT
```



First output file: « updated file »

```
>NA;Chromista;Bacillariophyta;Bacillariophyceae;Fragilariiales;Fragilariaceae;Fragilaria;Fragilaria_troluensis
GGACAGAAAGACCCATGAAGACTGTAGTCTGGAAATGGAAATTCGGGCTTTCTTGGCCAGCCTAGGTGGGAGGCGTTGAAATTTCTTCCGGGAAATCAGAGCCATCAGTGGAGAGCCACTCTGGGAAGCCT
>NA;Plantae;Chlorophyta;Chlorophyceae;Sphaeropleales;Selenastraceae;Raphidocelis;Raphidocelis_subcapitata
GGACAGAAAGACCCATGAAGACTGTAGTCTGGAAATGGAAATTCGGGCTTTCTTGGCCAGCCTAGGTGGGAGGCGTTGAAATTTCTTCCGGGAAATCAGAGCCATCAGTGGAGAGCCACTCTGGGAAGCCT
>PHYTOOL_example5;Chorda;Amphibia;Anura;Dendrobatiidae;Dendrobatiinae;Dendrobates;Dendrobates_tincunius;
ACTTGTCTTTAATTGAGGACTAGTATGAACGGCTTACGAAGACTACACTGTCTCTTTCTTAATCAATGAACCTAATCTCCCGTGAGAGAGCGGGATAAACCTATAGACGAGAGACCCATGCGMCT
```

Phytool v2

Phytool v2.R

- Taxonomy homogenization
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**Second output file: « logfile »**

```

what;modification
Fragilaria crotonensis;Genus_species already up to date
Kirchneria subcapitata>Raphidocelis subcapitata;updated ←
Dendrobates tinctorius;Genus_species not found ←
    
```

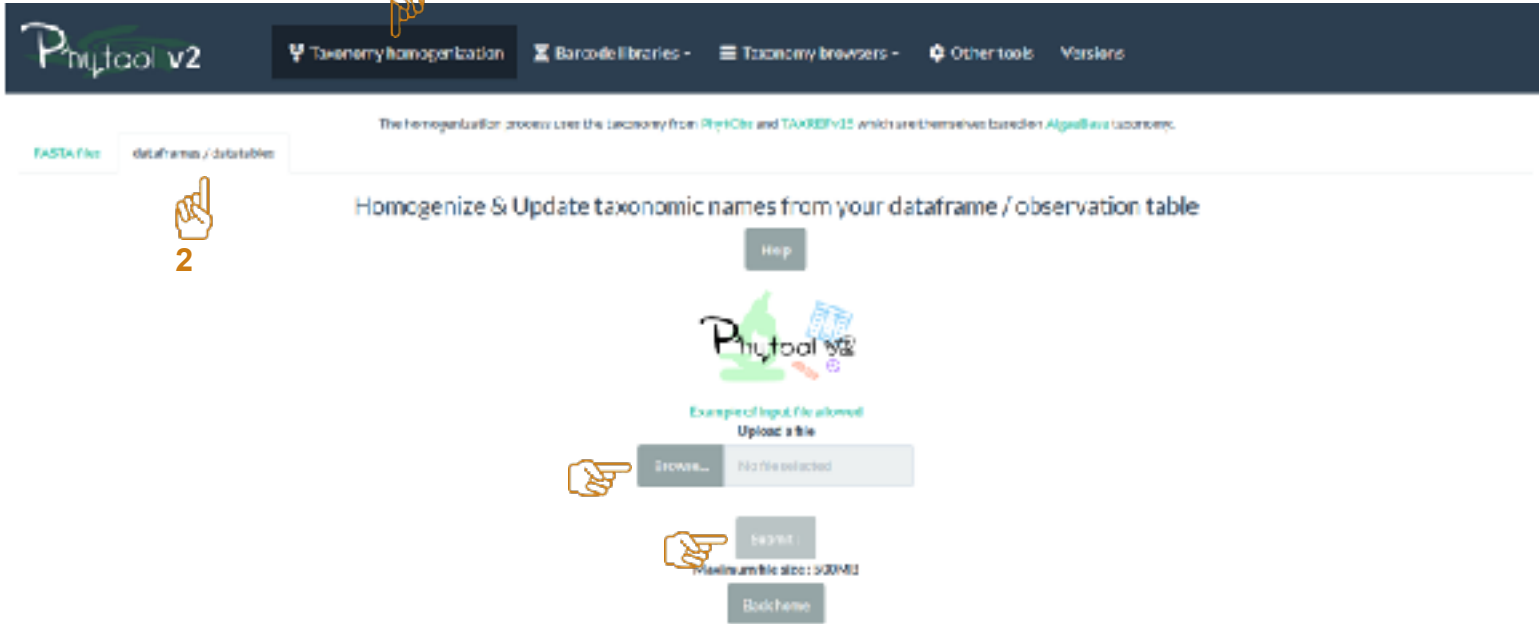


*Dendrobates tinctorius*

Phytool v2

Phytool v2.R

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Phytool v2

Taxonomy homogenization

Barcode libraries

Taxonomy browsers

Other tools

FASTA files

dataframes / datables

Homogenize & Update taxonomic names from your dataframe / observation table

Help

Phytool v2

Example of input file allowed

Upload a file

Browse... No file selected

Maximum file size: 500MB

Back home

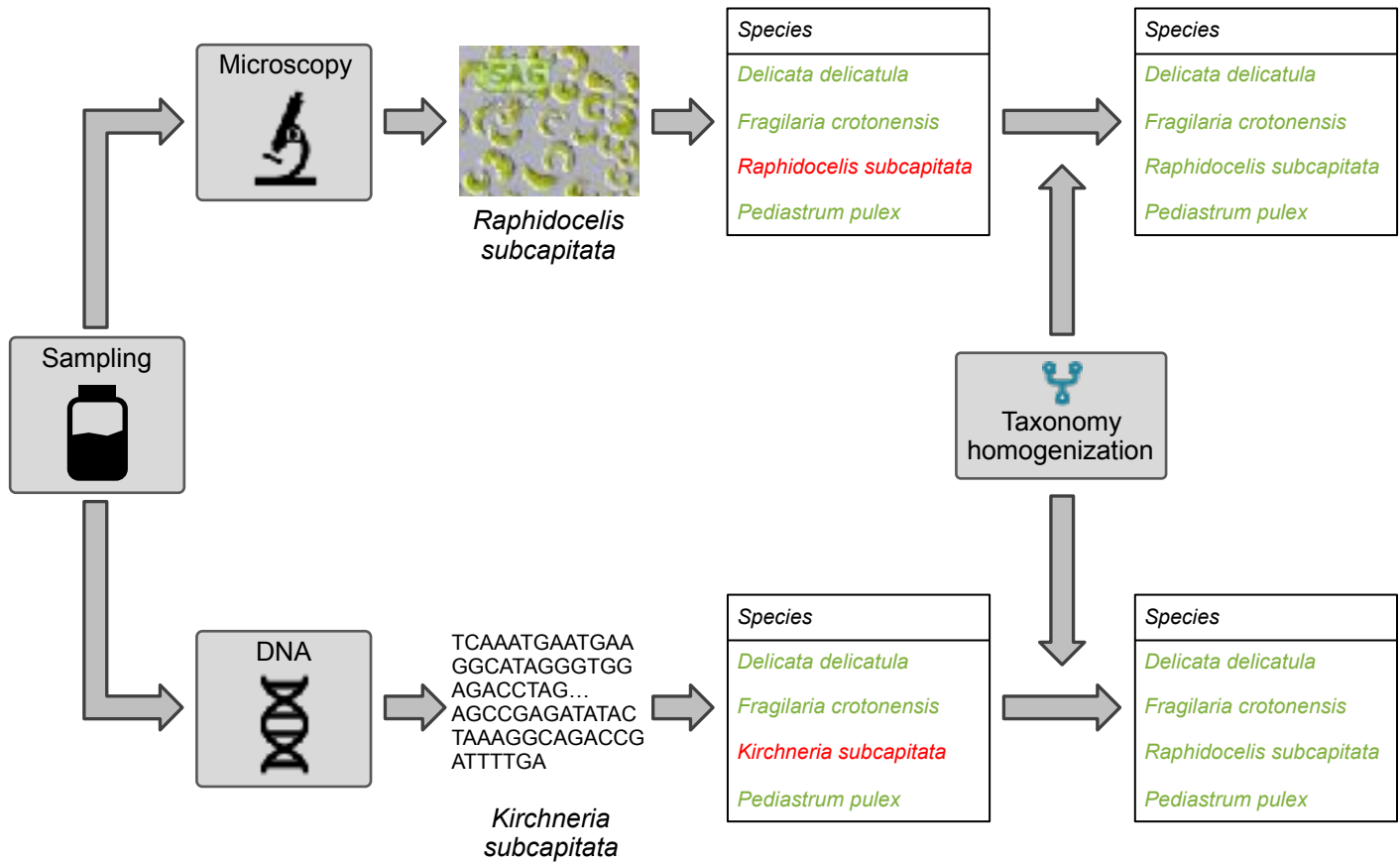
Your file (.csv; .txt) should look like:

	A	R	C	D
1	Family	Genus	Genus_species	Sampling_origin
2	Fragilariaceae	Fragilaria	Fragilaria crotonensis	Lake Geneva
3	Selenastreae	Kirchneria	Kirchneria subcapitata	Lake Geneva
4	Dendrobatiinae	Dendrobates	Dendrobates tinctorius	French Guiana

Phytool v2

Phytool v2.R

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Phytool v2

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Phytool v2

Taxonomy homogenization | Barcode libraries - | Taxonomy browsers - | Other tools | Versions

Reference library: Barcodes exploration **Left**

### rRNA 16S (SSU)

Columns to show/hide:

- Origin
- GenBank
- Kingdom
- Phylum
- Class
- Order
- Family
- Genus
- Genus species
- Status\_unknown

Download metadata: CSV (Excel)

Get the data (Excel)

For in-silico taxonomic assignment: Reference files (genomic data)

Show ID: - criteria

Search:

GenBank	Class	Order	Family	Genus	Genus species
EU554583.1.1461	Cyanophyceae	Oscillatoriales	Oscillatoriaceae	Phormidium	Phormidium bogovinum
FJ229498.1.1414	Cyanophyceae	Oscillatoriales	Oscillatoriaceae	Rhodospira	Rhodospira sp.
FN482342.1.1457	Cyanophyceae	Oscillatoriales	Oscillatoriaceae	Phormidium	Phormidium virgatum
GA529465.1.3277	Cyanophyceae	Synechococales	Heterotruncaceae	Heterotruncus	Heterotruncus calcicola
GI754203.1.4345	Cyanophyceae	Oscillatoriales	Oscillatoriaceae	Oscillatoria	Oscillatoria ovalata
HQ235981.1.1262	Cyanophyceae	Staurisococcales	Lynceaceae	Lynce	Lynce sp.
HQ247570.1.1427	Cyanophyceae	Nostocales	Microcoleaceae	Fortia	Fortia sp.
942#	Bacteriophyceae	Scenedescales	Scenedesaceae	Pseudonitzschia	Pseudonitzschia menziesii
1205#	Lincomycetes	Lymnocybales	Lymnocybaceae	Leptodinium	Leptodinium leptoide
234	Bacteriophyceae	Scenedescales	Scenedesaceae	Pseudonitzschia	Pseudonitzschia pseudonitzschiae





Phytool v2

Phytool v2.R

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Phytool v2

Taxonomy homogenization | Barcode libraries - | Taxonomy browsers - | Other tools | Versions

Reference library | Barcodes exploration

rRNA 16S (SSU)

Columns to show/hide:

- Origin
- GenBank
- Kingdom
- Phylum
- Class
- Order
- Family
- Genus
- Genus species
- Strain name

Download reference library (FASTA)

Reference file (GenBank data)

For in-silico taxonomic assignment

1

2

3

GenBank	Class	Order	Family	Genus	Genus species
EF754583.1.1451	Cyanophyceae	Oscillatoriales	Oscillatoriaceae	Planktonium	Planktonium bergedii
FJ229498.1.1414	Cyanophyceae	Oscillatoriales	Oscillatoriaceae	Rhodofila	Rhodofila sp.
F7485342.1.1457	Cyanophyceae	Oscillatoriales	Oscillatoriaceae	Planktonium	Planktonium virgatum
GA529465.1.3277	Cyanophyceae	Synechococcales	Heteronitellaceae	Heteronitella	Heteronitella caudata
GI754203.1.4345	Cyanophyceae	Oscillatoriales	Oscillatoriaceae	Oscillatoria	Oscillatoria ovalis
HKQ39581.1.1252	Cyanophyceae	Stauroneurales	Lynceaceae	Hylis	Hylis sp.
HKQ47570.1.1477	Cyanophyceae	Nostocales	Microchaetaceae	Fertilia	Fertilia sp.
942#	Bacterioidetes	Bacteriales	Bacteriaceae	Pseudomonas	Pseudomonas aeruginosa
1205#	Chlorophyta	Chlorophytales	Chlorophytales	Chlorococcum	Chlorococcum sp.
234	Bacterioidetes	Bacteriales	Bacteriaceae	Pseudomonas	Pseudomonas aeruginosa

Download complete barcode reference library...

Phytool v2

Phytool v2.R

- Taxonomy homogenization
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Phytool v2

Take taxonomy homogenization

Barcode libraries -

Taxonomy browsers -

Other tools

Versions

Reference library

Barcodes exploration

rRNA 16S (SSU)

rRNA 18S (SSU)

rRNA 23S (LSU)

rbcl

Show ID -> articles

Search

GenBank	King	Order	Family	Genus	Genus species
All	All	All	All	All	Filtered
MF276848346382115	Chlorophyceae	Sphaeropleales	Hydroclitaceae	Pseudopedicellstrum	Pseudopedicellstrum (HYDUL)
MF27686597844122436	Chlorophyceae	Sphaeropleales	Hydroclitaceae	Pseudopedicellstrum	Pseudopedicellstrum sp.
MF2768769325594838	Chlorophyceae	Sphaeropleales	Hydroclitaceae	Pedilicium	Pedilicium angustum
MF276877285655215588	Chlorophyceae	Sphaeropleales	Hydroclitaceae	Pedilicium	Pedilicium angustum
MF27688619938195598	Chlorophyceae	Sphaeropleales	Hydroclitaceae	Pedilicium	Pedilicium duplex
MF276891215670215876	Chlorophyceae	Sphaeropleales	Hydroclitaceae	Pedilicium	Pedilicium duplex
MF2769152325325767	Chlorophyceae	Sphaeropleales	Hydroclitaceae	Pedilicium	Pedilicium duplex
KY15405439446360675	Chlorophyceae	Sphaeropleales	Hydroclitaceae	Pedilicium	Pedilicium duplex
MF2769638865296031	Chlorophyceae	Sphaeropleales	Hydroclitaceae	Pseudopedicellstrum	Pseudopedicellstrum beryanum
MF276982199412206927	Chlorophyceae	Sphaeropleales	Hydroclitaceae	Pseudopedicellstrum	Pseudopedicellstrum beryanum

...Or select specific taxonomic rank

Phytool v2

Phytool v2.R

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Phytool v2

Taxonomy homogenization | Barcode libraries - | Taxonomy browsers - | Other tools | Versions

Reference library | Barcodes exploration

### rRNA 16S (SSU)

Origins: Kingdom, Phylum, Class, Order, Family, Genus, Species

*Pediastrum duplex*

Download data (FASTA)

4 hits selected

Reference file: species data

For Metatlas taxonomy assignments

GenBank	Order	Family	Genus	Species
MF276848346382115	Chlorophyceae	Sphaeroplexales	Hydroclithyceae	<i>Pseudopediastrum nitidum</i>
MF2768597844123436	Chlorophyceae	Sphaeroplexales	Hydroclithyceae	<i>Pseudopediastrum</i>
MF2768769325594858	Chlorophyceae	Sphaeroplexales	Hydroclithyceae	<i>Pediastrum</i>
MF276877285657215888	Chlorophyceae	Sphaeroplexales	Hydroclithyceae	<i>Pediastrum</i>
MF27688195937155788	Chlorophyceae	Sphaeroplexales	Hydroclithyceae	<i>Pediastrum</i>
MF276881915670215176	Chlorophyceae	Sphaeroplexales	Hydroclithyceae	<i>Pediastrum duplex</i>
MF2367152355375767	Chlorophyceae	Sphaeroplexales	Hydroclithyceae	<i>Pediastrum duplex</i>
KX13495439446380675	Chlorophyceae	Sphaeroplexales	Hydroclithyceae	<i>Pediastrum duplex</i>
MF2768828825295031	Chlorophyceae	Sphaeroplexales	Hydroclithyceae	<i>Pseudopediastrum beryllum</i>
MF27688219641230927	Chlorophyceae	Sphaeroplexales	Hydroclithyceae	<i>Pseudopediastrum beryllum</i>

### Phytool v2

#### Phytool v2.R

##### Taxonomy homogenization

- FASTA files
- dataframes / datables

##### Barcode libraries

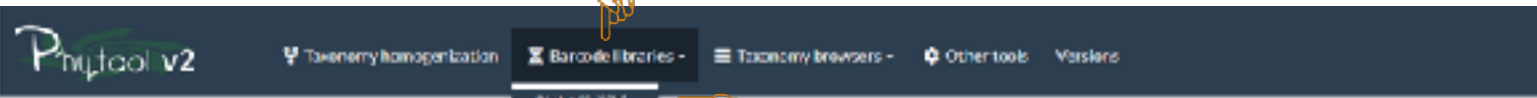
- rRNA 16S (SSU)
  - Reference library
  - Barcodes exploration
- rRNA 18S (SSU)
- rRNA 23S (LSU)
- rbcL

##### Taxonomy browsers

- Freshwater microalgae
- Complete microalgae

##### Other tools

- FASTA format rearranger
- FASTA delimiters rearranger



Phytool v2 Taxonomy homogenization Barcode libraries - Taxonomy browsers - Other tools Versions

Reference library Barcodes exploration **beta**

### rRNA 16S (SSU)

Choose a barcode library 16S  
Barcode available:  
v2-v4

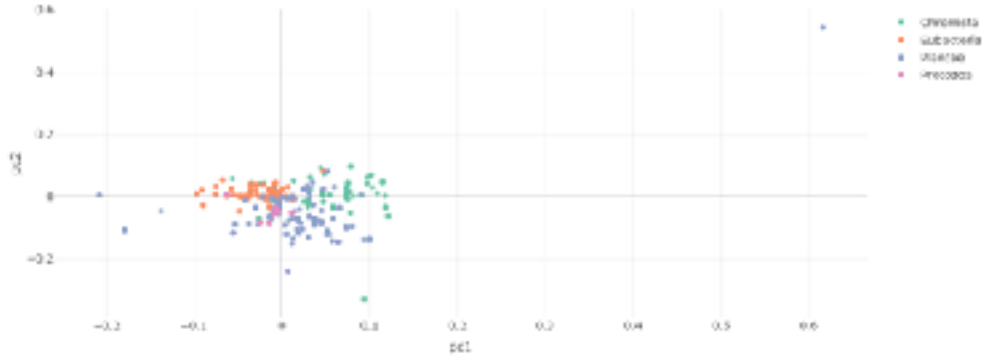
Corresponding palindromic:  
CTAAGG: GCGGAAATTCGCGCAATGG  
CTAAGG: GCGGAAATTCGCGCAATGG  
Max. 2 mismatches allowed

Choose a taxonomy browser to explore:  
Taxonomic ranks:  
Kingdom

Optional target specific bases:

target

- 1 rRNA 16S (SSU)
- 2 rRNA 18S (SSU)
- 3 rRNA 23S (LSU)
- 4 rbcL



Data shown on this page were curated from:



Phytool v2

Phytool v2.R

- Taxonomy homogenization
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Phytool v2

Barcode libraries -

- rRNA 16S (SSU) (pointed to by 1)
- rRNA 18S (SSU) (pointed to by 2)
- rRNA 23S (LSU)
- rbcl

Reference library | Barcodes exploration (pointed to by 3)

### rRNA 16S (SSU)

Choose a barcode for rRNA 16S:

Barcodes available:

v2-v4

Corresponding palindromic:

CTAAGTTC: GGGGAAATTCGGCAATGGG  
 CTAAGTTC: GGGGAAATTCGGCAATGGG  
 Max. 2 mismatches allowed

Choose a taxonomic rank to explore:

Taxonomic ranks:

- Kingdom (pointed to)
- Kingdom
- Phylum
- Class
- Order
- Family
- Genus
- Species

Legend:

- Chlorophyta
- Substantia
- Chlorophyta
- Chlorophyta

PC1 vs PC2 scatter plot

Download on this page were curated from:

silva | NCBI | PhyloRef

Display different taxonomic ranks



Phytool v2

Phytool v2.R

- Taxonomy homogenization
  - FASTA files
  - dataframes / datables
- Barcode libraries
  - rRNA 16S (SSU)
    - Reference library
    - Barcodes exploration
  - rRNA 18S (SSU)
  - rRNA 23S (LSU)
  - rbcl
- Taxonomy browsers
  - Freshwater microalgae
  - Complete microalgae
- Other tools
  - FASTA format rearranger
  - FASTA delimiters rearranger

Phytool v2

Taxonomy homogenization | Barcode libraries - | Taxonomy browsers - | Other tools | Versions

Reference library | Barcodes exploration **beta**

### rRNA 16S (SSU)

Choose a barcode library 16S:  
Barcode available:  
v2-v4

Consensus sequence:  
CTAAGTTC: GGGGAAATTCGCGCAATGGG  
CTAATGTC: GAGCAATTCGCGCAATGGG  
Max. 2 mismatches allowed

Choose a taxonomy browser to explore:  
Taxonomy browser:  
Phylum

Optional target clade to focus:  
oc:Chlorodactylophyta

target

- Metazoa
- Chloroda
- Chlorophyta
- Chlorococcales
- Cyanoophyceae
- Cyanobacteria
- Phaeocystis
- Chlorococcales
- Chlorophyta
- Metazoa
- Fungi
- Chlorophyta
- Freshwater algae
- Phaeocystis
- Metazoa

Target a specific clade...



Phytool v2

Phytool v2.R

- Taxonomy homogenization
  - FASTA files
  - dataframes / datables
- Barcode libraries
  - rRNA 16S (SSU)
    - Reference library
    - Barcodes exploration
  - rRNA 18S (SSU)
  - rRNA 23S (LSU)
  - rbcl
- Taxonomy browsers
  - Freshwater microalgae
  - Complete microalgae
- Other tools
  - FASTA format rearranger
  - FASTA delimiters rearranger

Phytool v2

Taxonomy homogenization Barcode libraries - Taxonomy browsers - Other tools Versions

Reference library Barcodes exploration **1**

rRNA 16S (SSU)

silva 16S (SSU) **2**

rRNA 18S (SSU)

rRNA 23S (LSU)

rbcl

Choose a barcode: rRNA 16S

Barcodes available:

silva

Corresponding primer(s):

CGAAG: CCGGAAATTCGCGCAATCG

CTAAGT: GATCAATGATGAGGATGCTATGCTG

Max. 2 mismatches allowed

Choose a taxonomy: rRNA 16S

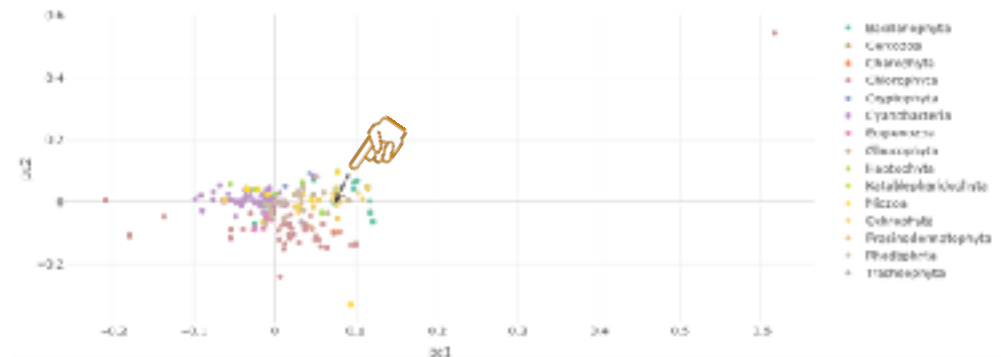
Taxonomic ranks:

Phylum

Optional target species name:

Cryptophyta **3**

Target



1 matching your selection.

Note: some species or points may overlap and this results in less species than expected (or different species name when hovering the point with the mouse)

Unfolded on this page were curated from:



...or a specific species



Phytool v2

Phytool v2.R

- Taxonomy homogenization
  - FASTA files
  - dataframes / datables
- Barcode libraries
  - rRNA 16S (SSU)
    - Reference library
    - Barcodes exploration
  - rRNA 18S (SSU)
  - rRNA 23S (LSU)
  - rbcl
- Taxonomy browsers
  - Freshwater microalgae
  - Complete microalgae
- Other tools
  - FASTA format rearranger
  - FASTA delimiters rearranger

Phytool v2

Taxonomy homogenization | Barcode libraries - | Taxonomy browsers - | Other tools | Versions

Reference library | Barcodes exploration **beta**

rRNA 16S (SSU)

Choose a barcode library: 16S

Barcode available: v2-v4

Consensus sequence:

```

CGAAGG: GGGGAAATTCGCGCAATGG
CTAATGRTGACGAAATGAGGATGCTATGKAAATTT
Max.2 mismatches allowed
    
```

Choose a taxonomy browser: complete

Taxonomic ranks: Phyllum

Optional target accession: *Cymbella brevistriata*

Target

1

2

3

1 matching your selection.  
 Note: some species or points may overlap and this results in less species than expected (or different species name when hovering the point with the mouse)

Download on this page were curated from:



Phytool v2

Phytool v2.R

- Taxonomy homogenization
  - FASTA files
  - dataframes / datables
- Barcode libraries
  - rRNA 16S (SSU)
    - Reference library
    - Barcodes exploration
  - rRNA 18S (SSU)
  - rRNA 23S (LSU)
  - rbcl
- Taxonomy browsers
  - Freshwater microalgae
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  - FASTA delimiters rearranger

Phytool v2

Taxonomy homogenization | Barcode libraries | **Taxonomy browsers** | Other tools | Versions

Freshwater microalgae | Complete microalgae

### Freshwater microalgae from PhytoObs

Columns to show:

- Kingdom
- Phylum
- Class
- Order
- Family
- Genus
- Genus/species
- Author
- Strain name
- rRNA16S
- rRNA18S
- rRNA23S
- rbcL

Download full data (.csv)

Download current selection (.csv)

View: 10 | 1000

SEARCH:

Genus	Genus/species	rRNA16S	rRNA18S	rRNA23S	rbcL
<input type="text" value="All"/>	<input type="text" value="All"/>	<input type="text" value="All"/>	<input type="text" value="All"/>	<input type="text" value="All"/>	<input type="text" value="All"/>
Chroocodytion	Chroocodytion ornatae	1	2		
Ulothrix	Ulothrix zonata		8		1
Sibirococcus	Sibirococcus bellieri	12	27	3	
Aphanizomenon	Aphanizomenon sp.		2		
Ulothrix	Ulothrix chlamyde				
Chlorella	Chlorella kuetzingii		1		
Chlorella	Chlorella pyrenoidosa		12		
Bostrychia	Bostrychia rufipes	1	11		1
Chlorella	Chlorella vulgaris				
Bostrychia	Bostrychia montana	1	3		1

Phytool v2

Phytool v2.R

- Taxonomy homogenization
  - FASTA files
  - dataframes / datables
- Barcode libraries
  - rRNA 16S (SSU)
    - Reference library
    - Barcodes exploration
  - rRNA 18S (SSU)
  - rRNA 23S (LSU)
  - rbcl
- Taxonomy browsers
  - Freshwater microalgae
  - Complete microalgae
- Other tools
  - FASTA format rearranger
  - FASTA delimiters rearranger

Phytool v2

Taxonomy homogenization | Barcode libraries - | **Taxonomy browsers -** | Other tools | Versions

Freshwater microalgae  
Complete microalgae

View: 10 - 20 items

Columns to show:

- Kingdom
- Phylum
- Class
- Order
- Family
- Genus
- Genus, species
- Author
- Strain name
- rRNA16S
- rRNA18S
- rRNA23S
- rbcL

Download full data / current selection:

Download Full Data (.csv)

0 rows selected

Download Current Selection (.csv)

Genus	Genus, species	rRNA16S	rRNA18S	rRNA23S	rbcL
All	Microcystis	All	All	All	All
Microcystis	Microcystis encopryta				
Microcystis	Microcystis marginata				
Microcystis	Microcystis ochracea				
Microcystis	Microcystis wuellerstorfi	13			
Microcystis	Microcystis viridis	14			
Microcystis	Microcystis aeruginosa	8			
Microcystis	Microcystis aeruginosa	211		29	
Microcystis	Microcystis zantedoni				
Microcystis	Microcystis diadema				
Microcystis	Microcystis stereosiphia				

Phytool v2

Phytool v2.R

- Taxonomy homogenization
  - FASTA files
  - dataframes / databses
- Barcode libraries
  - rRNA 16S (SSU)
  - Reference library
  - Barcodes exploration
  - rRNA 18S (SSU)
  - rRNA 23S (LSU)
  - rbcL
- Taxonomy browsers
  - Freshwater microalgae
  - Complete microalgae
- Other tools
  - FASTA format rearranger
  - FASTA delimiters rearranger

Phytool v2

Taxonomy homogenization Barcode libraries - Taxonomy browsers - Other tools Versions



FASTA format rearranger FASTA delimiters rearranger

This functionality enables to upload a fasta file with sequences spread over multiple 'rows/lines' and transform it to a fasta file with sequences filling just one sequence row.

```
> identifier_sequence_1
ACGATTACAGACTAGGACTACGACACATATC
AGACGAGGACTACTAGGACTACATCATCAT
CATACTACTACTACTACTGTACTACTAGGAC
TATCATCATCTTC
> identifier_sequence_2
GATGACCCGCCAGCTACGACACATATCAGAC
GAGGACTACTAGGACTACATCATCATCATAC
TACTACTACTACTACTGTACTACTAGGACTATCAT
CATCATCTTCAG
> identifier_sequence_3
ATTATCAGCCCAAGACACATCATTTTTATTGAC
CCAGACGACGAGTACTAGGACTACATCATCATC
ATCATACTACTACTACTACTGTACTACTAGG
AGTATGAAA
```



```
> identifier_sequence_1
ACGATTACAGACTAGGACTACGACACATATCAGACGAC
> identifier_sequence_2
GATGACCCGCCAGCTACGACACATATCAGACGAGGACT
> identifier_sequence_3
ATTATCAGCCCATCAGACATCATTTTTATTGACCCAGAC
```

CHOOSE A TITLE

Browser... Newline value: 100

↓ build

Save profile

Phytool v2

Phytool v2.R

- Taxonomy homogenization
  - FASTA files
  - dataframes / databases
- Barcode libraries
  - rRNA 16S (SSU)
  - rRNA 18S (SSU)
  - rRNA 23S (LSU)
  - rbcL
- Taxonomy browsers
  - Freshwater microalgae
  - Complete microalgae
- Other tools
  - FASTA format rearranger
  - FASTA delimiters rearranger

Phytool v2

Taxonomy homogenization Barcode libraries Taxonomy browsers Other tools Versions

FASTA format rearranger FASTA delimiters rearranger

This functionality enables to upload a fasta file and change the nature of delimiters in the identifier lines

```

> ID0001 Phylum | Class | Family | Genus species
ATCCGATTAGCTCTTAGCTACGGATCCGATCGATTAGCGA
> ID0002 Phylum | Class | Family | Genus species
CCATCTTACTCAGCTCTTATCCGATTAGCTCTTAGCTAC
> ID0003 Phylum | Class | Family | Genus species
CCCATGGATCATGGACTCCATTTTAAAATTCGAGTA
> ID0004 Phylum | Class | Family | Genus species
GATTGATTAAATCCATTAGCTCTTAGCTACGGATCCGATC
    
```

→

```

> ID0701 Phylum ; Class ; Family ; Genus species
ATCCGATTAGCTCTTAGCTACGGATCCGATCGATTAGCGA
> ID0702 Phylum ; Class ; Family ; Genus species
CCATCTTACTCAGCTCTTATCCGATTAGCTCTTAGCTAC
> ID0703 Phylum ; Class ; Family ; Genus species
CCCATGGATCATGGACTCCATTTTAAAATTCGAGTA
> ID0704 Phylum ; Class ; Family ; Genus species
GATTGATTAAATCCATTAGCTCTTAGCTACGGATCCGATC
    
```

Choose a fasta file

Browser...

Transform:

delimiter to modify:

Info:

Submit

Back home

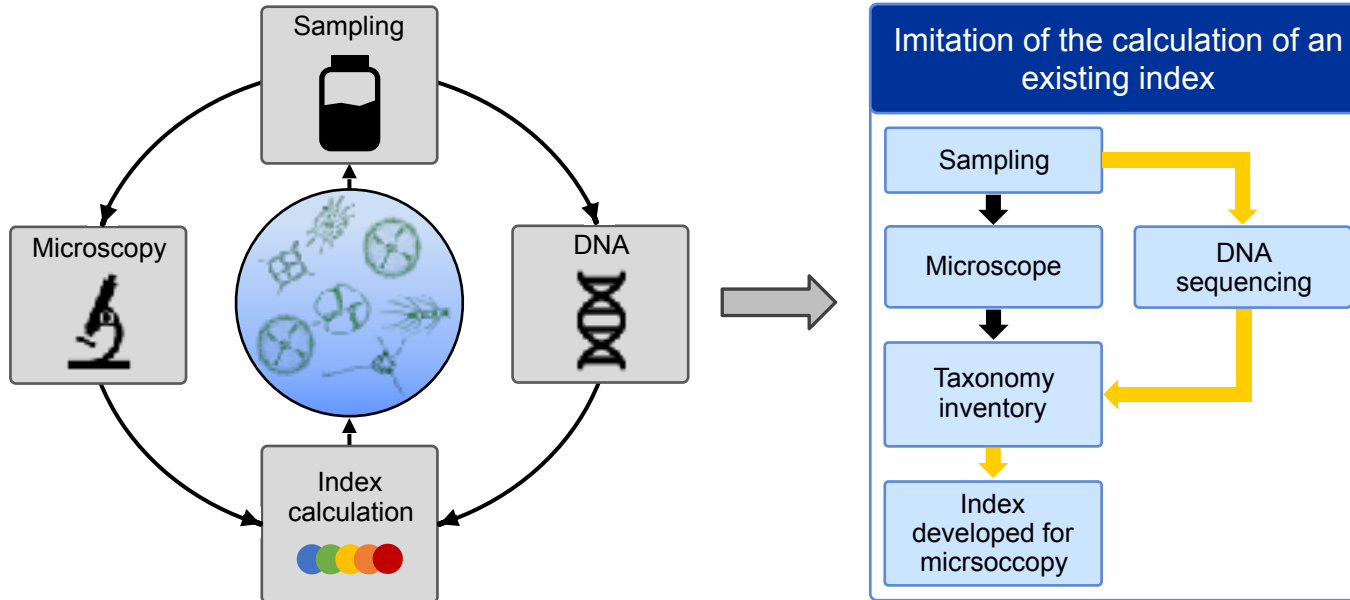


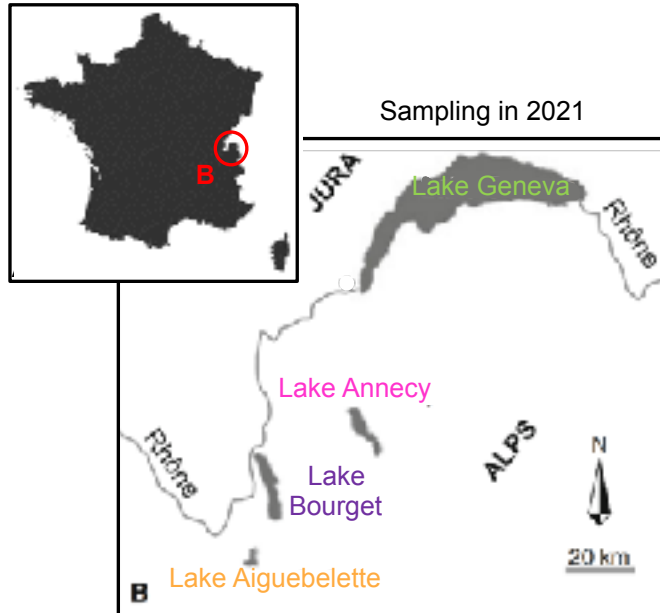
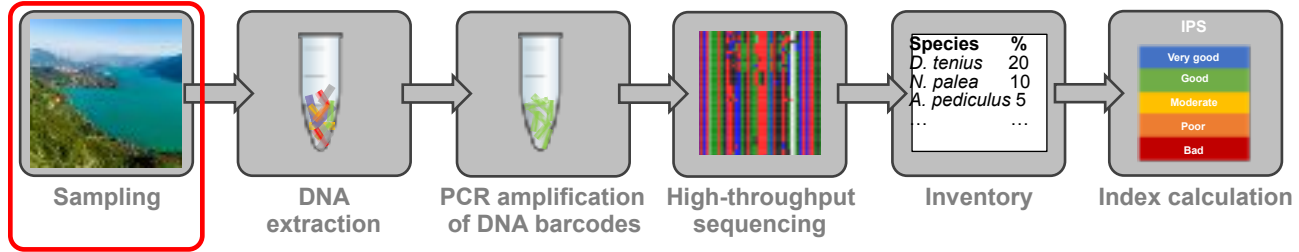
## Reminders

- 1- Phytool reference library
- 2- Tests on environmental samples 

# Assessing the relevance of DNA metabarcoding compared to morphological identification for lake phytoplankton monitoring

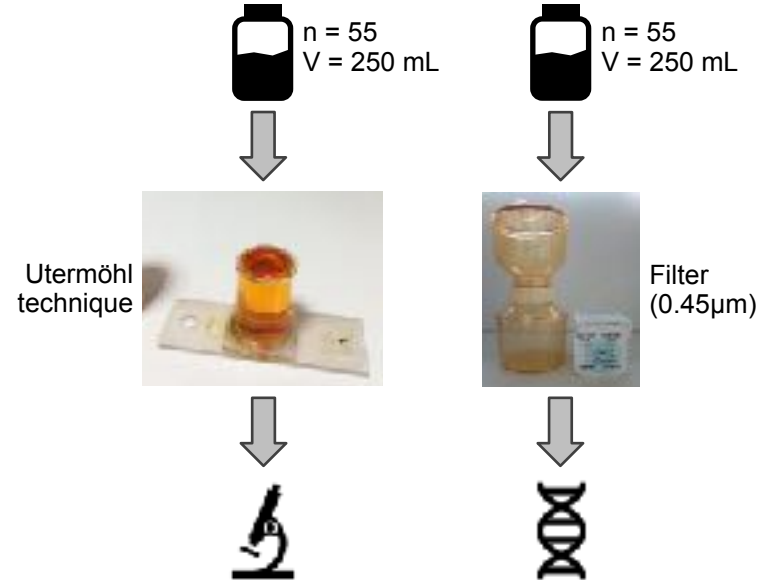
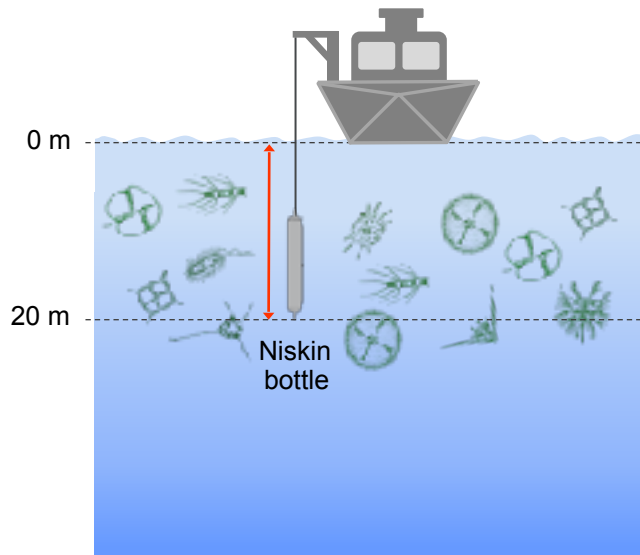
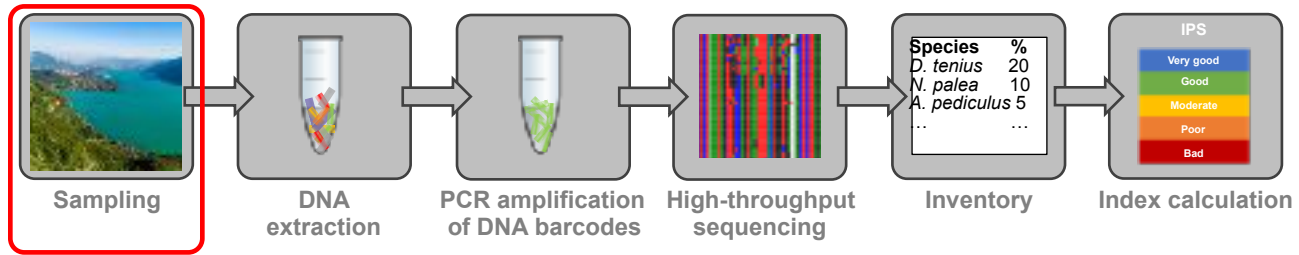
Nicolosi-Gelis M.M., A. Canino, A. Bouchez, I. Domaizon, C. Laplace-Treytore, F. Rimet, B. Alric

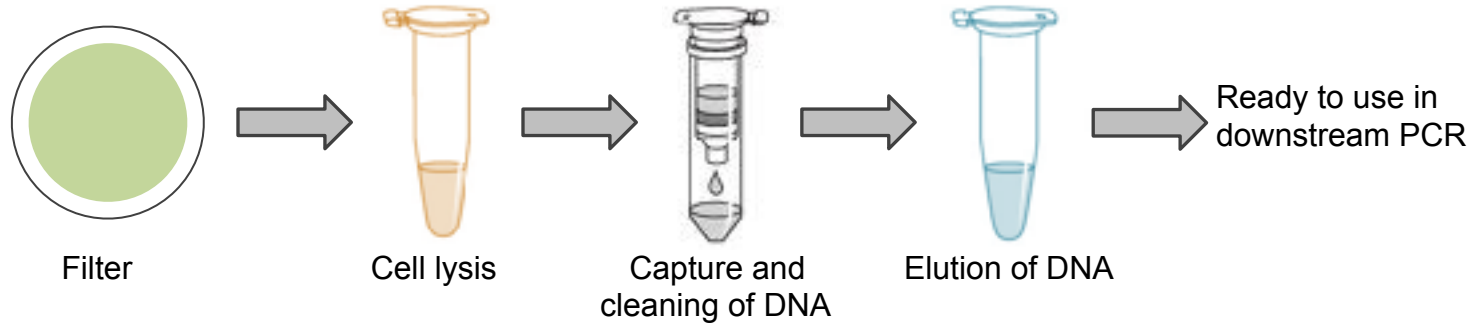
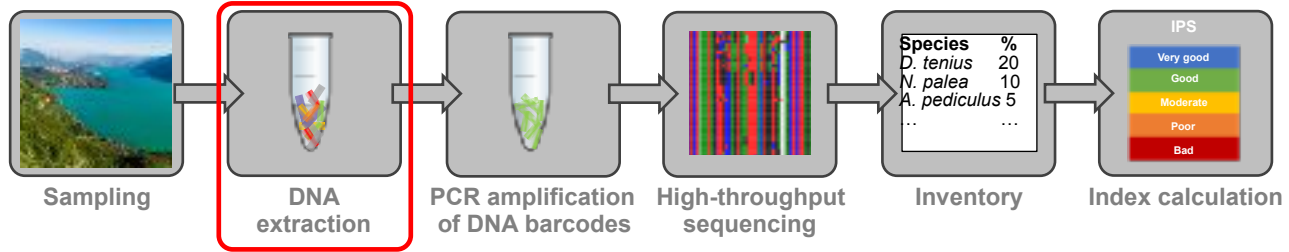


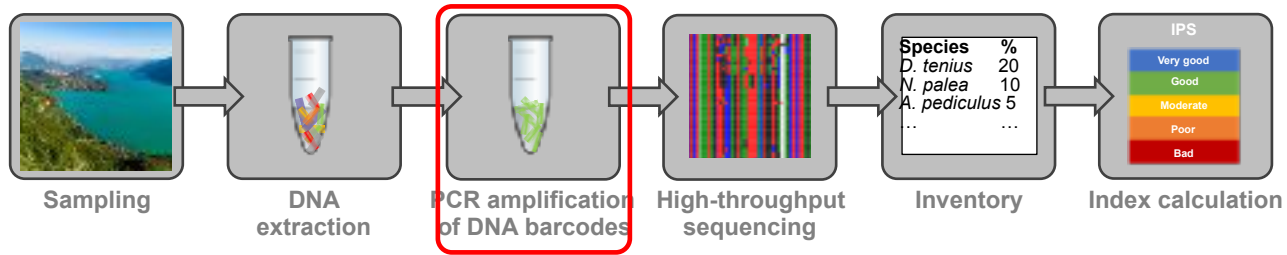


Max depth (m)	Trophic condition
310	Mesotrophic
145	Oligo-mesotrophic
82	Oligotrophic
70	Oligotrophic

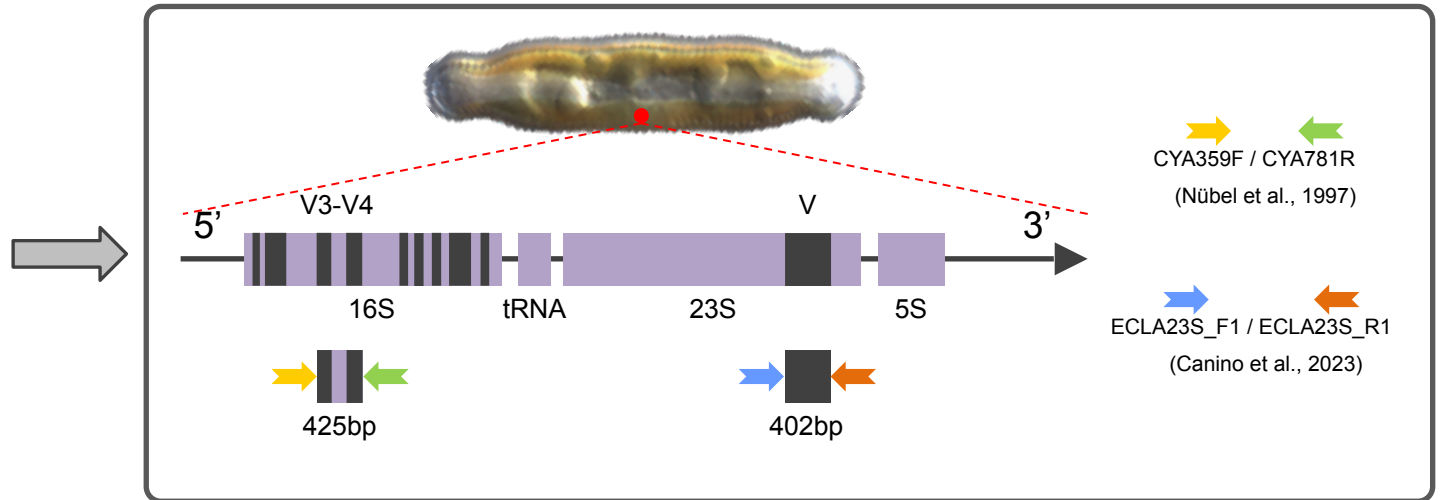


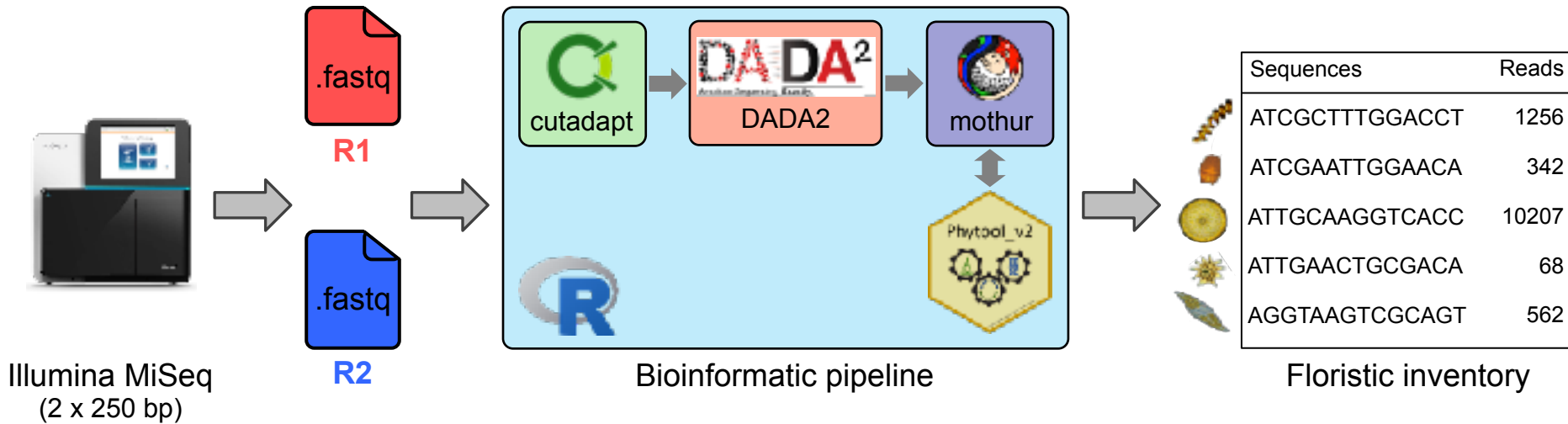
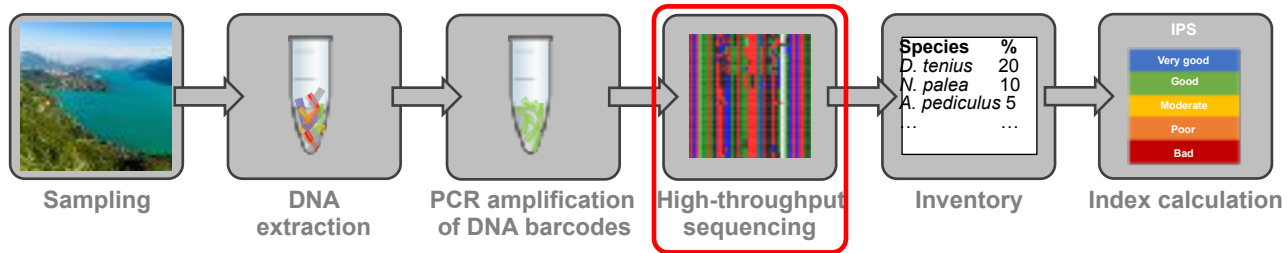


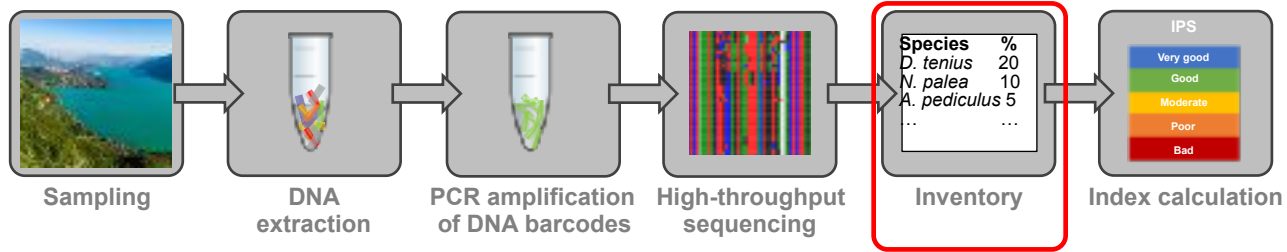




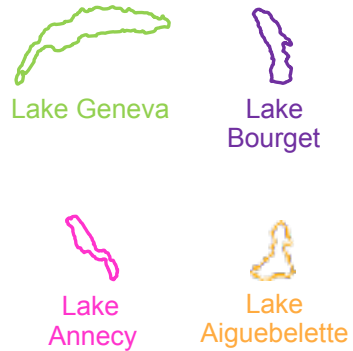
Thermal cycler PCR



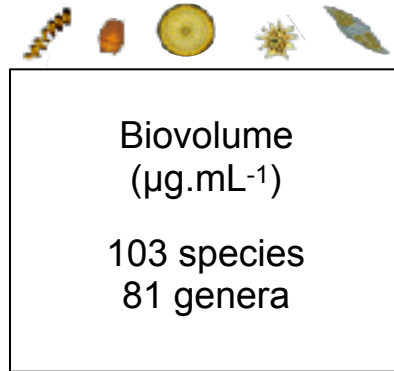




### Microscopy

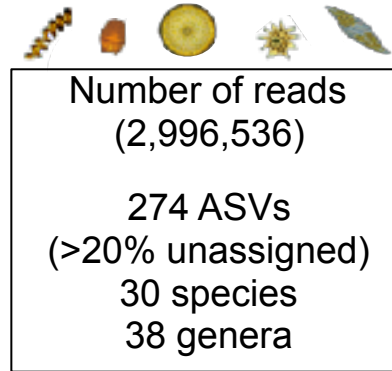


Sites / dates



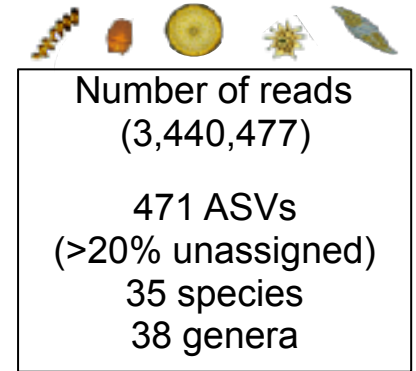
### 16S rRNA

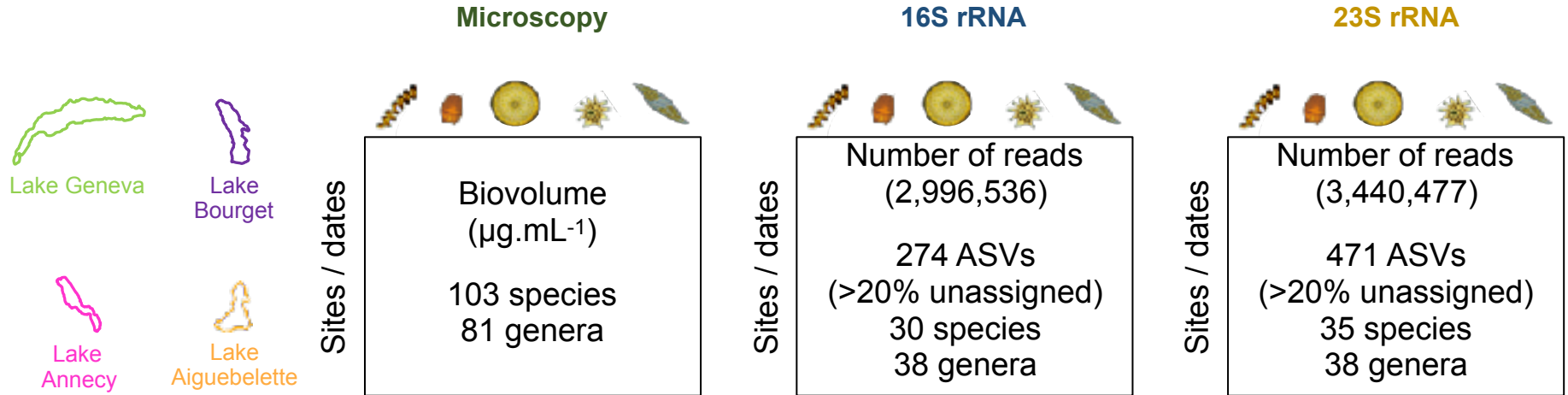
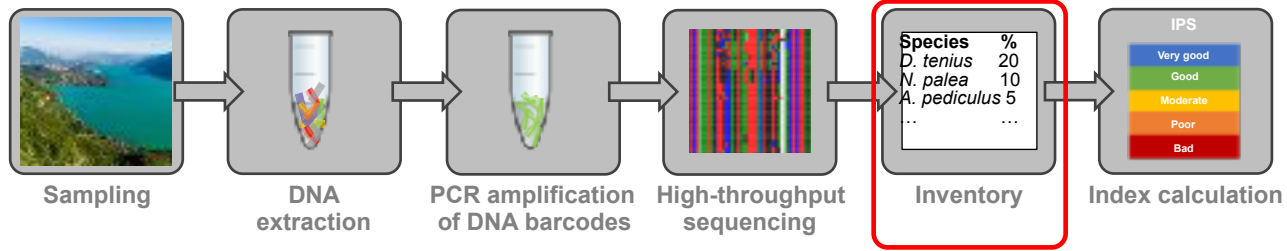
Sites / dates



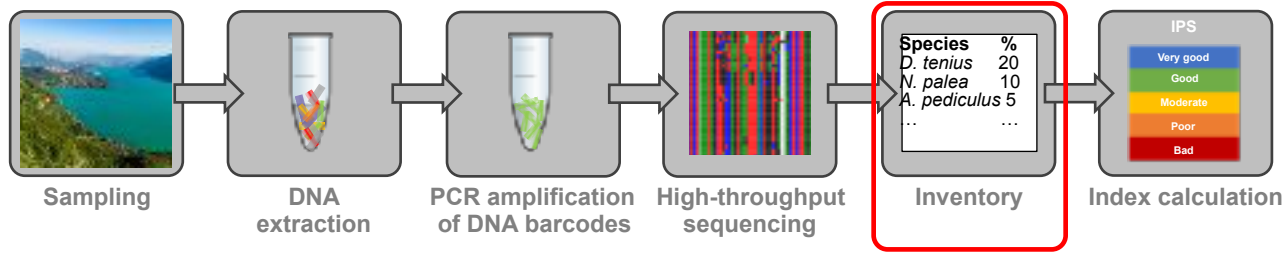
### 23S rRNA

Sites / dates



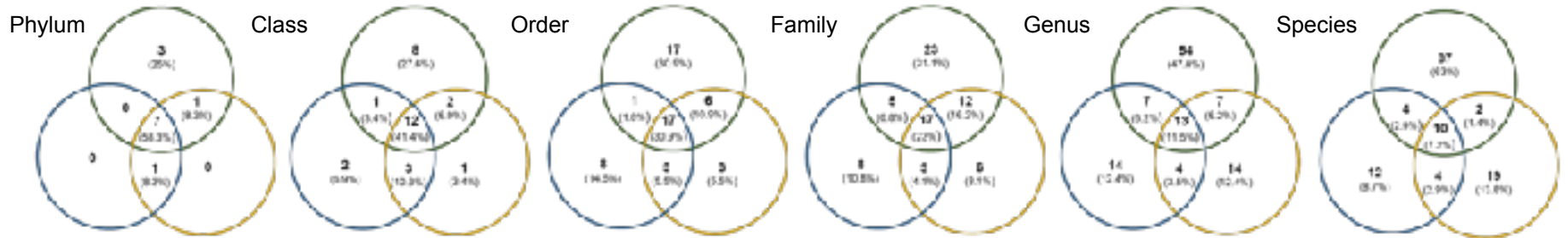


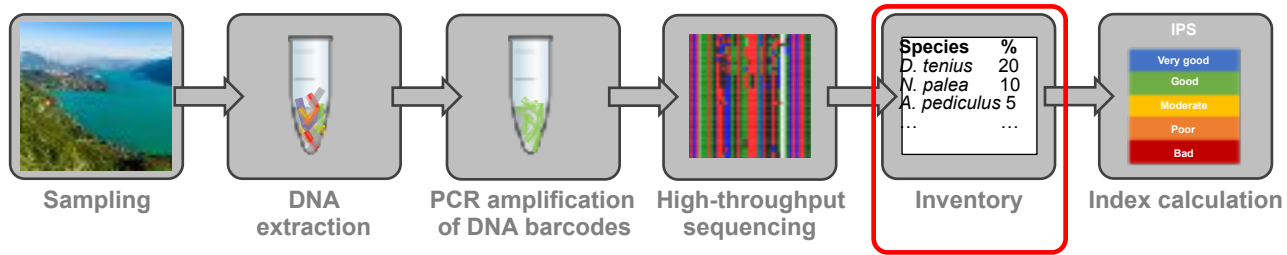
- Taxonomy-free: Number of ASVs is greater than the diversity in species identified by microscopy
- Assigned taxonomy: Number of species is lower than those obtained by microscopy



### Comparison of taxa detected

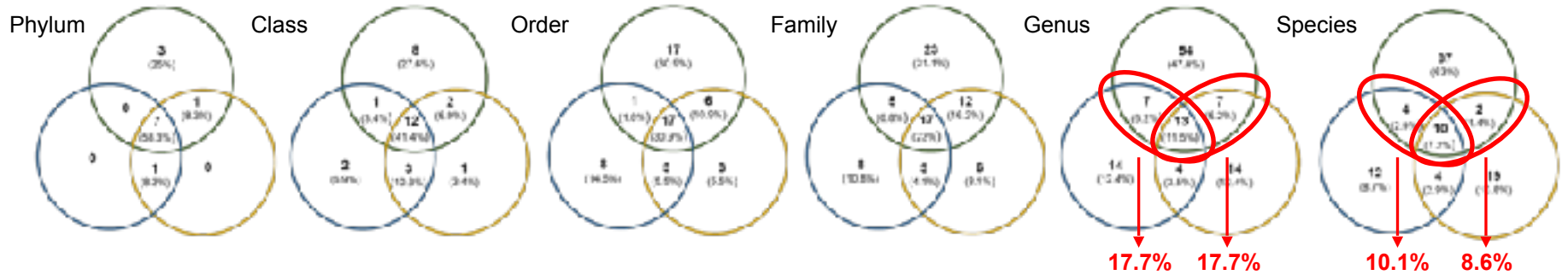
■ Microscopy (103 species)   
 ■ 16S rRNA (30 species)   
 ■ 23S rRNA (35 species)



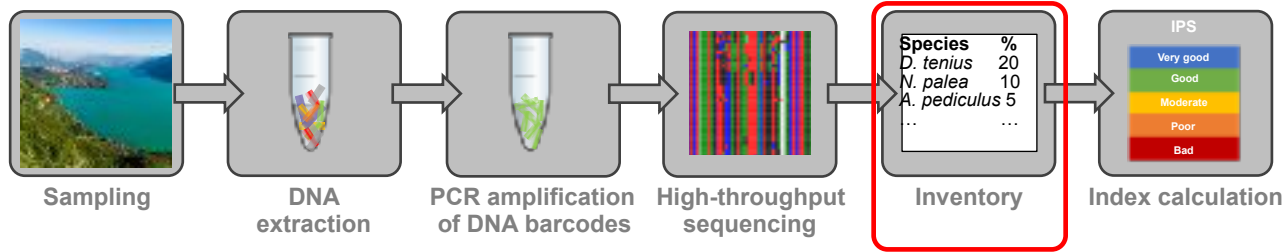


### Comparison of taxa detected

■ Microscopy (103 species)   
 ■ 16S rRNA (30 species)   
 ■ 23S rRNA (35 species)

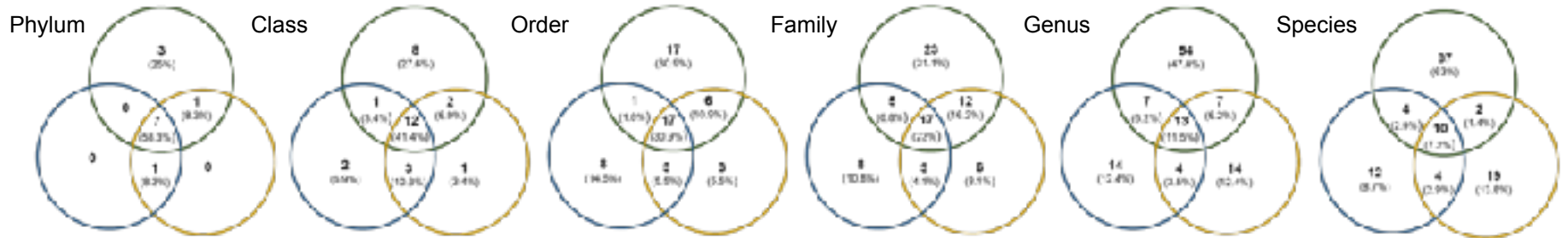




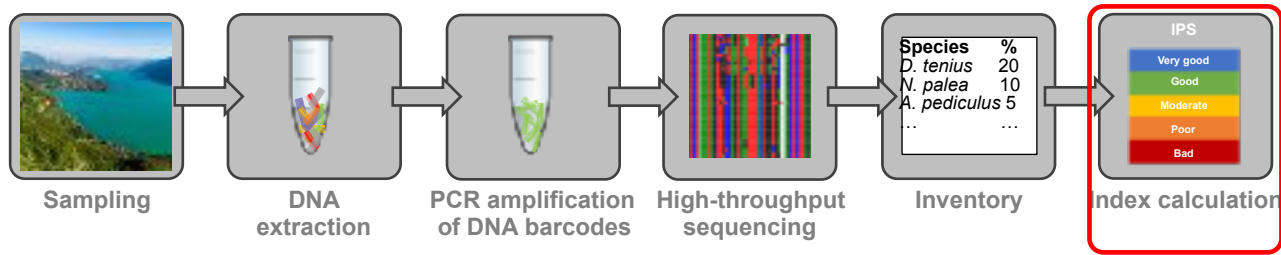


### Comparison of taxa detected

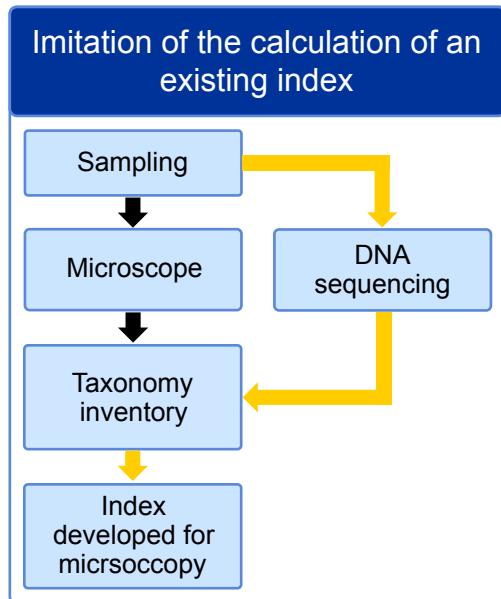
■ Microscopy (103 species)   
 ■ 16S rRNA (30 species)   
 ■ 23S rRNA (35 species)



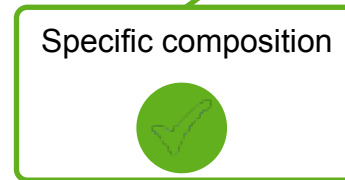
- Microscopy:**
- Different from species identified by metabarcoding
  - More numerous (many species have not barcode)
  - Larger (small species are poorly identified)

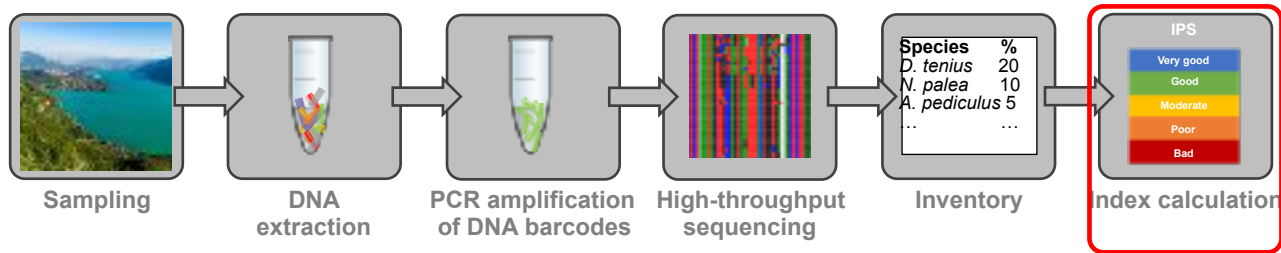


### Comparison of lake trophic status



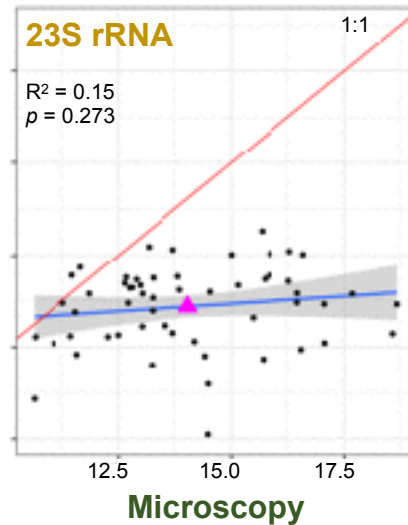
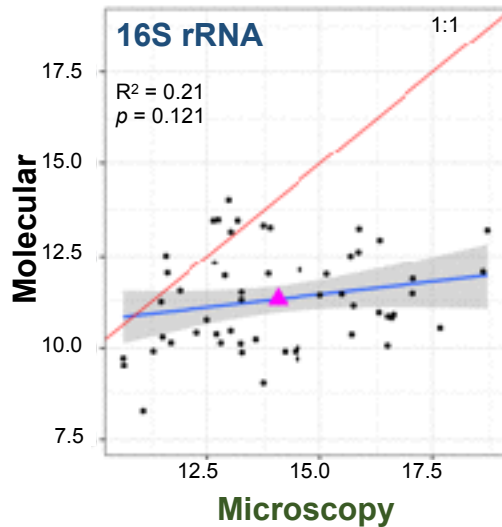
$$\text{IPLAC} = 0.7 \times \text{MCS}_{\text{nEQR}} + 0.3 \times \text{MBA}_{\text{nEQR}}$$

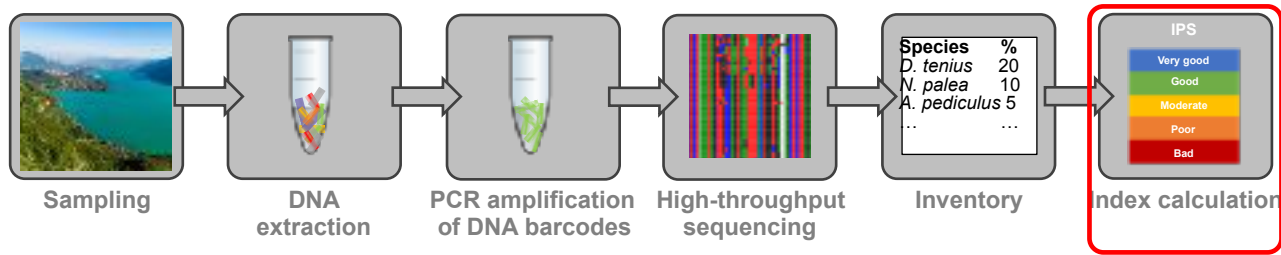




### Comparison of lake trophic status

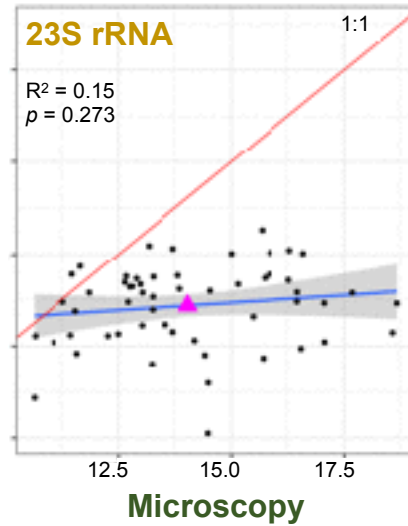
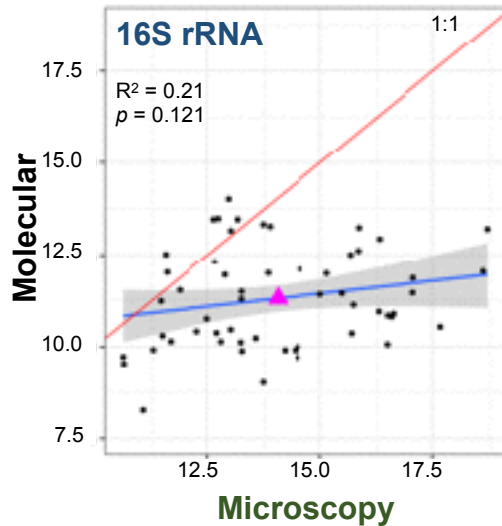
#### MCS metric



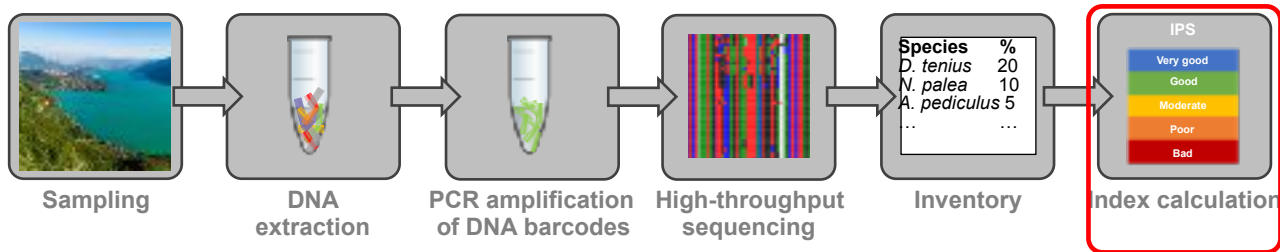


### Comparison of lake trophic status

#### MCS metric

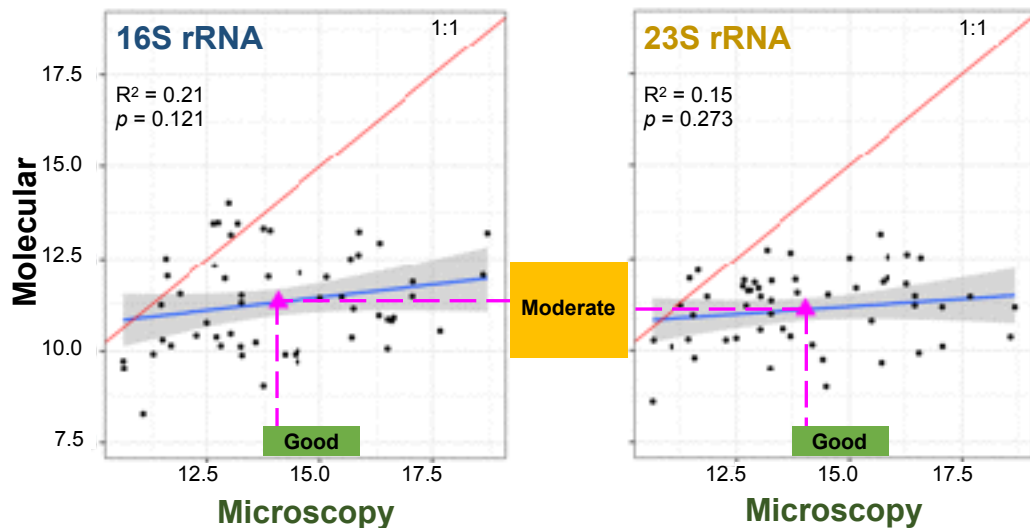


No correlation in the lake trophic status between the two approaches

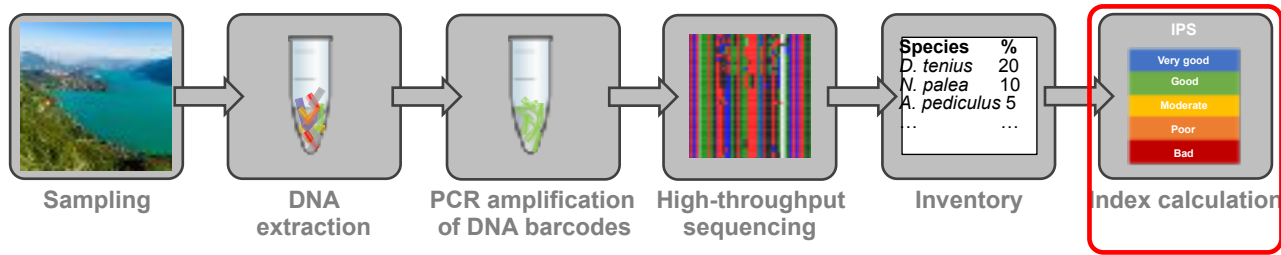


### Comparison of lake trophic status

#### MCS metric

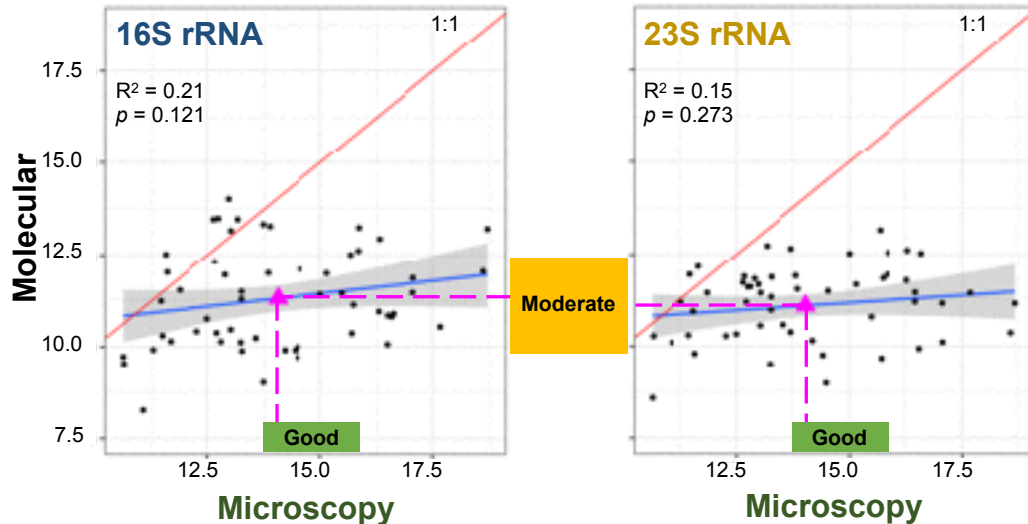


No correlation in the lake trophic status between the two approaches



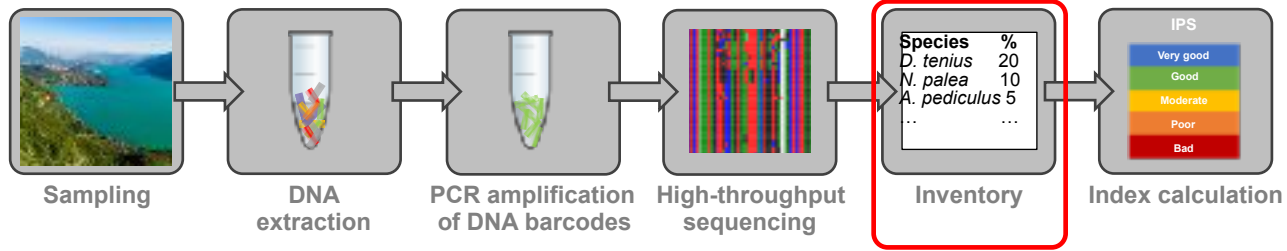
### Comparison of lake trophic status

#### MCS metric



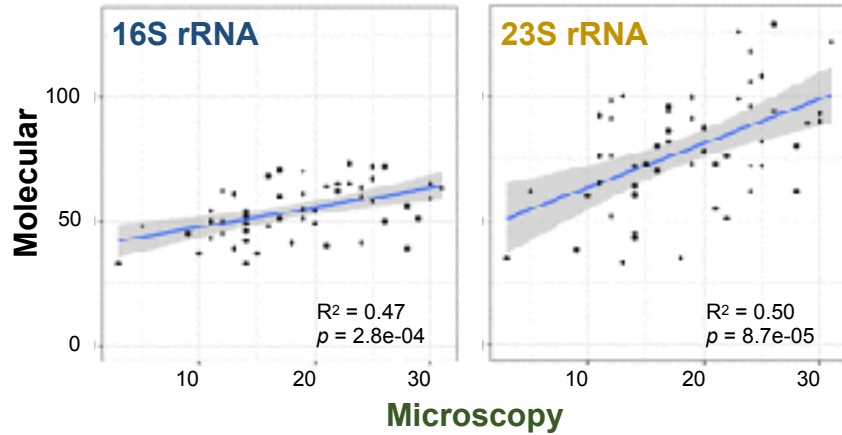
No correlation in the lake trophic status between the two approaches

- Too few species taken into account
  - 16S rRNA** 13 species (out of 30)
  - 23S rRNA** 14 species (out of 35)
  - Microscopy** 54 species (out of 103)
- Not the same dominant taxa

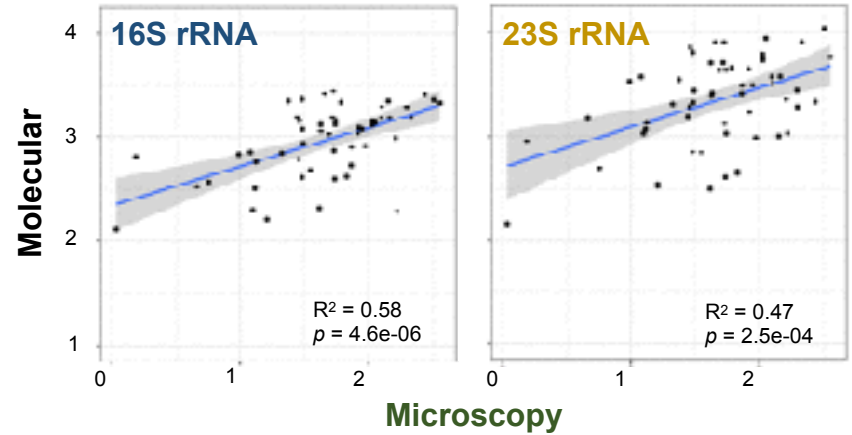


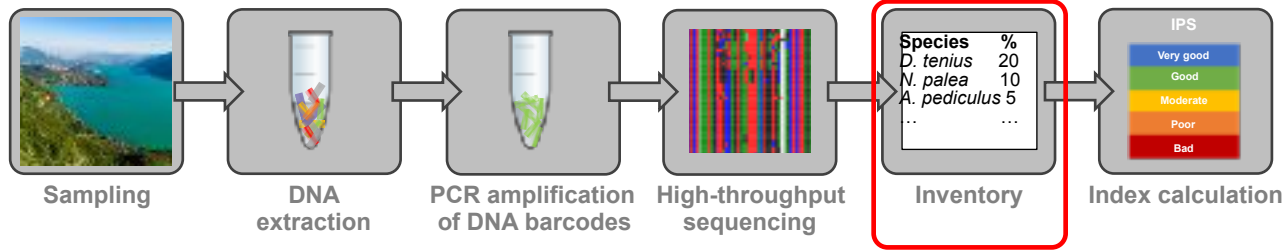
### Comparison of diversity metrics – Taxonomy-free

#### Species richness



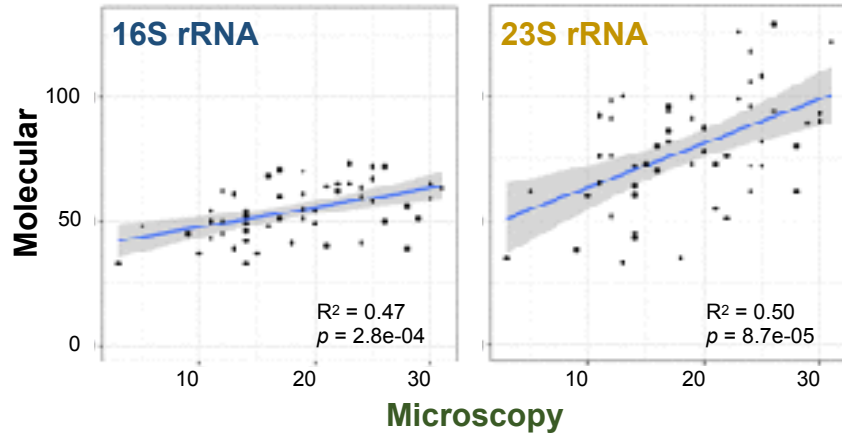
#### Shannon index



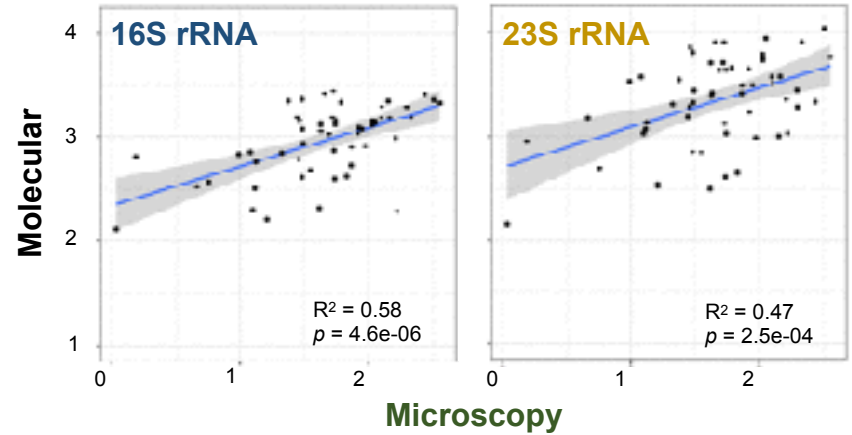


## Comparison of diversity metrics – Taxonomy-free

### Species richness

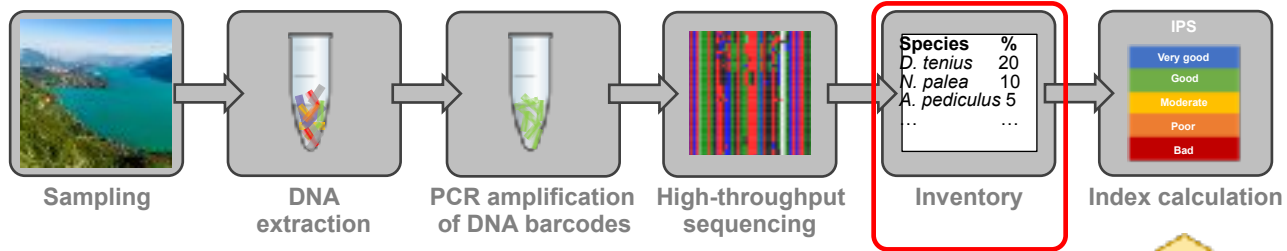


### Shannon index



Alpha diversity metrics obtained from two approaches are correlated

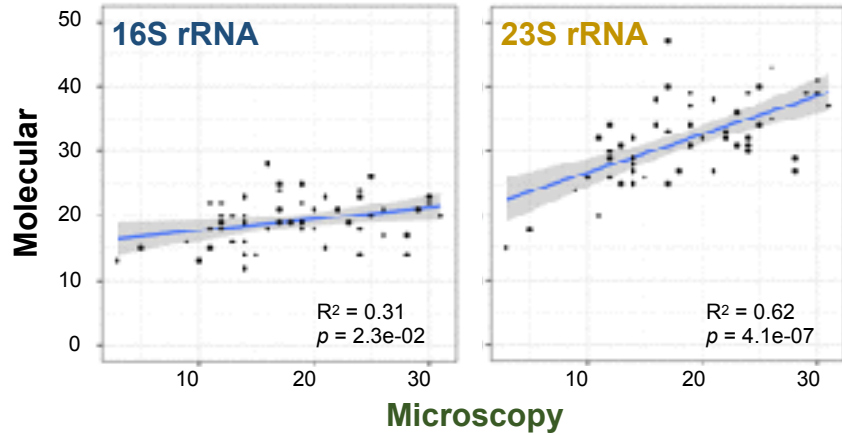




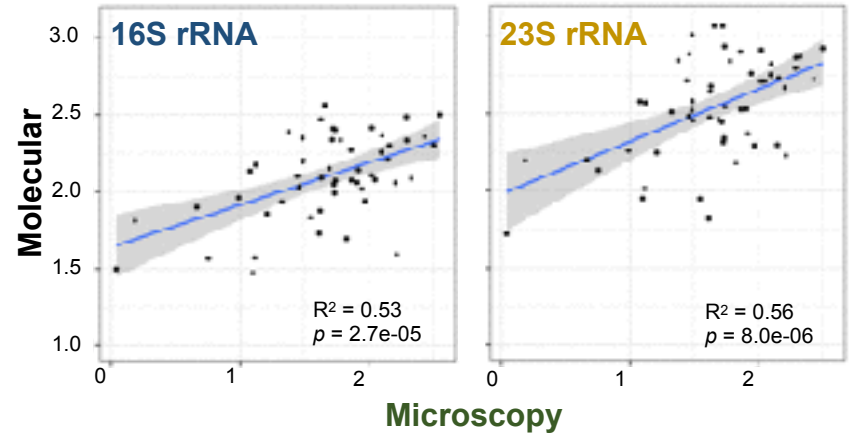
## Comparison of diversity metrics – Assigned taxonomy



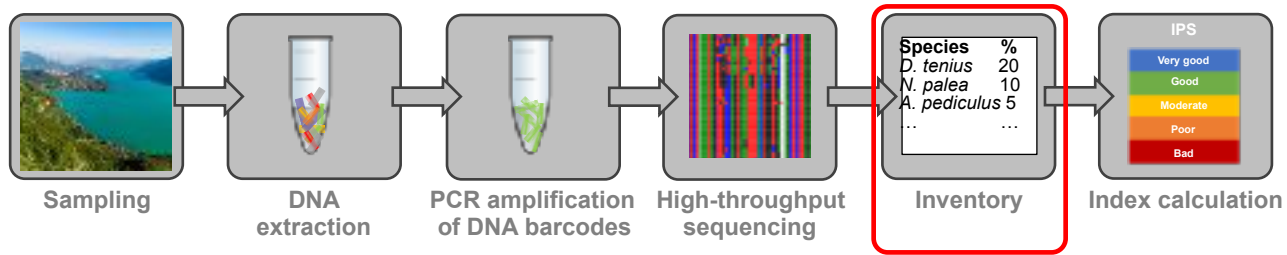
### Species richness



### Shannon index

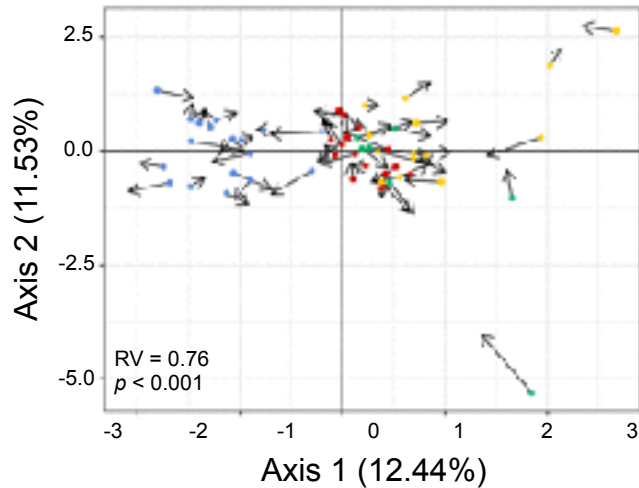


Trends in alpha diversity metrics are similar to those observed for taxonomy-free

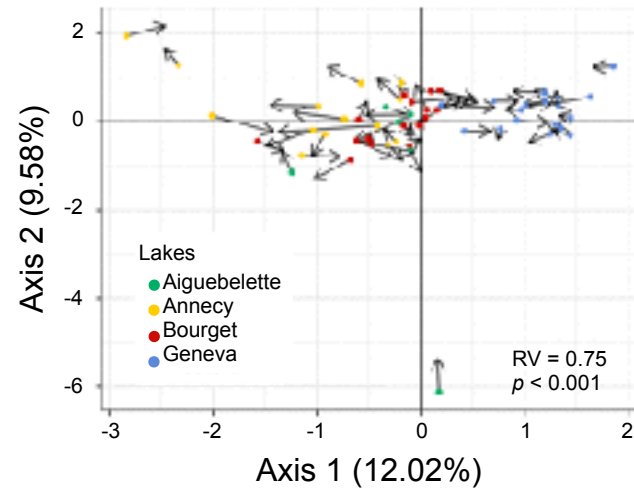


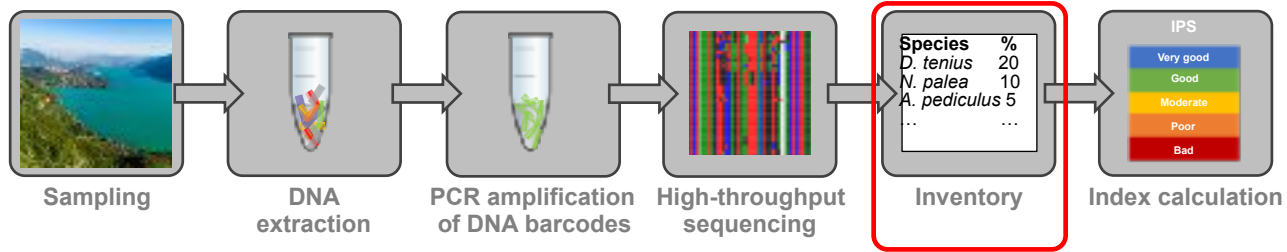
## Comparison of community structure – Taxonomy-free

### Microscopy vs. 16S rRNA

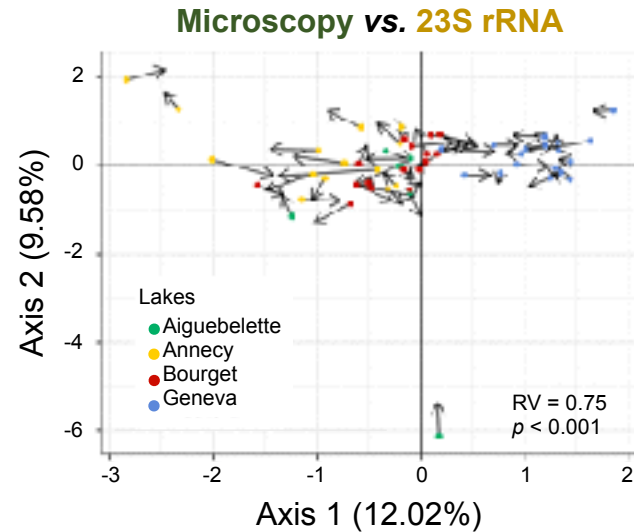
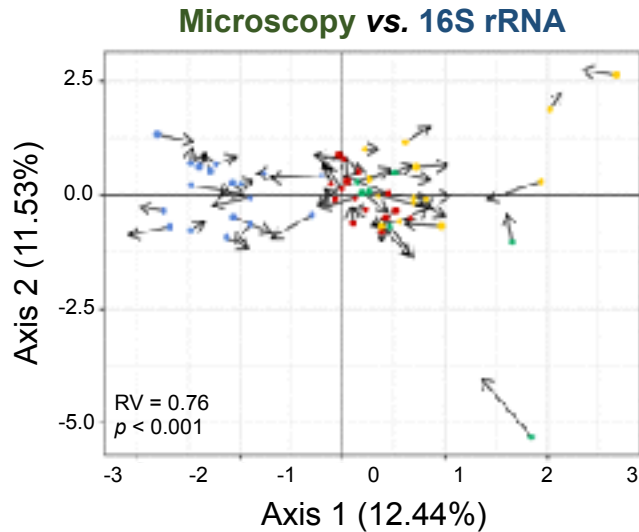


### Microscopy vs. 23S rRNA

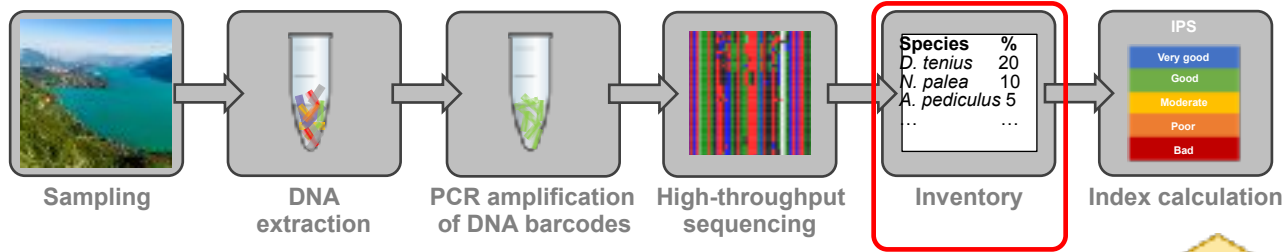




## Comparison of community structure – Taxonomy-free



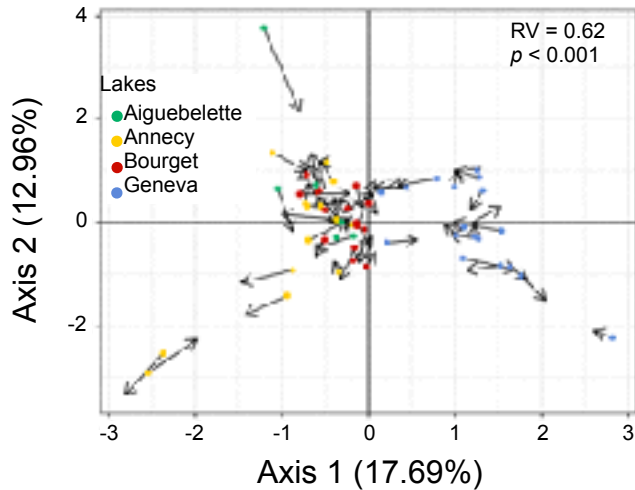
Congruence between assemblages identified by the two approaches



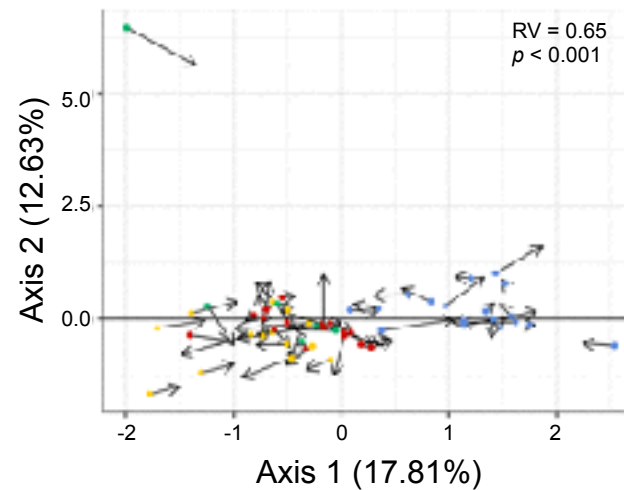
## Comparison of community structure – Assigned taxonomy



### Microscopy vs. 16S rRNA



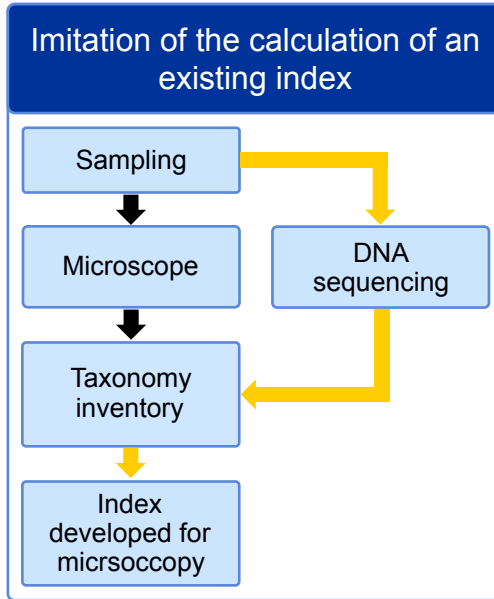
### Microscopy vs. 23S rRNA



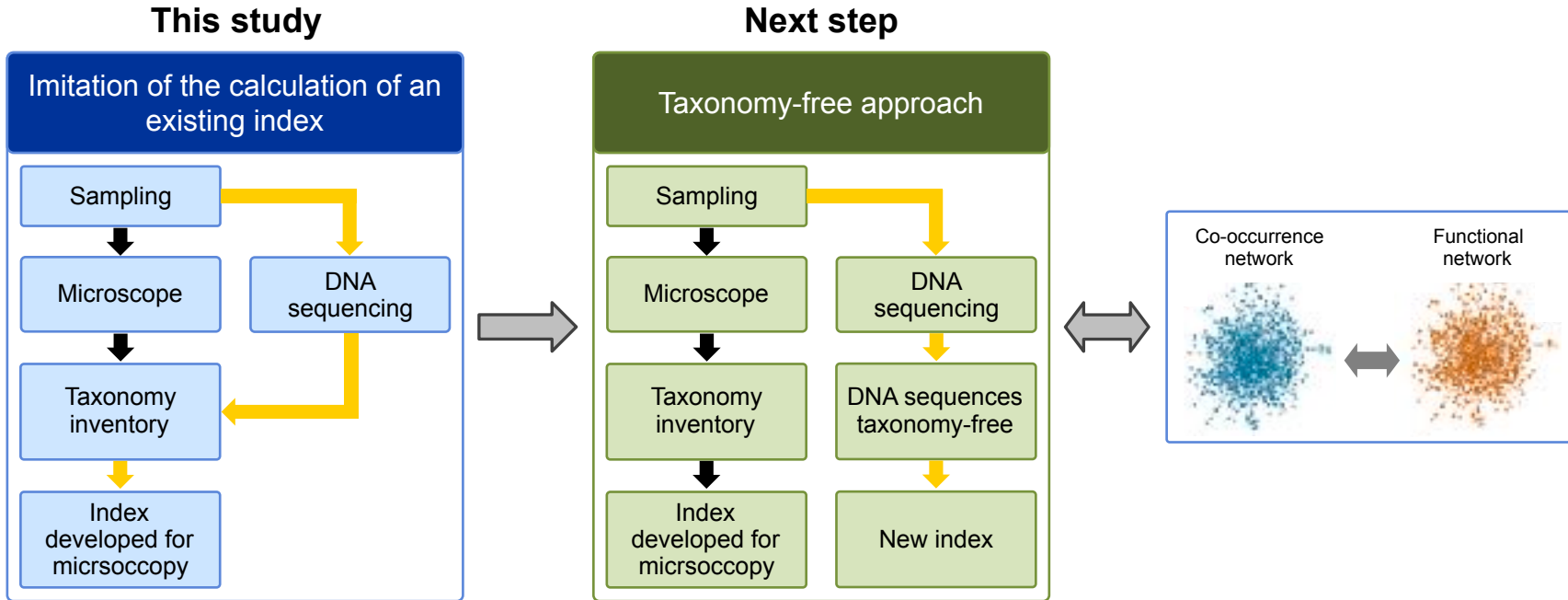
Congruence patterns are similar to those observed for taxonomy-free

## Conclusions and perspectives

### This study



## Conclusions and perspectives





# Questions?



