



Diatoms metabarcoding: Intercalibration

Agnès Bouchez

The INRAE logo is positioned at the bottom left of the slide. It consists of the letters "INRAE" in a bold, teal-colored, sans-serif font. The letter "A" is stylized with a circular element that resembles a leaf or a drop. 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.

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 with white clouds. 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.



'Ring Test'

Inter-laboratory test to compare wet lab protocols of diatom metabarcoding in view of a future standardisation



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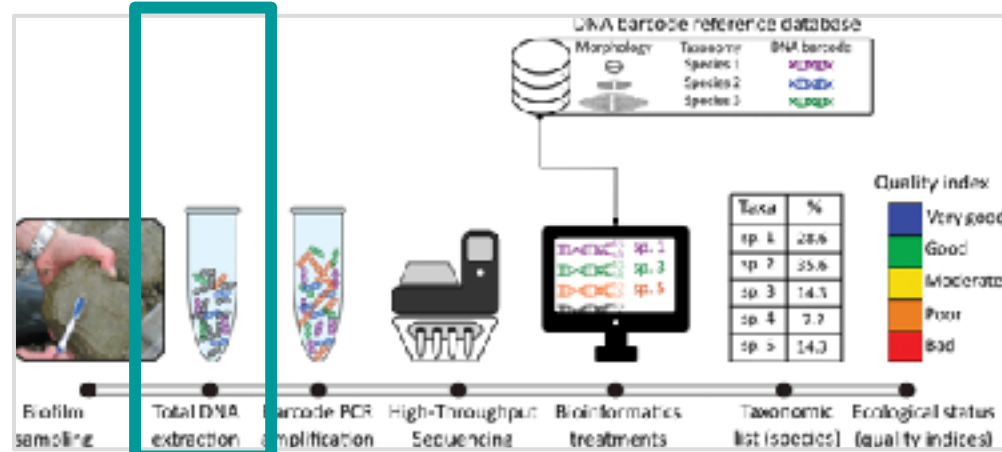


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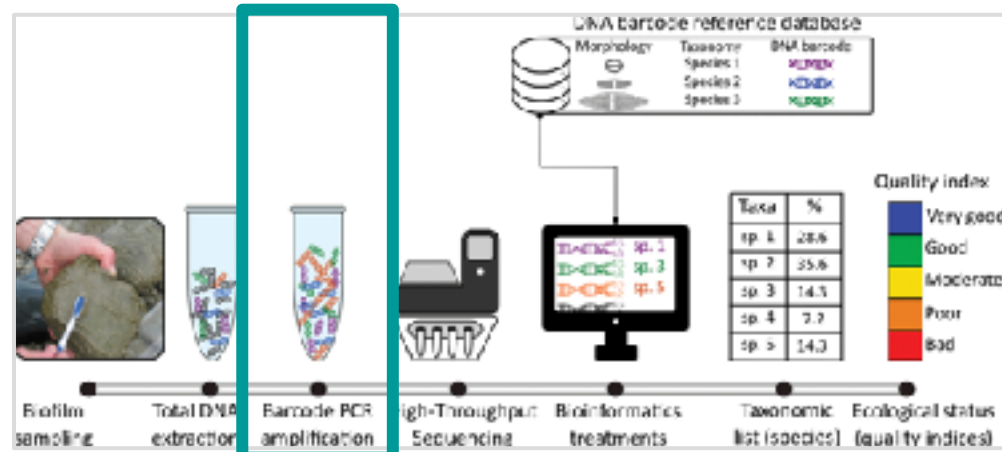
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➤ DNA extraction



➤ Barcode amplification



- **17 participants (A to Q)**
 - public/private
 - beginner/advanced
- **+ 1 Reference Laboratory (RL) - INRAE CARRTEL**

- **1 set of controlled samples**
 - 2 environmental samples : **1 lake + 1 river**
 - 2 artificial samples : **1 synthetic community + 1 mock community**

- **2 targeted steps**
 - DNA extraction
 - Barcode PCR amplification





« One for All » Protocol transfer (PCR, Taq Takara LA, *rbcL* barcode)

- 4 DNA extracts sent by Ref lab
 - 17 laboratories: 1 PCR per sample
 - 1 Ref Lab (RL): 3 PCR per sample
- PCR products sent by participants back to RL
- RL proceeds: sequencing library prep / sequencing (platform) / bioinformatics

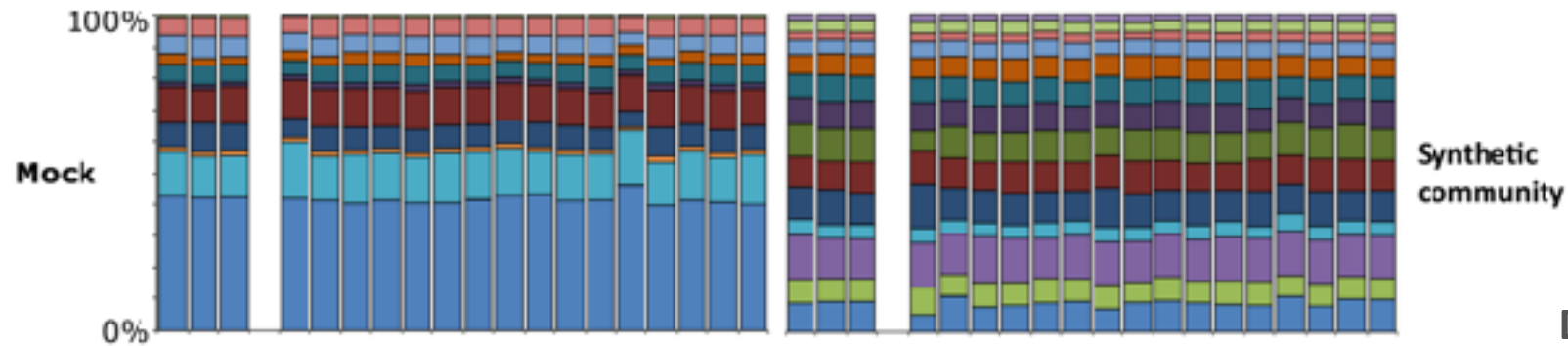
« All for One » Variability among protocols (DNA Extraction)

- 2 environmental samples (river/lake biofilm) sent by Ref Lab
 - 9 participants: 3 DNA extractions per sample
 - 1 Ref Lab (RL) : 3 DNA extractions per sample
- DNA extracts sent by participants back to RL
- RL proceeds: PCR / sequencing library prep / bioinformatics



« One for All » Protocol transfer (PCR, Taq Takara LA, *rbcL* barcode)

- 4 DNA extracts (1 common protocol)
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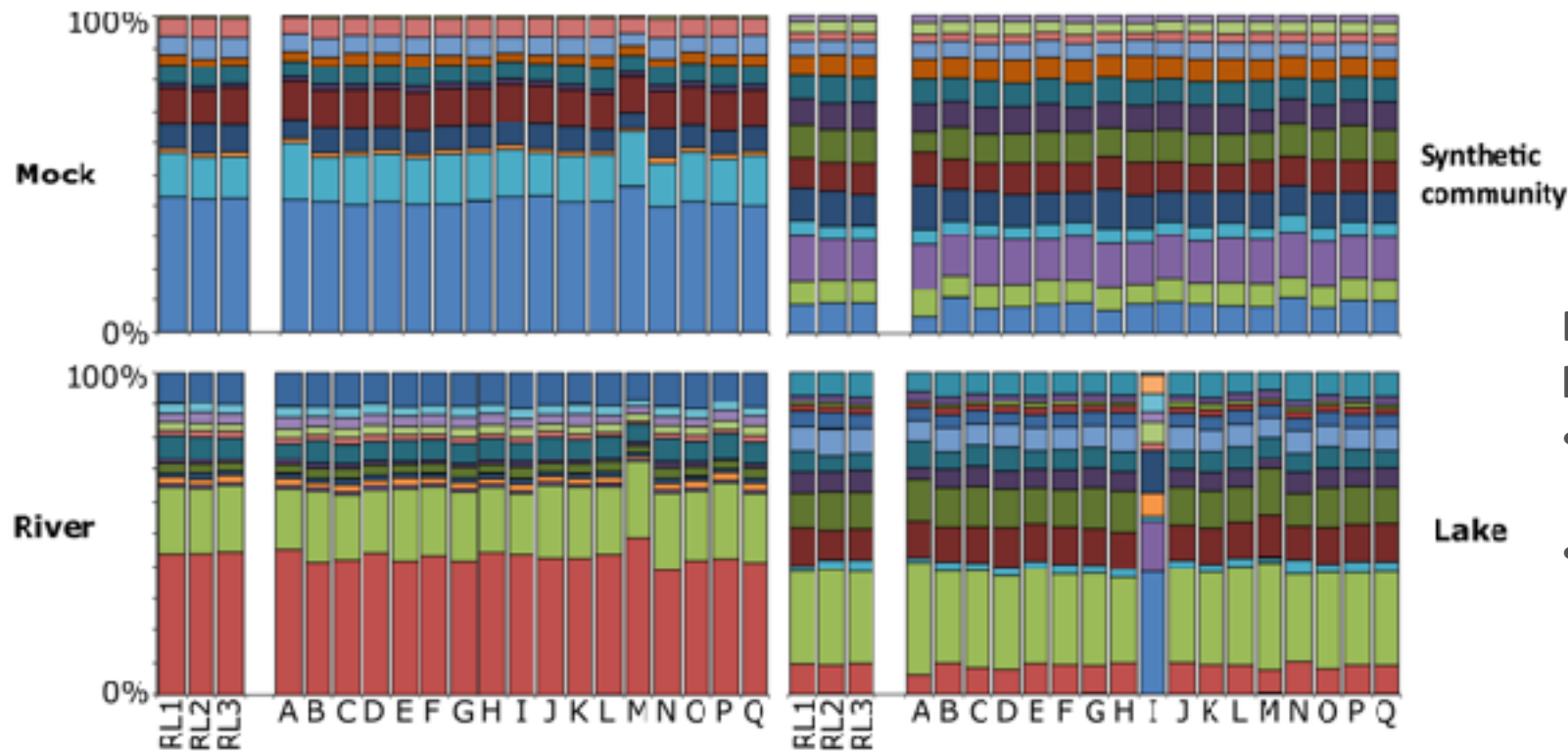


Diatom community composition is homogeneous between participants

- For mock/synthetic controlled samples

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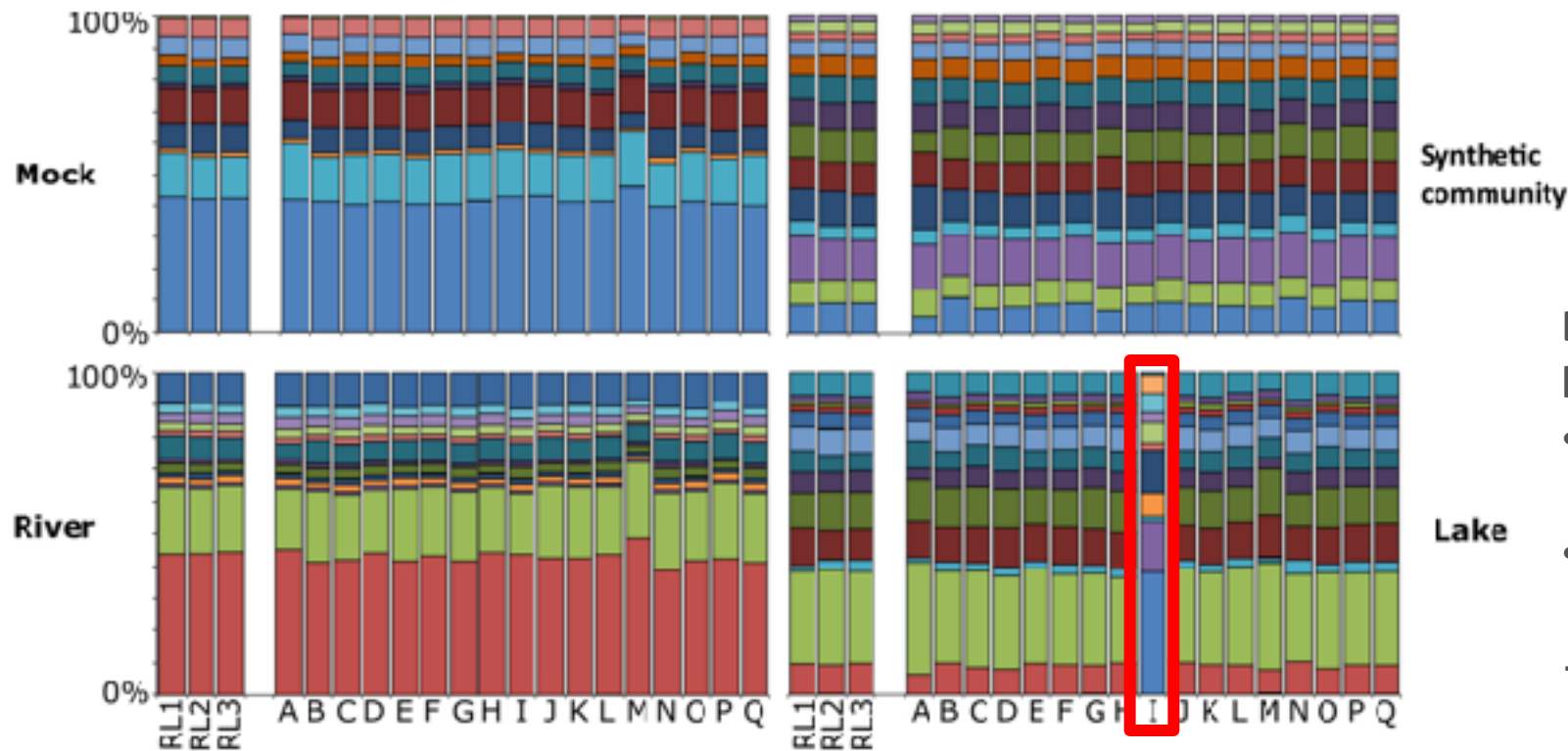


Diatom community composition is homogeneous between participants

- For mock/synthetic controlled samples
- For environmental samples

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Diatom community composition is homogeneous between participants

- For mock/synthetic controlled samples
- For environmental samples

→ **Protocol is easily transferable**

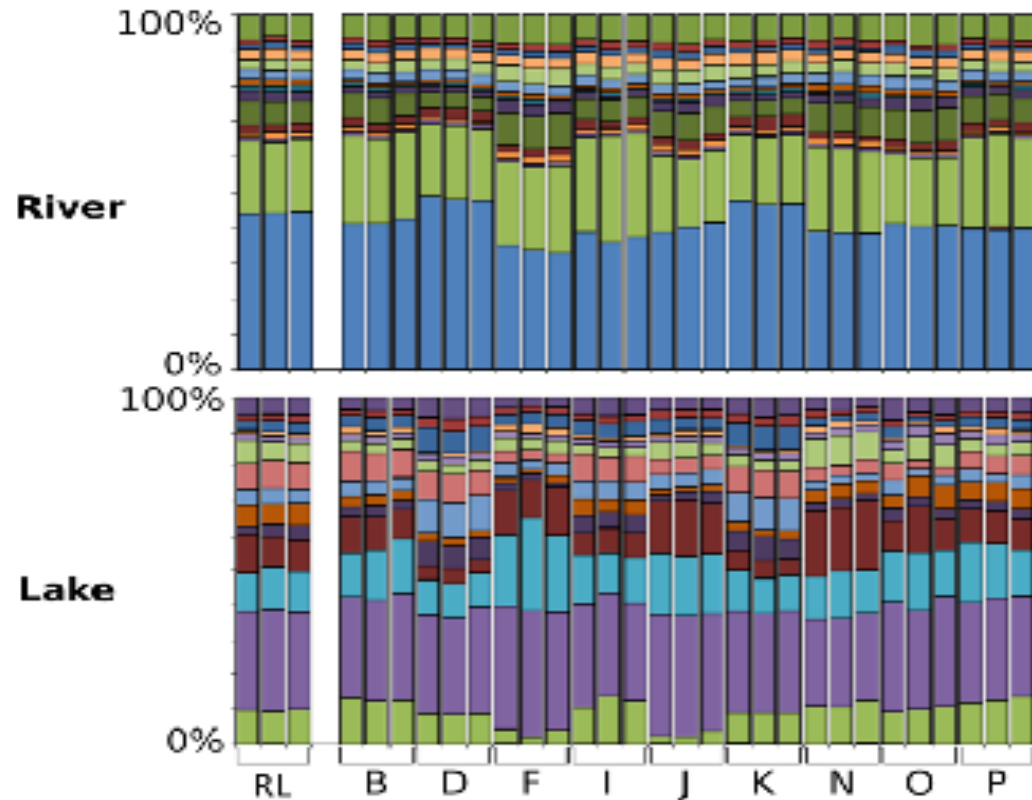
« All for One » Variability among DNA Extraction protocols

- 2 environmental samples (river/lake biofilm)
- 9 participants: 3 DNA extractions per sample
- 1 Ref Lab (RL) : 3 DNA extractions per sample

Participant	DNA extraction Method
RL	Macherey-Nagel NucleoSpin Soil
F	GenElute/home-made
D	Macherey-Nagel Nucleospin Plant Mini Kit
P	Qiagen Biofilm
O	Qiagen Powerlyzer Powersoil
I	Qiagen/home-made
J	Qiagen DNeasy Plant Mini Kit
K	Qiagen DNeasy Plant Mini Kit
B	Qiagen DNeasy PowerSoil
N	Machery-Nagel Nucleospin Soil kit with a precellys machine

« All for One » Variability among DNA Extraction protocols

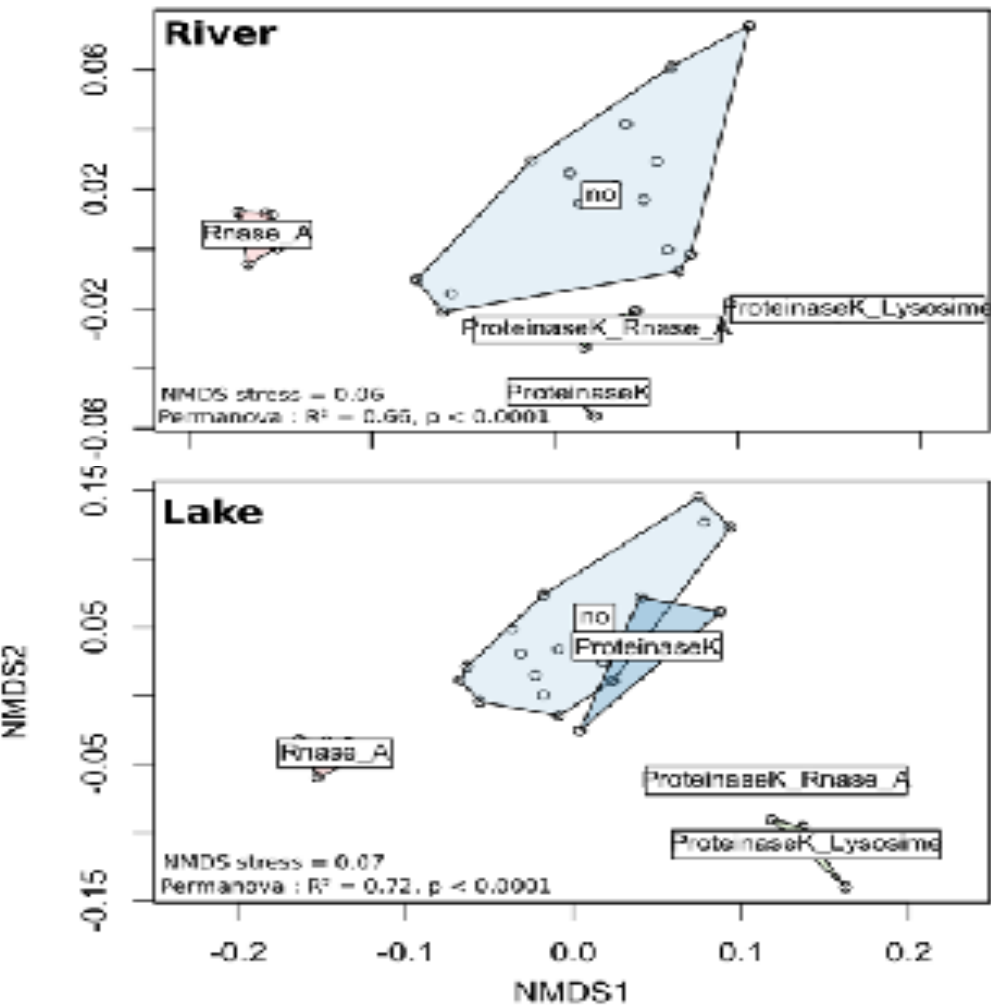
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- Similar species detected
- Variability on relative abundances (changes in sp. %)

« All for One » Variability among DNA Extraction protocols

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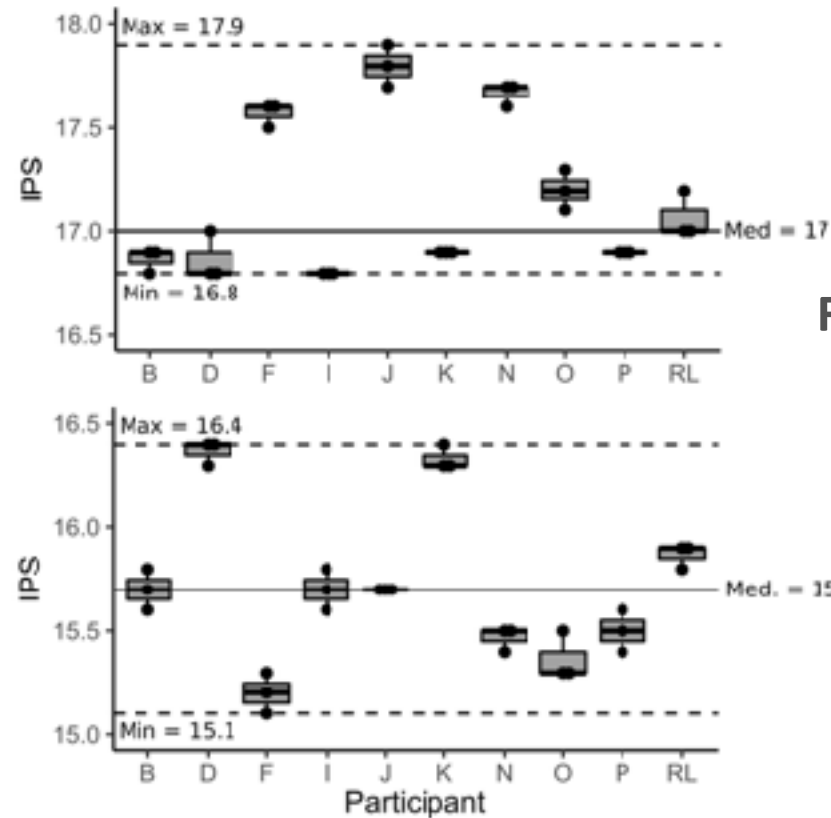
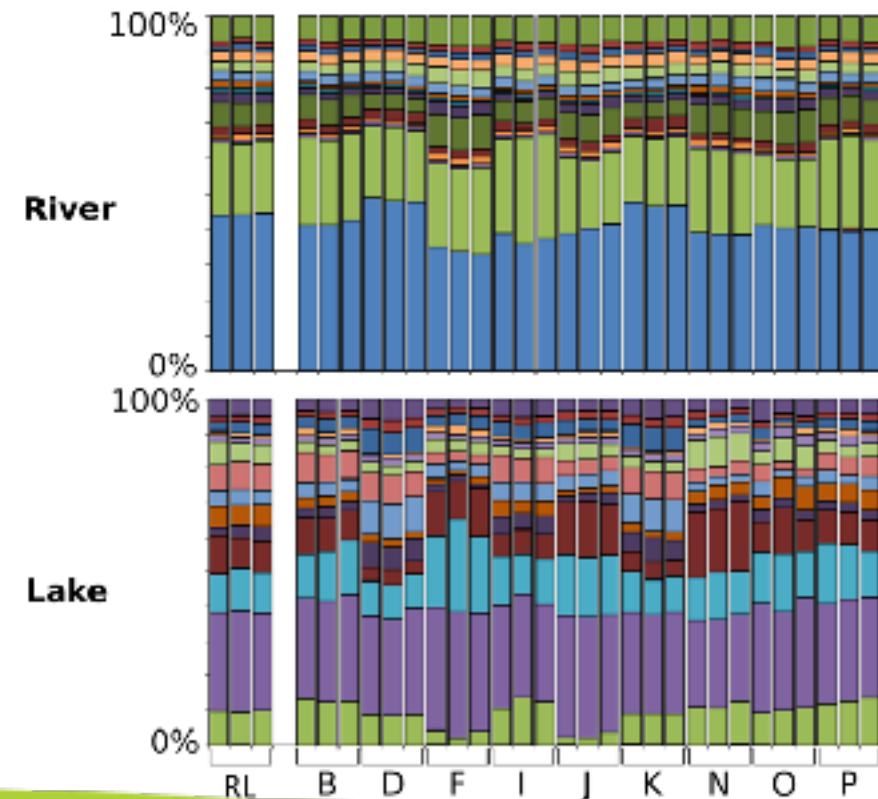


The variability in species % is due to:

- Processing lab
- DNA extraction method (lysis step)

« All for One » Variability among DNA Extraction protocols

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For Ecological Quality Assessment:

- No impact of sp % changes on IBD
- Moderate impact on IPS

→ All protocols can be used



Thanks to all participants !

<https://doi.org/10.3897/aca.4.e65142>

...paper coming soon (hopefully)



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Questions ?



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