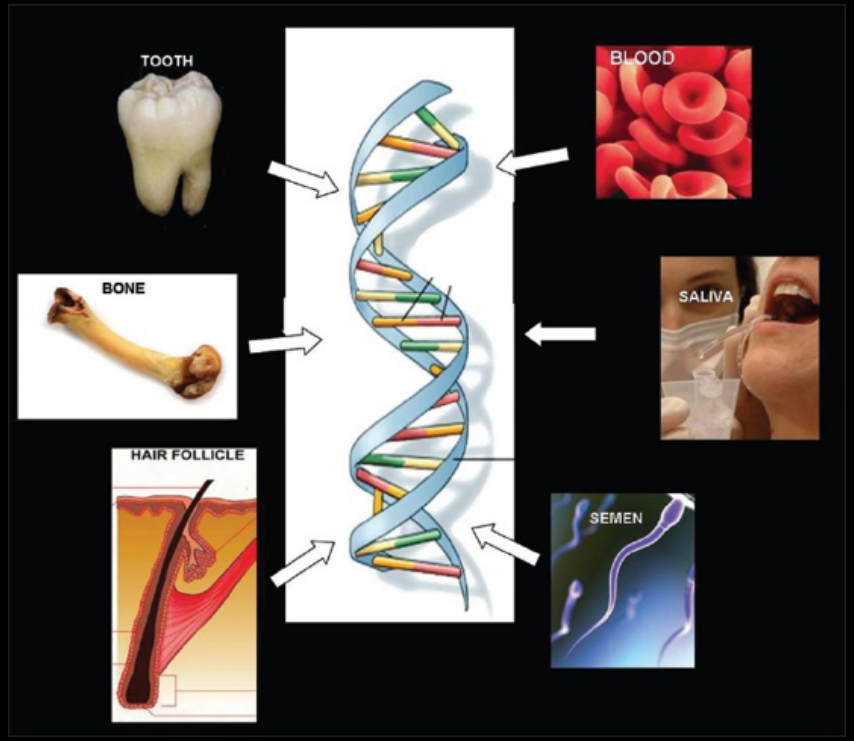
Welcome to DNAqua-Net's stakeholder workshop series

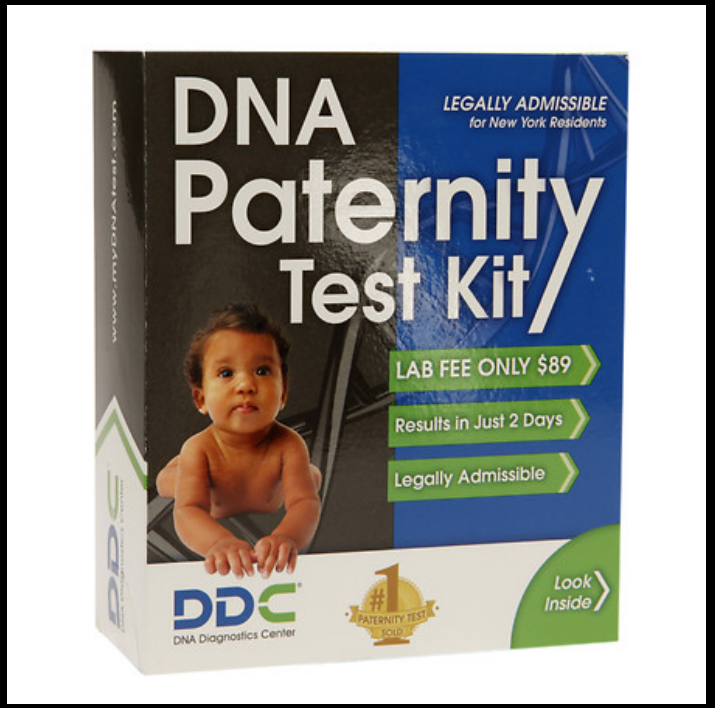
March 12th 2021

Prof. Dr. Florian Leese
University of Duisburg-Essen
Chair of COST Action DNAqua-Net

@dnaquanet

We trust genetic methods in various sectors of our life





What about biodiversity assessment and biomonitoring?

The European version of the obvious back in 2015/2016

MoU: „Advance the application of DNA-based tools for biodiversity assessments & develop a roadmap to include these in standardized bioassessments of aquatic ecosystems in Europe **and beyond**.“

DNAqua-Net
EU COST ACTION

EU COST Action DNAqua-Net (2016 – 2021)

The European version of the obvious back in 2015/2016

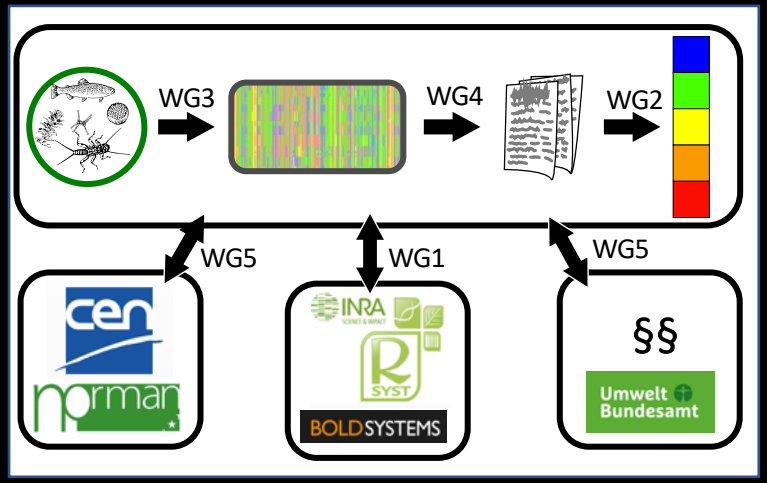
MoU: „Advance the application of DNA-based tools for biodiversity assessments & develop a roadmap to include these in standardized bioassessments of aquatic ecosystems in Europe **and beyond**.“

THIS IS NOT ONLY A RESEARCH QUESTION; COLLABORATION BETWEEN ACADEMIA & APPLICATION EXTREMELY IMPORTANT!

DNAqua-Net
EU COST ACTION

EU COST Action DNAqua-Net (2016 – 2021)

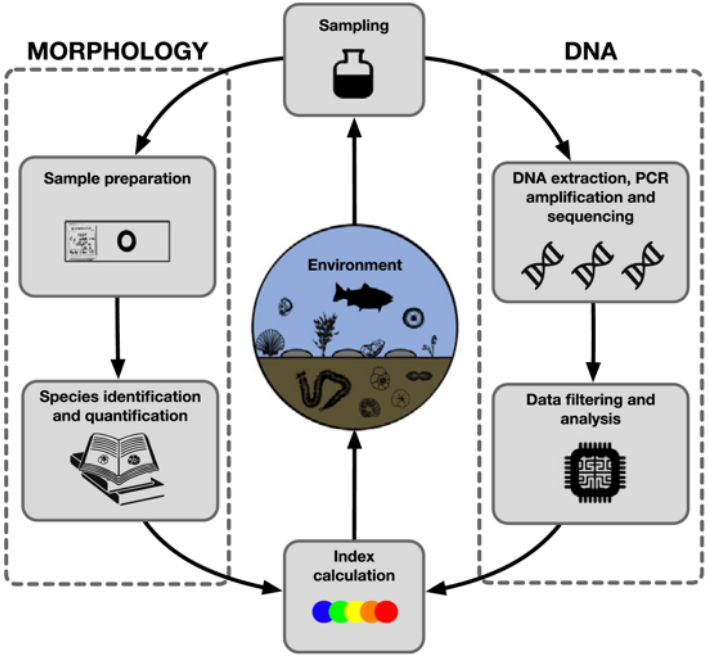
DNAqua-Net's vision



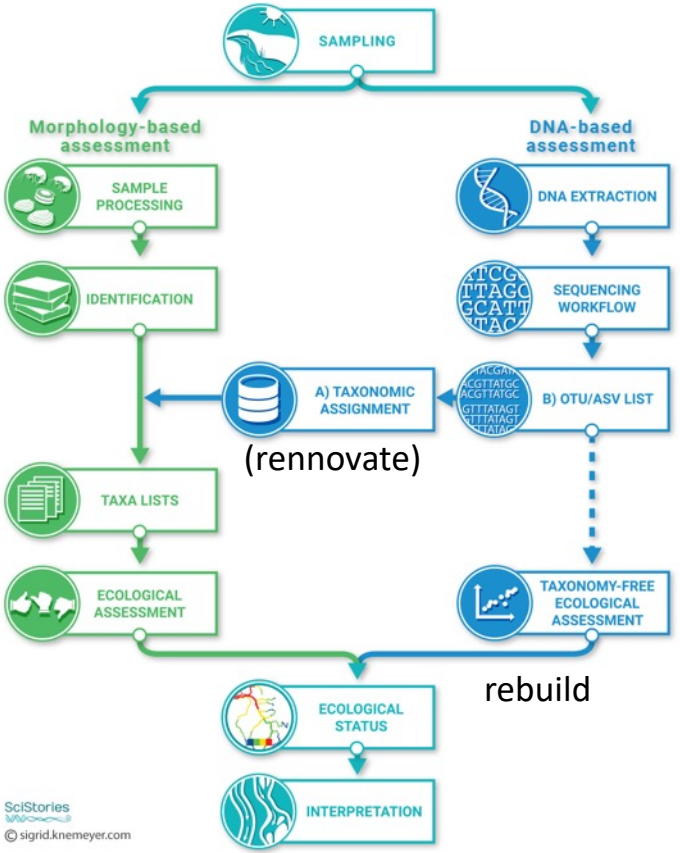
From research to application

- Between 400 & 600 members
- 49 countries
- >100 publications & stakeholder reports
- >50 exchanges, ~50 meetings / round tables

General Options



Pawlowski et al. (2018)



Contents lists available at ScienceDirect

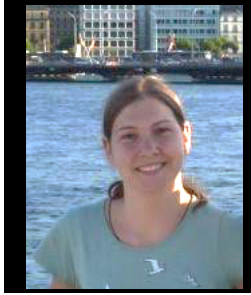
Science of the Total Environment

journal homepage: www.elsevier.com/locate/scitotenv

Review

DNA barcode reference libraries for the monitoring of aquatic biota in Europe: Gap-analysis and recommendations for future work

Hannah Weigand [a], Arne J. Beermann [b], Fedor Čiampor [c], Filipe O. Costa [d,e], Zoltán Csabai [f], Sofia Duarte [d,e], Matthias F. Geiger [g], Michał Grabowski [h], Frédéric Rimet [i], Björn Rulik [g], Malin Strand [j], Nikolaus Szucsich [k], Alexander M. Weigand [a,b], Endre Willassen [l], Sofia A. Wyler [m], Agnès Bouchez [i], Angel Borja [n], Zuzana Čiamporov[á], Piotr Gadawski [h], V[...], Lujza Keresztes [v], E[...], Daniela Maric Pfan[...], Marcos A.L. Teixeir[a]



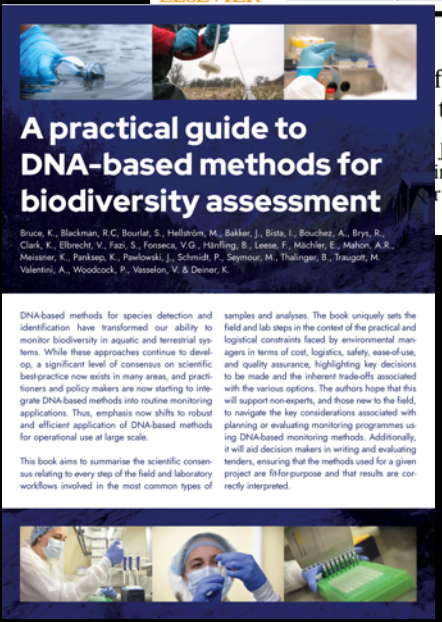
AND MANY MORE!

Contents lists available at ScienceDirect

Water Research

journal homepage: www.elsevier.com/locate/watres





for DNA-based identification into ecological the European Water Framework Directive

J.Iwan Jones [c], [...]
[...]ina Drakare [h], [...]
[...] [k], Patricia Mer[...]

Contents lists available at ScienceDirect

Science of the Total Environment

journal homepage: www.elsevier.com/locate/scitotenv

Review

The future of biotic indices in the ecogenomic era: Integrating (e)DNA metabarcoding in biological assessment of aquatic ecosystems

Jan Pawlowski [a,*], Ma[...] [b], Florian Altermatt [c], Laura Apothéloz-Perret-Gentil [a], Pedro Beja [d], [...]ero [e], Ang[...], [...]ipe [d], Ric[...], [...]ova-Mar[...], [...]et [g], Buk[...], [...]k [v], Jona[...]

1 **Revision and annotation of DNA barcode records for marine invertebrates: report of the**
2 **8th iBOL conference hackathon**
3
4 Adriana E. Radulovici[1*], Pedro E. Vieira[2,3], Sofia Duarte[2,3], Marcos A. L. Teixeira[2,3], Luisa M.
5 S. Borges[4], Bruce Deagle[5], Sanna Majaneva[6,7], Niamh Redmond[8], Jessica A. Schultz[1,9], Filipe
6 O. Costa[2,3*]
7


Where are the general/specific challenges?

Concept

- unrepresentative sampling
- new taxonomic / community information
  (e.g. terrestrial eDNA, gut content)
- abundance / biomass / copy-number vs. presence-absence data
- new reference conditions
- new metrics

Technology

- sample / storage conditions
  (e.g. preservation liquid, inhibitors)
- primer bias / PCR stochasticity
- misidentifications
  (e.g. wrong references, shared barcodes)
- reference database development
- non-corresponding taxonomy
  (e.g. between reference list and results)

Perception

- new 'units' to quantify biodiversity
- new technical language
- more complex / integrative settings

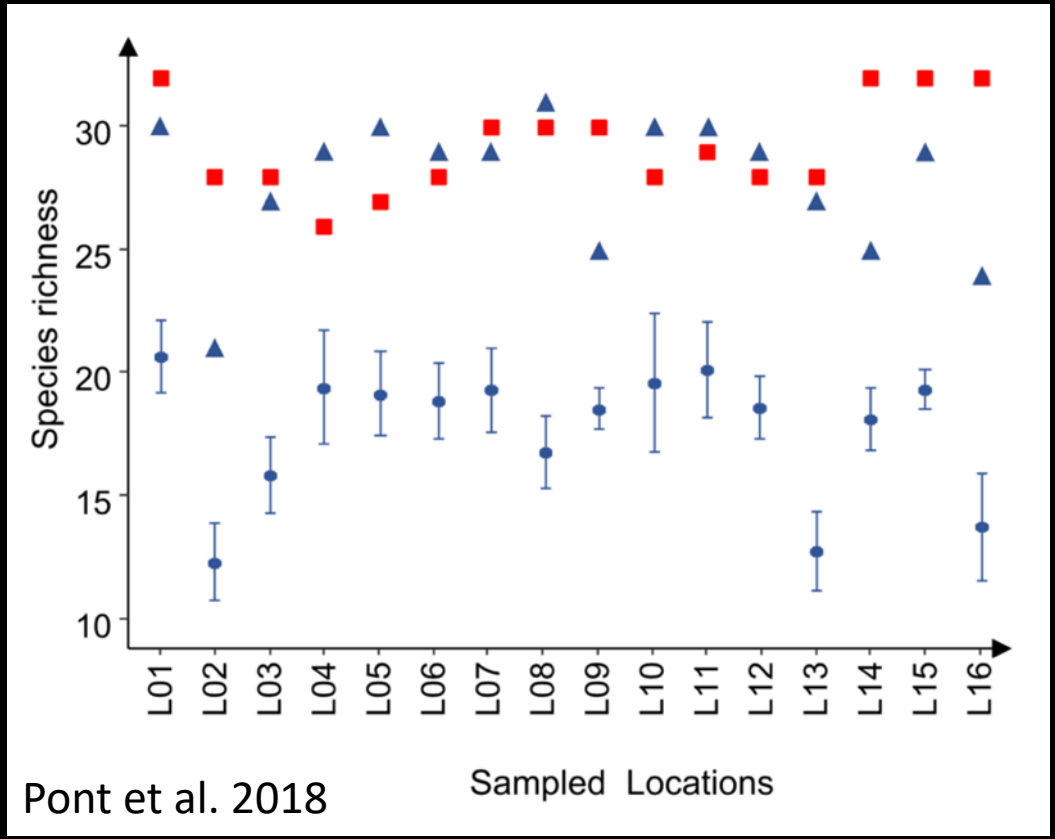
Economic & legal framework

- costs
- knowledge transfer
- legislative requirements
  (e.g. abundance data, intercalibration)

Leese et al. (2018)

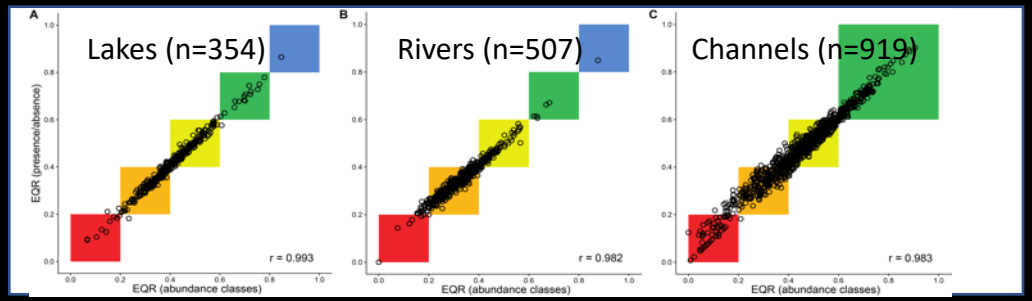
Comparability?

- Especially for deep rivers and lakes – better species representation using eDNA
- In particular benthic fish

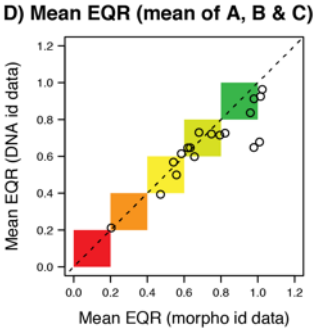


Pont et al. 2018

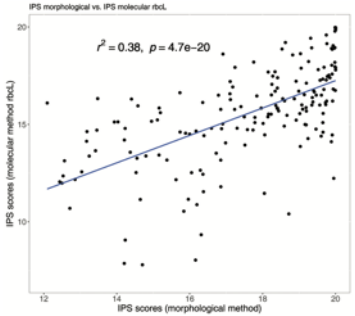
Abundance sometimes not of prime importance



Beentjes et al. (2018) MBMG



Elbrecht et al. (2017)



Baillet et al. (2018)

eDNA can reflect fish abundance / biomass in ponds!

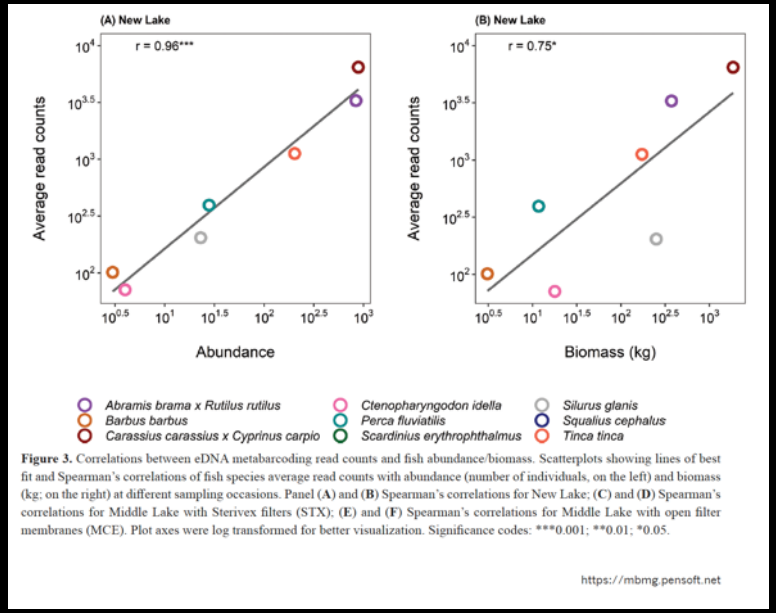


Figure 3. Correlations between eDNA metabarcoding read counts and fish abundance/biomass. Scatterplots showing lines of best fit and Spearman's correlations of fish species average read counts with abundance (number of individuals, on the left) and biomass (kg; on the right) at different sampling occasions. Panel **(A)** and **(B)** Spearman's correlations for New Lake; **(C)** and **(D)** Spearman's correlations for Middle Lake with Sterivex filters (STX); **(E)** and **(F)** Spearman's correlations for Middle Lake with open filter membranes (MCE). Plot axes were log transformed for better visualization. Significance codes: ***0.001; **0.01; *0.05.

https://mbmg.pensoft.net

MBMG
Metabarcoding & Metagenomics

Metabarcoding and Metagenomics 4: 97–112
DOI 10.3897/mbmg.4.56959

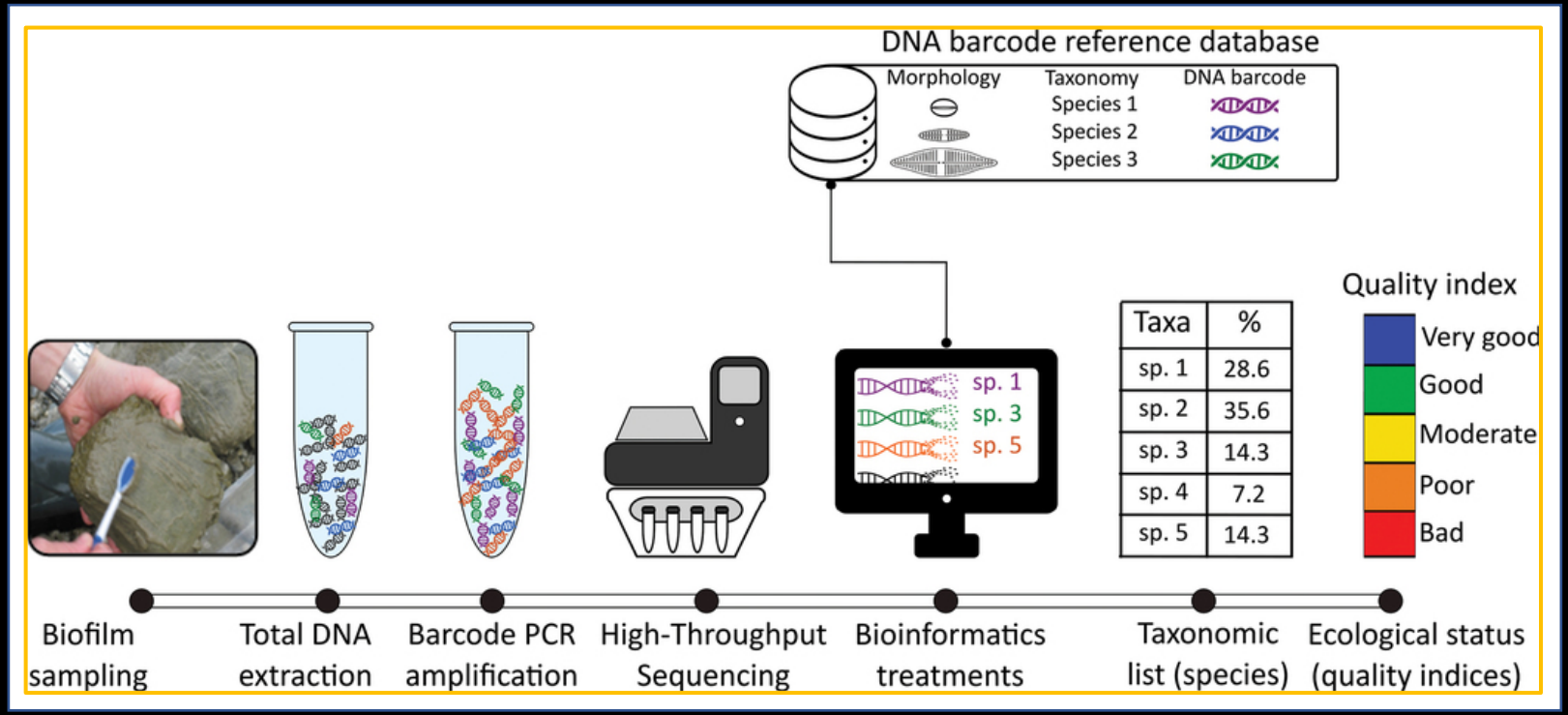
Research Article

Read counts from environmental DNA (eDNA) metabarcoding reflect fish abundance and biomass in drained ponds

Cristina Di Muri[1], Lori Lawson Handley[1], Colin W. Bean[2], Jianlong Li[3,4], Graeme Peirson[5], Graham S. Sellers[1], Kerry Walsh[6], Hayley V. Watson[1], Ian J. Winfield[7], Bernd Hänfling[1]

See also Ushio et al. 2019; Doi et al. (mult. ref), Li et al. (2020), Hänfling et al. (2016); Pont et al. (2018, 2020)

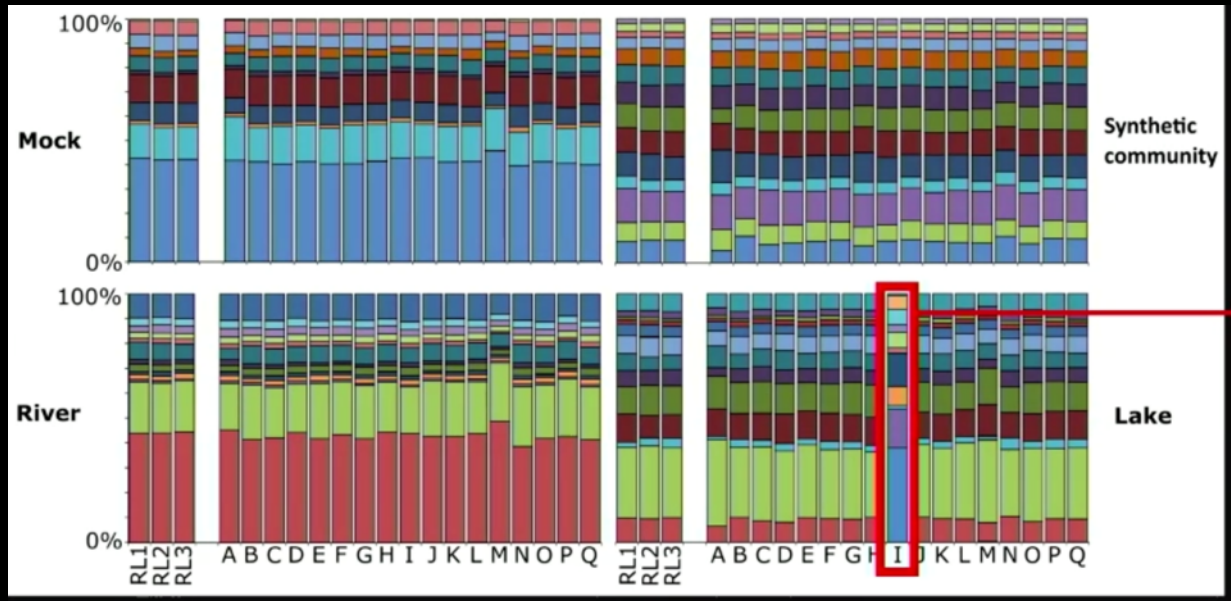
How comparable are the data?



Vasselon et al. 2019, MBMG

How comparable are the data?

- Fast, simple, cheap in application, robust & reproducible data to in form on pressures
- Few ring tests – standardisation needed, but results promising



Same Taq in all labs!

Error, Inversion of two samples (by RL or the participant). Removed from downstream analysis.

- 18 labs in 15 countries participated in diatom ring test

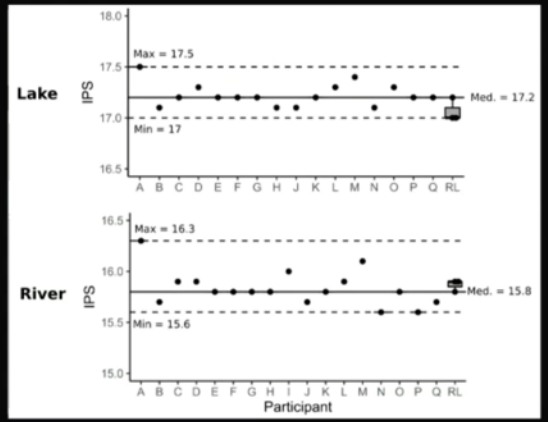
Source: V. Vasselon

How reliable are the data?

- Fast, simple, cheap in application, robust & reproducible data to in form on pressures

Ecological assessment using IPS diatom index

- IPS quality scores calculated using OMNIDIA 6



Q3 - Variability observed on IPS score is satisfactory (max diff. = 0.7 point)

Calculation of z-score using Lake and River IPS scores

- calculated for each participant : $z = (x - \mu) / \sigma$
- evaluates how far a participant result is from the mean

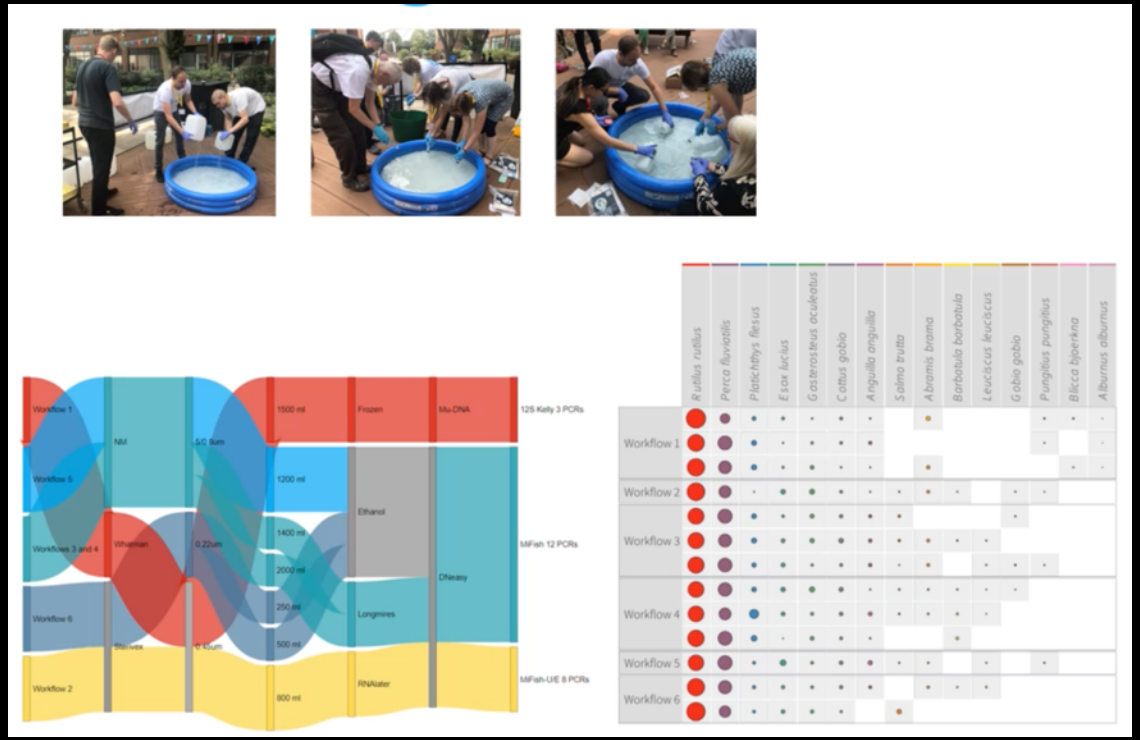
	Z-score	
	IPS_Lake	IPS_River
RL	-1,29	0,17
A	2,46	2,70
B	-1,00	-0,80
C	-0,14	0,37
D	0,73	0,37
E	-0,14	-0,22
F	-0,14	-0,22
G	-0,14	-0,22
H	-1,00	-0,22
I		0,95
J	-1,00	-0,80
K	-0,14	-0,22
L	0,73	0,37
M	1,60	1,53
N	-1,00	-1,38
O	0,73	-0,22
P	-0,14	-1,38
Q	-0,14	-0,80

$|z\text{-score}| \leq 2.0$ satisfactory
$2.0 < |z\text{-score}| < 3.0$ questionable
$|z\text{-score}| \geq 3.0$ unsatisfactory

Q3 - Ring test successful for PCR
no participant considered unsatisfactory

Source: V. Vasselon

How reliable are the data?



- Fish eDNA metabarcoding comparison
- 6 very different workflows and labs
- Very consistent results

Source: Kat Bruce

Co-designed validation studies are important now!

GeDNA

SEANDNAnet

Financed by Nordic Council of Ministers

JOINT DANUBE SURVEY 4

cen

EDNA-VALIDATION.COM

Infrastructure – DIY, or rely on public infrastructure

- Data storage
- Data processing
- Taxonomic assignment
- Ecological analysis / index calculation

EUROPEAN OPEN SCIENCE CLOUD

elixir

EGI

ENA
European Nucleotide Archive

DIAT.BARCODE

silva
high quality ribosomal RNA databases

LifeWatch ERIC

www.freshwaterecology.info
The Taxa and Autecology Database for Freshwater Organisms

Knowledge Transfer – consensus building!

https://dnaqua.net
https://dnaquahub.eu

→ DNAqua-Net WG3; Appearing soon!

Pawlowski et al. 2020: Available in 3 languages!


Countries
Disciplines
Cultures
Generations
Sustainable management of aquatic ecosystems
Ecosystem
Sampling
Laboratory work
WG3
WG3
Morphological identification
Bioinformatics, HPC & long-term digital preservation
WG4
WG5
Legal aspects management implementation
Taxa
Barcode databases
WG1
WG2
New indices
New metrics
Let’s work together / bridge gaps
Now let’s discuss at national level

Aims of this workshop

Aims

- Present the state-of-the-art of DNA and eDNA-based tools
- Discuss details (reference databases, quantification, taxonomic assignment, costs) for the purpose of routine monitoring
- Link actors in the field at national level

- Where do you see use of the methods in your country?
- What are main obstacles for the uptake of the methods?

→ Please perform in the survey