



DNA-based aquatic bioassessment in Europe and beyond: Chances and challenges

LifeWatch Meeting, Porto, February 26th 2020

Florian Leese

University of Duisburg-Essen, Germany

Chair of EU COST Action DNAqua-Net

German Barcode of Life

@leeselab @dnaquanet





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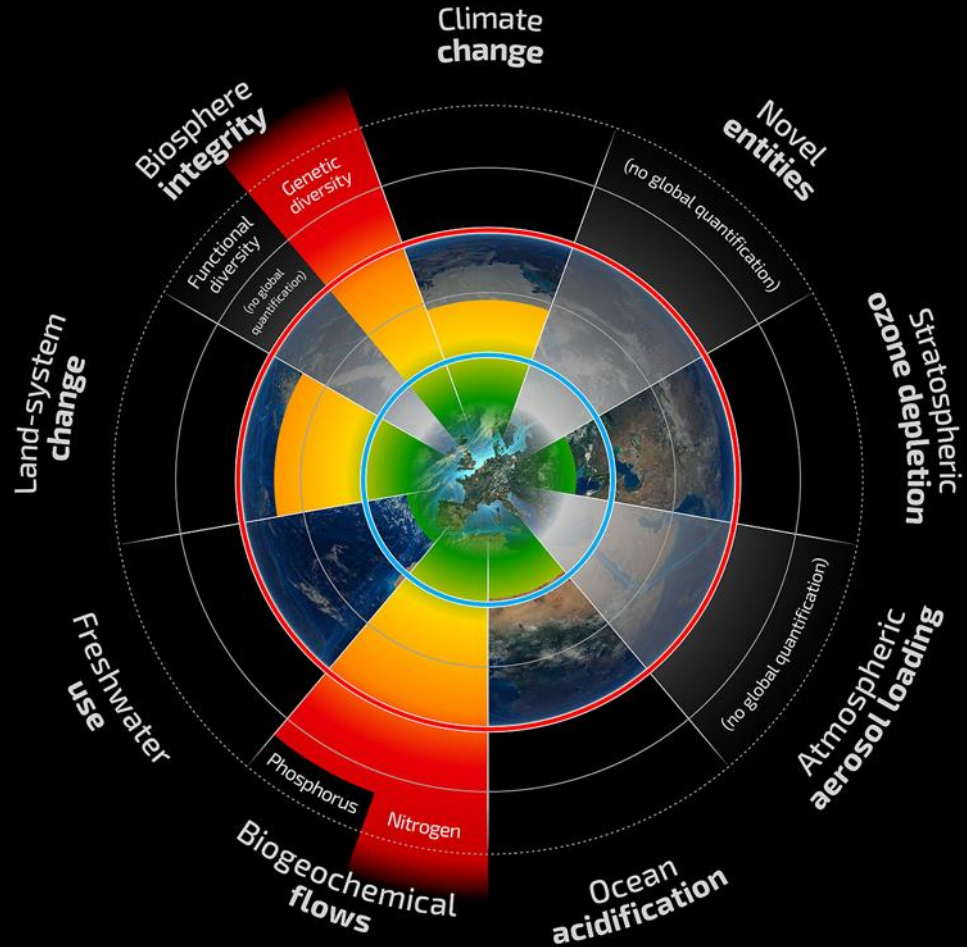
German Barcode of Life

@leeselab @dnaquanet



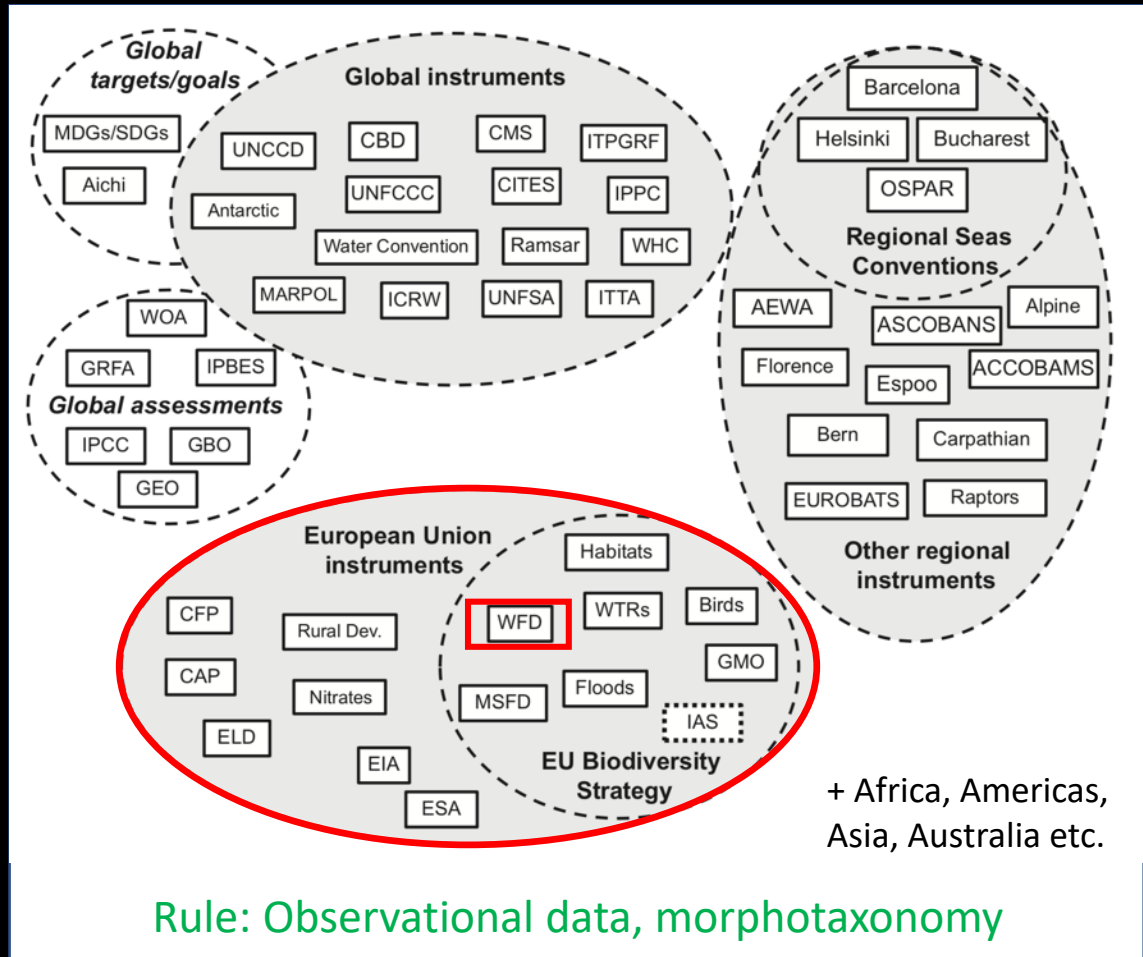
The Scene I: Pressing issues

- Biodiversity loss world-wide
- Freshwater biodiversity crisis most pronounced (WWF LPI)
- Loss of functions/services?



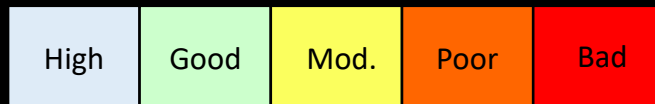
The Scene II: Environmental policies

'EU-biased view'



Example: EU Water Framework Directive

- Very advanced piece of environmental legislation (Directive 2000/60/EC) – inspired by CWA and more
- Aim: 2027 surface waters good status
- **Ecological** status as primary determinant of management needs
- >100,000 water bodies monitored - **long-term data**
- Decades of **intercalibration** (~340 formal EC decisions)
- **Published CEN/ISO standards** for sampling / analysis



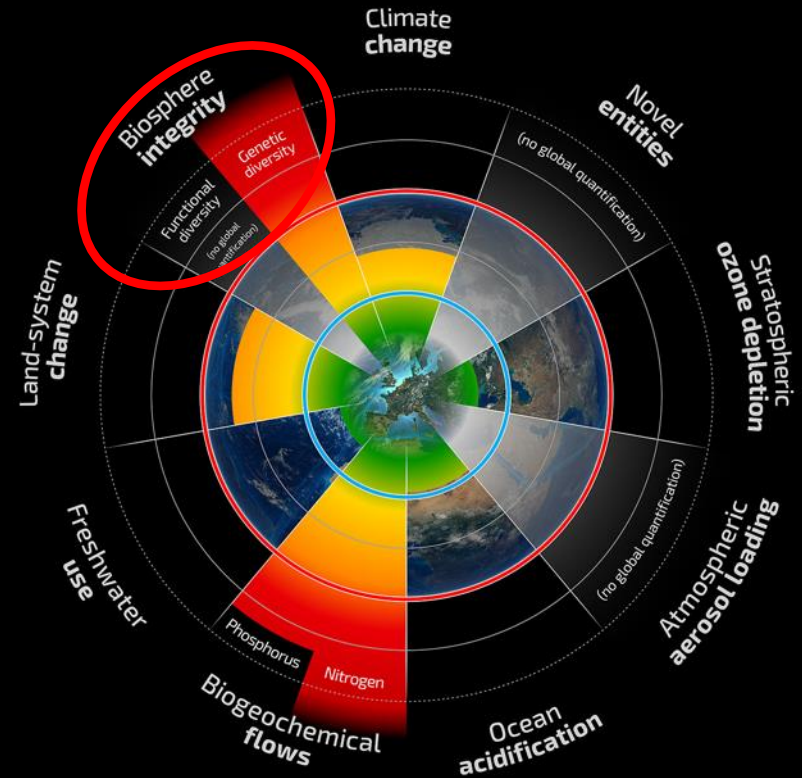
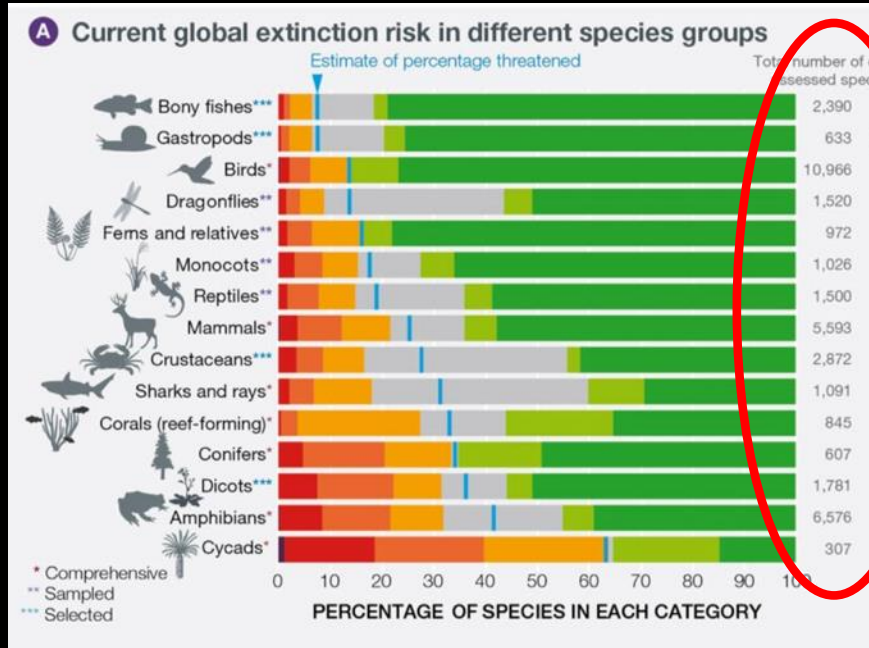
expensive

2000	Directive entered into force	Art. 2
2003	Transposition into national legislation Identification of River Basin Districts and Authorities	Art. 23 Art. 3
2004	Characterization of river basin: pressures, impacts and economic analysis	Art. 5
2006	Establishment of monitoring network Start public consultation (at the latest)	Art. 8 Art. 14
2008	Present draft river basin management plan	Art. 13
2009	Finalize river basin management plan including programme of measures	Art. 13, 11
2010	Introduce pricing policies	Art. 9
2012	Make operational programmes of measures	Art. 11
2015	Meet environmental objectives First management cycle ends Second river basin management plan & first flood risk management plan	Art. 4
2021	Second management cycle ends	Art. 4, 13
2027	Third management cycle ends Final deadline for meeting objectives	Art. 4, 13

Continuous monitoring
No deterioration

after <http://ec.europa.eu>

But we're only scratching the surface with our current approaches





- We need fast, reliable data about biodiversity change
- Greater resolution in space and time
- FAIR – findable, accessible, interoperable, reusable

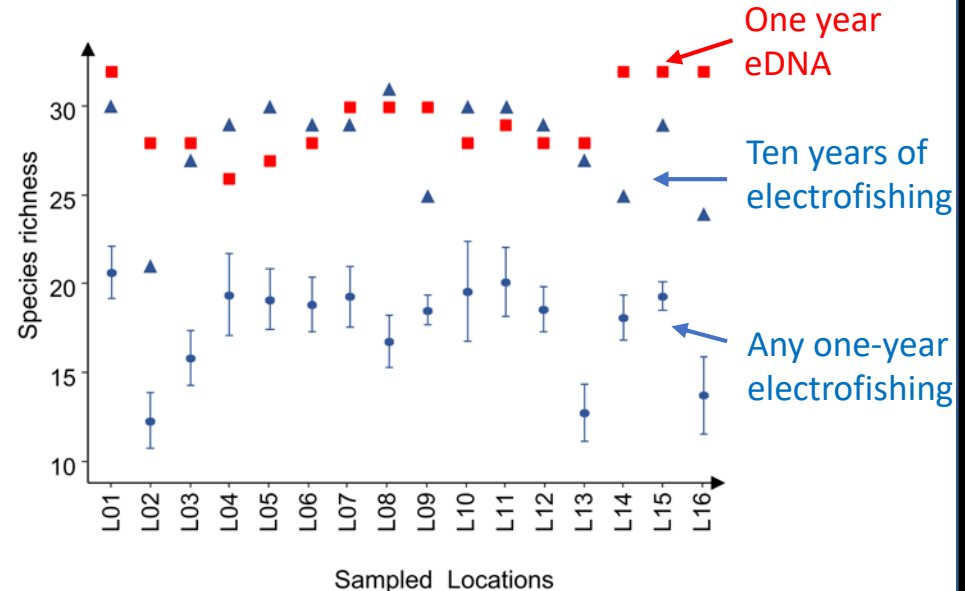
Genetic tools – right now especially eDNA metabarcoding – can

- provide a much more holistic picture of biodiversity
- microbial to macrobial life
- can identify new indicator species for stressors
- detects invasive / protected species reliably
- can identify intraspecific diversity changes
- works even with non-invasive samples (water, sediment...)
- depends less on human expertise
- DNA can be stored for later validation for decades

- eDNA analysis in a French stream (Rhône) shows great performance of eDNA for fish biodiversity assessments
- **Many such studies reported from many different countries!**

Environmental DNA reveals quantitative patterns of fish biodiversity in large rivers despite its downstream transportation

Didier Pont^{1,2,3}, Mathieu Rocle⁴, Alice Valentini^{1,2}, Raphaël Civade², Pauline Jean¹, Anthony Maire⁵, Nicolas Roset⁶, Michael Schabuss⁷, Horst Zornig⁷ & Tony Dejean^{1,2}



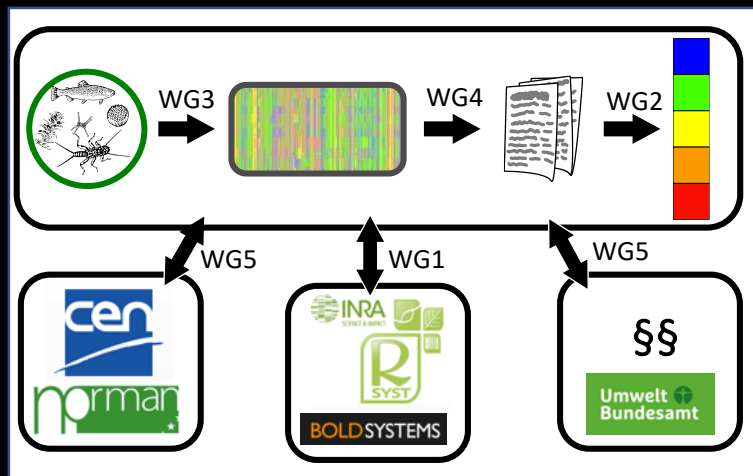


Advance the application of DNA-based tools for biodiversity assessments & develop a roadmap to include these in standardized bioassessments of aquatic ecosystems in Europe and beyond!

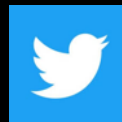


EU COST Action DNAqua-Net (2016 – 2020+)

DNAqua-Net's mission

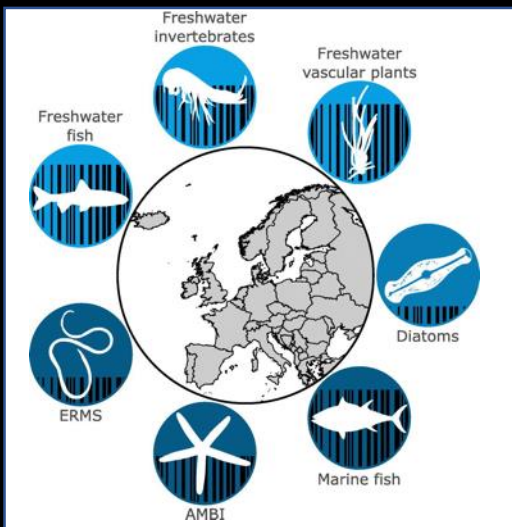


- ~600 members
- 49 countries (incl. US, Canada, China)
- >60 publications and stakeholder reports
- connects labs, countries, disciplines
- >55 exchanges, ~40 meetings / round tables
- funding until end of 2020 (options to extend)







@dnaquanet





- For fish and macroinvertebrates the European Operational Taxalists are often well-covered (JDS4: 90%, 81%)
- Priorities defined to close gaps
- Bratislava in February 2020 to continue to toward this goal (you're welcome)








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 Rulík ^g, Malin Strand ^j, Nikolaus Szucsich ^k, Alexander M. Weigand ^{a,b}, Endre Willassen ^l, Sofia A. Wyler ^m, Agnès Bouchez ^l, Angel Borja ⁿ, Zuzana Čiamporová-Zat'ovičová ^c, Sónia Ferreira ^a, Klaas-Douwe B. Dijkstra ^p, Ursula Eisdndle ^q, Jörg Freyhof ^r, Piotr Gadawski ^h, Wolfram Graf ^s, Arne Haegerbaeumer ^t, Berry B. van der Hoorn ^p, Bella Japoshvili ^u, Lujza Keresztes ^v, Emre Keskin ^w, Florian Leese ^b, Jan N. Macher ^p, Tomasz Mamos ^h, Guy Paz ^x, Vladimír Pešić ^y, Daniela Maric Pfannkuchen ^z, Martin Andreas Pfannkuchen ^z, Benjamin W. Price ^{aa}, Buki Rinkevich ^x, Marcos A.L. Teixeira ^{d,e}, Gábor Váró ^{ab}, Torbjørn Ekrem ^{ac,*}

Review

Implementation options for DNA-based identification into ecological status assessment under the European Water Framework Directive



Daniel Hering^{a,*}, Angel Borja^b, J.Iwan Jones^c, Didier Pont^d, Agnes Bouchez^e, Kat Bruce^g, Stina Drakare^h, Bernd Hänfliⁱ, Florian Leese^j, Kristian Meissner^k, Patricia Mergen^{l,m}, Yori Alfred Vogler^p, Martyn Kelly^q

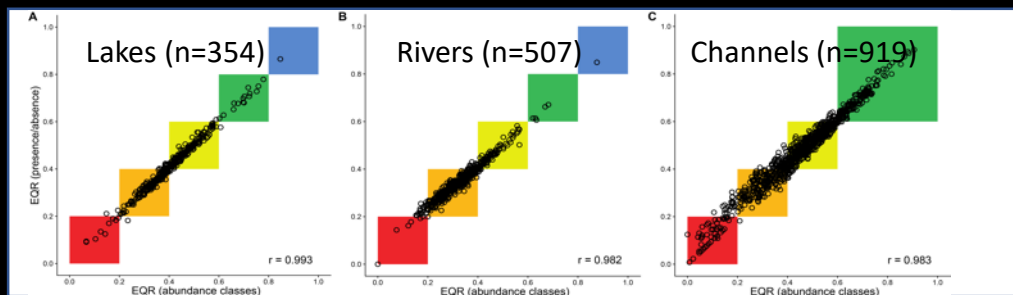


- Some low(er) hanging fruits!
- Key is intercalibration with the old methods
- Machine-learning helps a lot today!

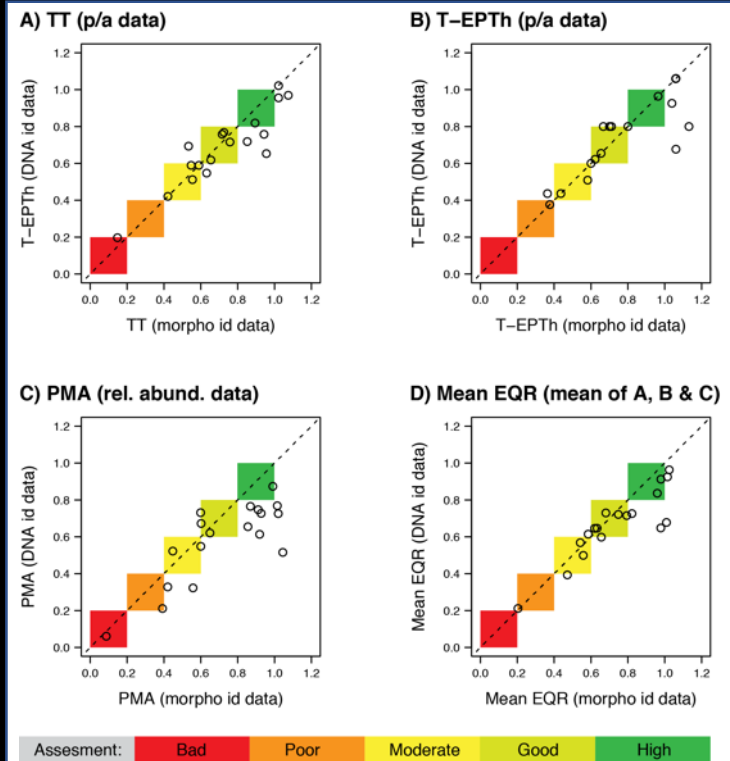
		1.1 sampling	1.2 errors	1.3 abundance	2.1 sensitive taxa	2.2 unassigned reads	3.1 uncertainty	4.1 EQR sensitivity	4.2 intercalibration	5.1 cost ratio	5.2 speed	6.1 animal well-being
phytoplankton	lakes, rivers	●	●	●	●	●	●	●	●	●	●	N/A
phytoplankton	TraC	●	●	●	●	●	●	●	●	●	●	N/A
phytobenthos	rivers	●	●	●	●	●	●	●	●	●	●	N/A
phytobenthos	lakes	●	●	●	●	●	●	●	●	●	●	N/A
macrophytes	rivers	●	●	●	?	●	●	●	●	●	●	N/A
macrophytes	lakes	●	●	●	?	●	●	●	●	●	●	N/A
macroalgae	TraC	●	●	●	?	●	●	●	●	●	●	N/A
angiosperms	TraC	●	●	●	?	●	●	●	●	●	●	N/A
invertebrates	rivers	●	●	●	●	●	●	●	●	●	●	●
invertebrates	lakes	●	●	●	●	●	●	●	●	●	●	●
invertebrates	TraC	●	●	●	●	●	●	●	●	●	●	●
fish	rivers	●	●	●	●	●	●	●	●	●	●	●
fish	lakes	●	●	●	●	●	●	●	●	●	●	●
fish	TraC	●	●	●	●	●	●	●	●	●	●	●

Fig. 1. Rating of the criteria for different BQEs and water categories. Large circles = high suitability of DNA-based identification; mid-sized circles = medium suitability; small circles = low suitability; N/A = not applicable. TraC: Transitional and Coastal waters.

Classical indices can be compatible with metabarcoding data



Beentjes et al. (2018) MBMG

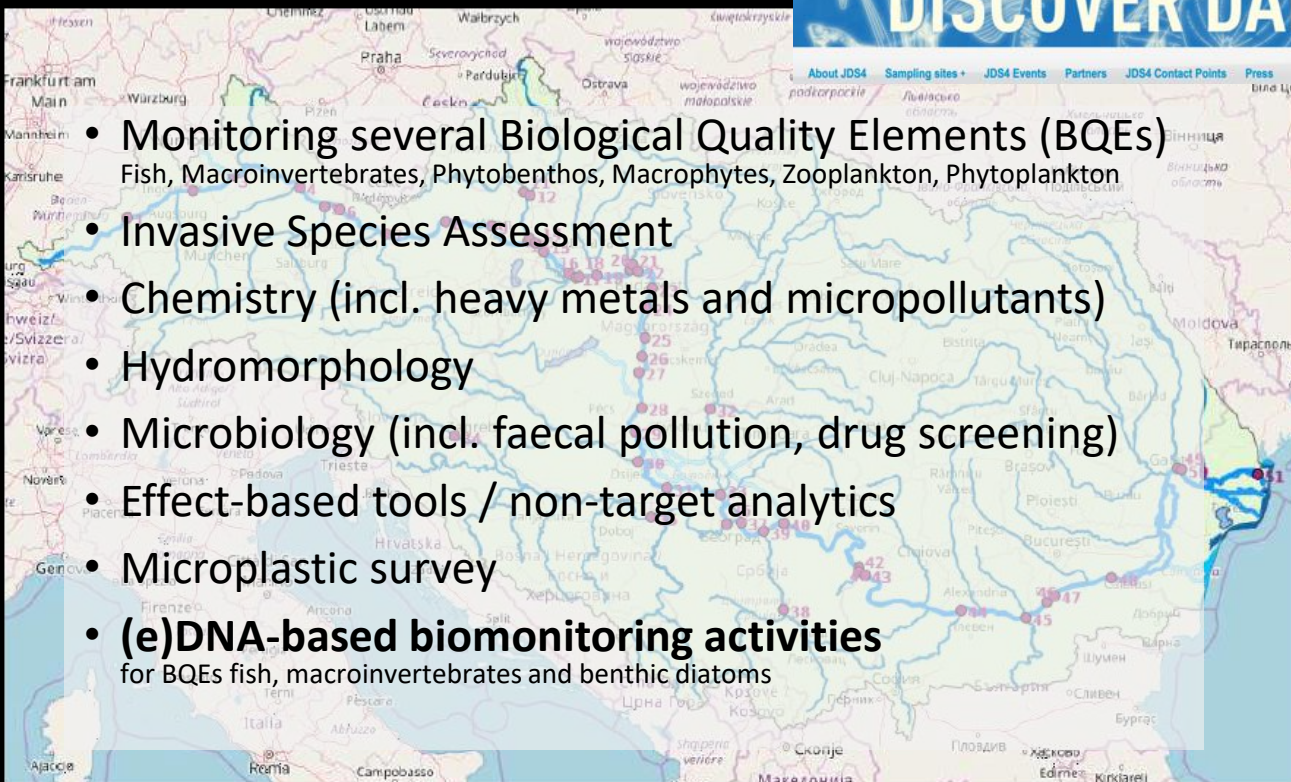


Elbrecht et al. (2017)

Boots on the ground & test



- Monitoring several Biological Quality Elements (BQEs)
Fish, Macroinvertebrates, Phytobenthos, Macrophytes, Zooplankton, Phytoplankton
- Invasive Species Assessment
- Chemistry (incl. heavy metals and micropollutants)
- Hydromorphology
- Microbiology (incl. faecal pollution, drug screening)
- Effect-based tools / non-target analytics
- Microplastic survey
- **(e)DNA-based biomonitoring activities**
for BQEs fish, macroinvertebrates and benthic diatoms



The future of biotic indices in the ecogenomic era

- Running in established legal frameworks – two step approach
- Use existing indicators; align genetic data
- Test, compare, calibrate, if not possible:
- **Develop new indices**



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Review

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



Jan Pawlowski ^{a,*}, Mary Kelly-Quinn ^b, Florian Altermatt ^c, Laure Apothéloz-Perret-Gentil ^a, Pedro Beja ^d, Angela Boggero ^e, Angel Borja ^f, Agnès Bouchez ^g, Tristan Cordier ^a, Isabelle Domaizon ^g, Maria Joao Feio ^h, Ana Filipa Filipe ^d, Riccardo Fornaroli ⁱ, Wolfram Graf ^j, Jelger Herder ^k, Berry van der Hooft ^l, J. Iwan Jones ^m, Marketa Sagova-Mareckova ⁿ, Christian Moritz ^o, Jose Barquin ^p, Jeremy J. Piggott ^q, Maurizio Pinna ^r, Frederic Rimet ^g, Buki Rinkevich ^s, Carla Sousa-Santos ^t, Valeria Specchia ^r, Rosa Trobajo ^u, Valentin Vasselon ^g, Simon Vitecek ^v, Jonas Zimmerman ^w, Alexander Weigand ^{x,y}, Florian Leese ^x, Maria Kahlert ^z

A new, permanent European Standards group

- Think standardisation issues
- Standardisation must not strip scientific innovation
- General ,contours', QA/QC, ring-tests, accreditation, blind-tests
- **eDNA: Water, Sediment [in progr.]**



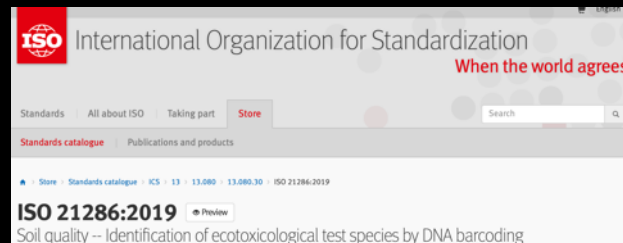
CEN/TC 230/WG28: DNA & eDNA methods Chairmen: Kristian Meissner (SYKE, FIN)

DECISION 646 (Brussels 17/2018) taken by CEN/TC 230 on 2018-06-08

Subject: CEN/TC 230 – DNA and eDNA methods

Dr. Kat Bruce will submit a draft for a NWIP on eDNA water sampling by November 2018. The NWIP will be submitted to CEN/TC 230 for the registration in the work program. Following a positive outcome, the working group on DNA and eDNA will be officially installed. SFS, AFNOR and NEN are investigating the provision of the secretariat for this new WG.

Activities at the ISO level as well (not water)



allgenetics

!! Open process – comments possible !!



Today
(and
beyond)



!Community!
more data, access,
better assessment

OCCURRENCE DATASET | REGISTERED JULY 12, 2018
BIOWIDE eDNA Fungi datasetPublished by [Danish Biodiversity Information Facility](#)

Tobias Frøslev • Rasmus Ejrnæs

DATASET PROJECT METRICS ACTIVITY DOWNLOAD HOME PAGE

30,091 OCCURRENCES 3 CITATIONS

The Biowide project (2014-2018) was a project aiming at collecting biodiversity data from 130 terrestrial sampling sites across Denmark. Data was collected with both classical means (observation and trapping) and by eDNA metabarcoding (sequencing of amplified marker genes). Data was also collected on environmental variables. Biowide (Biodiversity in Width and Depth) took place in collaboration between Århus University (main project holder) and the two major Danish natural history museums and the... [More](#)

Metadata last modified: July 12, 2018

Data last changed: December 12, 2018

Hosted by: [Danish Biodiversity Information Facility](#)

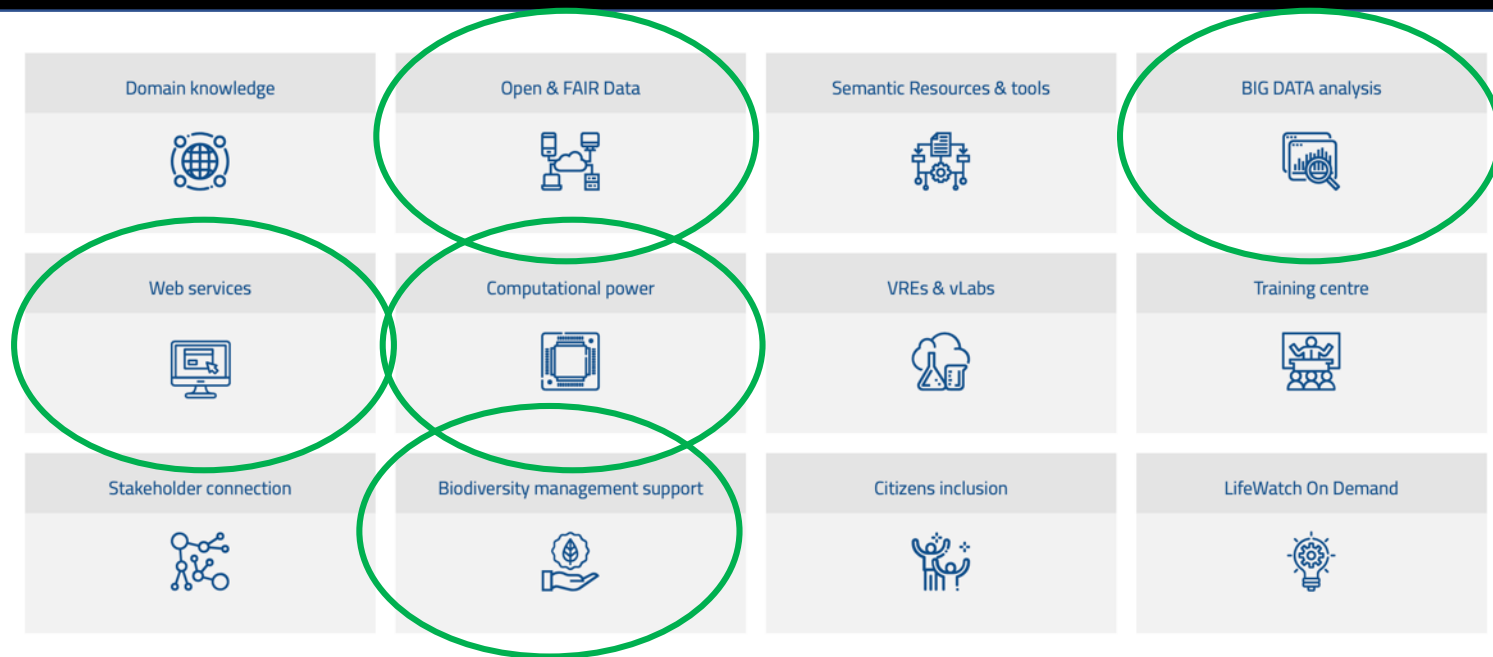
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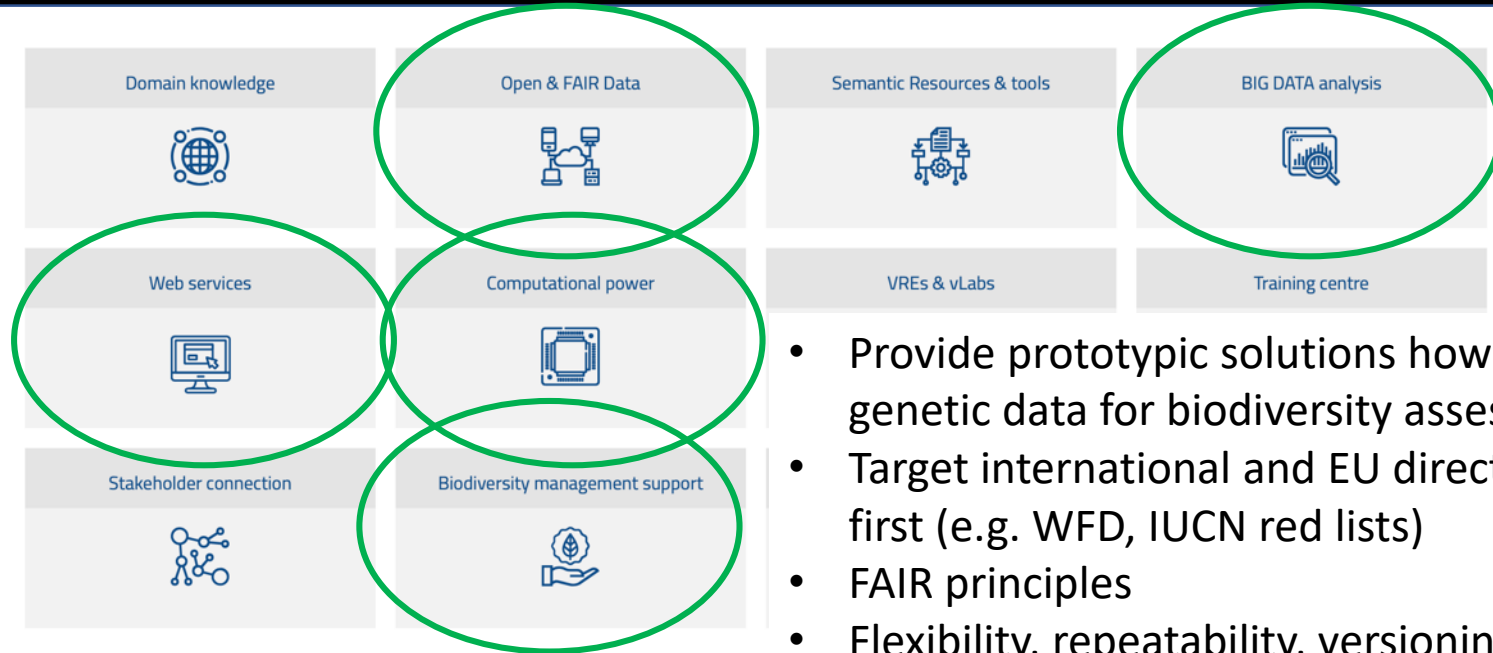
[How to cite](#) [DOI](#) 10.15468/nestbx 30,091
Occurrences 100%
With taxon match 100%
With coordinates 100%
With year

30,091 GEOREFERENCED RECORDS



- Go beyond GBIF (that already now allows eDNA records)
- Allow for the process chain from raw sequence submission (crawling) to biodiversity statistics and regulatory reporting standards (e.g. Ecological Quality Status Assessment as part of WFD – 2000/60/EC)





- Provide prototypic solutions how to use genetic data for biodiversity assessments
- Target international and EU directives first (e.g. WFD, IUCN red lists)
- FAIR principles
- Flexibility, repeatability, versioning



DNAqua-Net experts on site:

- Alexander Eiler (University of Oslo, Norway; eDNA solutions, Sweden)
- Sergei Põlme (University of Tartu, Estonia)
- Niklas Noll (Zoological Research Museum Alexander Koenig, Germany)
- Florian Mauffrey (University of Geneva, ID-Gene, Switzerland)



Further important notes:

- Check <https://dnaqua.net> for further information
- Welcome to Evian 15-18th 2020 (France) big bioassessment conference hosted by DNAqua-Net
- We have funds for short-term exchange (apply for an ,STSM')
- We host several workshops / round-tables / training schools – March 10th for ECOSTAT in Paris, EPA Dublin March 18th etc.

