Monitoring UK lake fish communities using eDNA

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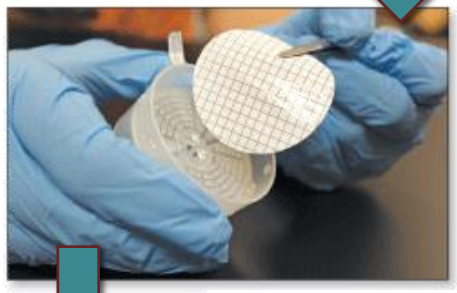
Environmental DNA (eDNA):

Cells, free-floating DNA (from sloughed skin cells faeces/urine, gametes, decaying matter)

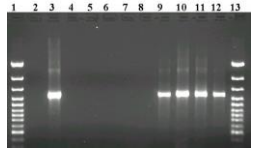
Water sampled & filtered (0.5-2L samples)



Extract DNA

Targeted detection:

- Species-specific primers
- Standard or qPCR



Whole community:

- eDNA metabarcoding
- Conserved primers
- Next generation sequencing

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Environment Agency

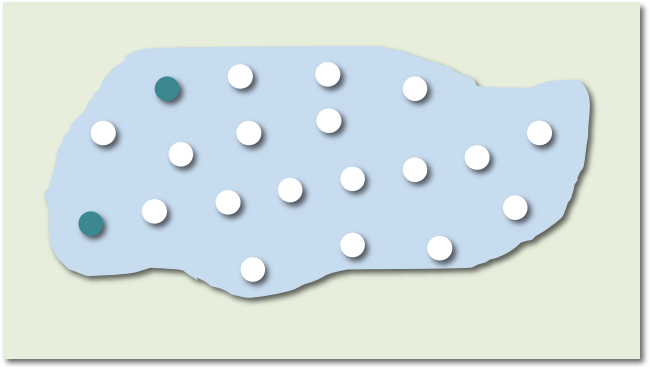
SEPA
Scottish Environment Protection Agency

Lake fish monitoring with eDNA metabarcoding

Hänfling et al. (2016) *Molecular Ecology*, **25**, 3101-3119

Li et al. (2019) *Journal of Applied Ecology,* **56**, 1232-1244

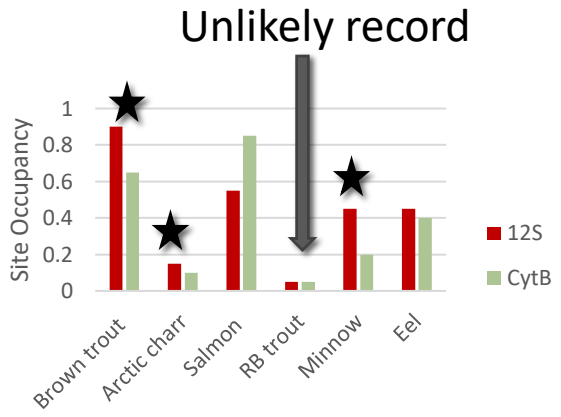
Lawson-Handley et al (2019), *Environmental DNA* **1**, 24-36



eDNA metabarcoding has low false negative rates

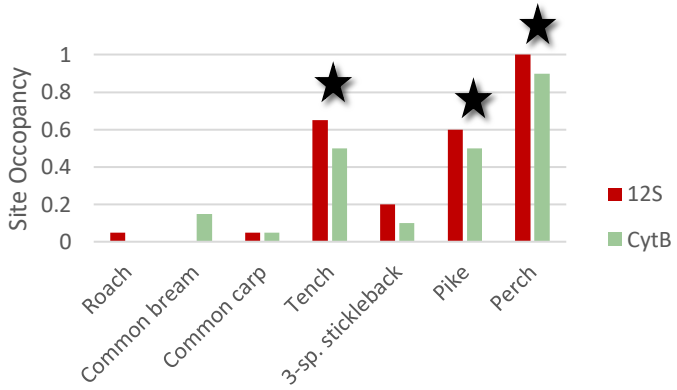
Highland lakes
e.g. Scottish Lochs,

Low alkalinity
oligotrophic
Deep



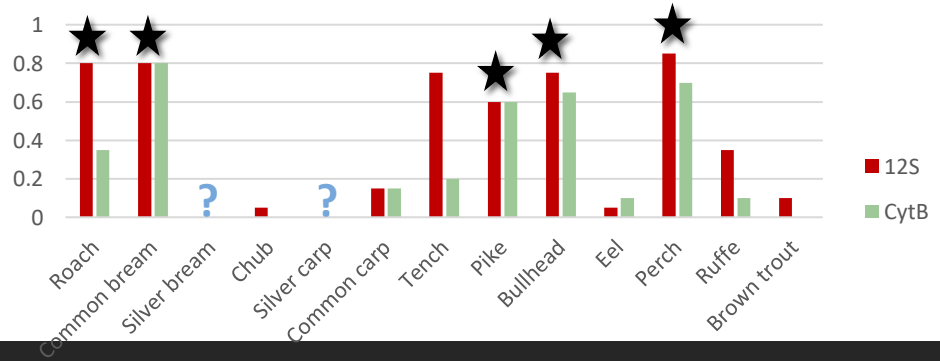
Lowland lakes
e.g. Cheshire Meres

Medium alkalinity
mesotrophic
shallow



Lowland lakes
e.g Thames Flood Plain

Low alkalinity
Very shallow
eutrophic



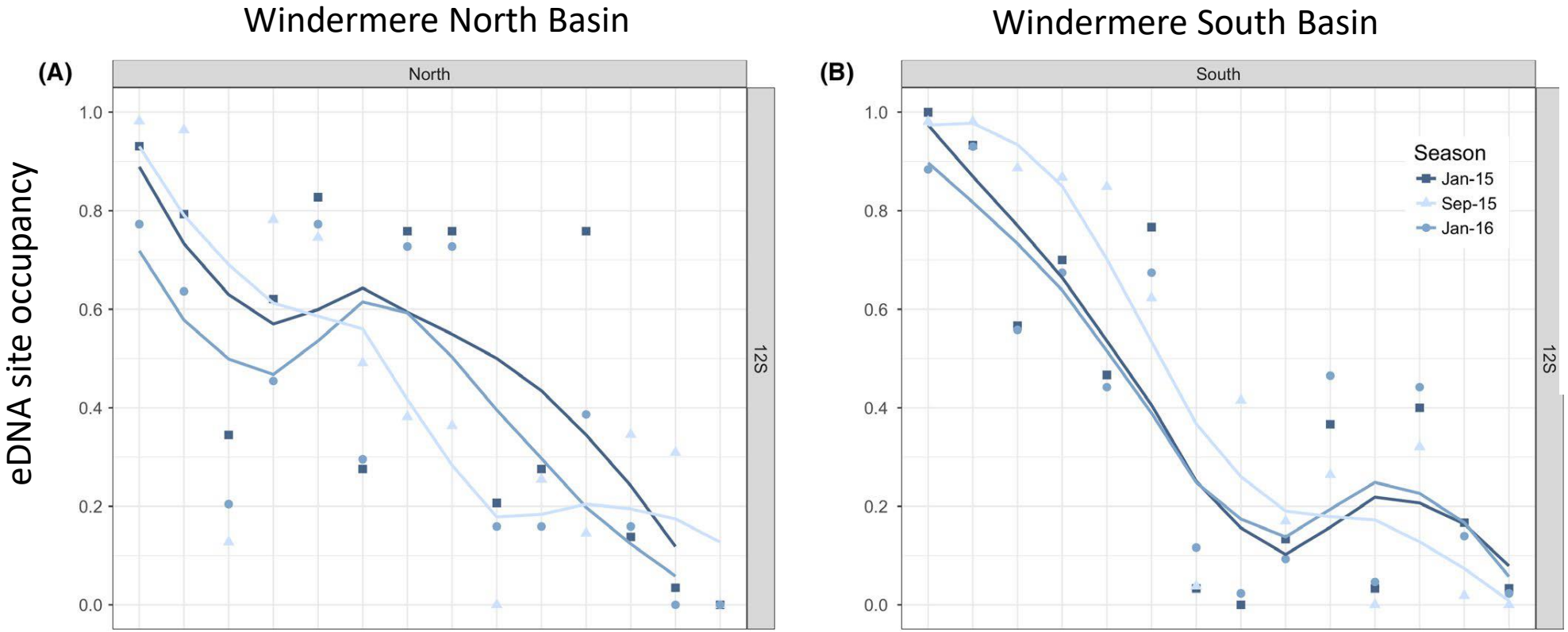
? = species detected at > 2 sites but at low abundance (below threshold) ★ = species detected in netting surveys

Implausible detections, “false positives”

- Contamination during sampling
- Contamination in the lab
- Tag-jumping during sequencing
- Bioinformatics/reference data base
- DNA contamination of the environment

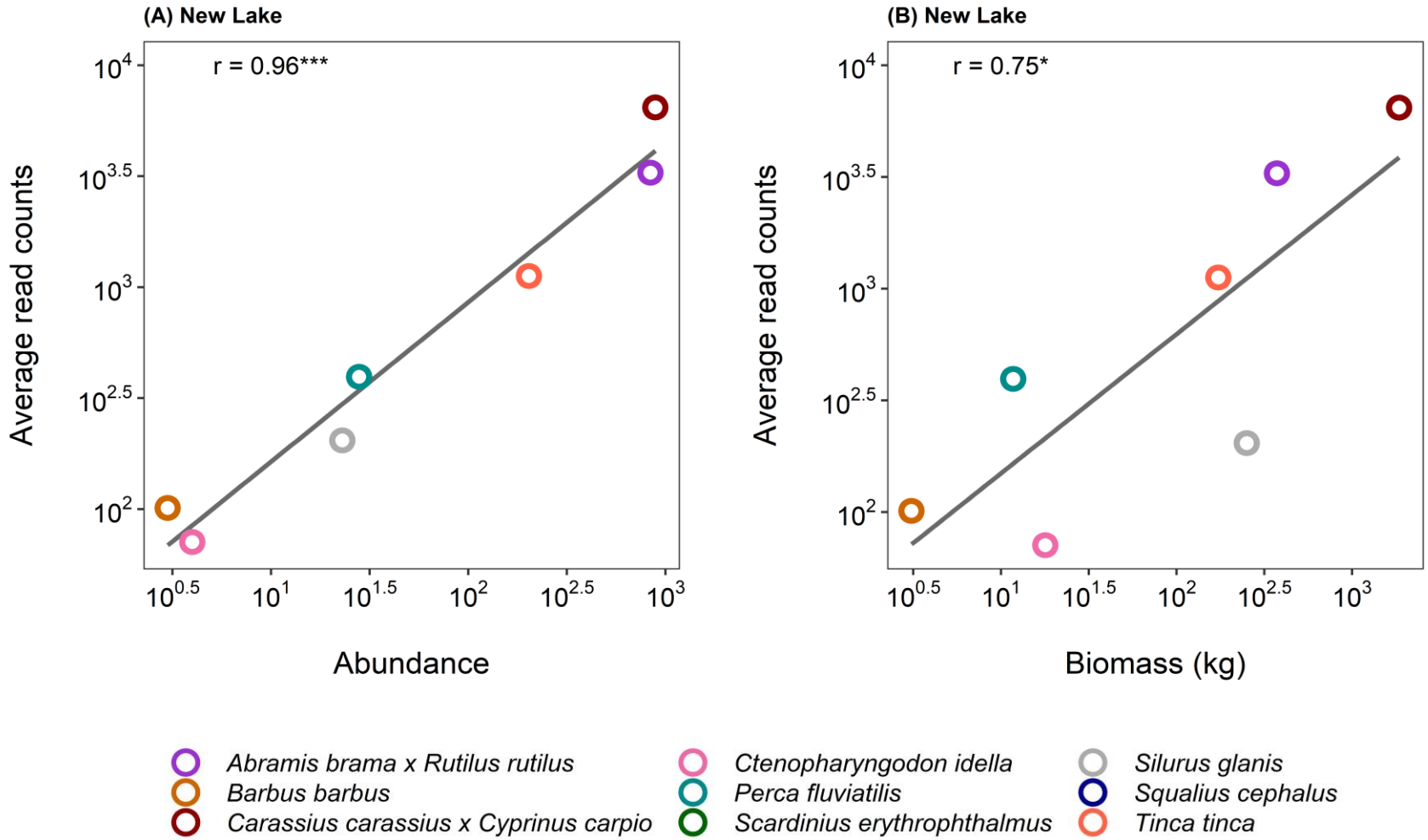
< 2% of all records in our data set

eDNA abundance reflects relative fish abundance (e.g. Windermere)



Species abundance rank based on long-term data

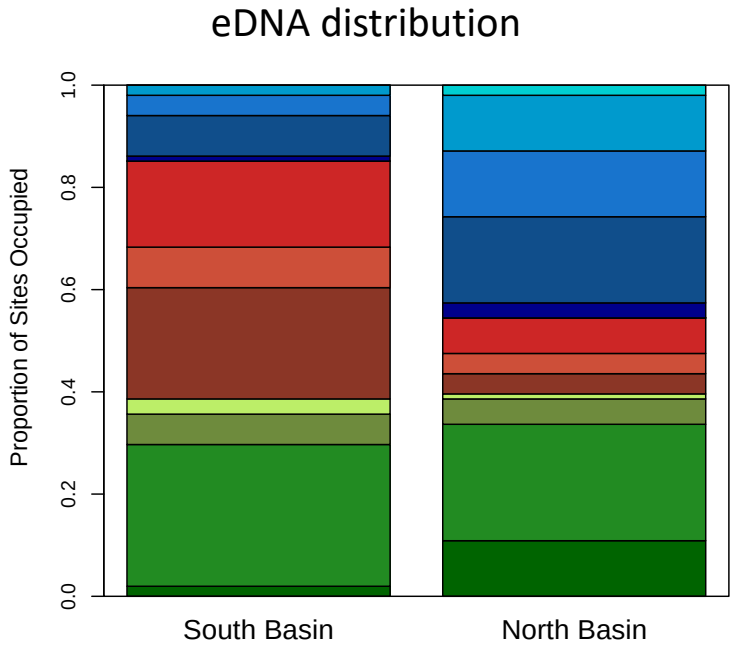
eDNA site abundance reflects relative fish abundance (drained fishing lake)



eDNA distribution reflects lake ecology

Oligotrophic-mesotrophic

Eutrophic-mesotrophic



Oligotrophic association
- S. salar
- P. phoxinus
- C. gobio
- S. trutta
- S. alpinus

Eutrophic association
- T. tinca
- S. erythrophthalmus
- R. rutilus
- A. anguilla
- A. brama

No association
- B. barbatula
- E. lucius
- P. fluviatilis
- G. aculeatus

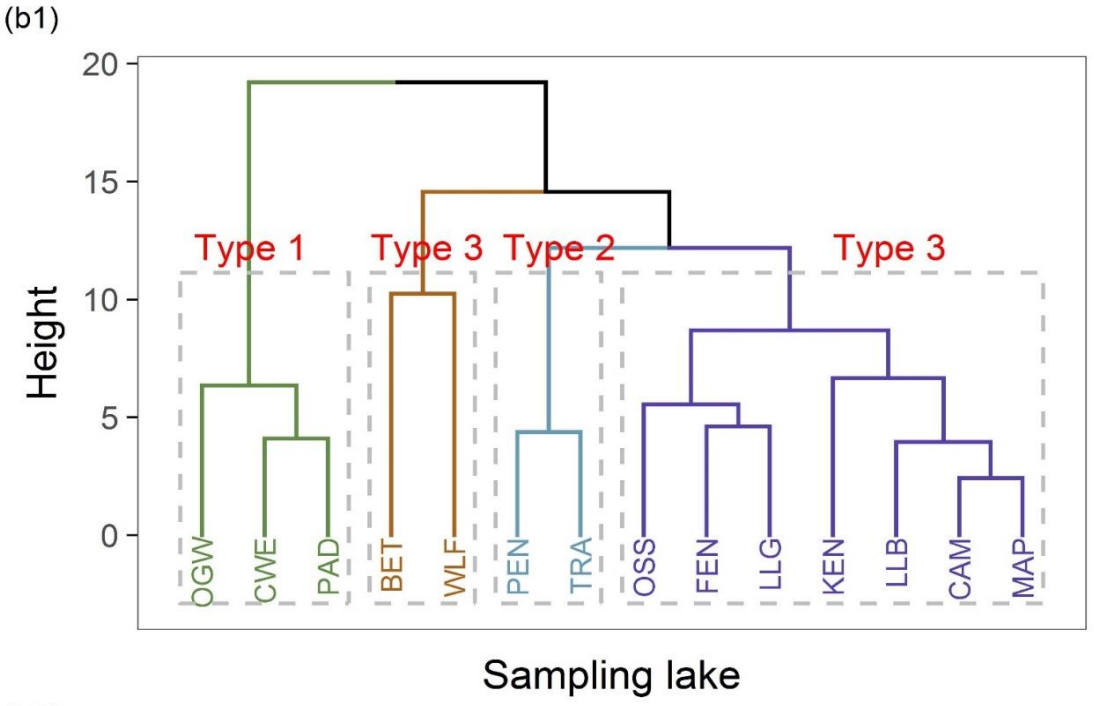
North basin contains a higher proportion of oligotrophic species

eDNA provides an accurate description of expected lake fish communities

eDNA metabarcoding of 14 Lakes in Wales and NW England

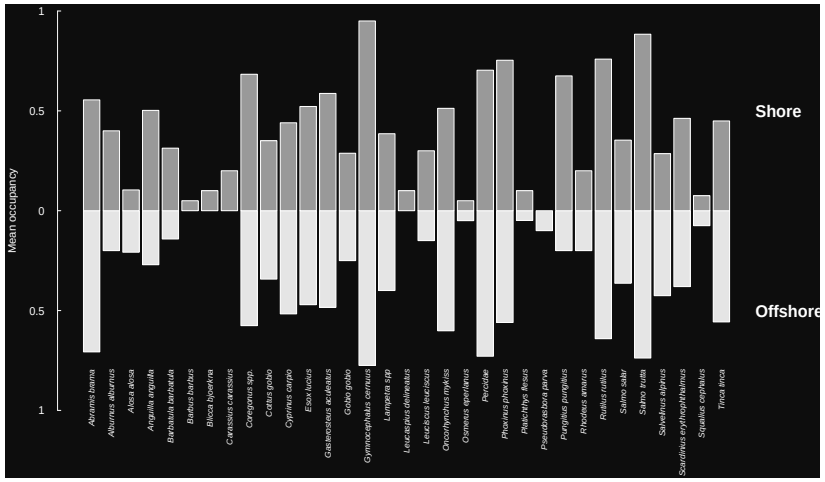
Pre-classified in 3 types

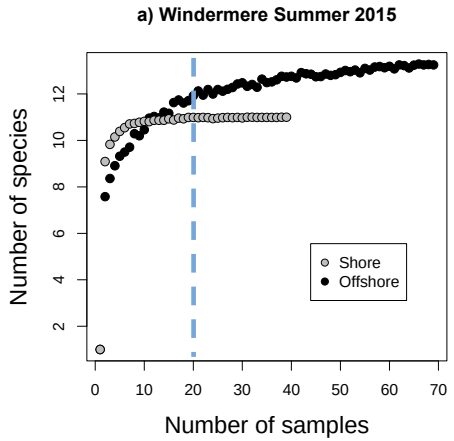
Type 1: Low alkaline deep upland lakes
Type 2: High alkaline shallow coastal lakes
Type 3: High alkaline very shallow inland lakes

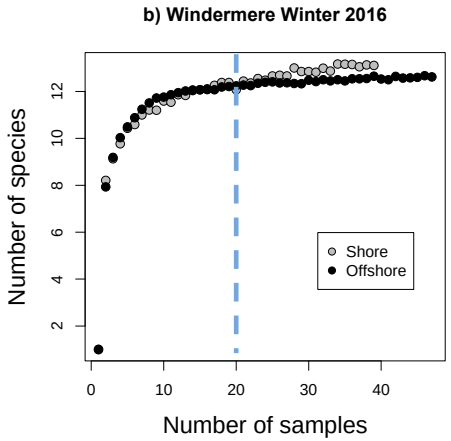


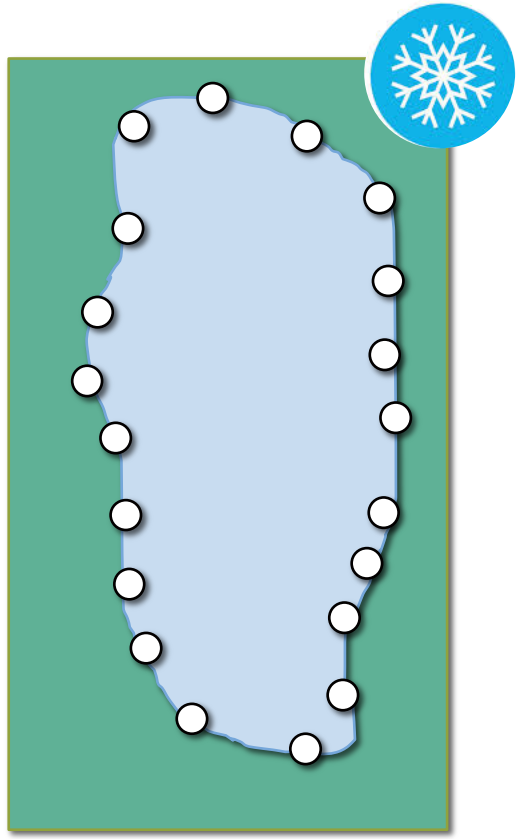
Recommended sampling strategy for UK lakes
(aim = biodiversity monitoring)

- Samples collected from the shore
- Winter sampling (November – February)
- 20 samples per lake (2 litres each)

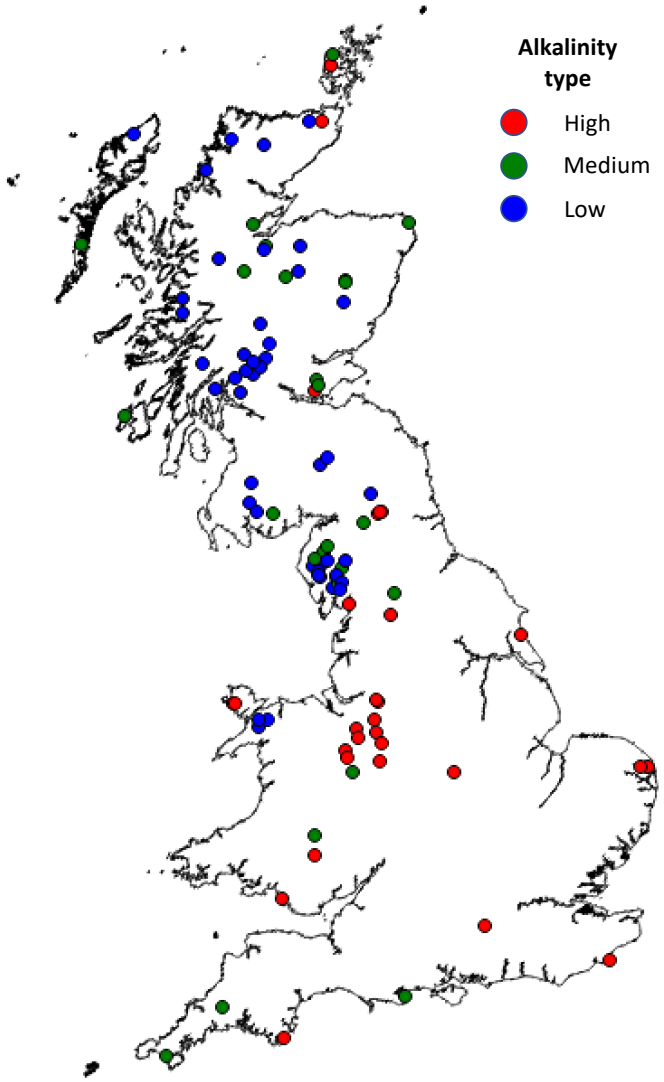








Building a data set of representative UK lakes

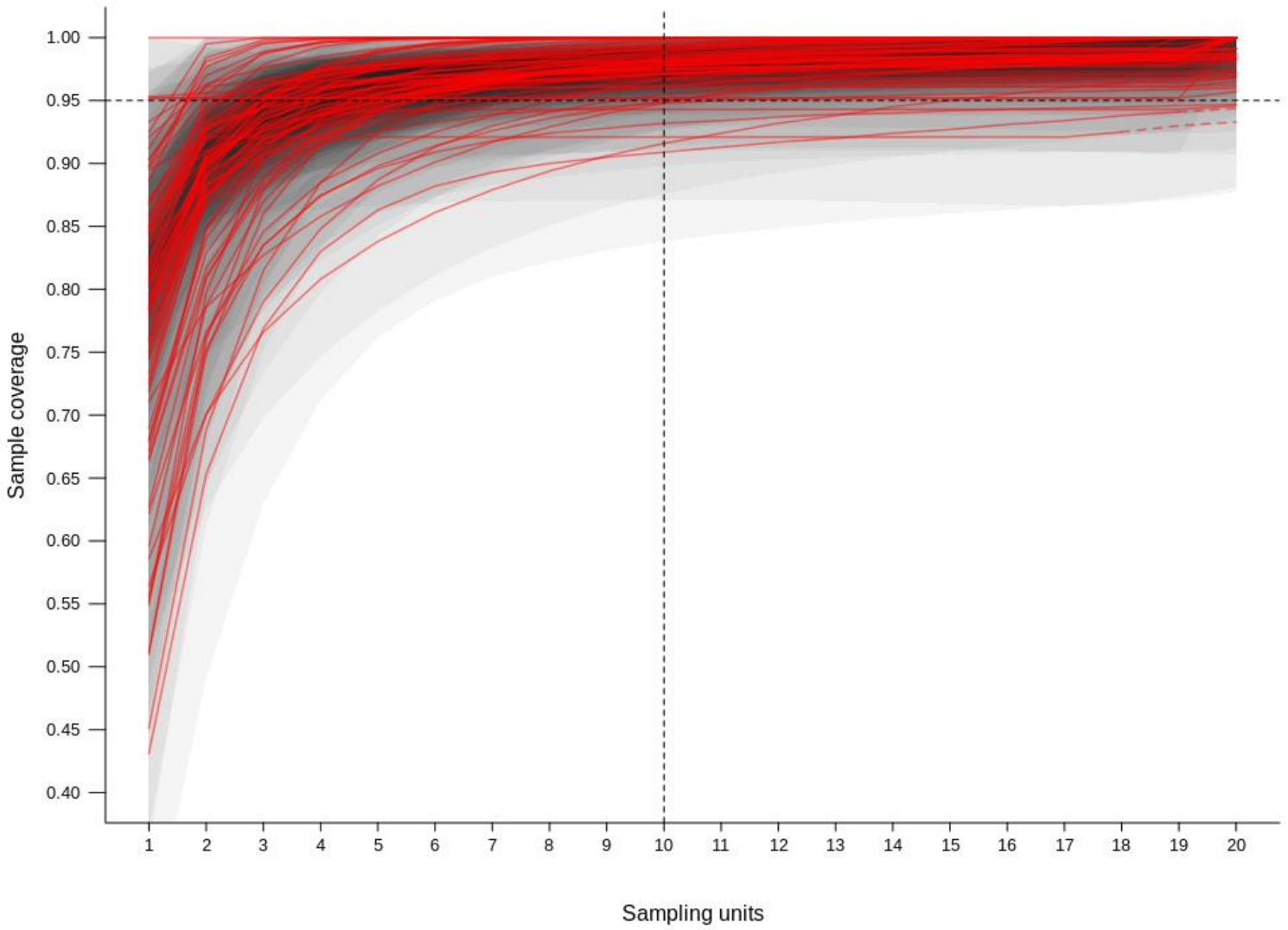


101 water bodies

- Wide geographical spread and coverage of lake types and status
- 28 lakes of “reference conditions”
- 40 fish taxa detected of which 16 restricted to <5% of sites
- Median richness 7 taxa per site (2-18).

Morpho-edaphic index:
Integrated measure of natural productivity
High = high alkalinity, shallow
Low = Low alkalinity, deep

Sample coverage, based on Chao & Jost (2013)



How many samples are needed to reach 95% sample coverage (sampling threshold)?

- Range: 1-25
- Mean = 5.7 (SD 4.7)

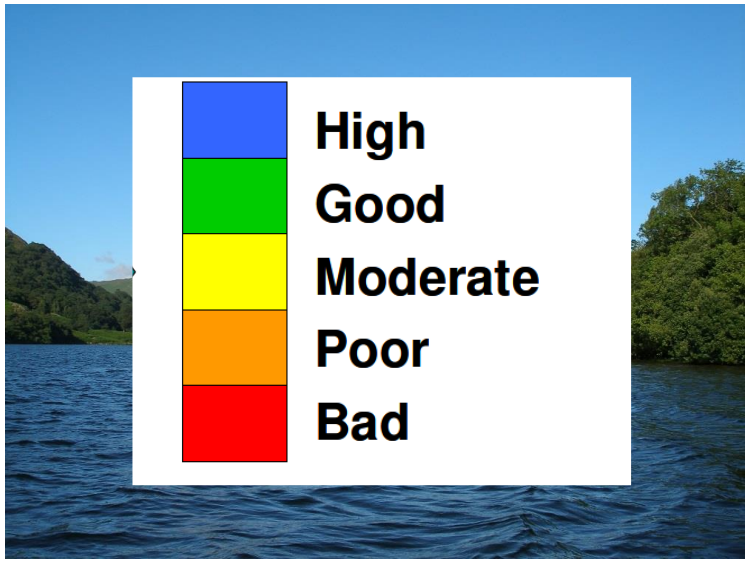
- 10 samples: 89% of 101 lakes
- 20 samples: 96% of 101 lakes

Sampling threshold *vs* **species richness**:
$r_s = 0.42$, $p < 0.05$

Sampling threshold *vs* **mean occupancy**:
$r_s = -0.83$, $p < 0.05$

Sampling threshold *vs* **lake size**:
$r_s = -0.09$, $p > 0.3$

Can we detect anthropogenic pressure using species relative abundance alone where there are few species?

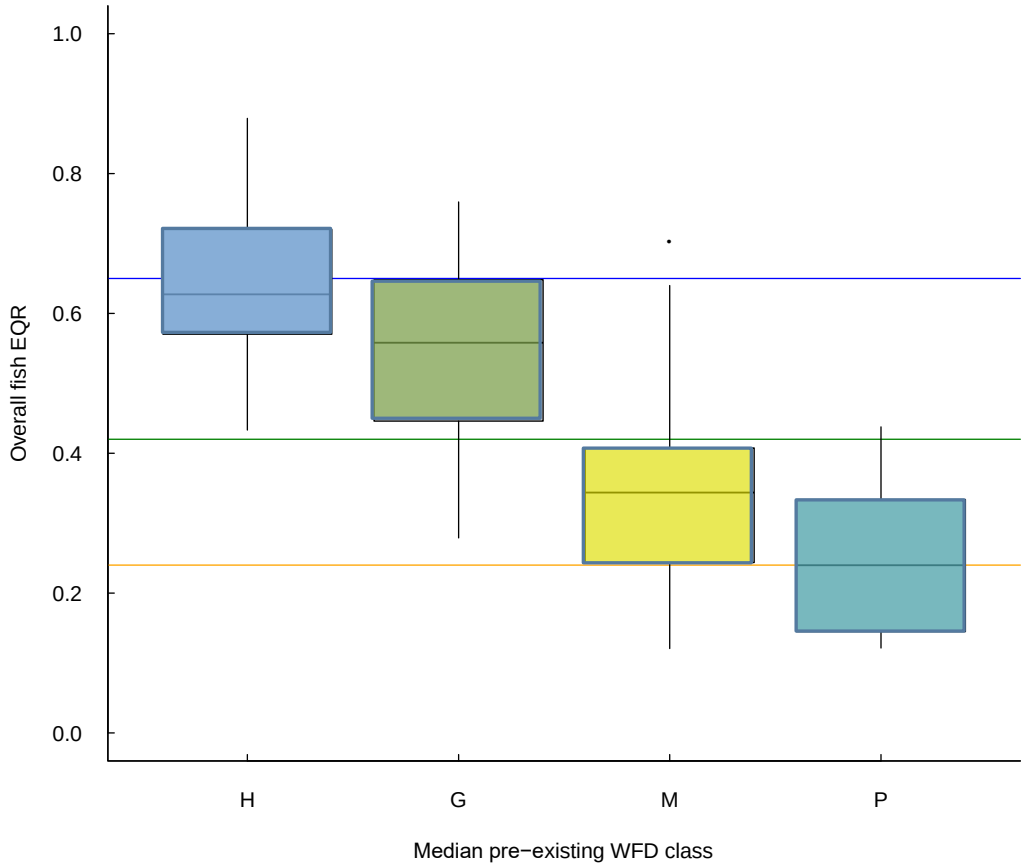


Analysis by Nigel Willby, Alan Law, Colin Bull, University of Stirling

Fish metrics considered for WFD tool

- Composition using **taxonomic data** – occupancy or read shares for 24 taxa found in >5% of sites
- Composition using **functional groupings/guilds** e.g. piscivores v insectivores, pelagic v littoral, phytophilous vs lithophilous. Limited utility
- **Taxon richness** per site
- Richness or read shares of **non-native taxa**
- Community index based on ranked position of each species on **eutrophication pressure axis** (ASPT for fish)

Deriving class boundaries on fish EQR scale



Class boundaries of fish tool positioned to maximise class agreement and minimize classification bias, based on 'typical' pre-existing WFD class (WoE, not 1oAo) for eutrophication sensitive BQEs

		fish class				
		H	G	M	P/B	sum
WFD median class	H	18	19	0	0	37
	G	7	18	7	0	32
	M	1	4	14	6	25
	P/B	0	1	2	4	7
	sum	26	42	23	10	101

54% same class, 99% +/- 1 class

Bias: -0.15 classes

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