

TGCATTTAGCT
TATCC AATATTCAGGATAAAC

UNIVERSITÄT
**DUISBURG
ESSEN**

CACCCTTACT
AAGAT
TCGGATTCTTAT
TATAGCCC
GGATA

C
GTCGGT

TCC
AACCCCCCA
CATTCTTT

TCT
TTACCC

TAA

ACAGATT
GGTAGC
TCA

GAGAGTGCAG
AGGGTTGATTGG
TGGTA GTGTTAGC
CAAAGAGCTCAAATT



The future of stream monitoring: DNA Metabarcoding!

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**AQUATIC
ECOSYSTEM
RESEARCH**



GeneStream

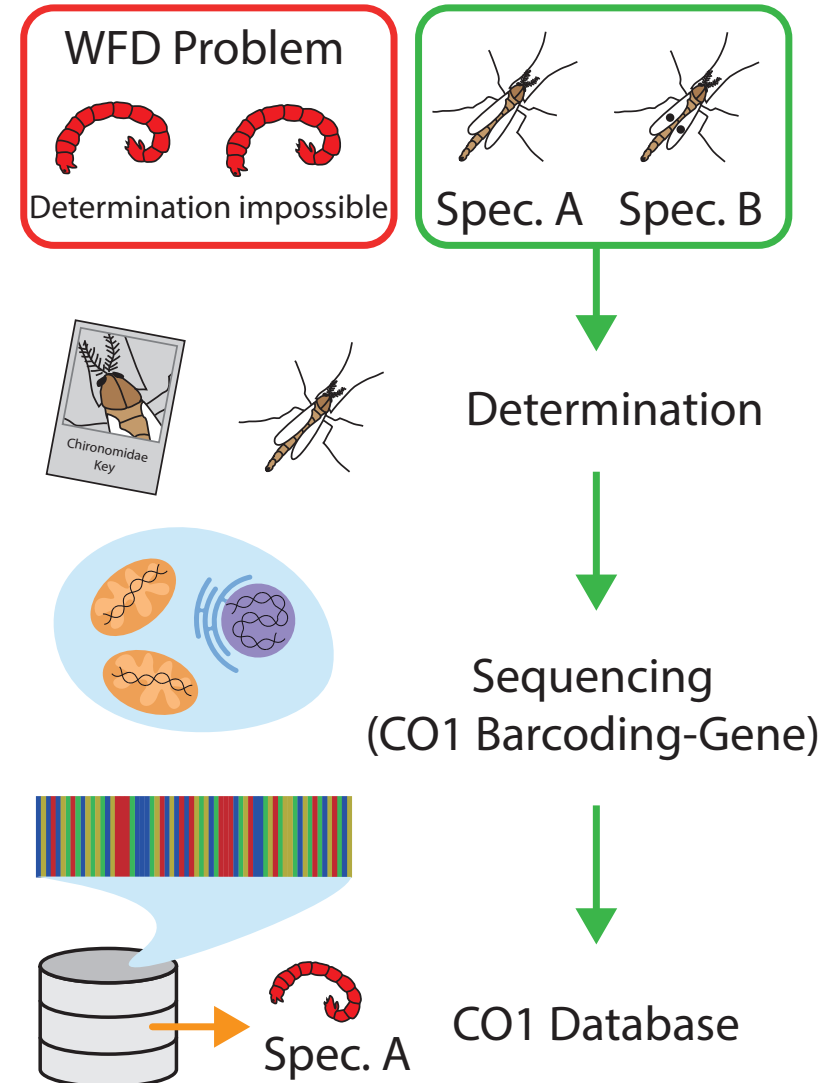
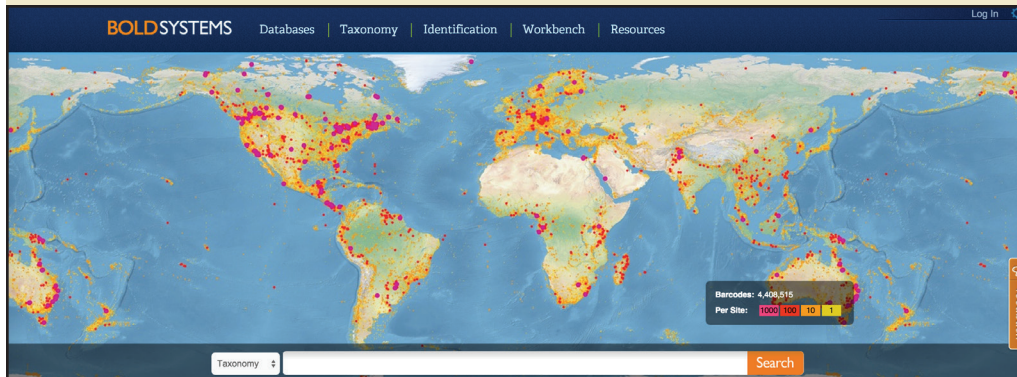
- Water assessment is based on the morphological identification of macroinvertebrates

	Morphology
Missidentification	occurs!
Taxonomic resolution	— — / + <small>taxon dependent</small>
Data comparability	— —
Speed	—
Abundance	+
Cost	+

- Misidentification -> problem for management



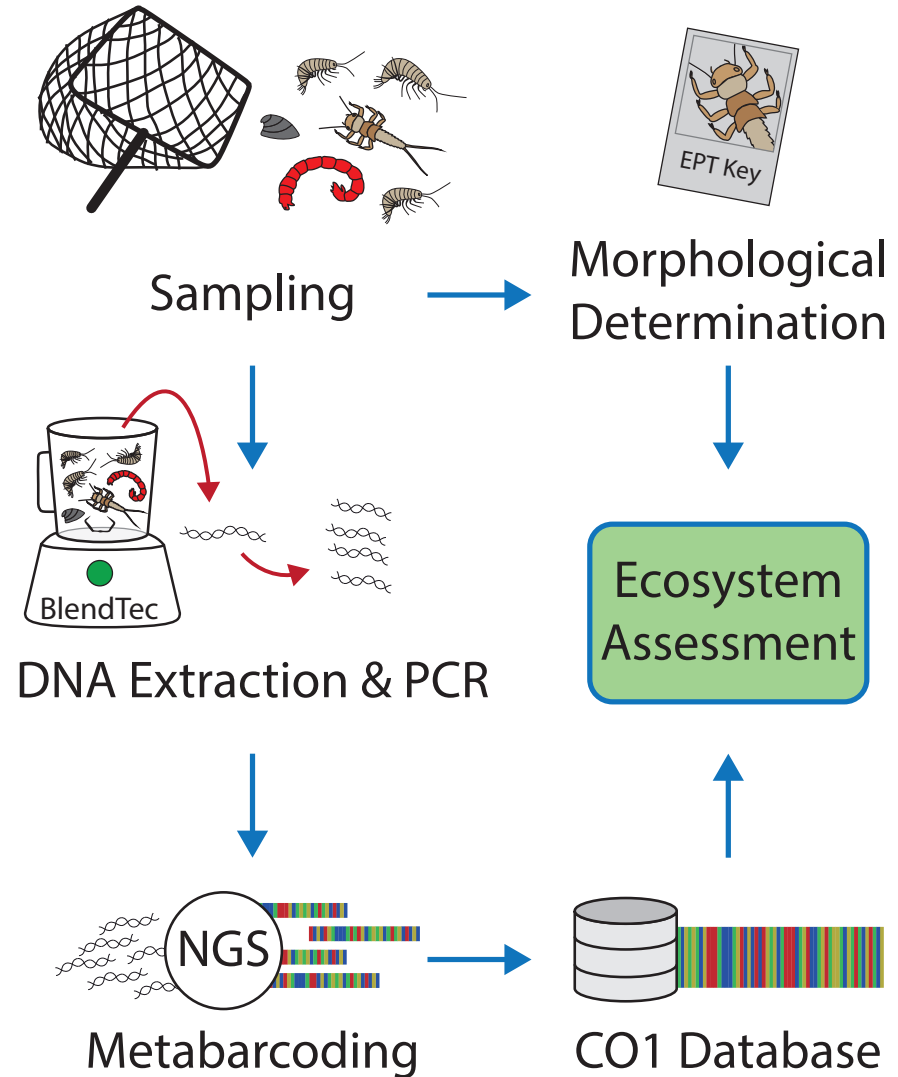
- DNA based identification of single specimens (expensive & time consuming)
- Morphological identification of imagines -> feed barcode into data base
- BOLD reference database -> 5 million sequences



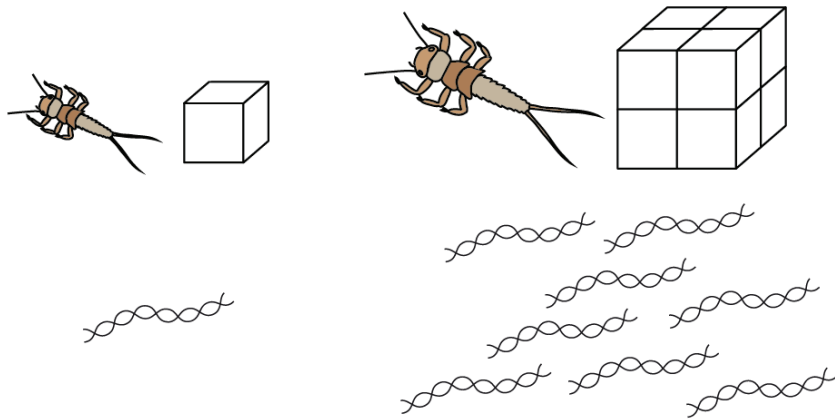
- **N**ext **G**eneration **S**equencing
- Generates millions of sequences



From sampling to the species level taxa list in less than a week!

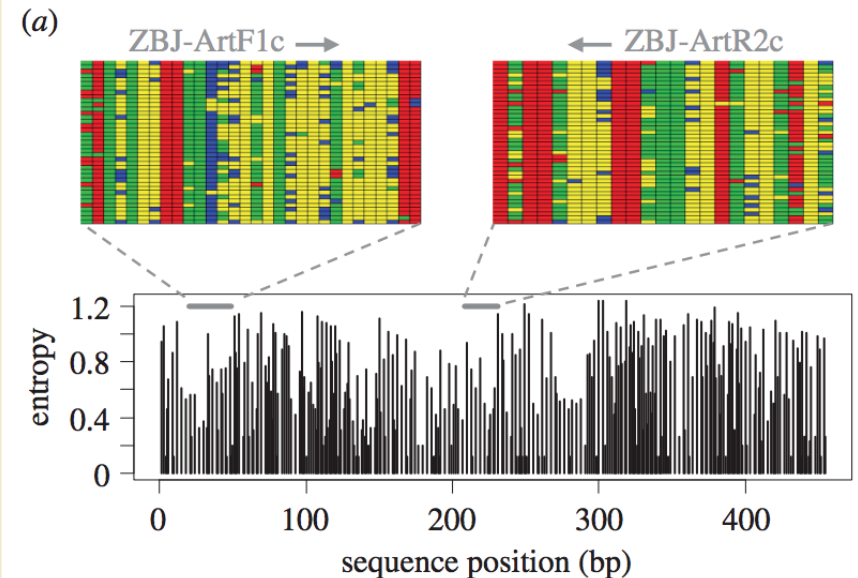


Different specimen biomass



Clear relationship between
sequence abundance and biomass
(within the same species)

CO1 Primer (binding site variability)



Deagle et al. 2014, Biol Lett.

---> Taxa detection primer dependent

Can metabarcoding estimate taxon biomass?

NO!



RESEARCH ARTICLE

Can DNA-Based Ecosystem Assessments Quantify Species Abundance? Testing Primer Bias and Biomass—Sequence Relationships with an Innovative Metabarcoding Protocol

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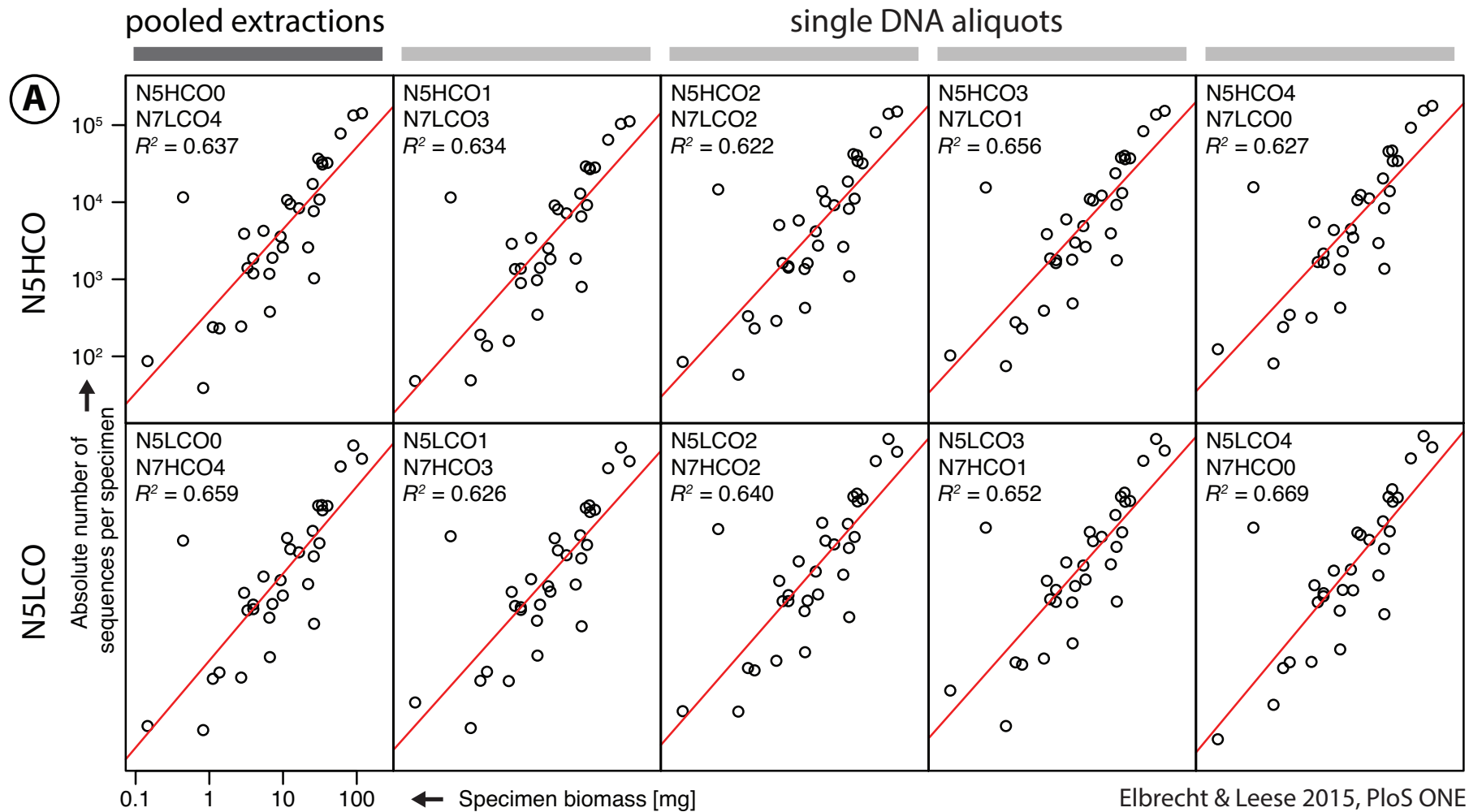
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Abstract

Metabarcoding is an emerging genetic tool to rapidly assess biodiversity in ecosystems. It



Experiment I: Biomass



Experiment II: Primer bias



Ephemeroptera:	8
Plecoptera:	4
Trichoptera:	15
Diptera:	8
Others:	17
Σ Taxa:	52

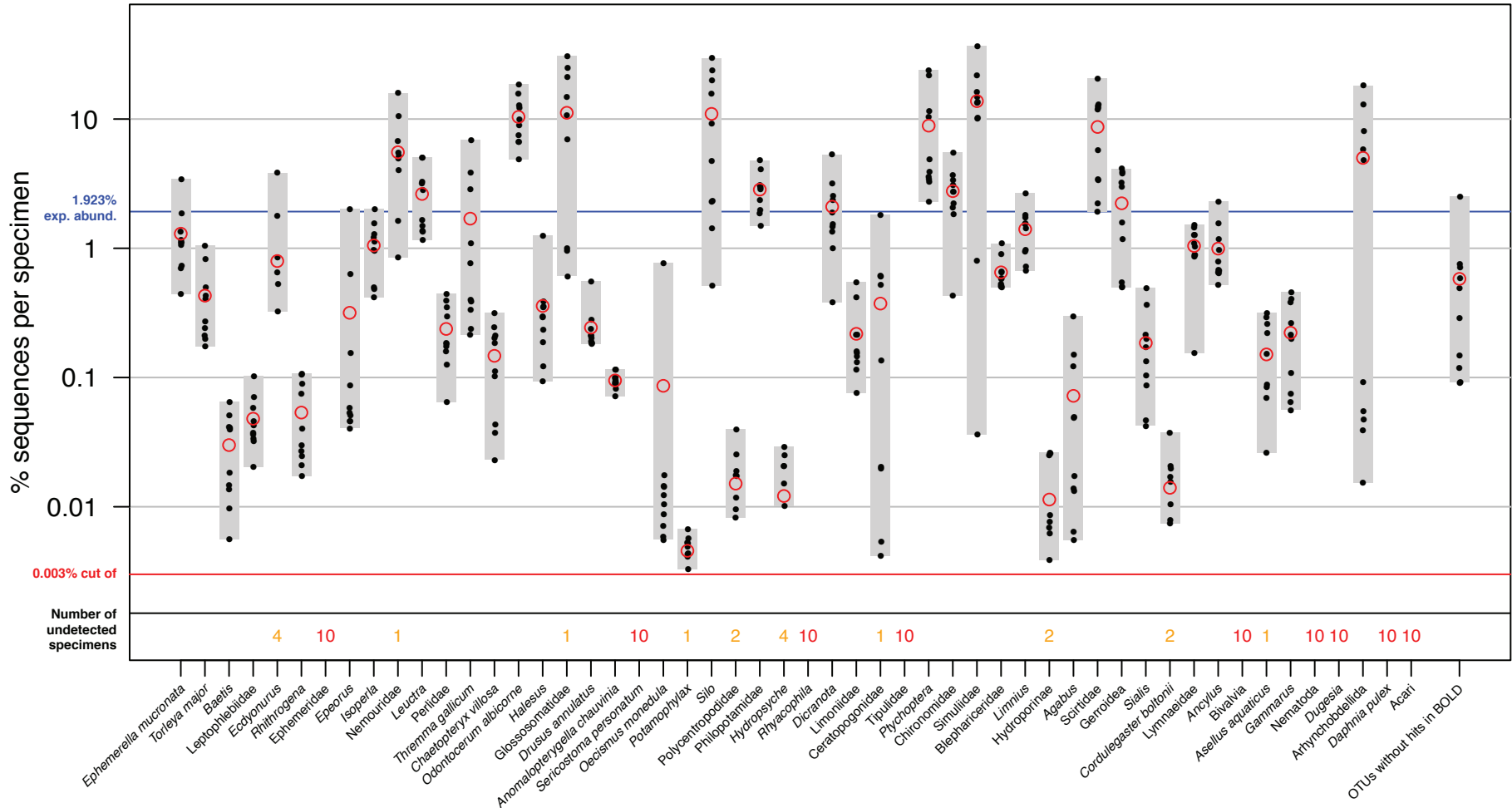


10 replicates

**Same amount of tissue
of each taxon**

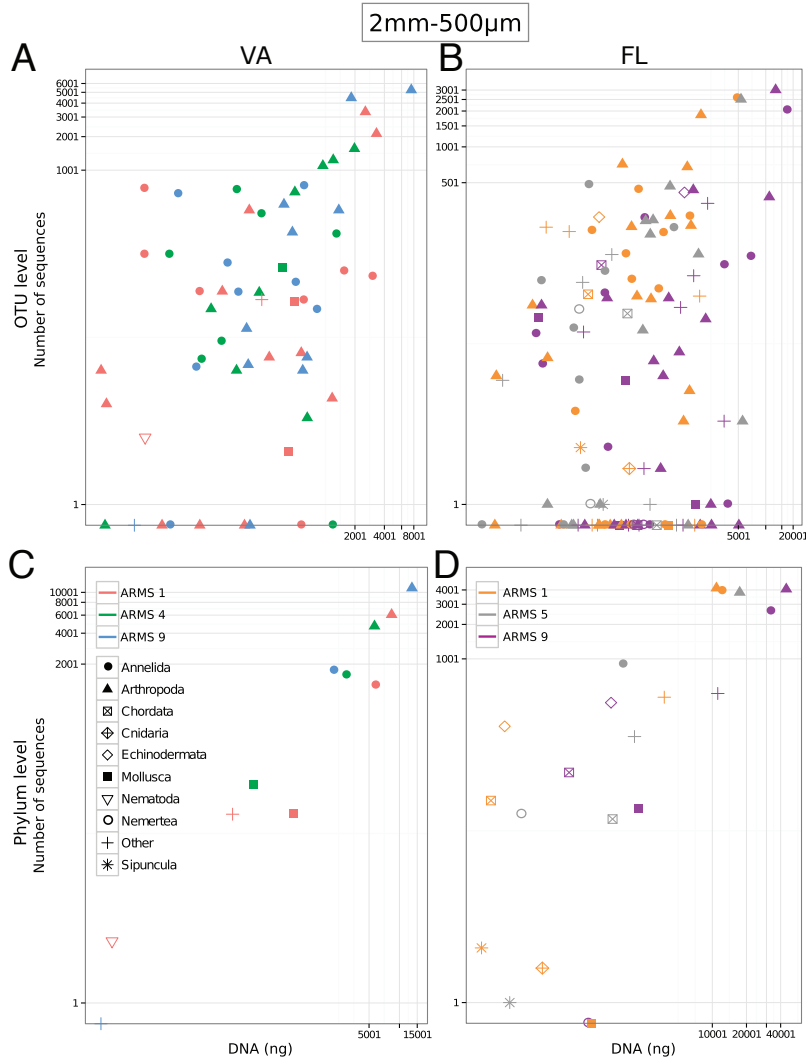
Elbrecht & Leese 2015, PloS ONE

Experiment II: Primer bias

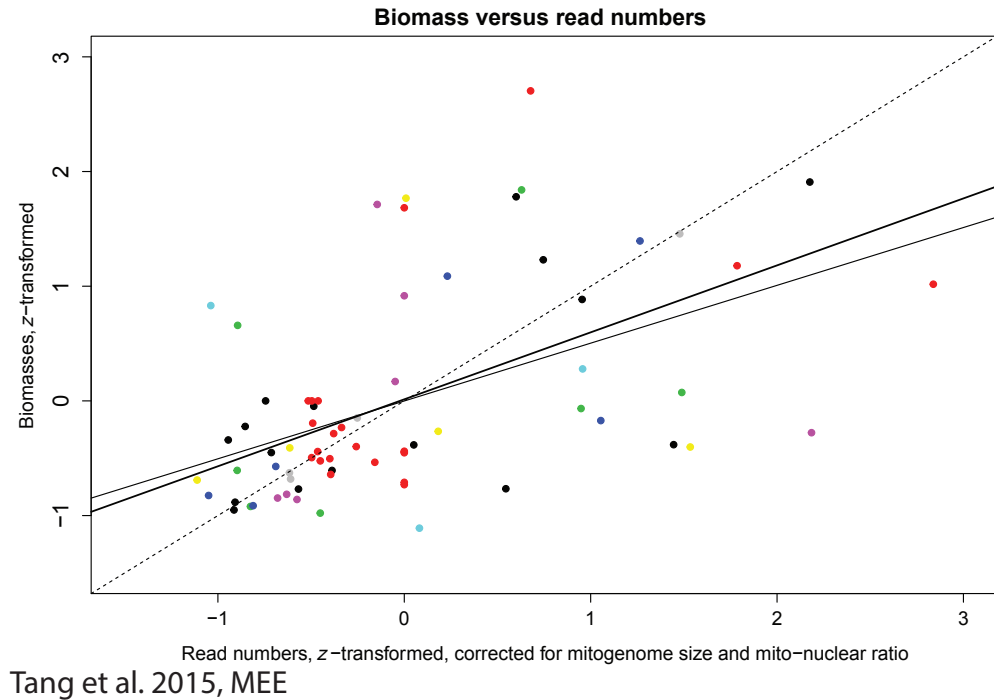


Elbrecht & Leese 2015, PloS ONE

Results confirmed by other studies

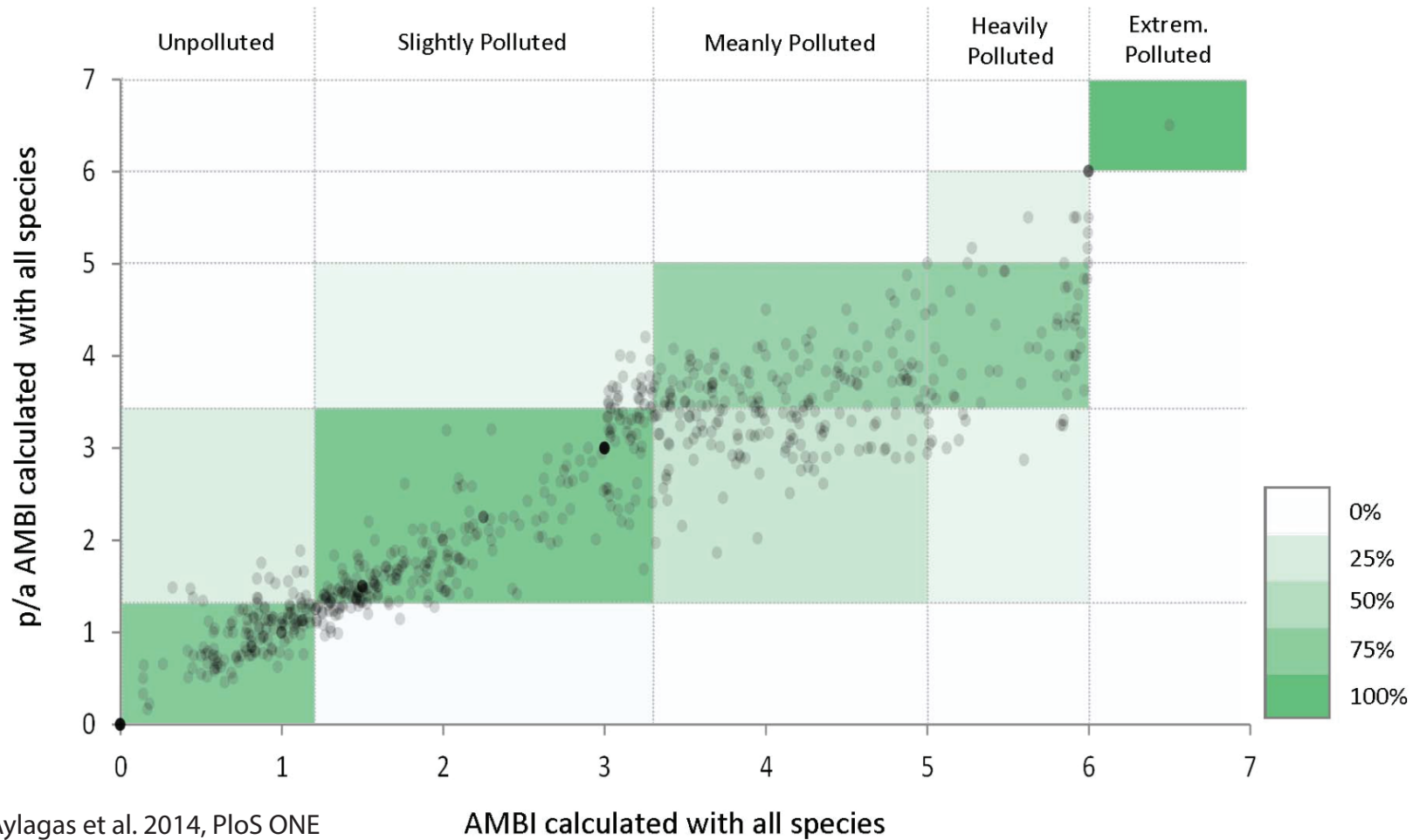


- ◀ Marine benthos
- ▼ Bees (metagenomics, PCR free!)



Abundance = does not look promising!

Is abundance necessary?



Aylagas et al. 2014, PloS ONE

AMBI calculated with all species

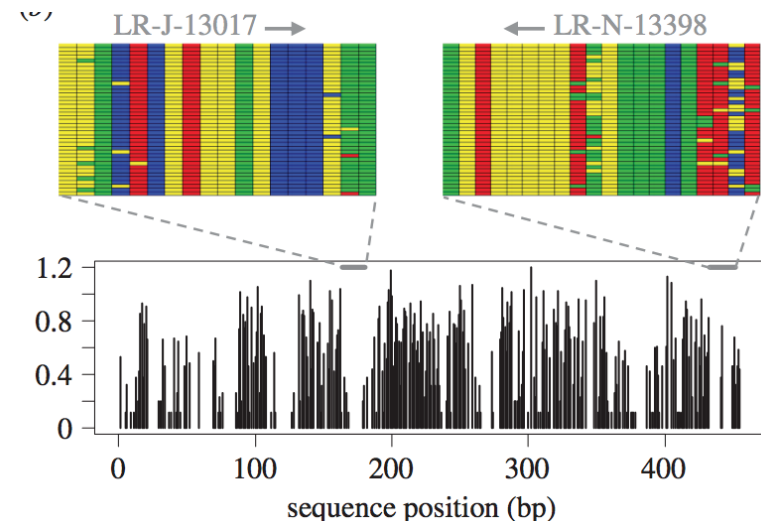
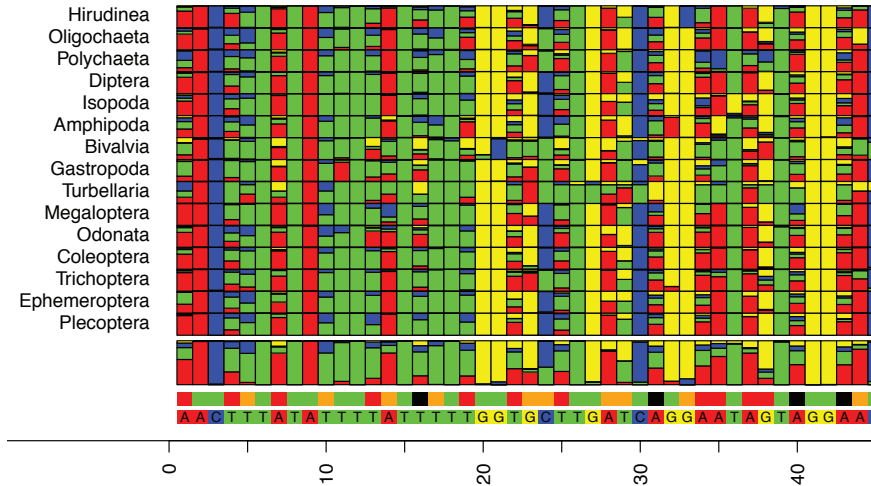
Abundance vs presence / absence = similar + species level identific. with DNA!

Optimised COI Primer

- Software: PrimerMiner
- Group specific primer
- OpenSource on GitHub
- 4 primer pairs

Alternative Markers

- 16S ribosomal marker
- DNA from Exp. II -> NextSeq
140.000.000 sequences
- lack of reference sequences

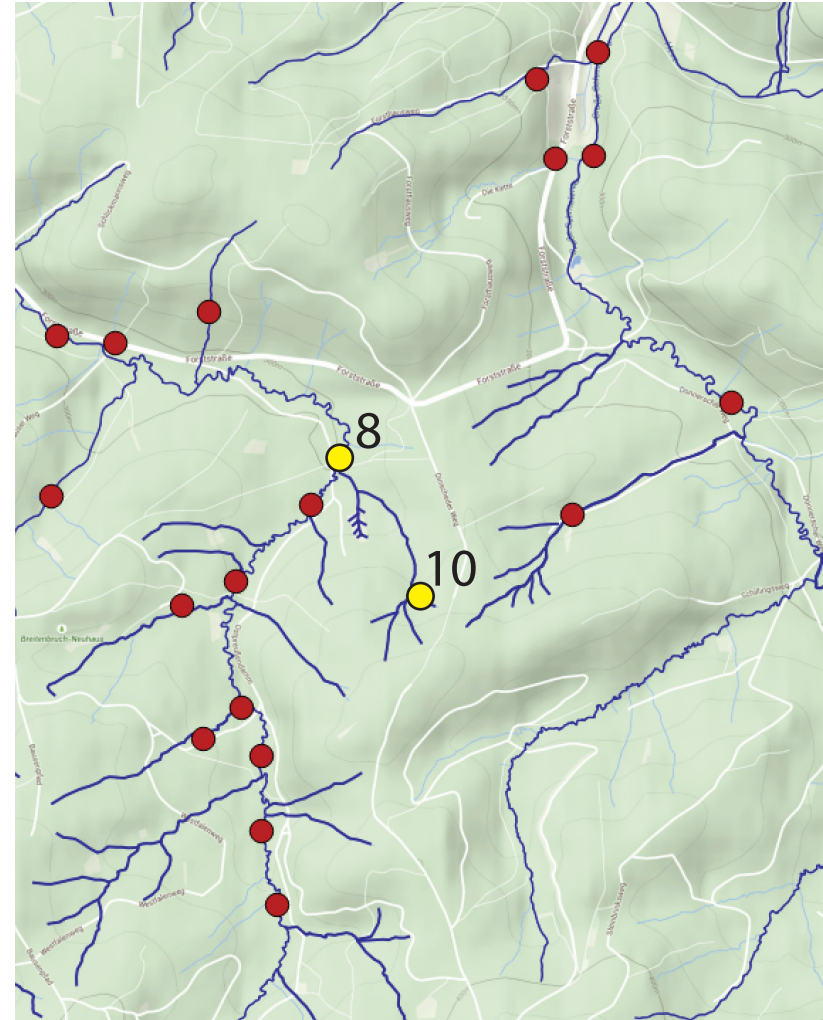


Deagle et al. 2014, Biol Lett.

Metabarcoding works!

	Morphology	Metabarcoding
Missidentification	occurs!	does not occur
Taxonomic resolution	--- / + taxon dependent	+ + taxon independent
Data comparability	---	+
Speed	-	+
Abundance	+	---
Cost	+	- cost is sinking

- No abundance data possible!
presence / absence data
- Upcoming:
metabarcoding of complete kick
samples from 20 sampling sites



5 kick samples per site - WFD

Involved people and partners

- Jannis Neuman
- Bianca Peinert
- Kristian Meissner
- Ralph Tollrian
- Rüdiger Wagner
- Xavier-Francois Garcia
- Wolfgang Wägele
- Arne Beermann
- Jan Macher
- Martin Sondermann
- Maria Gies
- Martina Weiss
- Hannah Weigand



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