2nd **meeting of the UK eDNA network**
University of Hull, 18th---19th September 2014

Organisers: Dr. Lori Lawson Handley and Dr. Bernd Hänfling, Evolutionary Biology Group, University of Hull.

Meeting Programme

Thursday 18th September

12.00-13.00	Registration and buffet lunch	Wilberforce East Concourse
13.00-13.10	Prof. Doug Wilson (EA)	Introduction to the UK eDNA network
13.10-13.30	Dr. Lori Handley (UoH)	Introduction to eDNA and the 2nd eDNA network meeting
Session 1: End---user needs (Chair Prof. Doug Wilson)		
13.30-14.00	**Invited talk:** Dr. Alice Hiley (EA)	Invasive species and WFD – how does eDNA fit in?
14.00-14.05	Dr Megan Ellershaw (NE)	What could or should Natural England be using eDNA for?
14.05-14.10	Dr Peter Brotherton (NE)	Developing a proficiency test for eDNA detection of European Protected Species - how and who?
14.10-14.15	Dr Laura Corrigan (EA)	The Potential for use of eDNA in WFD Transitional fish monitoring
14.15-14.20	Dr Tim Bean (CEFAS)	The potential of high throughput sequencing for Cefas: Evidence in marine science
14.20-14.25	Prof. Neil Boonham (FERA)	Experiences of offering eDNA services
14.30- 15.30	**Discussion 1:** End-user needs (Chairs Doug Wilson and Kerry Walsh)	
15.30-16.00	Coffee break Wilberforce East Concourse	
Session 2: Current applications (Chair Dr. Lori Lawson Handley)		
16.00-16.30	**Invited talk:** Prof. Stefano Mariani (Salford)	DNA Barcoding isn't dead: Implications for seafood traceability and biodiversity assessment.
16.30-16.35	Dr Naomi Ewald (FHT)	Using eDNA to develop a national citizen science-based monitoring programme for the great crested newt (*Triturus cristatus*)
16.35-16.40	Andrew Buxton (DICE)	Great crested newt eDNA research: the next steps
16.40-16.45	Phil Davison (CEFAS/Bournemouth)	Detection of non-native fish using e-DNA
16.45-16.50	Dr Helen Hipperson (ICL)	Species detection & density estimates of native & non-native species
16.50-16.55	Dr Jens Carlsson (UCD)	Lamprey in Ireland
16.55-17.00	Dr Larry Griffin (WWT)	Searching for relict populations of the tadpole shrimp *Triops cancriformis* – mud sample incubation; an imperfect and time consuming technique!

17.00-18.00	**Discussion 2:** Current applications (Chairs Dr. Lori Lawson Handley and Prof. Stefano Mariani)	
19.30 - late	**Conference dinner at KC Stadium**	

Friday 19th September

Session 3: Practical aspects of eDNA analysis (Chair Dr. Bernd Hänfling)		
9.00-9.10	Dr. Bernd Hänfling	Introduction to day 2
9.10-9.40	Invited talk: Dr. Helen Rees (ADAS)	eDNA – methodological variation and validation
9.40-9.45	Dr Tristan Hatton-Ellis (NRW)	Spatial issues with eDNA sampling in British rivers: a case study
9.45-9.50	Iliana Bista (Bangor)	Understanding the ecological relevance and temporal persistence of eDNA in a natural lake ecosystem.
10.00-11.00	**Discussion 3:** Practical aspects (Chairs Dr. Bernd Hänfling and Dr. Si Creer)	
11.00-11.30	Coffee Break Wilberforce East Concourse	
Session 4: The future: metabarcoding, novel applications and funding (Chair Dr. Lori Lawson Handley)		
11.30-12.00	Invited talk: Dr. Stephane Derocles (UoH)	Molecular approaches to describe food web structure: How? Why?
12.00-12.05	Dr Elizabeth Clare (QMUL)	Deconstructing the biggest food web ever investigated
12.05-12.10	Dr Melanie Sapp (FERA)	Benthic diatom profiling using molecular methods - preparing for high throughput
12.10-12.15	Alice Evans (Bangor)	Environmental DNA Metabarcoding for Rapid Assessment of Freshwater Biodiversity in Malaysia
12.15-12.20	Dr Matthew Shepherd (NE)	Soil Mesofauna Metabarcoding
12.20-12.25	Dr Xin Zhou (CNGB-BGI)	Towards PCR-free mito-metagenomics
12.25-1.30	**Discussion 4:** The future, wrap up session (Chairs Dr. Lori Lawson Handley and Dr. Bernd Hänfling)	
1.30-2.30	Lunch Wilberforce East Concourse and departure	

Topics for Discussion

Session 1: End---user needs (Chairs: Prof. Doug Wilson and Dr. Kerry Walsh)

End-user needs: What do end-users need from eDNA? What are the priorities? What are the concerns?

Meeting WFD and MSFD targets etc. with eDNA: How can eDNA help us meet those targets, and what do we need to do to ensure eDNA evidence is robust in a legal framework?

Invasive species monitoring: What are the priority species?

Biodiversity monitoring: What are the priorities?

Other priority applications: e.g. bioindicators?

Is there a gap between academics and end-users, and if so, what can we do to bridge that gap?

How should regulatory authorities respond to these new techniques?
What funding streams are available to meet end-user needs (can be continued in final session)?

Session 2: Current applications (Chairs: Dr. Lori Lawson Handley and Prof. Stefano Mariani)

Update on other current projects, ongoing or in the pipeline.

What lessons have we learned from current projects that we could take forward?

Citizen science approaches: uses and limitations?

Dealing with the data:

- o How is **biological record data** being collated and archived and how *should* it be collated and archived?
- o How is **DNA barcode data** being collated and archived and how *should* it be collated and archived?

Session 3: Practical aspects of eDNA analysis (Chairs: Dr. Bernd Haenfling & Dr. Si Creer)

How much do we understand about DNA shedding rates of different species and DNA persistence in the environment?

- o What are the key things we need to know to ensure eDNA evidence is robust?

What is the best way to obtain a representative sample, accounting for spatial and temporal variation etc.?

Water sampling and filtration issues:

- o How much water should be collected and how (e.g. peristaltic pump or hand held container)?

      o   What is the best approach for water filtering (e.g. filter sizes, dealing with sediment/inhibitors etc.)?

      o   What is the best approach for DNA capture: filtration vs precipitation?

What are the best methods for DNA extraction (should we all be using the same kit (PowerWater?) or do we need to do more testing to find the gold standard?

What is the best practice for water and DNA storage?

What quality control measures do we need to take to avoid contamination, false positives and false negatives?

Do we need to devise standardised methodologies: are they useful or could this hinder progress?

How can we improve estimates of biomass/abundance (i.e. make the method more quantitative)?

Dealing with data (if not dealt with in previous session)

Session 4: The future: metabarcoding, novel applications and funding (Chairs: Dr. Lori Lawson Handley & Dr. Bernd Haenfling)

Towards a quantitative method: Will we ever be able to obtain reliable estimates of abundance from eDNA? Where are the research gaps?

Moving from barcoding to metabarcoding – is this the more cost effective route?

Are there other areas where the eDNA approach might be useful? e.g. analysing relatedness of individuals based on e---DNA material such as faecal samples, mito---metagenomics.

The future of the eDNA Working Group:

Bidding for joint funding – how, where?

      o   Is there need for forming smaller interest groups (aquatic, terrestrial, fish, amphibians)?

      o   Linking up with groups across Europe

      o   Position paper, is the idea dead?

      o   Next meeting: where, when?