



Traps all Folks!

Combining multiple entomological traps with metabarcoding to maximise species detection

Ben S. J. Hawthorne¹, Darren M. Evans¹, Jordan P. Cuff¹,
and Larissa E. Collins²

¹: Network Ecology Group, Newcastle University, UK

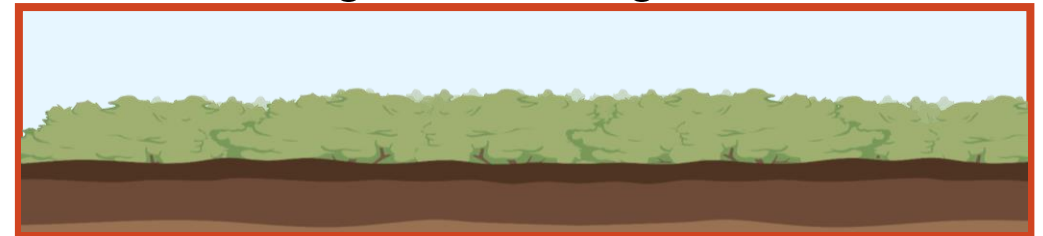
²: Fera Science Ltd., Sand Hutton, York, UK

- “Applying eDNA metabarcoding for the biomonitoring and assessment of Environmental Land Management schemes (ELMs)”
- Metabarcoding can increase depth and breadth of species identification
- First experiment: test efficacy of combining molecular methods with traps traditionally used for biomonitoring

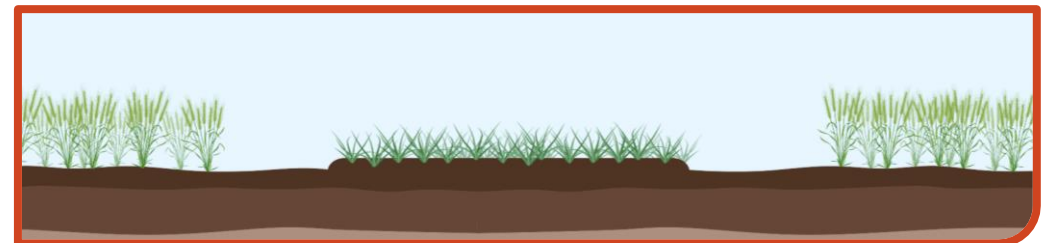
Buffering in-field ponds



Hedgerow management

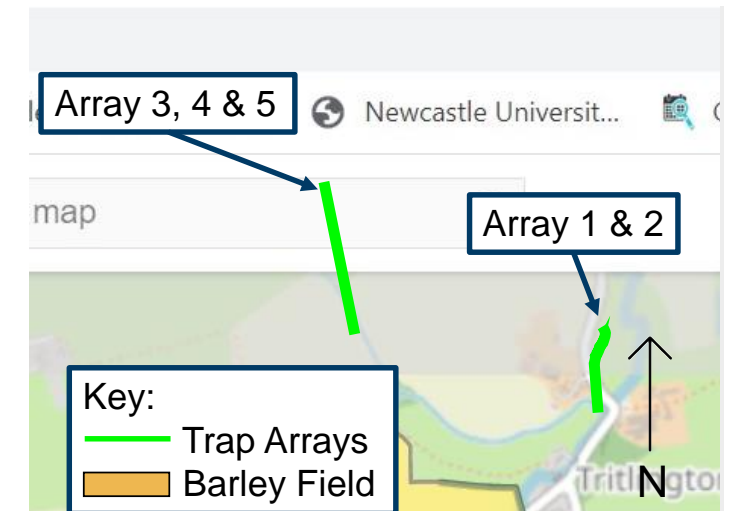
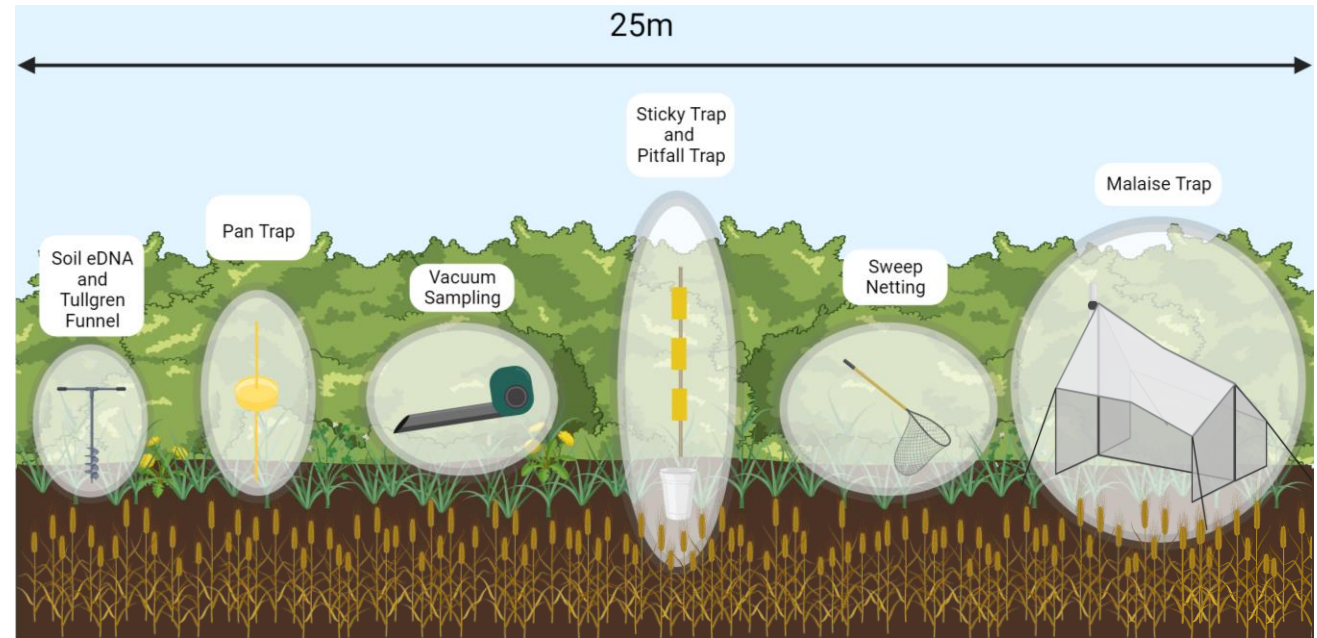


Beetle banks

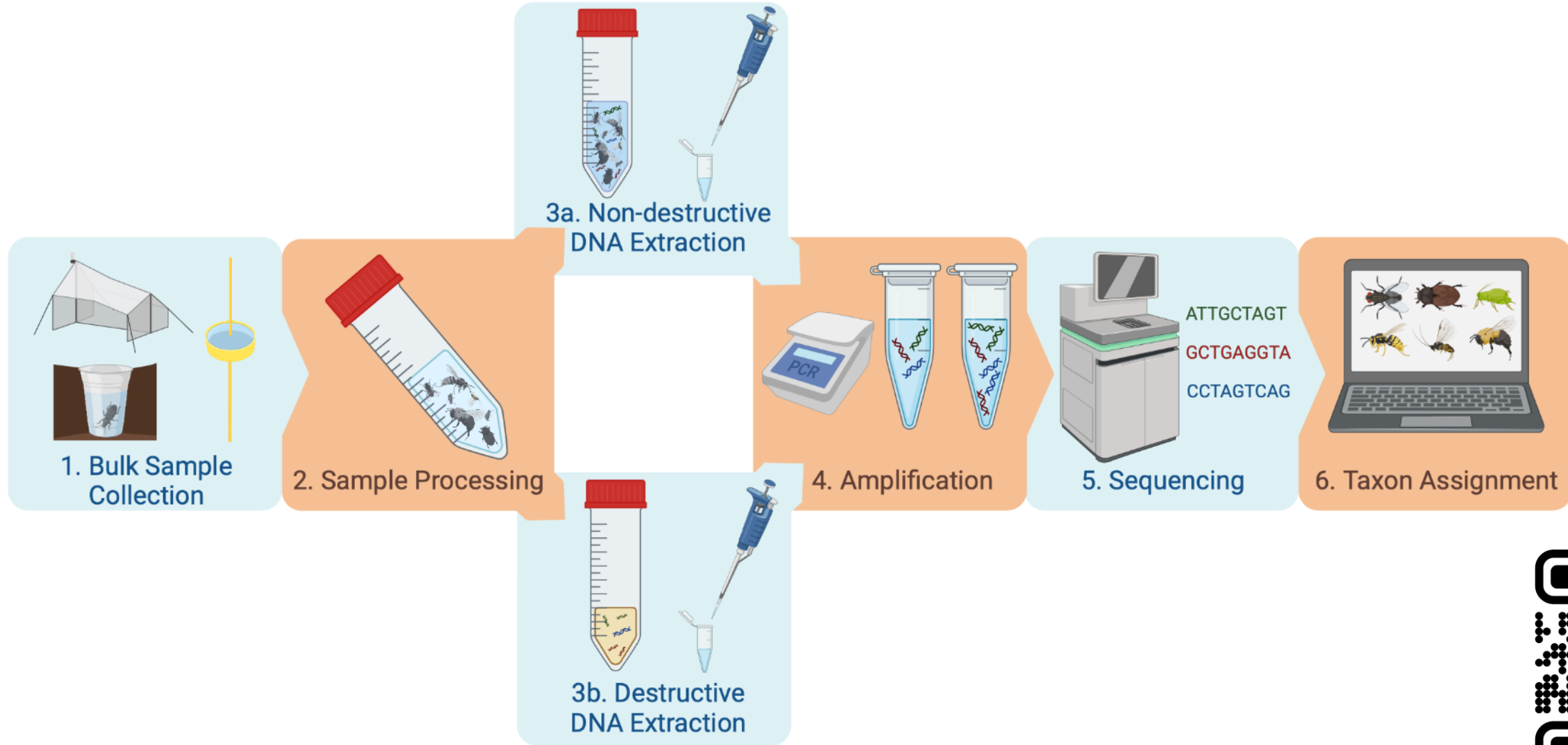


Method: Experimental Design

- Location: Cockle Park Farm, Morpeth, Northumberland
- Number of sampling methods: 8
- Arrays were spatially replicated 5 times, in grassy margins of spring-sown Barley fields, West-facing against mixed hedgerows.
- Sampling took place weekly over 6 weeks (10th July to 18th August); 3 weeks before and 3 weeks after harvest.



Method: Metabarcoding



Proposed Analysis

- Assessment of species overlap detected by each sampling method and compare diversity
- Focus on grouping by pests (e.g. herbivores and vectors of diseases) and beneficials (e.g. pollinators, natural predators, and parasitoids).
- Pre- and post- harvest comparison.
- Compare amount of effort required for each method?

