

Applying eDNA/Metabarcoding for the Biomonitoring and Assessment of Environmental Land Management schemes (ELMs)

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

¹: Network Ecology Group, Newcastle University, NE1 7RU, UK

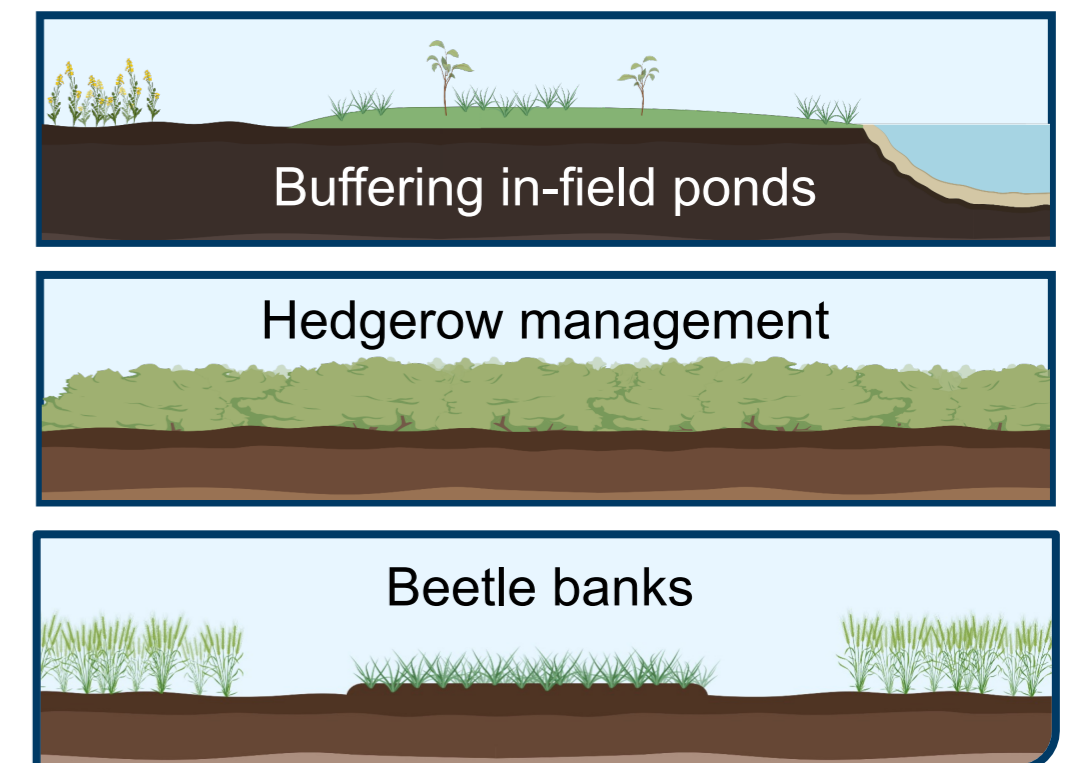
²: Fera Science Ltd., Sand Hutton, York, YO41 1LZ, UK

✉: B.Hawthorne2@newcastle.ac.uk 🐦: @BenSJHawthorne

Background

- The biodiversity crisis is a great threat to agriculture, due to the ecosystem services species deliver [1].
- ELMs are a UK Government scheme which aim to boost biodiversity, improve water quality and combat climate change [2].
- Metabarcoding has developed rapidly over recent years, making it a viable tool for identifying species in bulk samples [3].
- Assessing ELMs using metabarcoding could be a more efficient method for measuring biodiversity, with emphasis on pollinators, natural pest predators and crop pests.

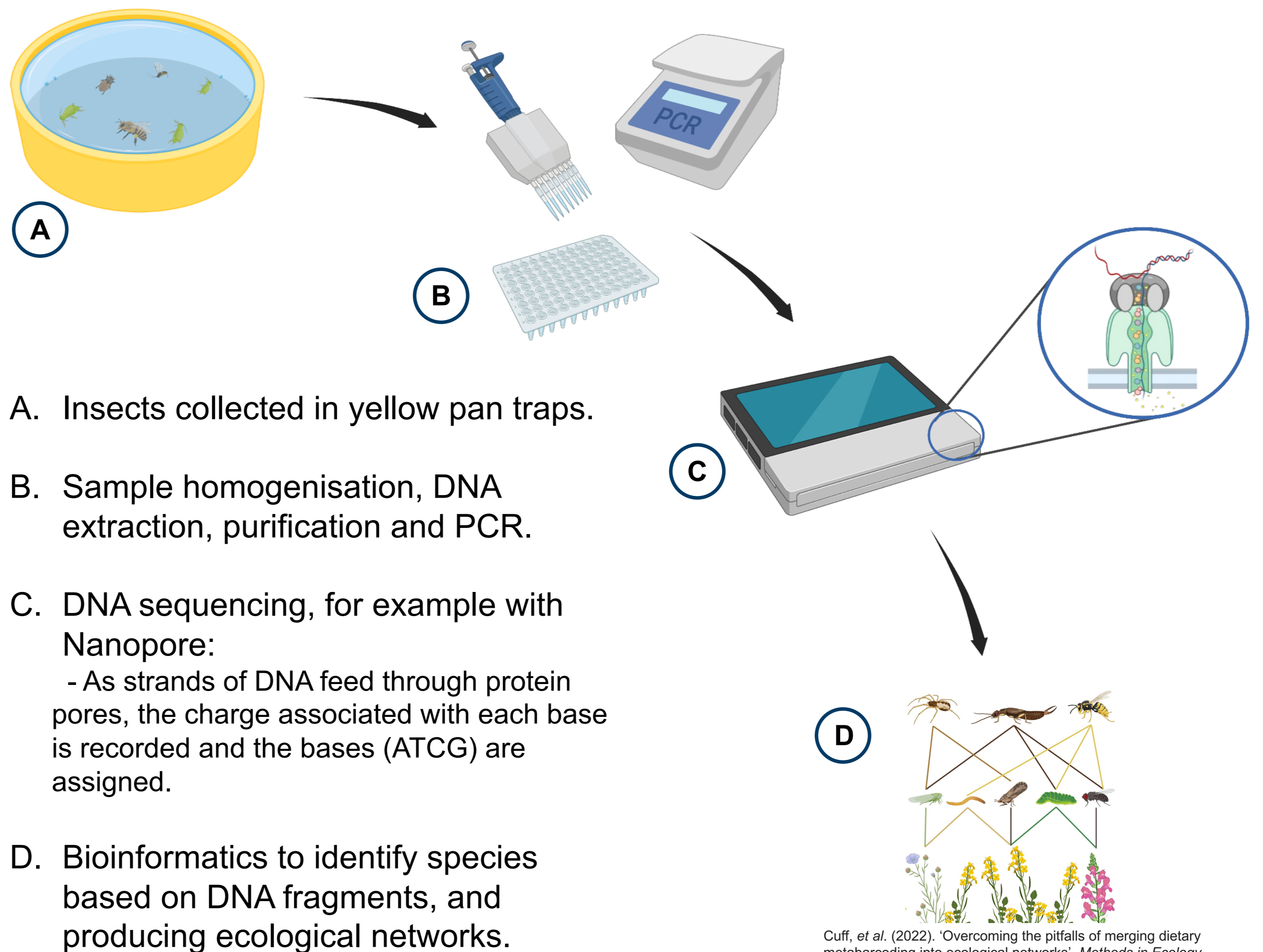
Examples of ELMs:



Aims

- How does insect biodiversity (pest and beneficial insects in particular) differ between managed crop and non-crop habitats?
- To what extent can eDNA metabarcoding be used as an agronomy tool for the biomonitoring and surveillance of pests and diseases?
- What are the spatial and temporal effects on insect natural capital?

Methodology



Syngenta: Operation Pollinator Wildflower Strips