eDNAPlus: A unifying modelling framework for DNA-based biodiversity monitoring

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DNA-based biodiversity surveys involve collecting physical samples from survey sites and assaying the contents in the laboratory to detect species via their diagnostic DNA sequences. DNA-based surveys are increasingly being adopted for biodiversity monitoring. The most commonly employed method is metabarcoding, which combines PCR with high-throughput DNA sequencing to amplify and then read `DNA barcode' sequences. This process generates count data indicating the number of times each DNA barcode was read. However, DNA-based data are noisy and error-prone, with several sources of variation. I will present a unifying modelling framework for DNA-based data allowing for most key sources of variation and error in the data-generating process (https://arxiv.org/abs/2211.12213). The model can estimate within-species biomass changes across sites and link those changes to environmental covariates, while accounting for species and sites correlation. I will demonstrate the new framework on a dataset of Malaise-trap samples and discuss matters of study design.