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Conference Abstract

Replicate DNA metabarcoding can discriminate seasonal and spatial abundance shifts in river macroinvertebrate assemblages

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Abstract

Metabarcoding is capable of delivering consistent and accurate fine-resolution biodiversity data, and offers great promise for improving aspects of environmental assessment and research. Even so, many ecologists are keen to make further inferences about species' abundances and the number of sequence reads has proven to be a poor proxy for abundance. The conservative interpretation has been to treat metabarcoding data as presence/absence, and although such data are less rich, occurrence and abundance are only different expressions of the same phenomenon. Interestingly if we assume the probability of detecting individuals is constant, it should be possible to use changes in the frequency of detection to infer changes in the underlying abundance. We tested the possibility that changes in the abundance structure of benthic macroinvertebrate communities could be recovered using replicated metabarcoding.

We conducted 5 monthly surveys from Jun-Nov 2019 at the Catamaran Brook, a small tributary of the Little Southwest Miramichi River in New Brunswick, Canada. Each survey collected 30 benthic samples divided between control and treatment cages that excluded

predatory fish. A further 6 samples were taken for traditional microscopic identification and counting.

Analysis of the metabarcoding data demonstrated that we could recover plausible changes in abundance from occurrence data, including significant responses to both seasonal dynamics and the experimental exclusion of predators. The microscopy samples merely confirmed that count data are highly stochastic, and therefore while specific estimates of expected abundance from our model are highly uncertain, they capture those differences we could validate. In summary, while we confirmed that occurrence data are more robust for routine bioassessment, it is possible to recover fine-resolution changes in abundance that can inform ecological studies using metabarcoding.

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