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"Competing pathways for equitable food systems transformation: Trade-offs and synergies"

Reducing the taxon bias in biodiversity data using robots, nanopore sequencing, and Ai identification tools for arthropods

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Abstract

Biodiversity science neglects hyperdiverse arthropod clades despite their importance with regard to terrestrial biomass, species diversity, and ecosystem services. In the talk, I will first document that more than half of the flying insect diversity in Malaise trap samples is concentrated in 20 family-level clades regardless of where the samples were collected. I then demonstrate how little we know about most of these arthropods clades by comparing the species richness in quantitative samples with the number of described species. This leads to the conclusion that we need new techniques for these taxa. At the Center for Integrative Biodiversity Discovery of the Natural History Museum in Berlin we have collaborated with colleagues from the Karlsruhe Institute of Technology to develop a robot ('DiversityScanner') for tackling abundance and efficient DNA barcoding techniques for tackling species richness. The DiversityScanner detects, images, and measures individual specimens before they are placed into microplates for barcoding with rapid and costeffective techniques involving Nanopore sequencers. After assigning images to species based on DNA barcodes, we can start to train Convolutional neural networks (CNNs) for all taxa with more than 100 images. The goal is delivering AI tools for large numbers of common species so that they become identifiable for everyone based on images. The power of the approach will be discussed for a few examples from tropical and non-tropical environments. One goal is to dramatically increase the number of species that can be described and make all the new species identifiable via a range of different techniques.

Keywords: Biodiversity

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