

Exploring Biodiversity with Next Generation Sequencing

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Abstract:

Just as the unique pattern of bars in a universal product code identifies each consumer product, a DNA barcode is a unique pattern of DNA sequence that can help identify species. Metabarcoding uses Next Generation Sequencing to analyze hundreds of thousands of DNA barcodes from complex mixtures of DNA—representing microbes (microbiomes) or environmental DNA. Dr. Nash will describe the programs, protocols, and infrastructure he has developed to support affordable metabarcoding by students, allowing them to learn molecular biology and bioinformatics while studying biodiversity.

Bio:

Bruce Nash holds a Ph.D. in medical and molecular genetics from the University of Toronto, where he studied the genes that guide axonal growth cones and migrating cells during development. After completing a postdoctoral position at the University of Oregon he joined the DNA learning Center at Cold Spring Harbor Laboratory, where he develops, disseminates, supports and teaches high school and college level curricula. While at the DNALC, he has developed approaches that support authentic research by students using RNA interference, DNA barcoding, and metabarcoding. In each case, this curriculum is designed to integrate bioinformatics, molecular biology, and the flexibility to support many research projects with unified methods.