DNA Technologies for Biodiversity Management

DNA technologies and applications to improve our ability to measure, understand, and protect global biodiversity

Convention on Biological Diversity

Japan Biodiversity Fund 生物多様性日本基金

international BARCODE OF LIFE

Introduction

Applying DNA technologies to real-world problems such as pest and disease control, food production and safety, resource management, and conservation can impact how society interacts with biodiversity.

DNA analysis makes it possible to identify animals, fungi and plants quickly and inexpensively. Its application for species identification of endangered wildlife, quarantine pests, and disease vectors allows enable researchers, enforcement agents, policymakers, and consumers to make informed biodiversity management decisions.

Researcher with cyclone spore sampler in Uppsala, Sweden (Photo: LIFEPLAN project)

DNA barcodes can be used to combat illegal wildlife trade.

DNA barcode training in Canada (Photo: iBOL Consortium)

Assessing arthropod diversity in a nature reserve. (Photo: iBOL Consortium)

DNA Technologies: From Concept to Conservation

Canadian evolutionary biologist Prof. Paul Hebert introduced DNA barcoding in 2003, transforming the field of biodiversity science.

Robotics automate and accelerate DNA analysis. (Photo: iBOL Consortium)

DNA barcoding – a term describing the use of sequence variation in short, standardized gene regions to discriminate species. In the case of the animal kingdom, the barcode region is a 648 base pair segment of the mitochondrial cytochrome *c* oxidase I gene. Developed by Canadian evolutionary biologist, Dr. Paul Hebert, DNA barcoding has been adopted by researchers and natural history enthusiasts worldwide. Because DNA barcoding requires only basic lab infrastructure, it's a cost-effective and efficient tool for specimen identification and species discovery.

Hebert's research group at the Centre for Biodiversity Genomics (CBG) at the University of Guelph has developed the infrastructure required to scale up DNA barcoding. By coupling its globally renowned informatics platform (BOLD – Barcode of Life Data System) with advanced imaging technologies, liquid handling robots, and high-throughput sequencers, the CBG is accelerating the production of biodiversity data at a time when science and society need this information to address biodiversity loss.

The CBG also hosts the Secretariat for the International Barcode of Life (iBOL) Consortium which includes research organizations in 40 nations. iBOL provides scientific and technical expertise and supports capacity-building activities in developing countries. It also aids the generation and sharing of biodiversity knowledge among Parties to the Convention on Biological Diversity (CBD) and relevant stakeholders and organizations.

DNA Technologies: Recent Advances

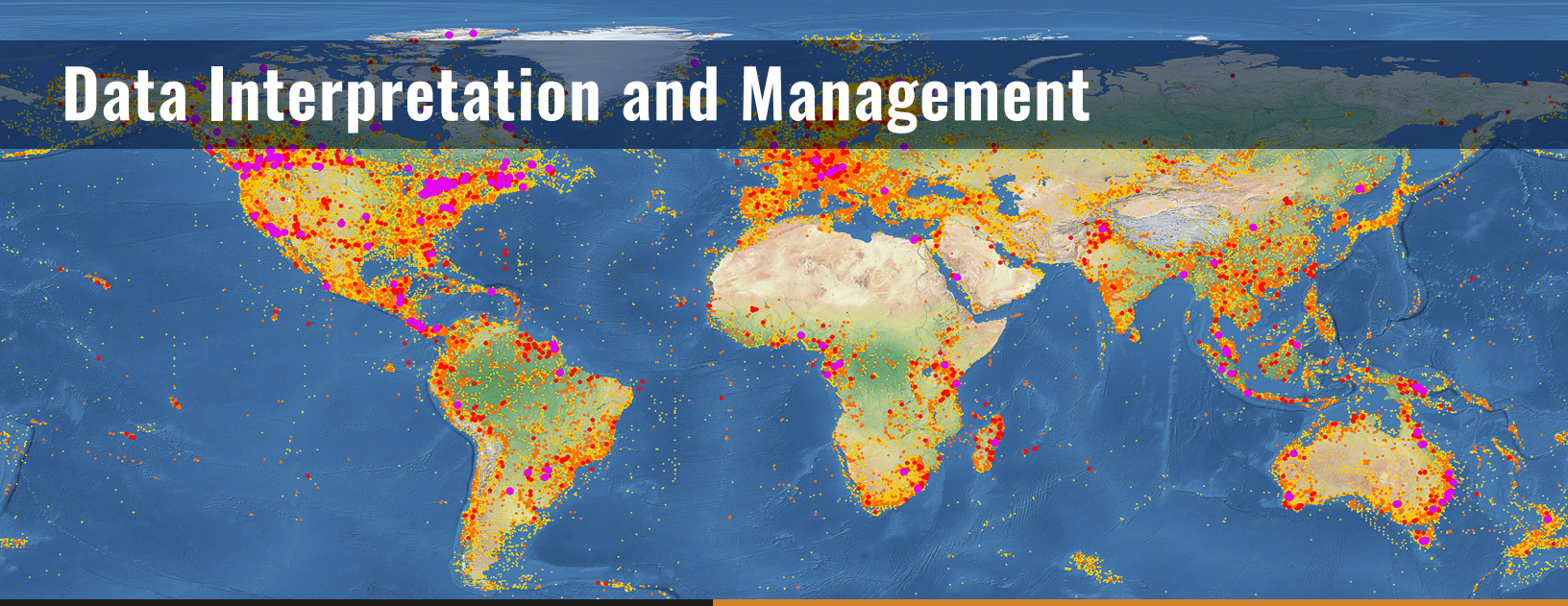
DNA metabarcoding allows researchers to barcode both bulk samples of organisms and eDNA collected from environmental samples such as water, snow, soil, and even air. Using high throughput sequencing (HTS) technologies, this method allows researchers to detect the presence of organisms through DNA shed into the environment. A single HTS instrument can process samples containing millions of specimens in a month, making metabarcoding a very cost-effective method for tracking shifts in species distribution and diversity.

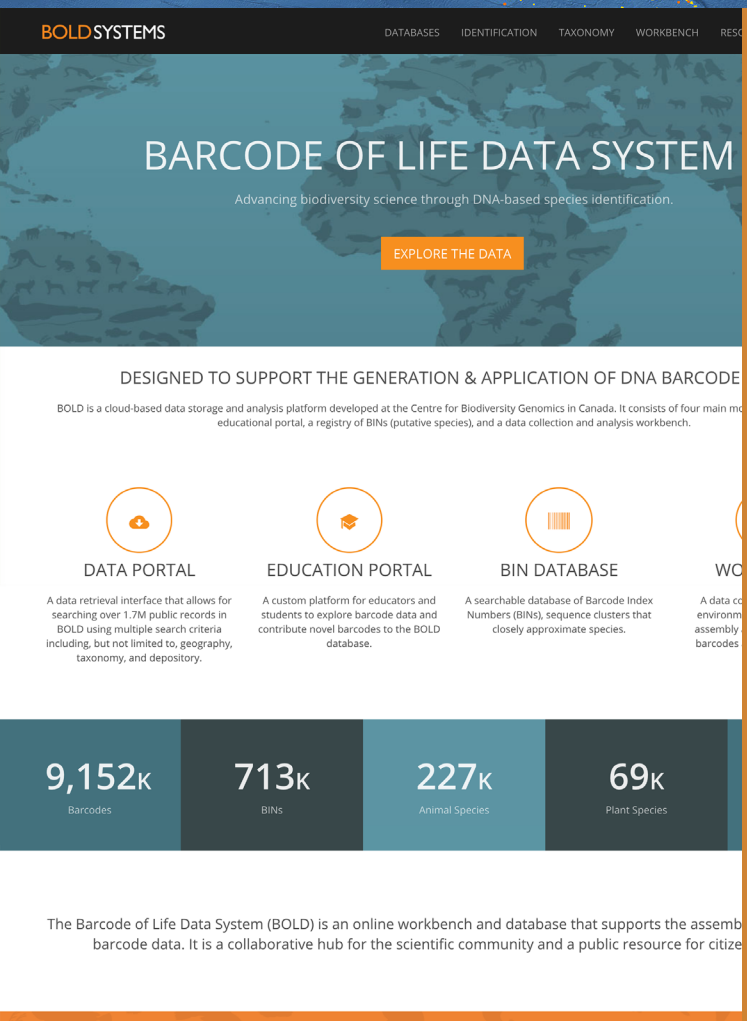
Many metabarcoding studies assess diverse eukaryote lineages including aquatic and terrestrial arthropods, vertebrates, pollen, and fungi. These technologies will eventually make it possible to track all species present within an ecosystem. This novel method continues to grow in popularity as an integral research tool for many global biodiversity management and conservation programs.

STREAM (Sequencing the Rivers for Environmental Assessment and Monitoring) is a collaboration between WWF-Canada, Environment and Climate Change Canada, the University of Guelph and Living Lakes Canada. It is supporting community groups in monitoring the quality of aquatic habitats by employing metabarcoding to identify the organisms resident in each habitat.

Above: Community members in British Columbia, Canada review data as part of the STREAM project.
Below: Researchers use kick nets to assess benthic invertebrates in freshwater (Photos: Living Lakes Canada)

Data Interpretation and Management



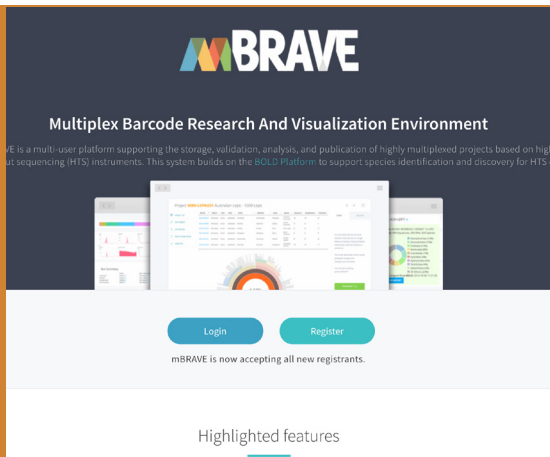


BOLD

Both DNA barcoding and metabarcoding rely on access to a comprehensive DNA barcode reference library so each sequence can be assigned to its source species. BOLD is the global repository for DNA barcode data. It is an essential resource for DNA-based identification and shares data with other public databases, including GenBank. BOLD is unique as it couples genomic data with specimen information, making it possible to validate taxonomic assignments for the specimen records that comprise the library. It also offers analytical tools that provide easy access to DNA-based identifications. Although BOLD now holds records for nearly a million species, this coverage needs to be expanded at least 10-fold to support global application of metabarcoding.

mBRAVE

Building on BOLD, the Multiplex Barcode Research and Visualization Environment (mBRAVE) is a multi-user platform supporting the storage, validation, analysis, and publication of data gathered by high-throughput sequencing (HTS) instruments. mBRAVE supports species identification and discovery for HTS data.



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To learn more about DNA technologies and applications, please visit:

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