

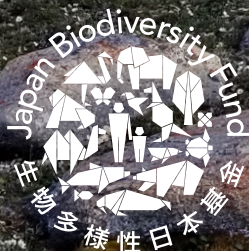


DNA Technologies for Biodiversity Management

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



Convention on
Biological Diversity



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.

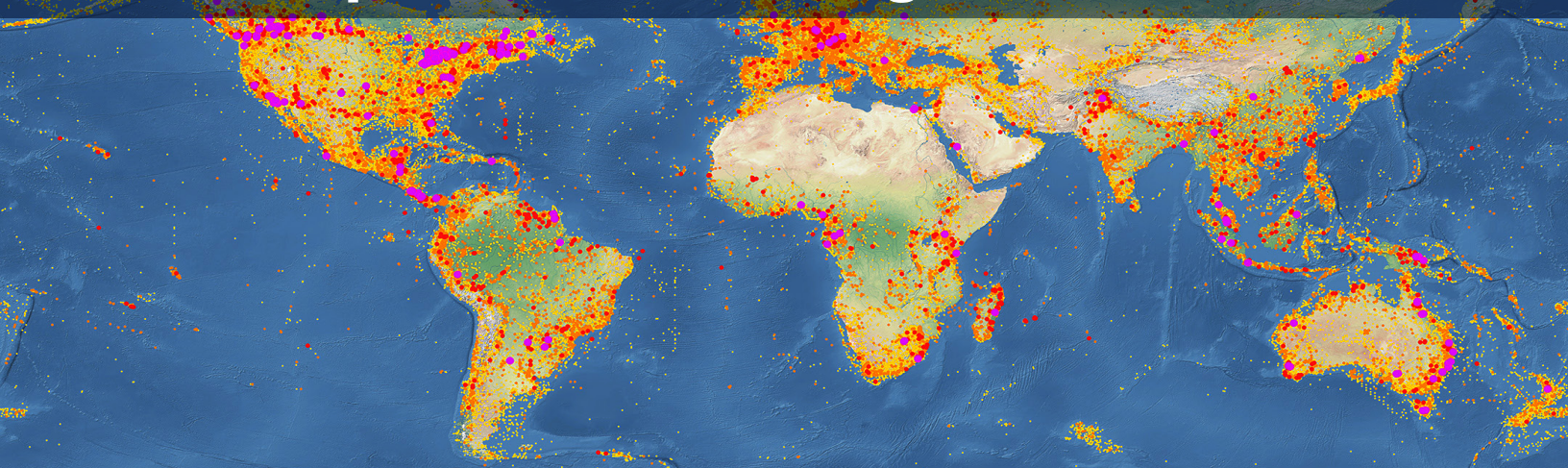


Above: Community members in British Columbia, Canada review data as part of the STREAM project.

Below: Researchers use kick nets to assess benthic invertebrates in freshwater (Photos: Living Lakes Canada)



Data Interpretation and Management



BOLDSYSTEMS

DATABASES IDENTIFICATION TAXONOMY WORKBENCH RESOURCES

BARCODE OF LIFE DATA SYSTEM

Advancing biodiversity science through DNA-based species identification.

EXPLORE THE DATA

DESIGNED TO SUPPORT THE GENERATION & APPLICATION OF DNA BARCODE

BOLD is a cloud-based data storage and analysis platform developed at the Centre for Biodiversity Genomics in Canada. It consists of four main modules: a data portal, an educational portal, a registry of BINs (putative species), and a data collection and analysis workbench.



DATA PORTAL

A data retrieval interface that allows for searching over 1.7M public records in BOLD using multiple search criteria including, but not limited to, geography, taxonomy, and depository.



EDUCATION PORTAL

A custom platform for educators and students to explore barcode data and contribute novel barcodes to the BOLD database.



BIN DATABASE

A searchable database of Barcode Index Numbers (BINs), sequence clusters that closely approximate species.



WORKBENCH

A data collection and analysis platform for environmental DNA (eDNA) and other high-throughput sequencing (HTS) data.

9,152k

Barcodes

713k

BINs

227k

Animal Species

69k

Plant Species

The Barcode of Life Data System (BOLD) is an online workbench and database that supports the assembly and analysis of DNA barcode data. It is a collaborative hub for the scientific community and a public resource for citizen scientists.

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.

mBRAVE

Multiplex Barcode Research And Visualization Environment

mBRAVE is a multi-user platform supporting the storage, validation, analysis, and publication of highly multiplexed projects based on high-throughput sequencing (HTS) instruments. This system builds on the BOLD Platform to support species identification and discovery for HTS data.



Login

Register

mBRAVE is now accepting all new registrants.

Highlighted features



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

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