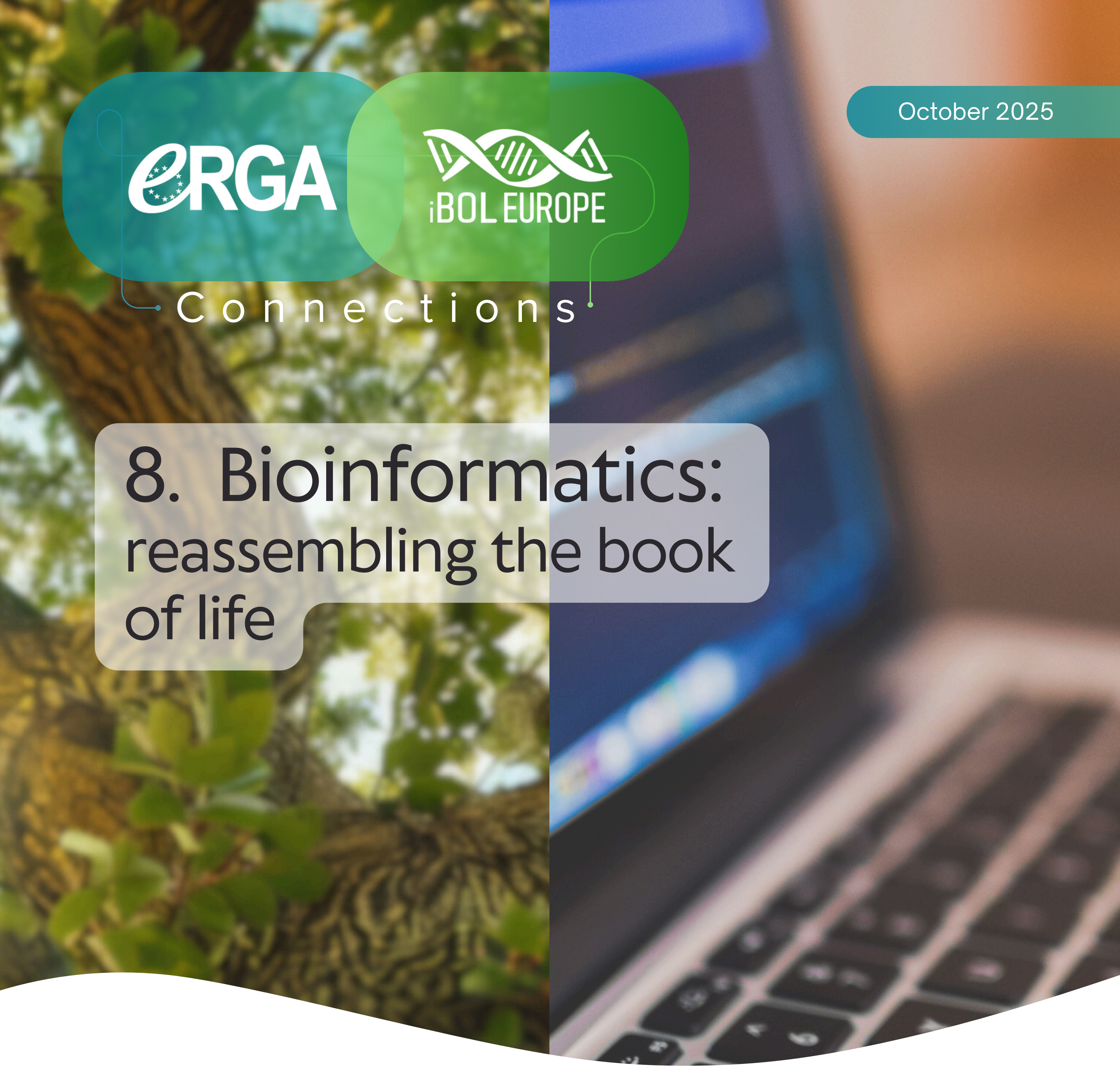

October 2025

ERGA

iBOL EUROPE

Connections

# 8. Bioinformatics: reassembling the book of life

The European Reference Genome Atlas (ERGA) and the European node of the International Barcode of Life (iBOL Europe), two international communities of scientists brought together under the Biodiversity Genomics Europe Project, are joining forces for a series of blog posts that explore the fascinating world of Biodiversity Genomics and the intersection of their communities.

Biodiversity Genomics Europe
BiodiversityGenomics.eu

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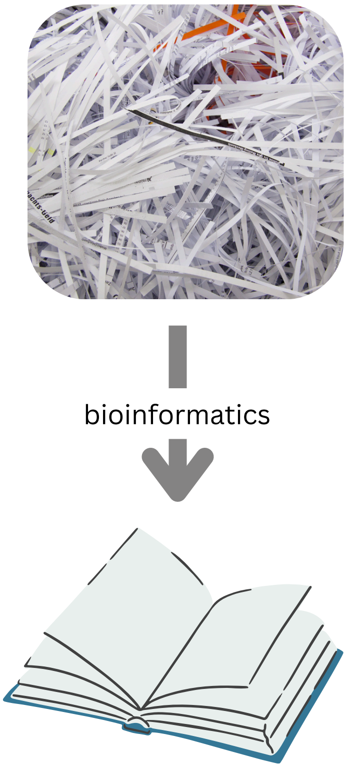
# **Bioinformatics:** reassembling the book of life

BY CHIARA BORTOLUZZI, KASIA FANTONI, CHRISTIAN DE GUTTRY AND LUISA MARINS

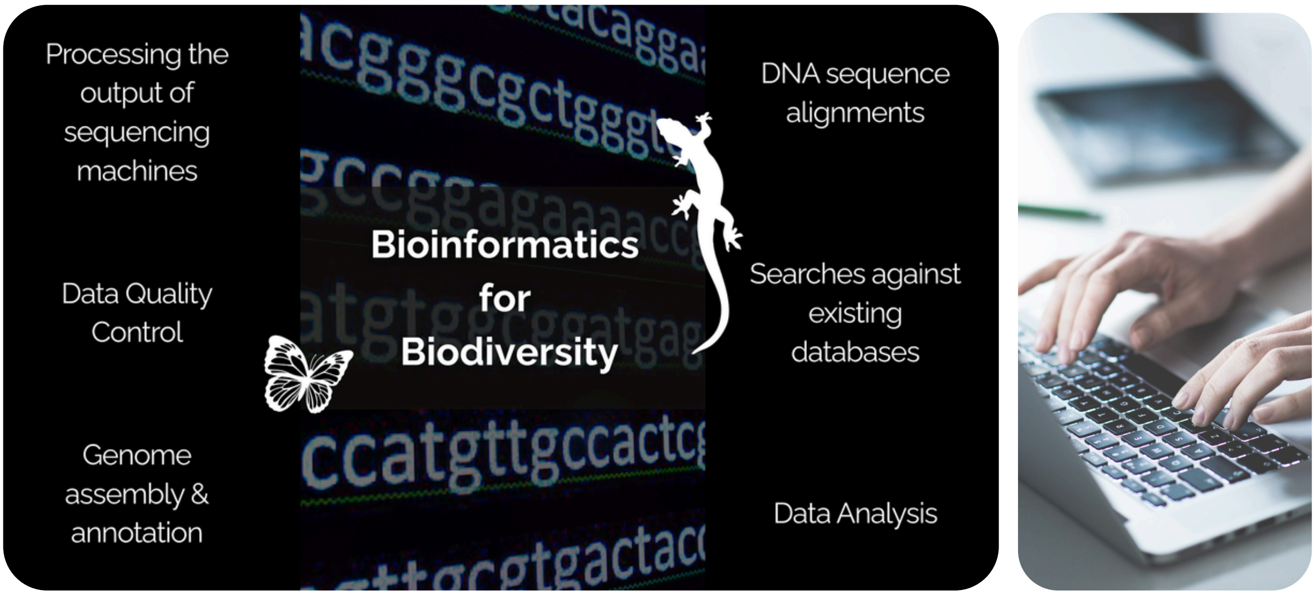
So far, we have said that DNA is like a book. Barcodes help us identify which book it is, while reference genomes let us read every page. But here is the catch! By the time DNA gets to the computer, the book has been turned into tiny strips of paper, millions of them! That is what sequencing does. Bioinformatics is the clever computer work that puts those strips back together so we can understand the story inside.



Imagine you have run your favourite novel through a photocopier that chops it into confetti. For barcoding, we only need a small paragraph to recognise the title, which is quick and handy for keeping track of species. For a reference genome, we want the whole book back, in the right order, with chapters and page numbers. That is a bigger puzzle! The computer checks overlaps, matches patterns, and uses extra clues (like “these pages were stapled together”) to rebuild the book.

A useful genomic database is like a well organized library. Photo by khouwes from Getty Images Signature.

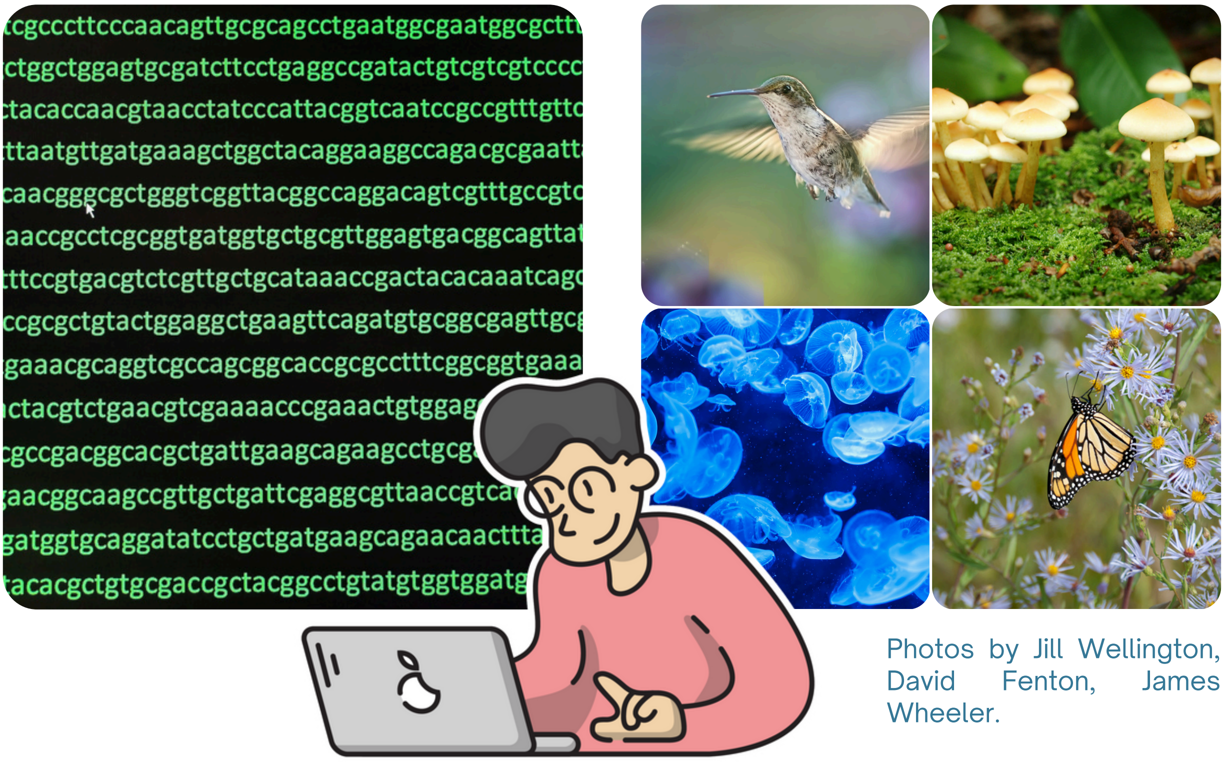
Bioinformatics grew up when biologists teamed up with computer scientists. Early on, people wrote programs to line up short DNA pieces and spot similarities. As DNA reading got faster and cheaper, the puzzles got bigger. Today, scientists use step-by-step “recipes” called pipelines so that the same work can be repeated and checked by others, like sharing a cake recipe that actually bakes the same cake in someone else’s oven.



Examples of some common bioinformatics tasks when working with genomic data from across the tree of life.

Files have funny names, computers complain if you mistype a letter, and everyone learns to keep organized notes. But when the final picture appears, “these insects are here this month” or “this species has a health problem we can fix”, it is worth the effort.

For iBOL Europe, good bioinformatics means reliable barcodes to identify species and watch nature change. For ERGA, it means high-quality genomes that help explain how species survive, adapt, or struggle, and what knowledge can guide protection and better decisions. The two fit together: barcodes tell us who is there, and genomes help us understand how they work.



Photos by Jill Wellington, David Fenton, James Wheeler.

Bioinformatics turns thousands of DNA pieces into useful answers. It is the friendly computer detective that helps scientists, parks, and communities see the living world more clearly. Next time, we will show how those answers are used in real decisions, from nature monitoring to practical conservation, so the story we have rebuilt can lead to a happier ending for wildlife.