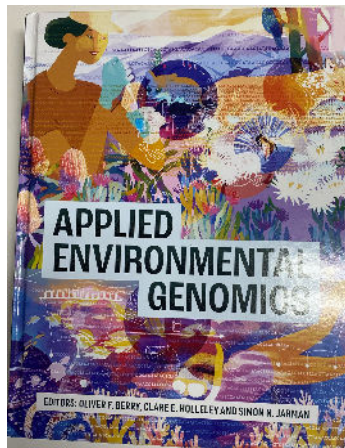


## BOOK REVIEW

Eds. Oliver F. Berry, Clare E. Holleley and Simon N. Jarman  
Hardback, December 2023, \$200 ISBN: 9781486314928, 368 pages  
Publisher: CSIRO Publishing. Colour plates, Illustrations, Photographs



The book consists of 6 themed sections, 27 chapters and 352 pages, focusing on new applications of genomic technologies to environmental problems. The introduction is informative, briefly providing the definition of environmental genomics, the challenge of environmental management, and how relevant genomics are to environmental management. Every chapter contains an abstract and ends with discussion topics stimulating readers to brainstorm future research directions.

Section A, “Biodiversity”, deciphers the intersection of metabarcoding surveys and biodiversity. It comprises 5 chapters, of which Chapter 1 teaches the significance of experimental design and sampling methods. It presents a guide to design eDNA metabarcoding surveys, covering eight areas of eDNA metabarcoding research: air, plant-pollinators, soil, diet, microbiome, freshwater, estuarine and marine. Then, chapter 2 covers post-sequencing analyses alarming that eDNA metabarcoding data can be distorted and contain artefacts. Examples, as well as the use of metabarcoding for ecological studies, are involved in the other three chapters.

Section B, “Life history and population biology”, containing 8 chapters, centres around headway and utilisation of biomarkers to characterise individual or population biology, involving lifespan estimation, epigenetic clocks, sex determination, wildlife abundance and population viability. Perspective utilisation of reference whole genome assemblies, to achieve insights into diseases and optimal strategies and addressing them, is explored through the case study of the Tasmanian devil and an infectious clonal cancer.

Section C, “Adaptation and change”, broadens the metagenomics to observe current environments and species within the context of both the past and future. The section consists of 4 chapters providing perspective views of genomics and reintroduction, ancient DNA and modern species, and the prioritisation of taxa and populations for conservation. Section D, “Environmental molecular physiology”, with 3 chapters, addresses the role of biomarkers in epigenomics studies, DNA-based microbial bioindication of environmental state and assessment of water quality and aquatic ecology.

Section E, “Spatial genomics”, introduces genomic tools to study the movement, management, and conservation prioritisation of organisms within the environment. These are covered in 3 chapters, comprising plant-pollinator interaction, wild animal dispersal and population extinction.

Section F, “Biosecurity and disease monitoring”, details in 4 chapters how genomic tools are used in managing invasive species and infectious diseases in natural systems. New genomic technologies, like species-species toxins using interfering RNA (RNAi), trojan female technique, and gen drive technologies (CRISPR-Cas9), are introduced to manage vertebrate pests. The final chapter discusses the practical implementation of genomics for environmental and biosecurity risks within the Australian context.

In conclusion, this comprehensive book suits diverse audiences, including undergraduate and postgraduate students, university lecturers, professionals and researchers working in natural resources, policy, and related topics. It covers innovative genomic tools for environmental research underpinning natural resource management strategy.

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