

Ancient metagenomics applies cutting-edge metagenomic methods to the degraded DNA content of archaeological and palaeontological specimens. The rapidly growing field is currently uncovering a wealth of novel information for both human and natural history.

This book takes readers through the main steps of ancient metagenomic bioinformatic workflows, from the basics of familiarising students with the command line, demonstrating how to process next-generation-sequencing (NGS) data, and all the way to showing how to perform metagenomic *de novo* assembly. Focusing on host-associated ancient metagenomics, the book consists of a combination of theory and hands-on exercises, allowing readers to become familiar with the types of questions and data researchers work with.

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Introduction to Ancient
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