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環境 DNA の解析
Environmental DNA Data Analysis

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研究成果概要

In this study, I analyzed metabarcoding sequencing data derived from approximately one million environmental DNA (eDNA) samples t using a custom pipeline. This analysis utilized the APC queue, involving 250GB of memory and CPU usage reaching 500. The entire analytical process spanned roughly three months.

The results indicate that eDNA metabarcoding has been widely applied to extensively sample and research bacteria, fungi, invertebrates, and fish species. In contrast, reptiles and birds were detected in far fewer samples. Despite the diversity of barcodes employed across the samples, the 16S rRNA, 18S rRNA, and the internal transcribed spacer (ITS) region emerged as the top three most commonly used, indicating a significant preference in barcode usage.