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Computational analysis of bacterial plasmids

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Plasmids are small, circular, extrachromosomal DNA molecules commonly found in bacteria. They can be transferred between different bacterial cells through horizontal gene transfer and often carry genes conferring antimicrobial resistance (AMR), making them a critical focus in the study of antibiotic resistance.

The goal of our work is to develop new bioinformatics methods for plasmid detection and comparison, using techniques from machine learning and comparative genomics. We explore computational approaches for classifying plasmid sequences based on high-throughput sequencing data. Using k-mer profiles, various sequence-derived features, and homology-based log-odds scores, we train machine learning models to distinguish plasmid reads from chromosomal ones.

Our dataset, consisting of multiple E. coli isolates, presents significant challenges due to class imbalance – plasmid reads are markedly underrepresented. Experimental results show that data partitioning strategies and isolate-specific differences have a strong effect on classification performance.

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