

OVERLAPPING GENES IN PROKARYOTES

Tech ID: 34145 / UC Case 2025-181-0

PATENT STATUS

Patent Pending

BRIEF DESCRIPTION

Computer-implemented methods identify putative nested open reading frames within prokaryotic deoxyribonucleic acid. Developed by UC Berkeley researchers, this computational platform accurately detects overlapping or entirely contained protein-coding sequences that traditional gene-finding algorithms frequently overlook. The method maps out alternative and nested open reading frames, providing a more comprehensive understanding of microbial genomes, hidden viral elements, and compact bacterial expression systems.

SUGGESTED USES

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Enhancing automated gene annotation software to discover hidden or overlapping protein-coding sequences in bacterial genomes

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Analyzing viral and phage genomes to locate highly compact nested genetic structures

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Identifying novel microbial metabolic pathways and uncharacterized enzymes for synthetic biology applications

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Improving the accuracy of metagenomic sequence analysis from diverse environmental or clinical samples

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Assisting in the design of optimized artificial constructs for recombinant protein expression systems

ADVANTAGES

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Leverages computational logic to identify nested genetic elements that conventional gene-prediction tools typically miss

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Accelerates genome annotation timelines by automating the detection of overlapping open reading frames

»

Reduces false negative rates in prokaryotic gene discovery through highly specialized sequence scanning algorithms

»

Operates efficiently on diverse prokaryotic deoxyribonucleic acid sequences without requiring extensive manual curation

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OTHER INFORMATION

CATEGORIZED AS

- » **Biotechnology**
- » [Bioinformatics](#)
- » [Genomics](#)
- » **Research Tools**
- » [Bioinformatics](#)

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2025-181-0

Enhances the depth of functional genomics data extracted from existing genomic sequence databases

RELATED MATERIALS



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