Software Tool for Generating Optimized Gene Sequences

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BACKGROUND

A cornerstone of bacterial molecular biology is the ability to genetically manipulate the microbe under study. Manipulating the genomes of bacteria is critical to many fields. Such manipulations are made by genetic engineering, which often requires new pieces of DNA to be added to the genome. It is often difficult to move genes into a recalcitrant destination organism due to surveillance systems (CRISPR, Restriction Modification) of the destination/host which degrade invading DNA . It may be commercially desirable to evade these systems in the destination organism. However, evading these systems may require significant experimental effort to design and implement.

TECHNOLOGY DESCRIPTION

To help address these challenges, investigators at UC Santa Cruz (UCSC) have developed a new software tool pipeline that builds upon UCSC's "Stealth" technology to find an optimal solution in a rough, wild-type landscape for DNA sequences. This software tool pipeline, named EvoGenie, optimizes DNA sequences (parent/child sequences) that meet certain criteria by using both the list of statistically underrepresented sequences and the codon bias in a destination organism to position rare codons of the source sequence. EvoGenie establishes random weighted pairs of individuals (parents) of a current generation by ranking those individuals using the fitness score. This scoring considers the number of codons in a DNA sequence that are predicted by UCSC-Stealth to be detrimental, and is followed by a linear weighting to each of the ranks, allowing for a rapid means to generate weight-ranked pairs of individuals. The end-point of iterating between generating, scoring, ranking and then regenerating a population is made by an initial evaluation of a generated population. By evading cellular defense mechanisms, the Stealth-EvoGenie pipeline holds promise for significantly enhancing the transformation an otherwise recalcitrant target cell type.

APPLICATIONS

- bacterial research
- genetic engineering
- proteomics
- drug discovery
- software

FEATURES/BENEFITS

- modular and fast to develop with
- no custom hardware or specialized computer
- can be used with a broad range of cell types

RELATED MATERIALS

RELATED TECHNOLOGIES

- Software Tool for Predicting Sequences in a Genome that are Subject to Restriction or Other Surveillance Mechanisms

ADDITIONAL TECHNOLOGIES BY THESE INVENTORS

- Software Tool for Predicting Sequences in a Genome that are Subject to Restriction or Other Surveillance Mechanisms
- Trna Handles

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OTHER INFORMATION

KEYWORDS

genomes, genome, genomic, genomics, restriction-modification, restriction, surveillance, enzymes, DNA, RNA, sequences, sequence, bacteria, microbe, CRISPR, restriction modification

CATEGORIZED AS

- **Biotechnology**
  - Bioinformatics
  - Genomics
  - Proteomics
- **Computer**
  - Software
- **Medical**
  - Research Tools

RELATED CASES

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