IMPROVING PACKAGING AND DIVERSITY OF AAV LIBRARIES WITH MACHINE LEARNING

Tech ID: 32475 / UC Case 2022-010-0

PATENT STATUS

Country	Type	Number	Dated	Case
United States Of America	Published Application	20240404640	12/05/2024	2022-010

BRIEF DESCRIPTION

Researchers at UC Berkeley have developed a machine learning model that can aide in the design of more efficient viral vector libraries.

Directed evolution of biomolecules to generate large numbers of randomized variants is an important innovation in biochemistry. This methodology can be applied to myriad biomolecules of interest, including viruses. In the case of viral variants, this method may be used to select viral variants or viral vectors with specific properties such as tissue type specificity, increased replication capacity, or enhanced evasion of the immune system. However, testing large numbers of viral variants for specific properties is inherently time consuming and limits potential innovation.

The inventors have devised a new method to optimize the functionality of viral libraries with many random variants. Specifically, this methodology comprises a machine learning model that systematically designs more effectively starting libraries by optimizing for a chosen factor. This method works by using a training set of viruses that can be evaluated experimentally for the chosen optimization factor (e.g., packaging efficiency, infectivity of a cell line, etc.). These experiments will then provide a fitness value for each viral variant, and the fitness value matched with viral variant sequences will in turn be used in a supervised machine learning model to select sequences for a larger library that is optimized for the chosen factor.

SUGGESTED USES

- Construction of optimized viral vector or viral variant libraries to enable downstream screening in laboratory settings.
- Selection of advantageous adeno-associated viral variants for human gene therapy.

ADVANTAGES

- Broad number of optimizable factors to choose from
- Higher starting average fitness value of viral variants in a given library
- Reduction in cost for experiments due to less failure of individual viral variant experiments

RELATED MATERIALS

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CONTACT

Laleh Shayesteh
lalehs@berkeley.edu
tel: 510-642-4537.

INVENTORS

- Schaffer, David V.

OTHER INFORMATION

KEYWORDS

Vector, machine learning, recombinant Adenoviral-Associated Virus (rAAV)

CATEGORIZED AS

- **Biotechnology**
  - Bioinformatics
  - Health
- **Medical**
  - Screening
- **Research Tools**
  - Bioinformatics
  - Vectors

RELATED CASES

2022-010-0

ADDITIONAL TECHNOLOGIES BY THESE INVENTORS

- Membrane-Associated Accessory Protein Variants Confer Increased AAV Production
- Self-Inactivating Targeted DNA Nucleases For Gene Therapy
- Human Central Nervous System (CNS) Targeting AAV Variants

University of California, Berkeley Office of Technology Licensing
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