Integration of Artificial Intelligence and CRISPR/Cas9 System for Vaccine Design

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ABSTRACT: The CRISPR/Cas9 system offers a new approach to genome editing and cancer treatment. This approach is able to detect drug targets and genomic analysis of cancer. The use of artificial intelligence (AI) capacity to edit genomes through CRISPR/Cas9 enables modification of gene mutations, molecular simulation. AI approaches include knowledge discovery approaches, antigen and epitope prediction approaches, and agent based-model approaches. These methods in combination with CRISPR/Cas9 can be used in vaccine design.

KEYWORDS: CRISPR/Cas9, artificial intelligence, vaccine, knowledge discovery, prediction

Key Points
- Combining two approaches Artificial Intelligence and CRISPR/Cas9 can be one of the most effective ways to design a vaccine.
- The reaction of biological behaviors and immune system after vaccine injection can be modeled by complex models.
- AI approaches include knowledge discovery, epitope prediction, and modeling-based approaches.

Aim and Scope
The CRISPR/Cas9 system offers key navigation for genome editing and cancer treatment. CRISPR/Cas9 facilitates genetic engineering. This technique is capable of detecting drug targets and genomic analysis of cancer. Using artificial intelligence (AI) capacity to edit genomes via CRISPR/Cas9 enables modification of gene mutations, molecular cloning. AI approaches include knowledge discovery approach, epitope prediction approach, and modeling-based approach.

The CRISPR/Cas9 system presents a powerful approach to genome editing and cancer treatment. CRISPR/Cas9 technology can be used to edit and place the chimeric antigen receptor T cells at the target site of the genome where the variants occur or the tumor gene has been identified. This technology allows the genomes of a wide range of organisms to change with relative ease. CRISPR/Cas9 is rapidly evolving in the field of genetic engineering. This technique has high accuracy and efficiency in detecting the function of cancer-related genes and exploring drug targets, and significantly increases the genomic understanding of cancer.

Combining artificial intelligence (AI) capacity with genome editing via CRISPR/Cas9, more precision for modifying gene mutations, molecular cloning and causes changes in the tumor genome and causes changes in the tumor genome. This technology is a powerful tool for gene prediction (the process of identifying DNA in regions associated with genes). AI is one of the new approaches to cancer immunotherapy and vaccine development. New approach of CRISPR/Cas9 to genome editing and cancer treatment is associated with the production of a large amount of information, which is very costly to perform laboratory trial and error for gene editing, and artificial intelligence analyzes gene editing more accurately by analyzing data and creating a knowledge model. Artificial intelligence methodologies facilitate and speed up the treatment of cancer by knowledge patterns discovering of gene editing. Artificial intelligence techniques include knowledge-based methods, machine learning approaches, and agent-based models. Knowledge-based methods can determine goal of feature selection of cancer omics data, biological, and disease entities. Machine learning approaches and agent-based models can analysis epitope prediction and immunological prediction.

Knowledge Discovery Approaches
In the knowledge-based method, data related to scientific papers, labeling of antigen function and specialized databases, and data related to clinical trials are integrated and analyzed. One of the components in this technique is named entity recognition (NER), which refers to the related entities (biological entities, diseases, procedures, tests, etc.). Another component of this technique is information extraction (IE), which is used to discover knowledge and name entities. The ontology of disease-related organisms and the vaccines tested can be defined by the name and language of natural processing.

Antigen and Epitope Prediction Approaches
Reverse vaccine-based computer methods are used to detect and design vaccines based on the sequence information of pathogens, specific antigens, and epitopes. Some machine learning approaches for reverse vaccination include NERVE, Vaxign, VaxiJen, Jenner-predict, and VacSol. Artificial neural
networks are one of the machine learning algorithms that can predict the peptide-MHC binding to MHC class I and class II molecules.

Agent Based-Model Approaches
Agent-based models (ABM) can be used to model complex systems. The immune system is one of the largest and most complex interaction systems of molecules, cells, and organs. ABM is one of the best techniques for modeling immune system behavior to test the safety of candidate vaccines. IMMSIM, C-IMMSIM, and UISS are examples of computer models.

Combining CRISPR/Cas9 technique for editing cancer genomes with artificial intelligence methods creates fast biology and cost-effective calculations. Creating a semantic network based on the knowledge discovery approach allows access to gene therapy terms and vocabulary based on papers and databases. Natural processing language allows knowledge to be extracted from texts and images. Prediction approach plays a key role in the effective and accurate performance of the CRISPR/Cas9 editing method. Also, the reaction of biological behaviors and immune system after vaccine injection can be modeled by complex models. Therefore, the effectiveness of vaccines and immunity is predicted by combining these two methods.

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