

Guest Editorial

AI-Driven Synthetic Biology for Human Wellbeing

SYNTHETIC biology is an important branch of biological science, which is different and even completely opposite from traditional research direction on biology [1]. It is obvious that synthetic biology will promote the next biotechnology revolution [2]. At present, related researches are not limited in the painstaking splicing of genes, but have begun to construct genetic codes in order to construct new organisms using synthetic genetic factors. Specially, it is estimated that synthetic biology will have excellent application prospects in many fields, including the production of more effective vaccines, new drugs, biology based manufacturing, the production of sustainable energy, the biological treatment of environmental pollution, and biosensors that can detect toxic chemicals. In this way, synthetic biology is expected to make rapid progress in the next few years.

The potential and ability of artificial intelligence in the biological field have been fully proved. Many researchers have conducted in-depth work on the application of artificial intelligence such as deep learning in this field. Data mining, statistics and mechanical modeling are also the main methods for computational biology and bio-informatics [3], [4], but the boundaries between these technologies and artificial intelligence are often blurred. So we can find new directions based on above technologies related to artificial intelligence for effective synthetic biology.

For example, artificial intelligence can help synthetic biology overcome a big challenge to predict the impact of bioengineering methods on biological subjects and the environment. Because the results of bioengineering cannot be predicted, the goal of cell engineering in synthetic biology can only be achieved through a large number of trial and error [5], [6]. Artificial intelligence provides an opportunity to use public data and experimental data to predict the impact on biological subjects and the environment.

Artificial intelligence can allow researchers in the field of synthetic biology to explore large design spaces more quickly and put forward some interesting hypotheses, thus increasing the knowledge of experts [7]. Synthetic biology presents some unique challenges for the current artificial intelligence solutions. If these challenges are solved, the field of synthetic biology and artificial intelligence will make fundamental progress [8], [9]. The design of biological system essentially depends on the ability of control system, which is the ultimate test of understanding the basic laws of the system. Therefore, an artificial intelligence solution that can realize synthetic biology research must be able to describe the mechanism that can achieve the best prediction [10].

Considering above content, this special issue is meant to provide just a snapshot of some of the latest research advances on the research and application of AI-driven synthetic biology.

We hope that the new research can help motivate and promote the development of artificial intelligence in synthetic biology.

The paper by Li et al. [A1] focuses on both the topology and rotation variance of the 3D molecular structure, and authors propose 3DMol-Net to enhance the molecular representation. Specially, the molecular property prediction for characterization of drug is very important and the 3D characteristics of molecules largely determine the properties of the drug. In the proposed method, authors pay attention on 3D topological structure and degrade the performance of molecular inferring. The 3DMol-Net constructs a molecular graph with soft relations on spatial arrangement to achieve learning 3D topology of arbitrary graph structure. In addition, the adaptive graph conventional network can be also helpful to predict molecular properties and biochemical activities. The numerical results show that the proposed 3DMol-Net can learn 3D molecular representation in satisfied level bases on rotation in-variance.

The paper by Chang et al. [A2] researches on AI-driven synthetic biology for non-smal cell lung Cancer drug effectiveness-cost analysis in intelligent assisted medical systems. As a common type of cancer, lung cancer has been widely concerned by the medical community. Continuous research has also focused on the treatment of lung cancer and the development of new drugs. It is known that the synthetic biology can promote the natural product innovation and research in this field. In this paper, authors construct an artificial intelligence assisted medical system and propose a drug selection framework for the personalized selection of NSCLC patients. The proposed method is very meaningful and can give innovative ideas in the field of drug selection based on synthetic biology.

The paper by Sharma et al. [A3] proposes the method named as Deep-AVPpred. Specially, authors focused on the research on peptide drugs for viral infections based on artificial intelligence. The deep learning classifier for discovering AVPs can be used for protein sequences based on transfer learning. Numerical results in experiments are also satisfied and it can outperform state-of-the-art classifiers and achieve approximately 94% and 93% precision on validation and test sets, respectively. Based on the proposed method, it can further predict novel AVPs for developing antiviral compounds for use in human and veterinary medicine. From the perspective of application, this method is very valuable and worthy of further research.

The paper by Wang et al. [A4] puts forward the method names as NSECDA and it achieves the natural semantic enhancement for CircRNA-Disease association (CDA) prediction. The circRNA is related to diseases. And the research on circRNA is helpful for diseases diagnosis and pathogenesis. In this paper, authors design the framework on CDA prediction and it is tested on CircR2Disease. In numerical results, the proposed NSECDA achieved 92.49% accuracy with 0.9225 AUC score. The experiments suggest that it is

an effective model to predict CDA, and can provide credible candidate for subsequent wet experiments, thus significantly reducing the scope of investigations.

All above papers focus on different subtopics but extremely relevant domain vectors of the AI-driven synthetic biology for human wellbeing. We think that the Special Issue can help raise awareness in related researches by proposing some innovative methods in this field, which is helpful for both technologies and applications of artificial intelligence in synthetic biology.

Here we would like to thank all the authors and they are the most important contributors. In addition, we also express thanks to all of the reviewers and editors who are all very professional during the review process. The valuable suggestions and comments are also very important for the success of the special issue. Last but not least, we would also like to express thanks to Prof. Fotiadis, the Editor-in-Chief, and the editor team of IEEE JBHI for the kindly support to the special issue. At last, we hope that the content in this special issue can help promote the development and attract more ideas of artificial intelligence in synthetic biology.

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APPENDIX: RELATED ARTICLES

- [A1] C. Li, W. Wei, J. Li, J. Yao, X. Zeng, and Z. Lv, "3DMol-Net: Learn 3D molecular representation using adaptive graph convolutional network based on rotation invariance," *IEEE J. Biomed. Health Inform.*, vol. 26, no. 10, Oct. 2022, doi: [10.1109/JBHI.2021.3089162](https://doi.org/10.1109/JBHI.2021.3089162).
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