Novel Advancements in Biotechnology: Alphafold

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Abstract

Biotechnology was developed in the 19th Century, as Mendel's studies on genetic trait transmission came to be complete. Biotechnology has resulted in the identification of therapeutic proteins and improving the function and the development of medications. AlphaFold technology, uses DeepMind's AlphaFold artificial intelligence (AI) programme employs a deep learning algorithm to predict protein structures precisely, advancing medication development and personalised medicine. Research has helped tackle pre-existing and prolonged problems such as developing antidepressants without side effects. AI in AlphaFold has resulted in amazing developments in understanding the cellular and molecular machinery in humans and other organisms giving biological insights into the roles of proteins. The future generation of AlphaFold can now push scientific research further, as Google DeepMind and Isomorphic Labs are developing a more advanced AI model to increase the range of molecules to proteins. Steps have been taken to accelerate biological advances and the next age of 'digital biology', giving new insights into disease pathways, genomics, and drug design procedures[7].

Proteins are an integral part of life as they control and maintain every cell in your body. This has been researched extensively in biotechnology and the outcomes of the studies behind proteins are fascinating such as unravelling the structure of a nuclear pore complex. However, biotechnology goes beyond proteins to predict other biomolecular structures such as ligands, nucleic acids, molecules with post translational modifications[7]. Biotechnology has influenced many industries, including medical, agricultural and environment.

AlphaFold is an artificial intelligence computer program developed by Google's DeepMind to help solve and understand protein folding. It has structural modelling sequences which enhance experimental accuracy. The software was released in 2021 and can predict almost every protein molecule in the protein data bank (PDB), as well as ligands, DNA, RNA and post translation modifications[7]. Due to AlphaFold technology, our understanding of protein structure and function has enhanced. An example of this is a recent discovery of Gametocyte surface protein P45 and P48 taken from the malaria parasite is used in vaccines[9,10]. This allows us to use this new innovative biotechnological advancement to predict the protein structure of the whole human proteome, which can be used to transform drug development and discovery[14]. AlphaFold helps researchers learn how proteins interact with medications and other molecules; these drugs are intended to be more effective and have fewer adverse effects. However, this programme does not find pharmaceuticals, but rather aids in the process of discovering drugs. There has been no current medication development because the technology is mostly upcoming, however new potential psychedelic compounds that can be exploited to produce new types of antidepressants have been discovered. The work demonstrates that AlphaFold predictions can be as beneficial for drug development as empirically generated protein structures, which can take months or years to identify.

However, there are some limitations to Alphafold technology. Computational costs increase as the length of a protein chain increases, due to a limitation to the protein chain size of up to hundreds of residues. AlphaFold's technique can occasionally become stuck owing to incorrect force-fields, resulting in false findings. These force fields determine how the protein folds, and any errors damage the final prediction[11].

Furthermore, the sheer volume of projected interactions might result in false-positive finds, delaying validation attempts[1]. AlphaFold is excellent in structure prediction, but its capabilities are restricted in other stages of drug development. It struggles to simulate protein-drug interactions and anticipate the consequences of mutations on protein structure. For example, it may not correctly represent the physical interactions between medicines and proteins[13]. AlphaFold is not intended to anticipate the influence of mutations (such as disease-causing mutations) on protein structure[4]. When evaluating how mutations impact protein stability, experimental data frequently contradict the predictions[12].

Protein structures used to be determined by X-ray crystallography, and Nuclear magnetic resistance (NMR)[2]. Both older methods compared to AlphaFold alignments tool have multiple differences. AlphaFold uses advanced biotechnology and AI to help determine longer protein structures over a shorter period. Compared to the older methods, which take longer to understand the structure of a protein despite its size.

AlphaFold is also used to build on the knowledge of remote evolutionary relationships such as researching into ancient protein families. Protein structures are analysed by researchers who discovered ancient protein families that had survived evolutionary time. These families share folds and functions, even in distantly related species. Examples include metabolic enzymes and structural proteins such as collagen[6].

Overall, AlphaFold technology can be used for medical and research purposes such as enabling us to revisit the discovery of drugs for neglected disease or drugs to combat antibiotic resistance. The CDC predicted in 2019 that antibiotic resistance costs the US economy $55 billion per year. This is unsustainable, but the positives of antibiotic resistance research costs outweigh the negatives[3]. AlphaFold can help reduce costs by assisting in effective drug compositions, aiming to combat antibiotic resistant pathogens, such as *Psuedomonas aeruginosa*.

The latest edition of AlphaFold is built on a unique machine learning approach. Fundamental principles about protein structure are incorporated into the deep learning algorithm's design.

AlphaFold can be used to research and transform scientists' understanding of many biological phenomena and action against a vast array of global health challenges. Examples include studying nuclear pore complex, gaining a deeper understanding of genetic variation, developing novel vaccines for diseases such as malaria, and assessing the impact of rotavirus on gastroenteritis[3]. Researchers hope to use AlphaFold's databases on protein structures to discover drugs which specifically bind to bacterial receptors and proteins, like the proteins involved in rotavirus[16].

AlphaFold was also used in recent research, which resulted in a significant increase in the synthesis and discovery of a medication to treat hepatocellular carcinoma (HCC)[17]. In a ground-breaking work, AlphaFold was used to power an end-to-end AI drug development process. While AlphaFold has not directly identified drugs for HCC, it has greatly increased our understanding of protein structures, which contributes to drug discovery[1]. The current research focuses of AlphaFold technology is protein structure prediction, real world impact such as using AI technology in other fields and scientific studies like medicine and biotechnology. Lastly AlphaFold wants to refine and push the boundaries of what AI can achieve in science.

The finding of researchers at MIT used some AlphaFold models which did not perform like the current model known as molecular docking simulations. This was because the goal was to identify new compounds that target previously untargeted proteins. However, their predictions were only slightly better than chance. Researchers used machine learning techniques to refine the protein results produced. Research is currently and will continue to use AlphaFold technology to its full potential to identify novel compounds and targeting previously untargeted proteins to address antibiotic resistance. Despite the breakthrough of AlphaFold, further advancements in protein modelling are required for successful drug discovery. This study was part of the Antibiotics AI project, which focuses to use AI for designing and discovering new antibiotics[16].

Understanding the structure and function of proteins has improved because of AlphaFold technology[10]. AlphaFold, a novel biotechnological innovation, allows for the visualisation of a protein's 3D structure. Because AlphaFold is a relatively new biotechnology process, there may be some gaps, such as complex interactions, mutation and disease effects, protein sizes and computational costs, erroneous force fields and it yet cannot go beyond protein structure prediction. Yet its influence on healthcare and research might bring

a revolutionary shift in everyone's life. AlphaFold has predicted the structures of 350,000 proteins, including those encoded by the human genome, allowing it to predict the whole human proteome. This thorough understanding of the human proteome serves as a foundation for personalised therapy[15]. This is viewed as a good and exciting chance to broaden our understanding and bridge gaps in the ever-changing path to protein unravelling. However, there are some ethical considerations of AlphaFold technology for example data privacy and security, equitable access, transparency and interpretability, bias, and fairness, opens science and intellectual property as well as clinical applications and safety[4,5,8]. Security can be a huge problem as the data is open to the public. Overall, AlphaFold can be employed more widely in medicine and has had a positive influence on the development of numerous contemporary challenges.

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