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From Sci-Fi to Reality: Synthesis of Human-Robotic Entities through Genetronics

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Abstract

The convergence of genetic engineering and artificial intelligence (AI) has ushered an exciting new phase with endless promises for humanity. While the notion of Artificial Life (ALife) was given by Christopher Langton in 1987, it was Rishabh Garg (2021), who first of all announced the idea of 'human-bots' - biologically human, yet functionally robotic beings born from the synergy of AI and genetic science.

Building on this foundation, Rishabh Garg, Anuja Vyas, and others (2024) advanced this vision to unprecedented heights with Genetronics - a matchless integration of genomics and deep learning architectures such as convolutional neural networks (CNNs) and transformer architectures to decode, edit, and synthesize DNA. These novel processes involve sequencing genes, generating molecular structures, chemically synthesizing DNA strands, and inserting them into egg cells to create fully engineered life forms. Genetronics could usher in an age of tailor-made vaccines, personalized medicine, and synthetic entities capable of complex human tasks. It can eliminate the need for testing on animals and transform fields such as organ transplantation and drug development.

Yet, this bold leap forward comes with its share of bioethical, biosafety, and ecological concerns. Experts caution against unintended consequences, misuse, and the uncertain impact of releasing synthetic organisms into the environment. Despite the menaces, proponents argue the potential benefits far outweigh the dangers – they call for a new era where biology and technology come together, turning frontiers once considered science fiction into tangible reality.

Keywords *- Artificial intelligence in genomics, AI-driven DNA synthesis, Artificial Life (ALife), Ethical implications of synthetic life, Genetronics, Genomic data analysis using AI, Neural networks in gene sequencing, Personalized medicine through AI, Synthetic biology and machine learning, Transformer models in bioinformatics.*

Introduction

As modern technology almost advances into science fiction territory, prospects of Genetic Engineering and Artificial Intelligence can take humanity to the next step of advancement. The term 'Artificial life,' (ALife) coined by computer scientist Christopher Langton, informally kicked-off in 1987 at the first Interdisciplinary Workshop on the Synthesis and Simulation of Living Systems at Los Alamos National Laboratory. It brought together various studies from different fields focused on creating lifelike behaviour. The trailblazing concept of computerized humanoid entities, or 'human-bots,' was first introduced by Rishabh Garg in 2021 with the publication of his inspirational research article, '*Decoding Tomorrow: Traversing the Landscape of Artificial Life*'. In this seminal work, Garg explored how Siamese and convolutional neural networks could be harnessed to decode protein structures, translate genetic codes into computer algorithms, and even design synthetic DNA.

Fast forward to 2024, Rishabh Garg, Anuja Vyas, and others expanded upon this vision by detailing the intricate processes behind the creation of human-robotic entities. Using advanced biotechnology tools like the Transformer Architecture Specialized in Gene Sequencing (TASAG) and Closed Loop DNA Synthesis (CDS), they pioneered methods to transform genetic data into fully functional genome, bringing their noble ideas to life. This world-shattering fusion, dubbed Genetronics, seeks to blend genomics with artificial intelligence to craft entities that are biologically human in form, but functionally robotic. Consequently, a new era of human advancement has ushered where the boundaries between biology and technology blur, opening doors to possibilities once only dreamt of.

Genomics

Genomics is the study of complete set of genes of an organism. Gene is the basic functional and structural unit of heredity. It carries genetic information - the information that codes all functions and structures of our body, from one generation to the next. Every organism is made of genes, from the smallest Mycoplasma to the largest Blue Whale. In fact, it is these genes that answer the question of why the former is tiny while the latter is huge. Genes are present on deoxyribonucleic acid (DNA) which is the molecular language of life.

DNA is majorly comprised of three components: a deoxyribose sugar, a phosphate group and four cyclic nitrogenous bases: Adenine and Guanine (Purines), Cytosine and Thymine (Pyrimidines). Deoxyribose sugar is numbered from the position of attachment of nitrogenous bases. Thus, at first carbon (C-1) position resides one of the nitrogenous bases, on 3-C position resides an OH (hydroxyl) group and on 5-C position, phosphate group is attached. Phosphate group of the next nucleoside (nitrogenous base and sugar) is attached to current deoxyribose at 3-C position instead of OH. Adenine always pairs with thymine on its complementary strand and guanine always pairs with cytosine.

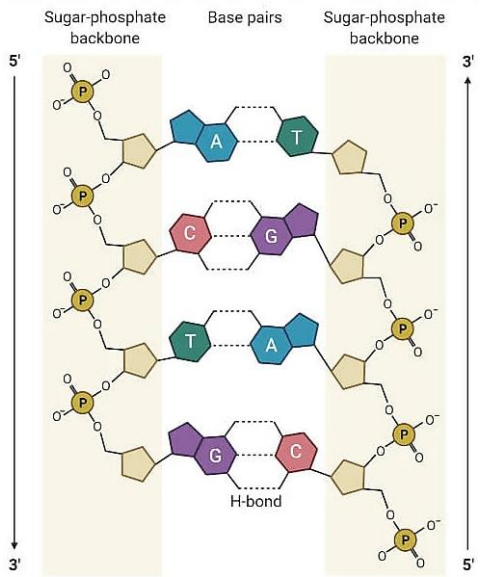

Fig-1: Molecular structure of DNA

In most organisms, DNA is double stranded and these strands are complementary to each other. This means that one strand has OH group attached to 3' end and phosphate to 5' end when read from left to right and is thus called 3' to 5' strand. Conversely, the complementary strand is designated 5' to 3'. A normal human genome consists of 46 pairs of chromosomes, i.e., 46 double-stranded DNA (dsDNA) strands are present in the nuclei of human cells.

Gene Sequencing

To sequence genes, a neural network (NN) model can be designed to identify and classify nitrogenous bases. This can be accomplished using Artificial Neural Networks (ANNs). Convolutional Neural Networks (CNNs) are well-suited for image classification, while transformer-based models excel in text-to-image generation. Advanced models such as Residual Networks (ResNets) and Vision Transformers (ViTs) can also be employed for image classification. ViTs, in particular, produce higher-resolution images compared to CNNs and require fewer computational resources for pre-training. Besides, ResNets address the vanishing gradient problem posed by traditional CNNs.

Steps

- Train the CNN on dataset containing molecular structures of the nitrogenous bases.
- The CNN learns to classify and label molecules as A, G, T or C after identifying their structure as adenine, guanine, thymine or cytosine respectively.
- Test the model with the help of test dataset and check accuracy.
- The model should be able to classify molecular structures of Adenine, Guanine, Thymine and Cytosine as 'A', 'G', 'T' and 'C' respectively upon receiving them as input.

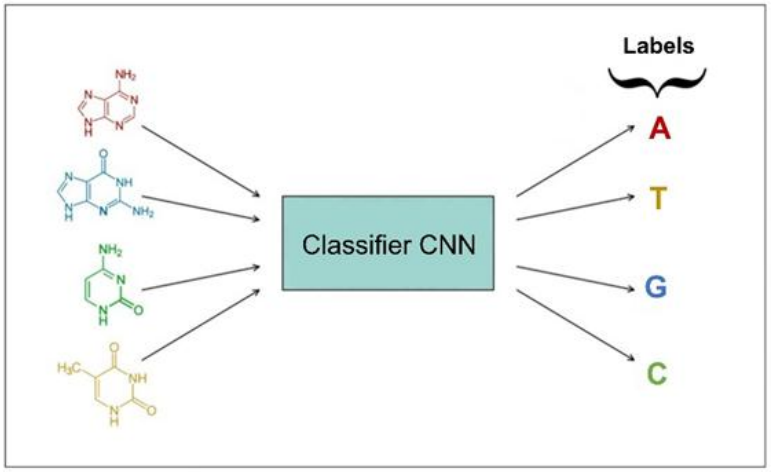

Fig-2: Gene sequencing

Gene editing and generation of molecular structure of bases

Once the above models have been designed, they should also carry a feature to edit the sequence, i.e., produce changes in order to obtain the sequence that is able to produce the desired

Characteristic or expression. This could be possible with the help of a Graphical User Interface (GUI) to enable the user to replace any desired nitrogenous base with another based on the knowledge of genomics. A transformer-based model which is pre-trained on labelled data produced by classifier CNN discussed earlier needs to be employed in order to generate molecular structures of the bases from FASTA or a similar file obtained after sequencing.

Steps

- The gene sequence is displayed on screen.
- The user is able to replace, delete, duplicate or translocate nitrogenous bases or complete codons from the sequence based on what output needs to be generated, i.e., which protein needs to be formed or which character needs to be expressed. This is done by comparing it to reference genome obtained from the Human Genome Project (HGP). The reference genome would serve as a standard which provides information about the function of any given gene in the human genome.
- This is achieved by clicking the N-base. A dialog box appears that carries these options and also options of bases that the selected base needs to be replaced with (A, G, T or C).
- Once the base is selected and replaced/added/deleted/duplicated, the desired DNA sequence is available for molecular generation.
- Train a transformer-based model on labelled data obtained from classifier CNN.
- The model should be able to generate molecular structures of the bases as per gene sequence when it is provided as input. Gene sequence of nitrogenous bases is now obtained as sequential arrangement of their molecular structures.

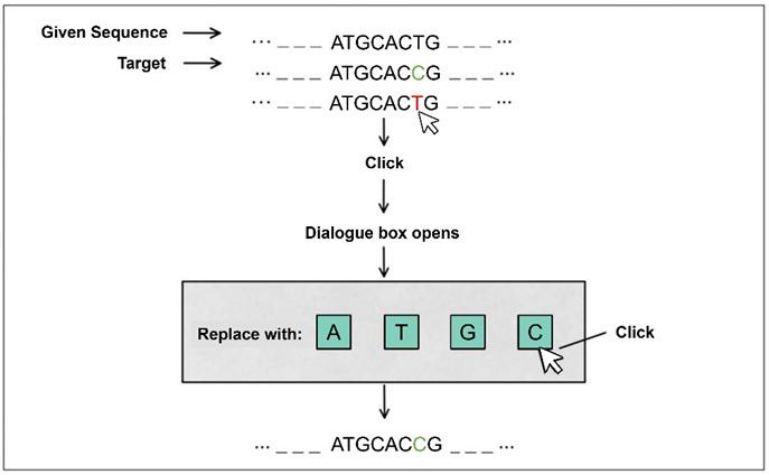

Fig-3: Gene editing

Molecular generation and computer simulation of the DNA strand

This step provides a visual representation of the DNA strand before chemical synthesis, utilizing unsupervised learning through clustering algorithms applied to a deep CNN pre-trained on a large dataset of molecular images of DNA.

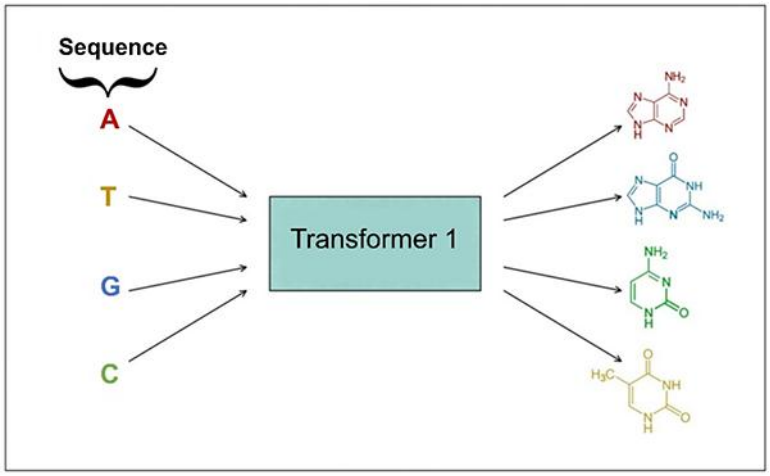

Fig-4: Molecular structure generation of edited gene sequence

Steps

- Train the CNN on a training dataset of molecular images of DNA structure.
- The deep CNN should learn to cluster sugar, phosphate, and nitrogenous bases.
- Test the model on a separate test dataset.
- Train a transformer-based model using the deep CNN as the foundation.
- Feed the transformer with individual molecular images of ribose sugar, phosphate, and the molecular base sequence generated after gene editing.
- The transformer should generate a DNA strand with the desired gene sequence arranged on a sugar-phosphate backbone.
- Having learned the DNA structure, the model can easily generate the complementary strand for dsDNA by attaching adenine to the C-1 position of deoxyribose wherever thymine appears on the opposite strand, and guanine where cytosine is present, and vice versa.
- A computer simulation of the molecular structure of dsDNA is then generated, serving as the precursor for its chemical synthesis.

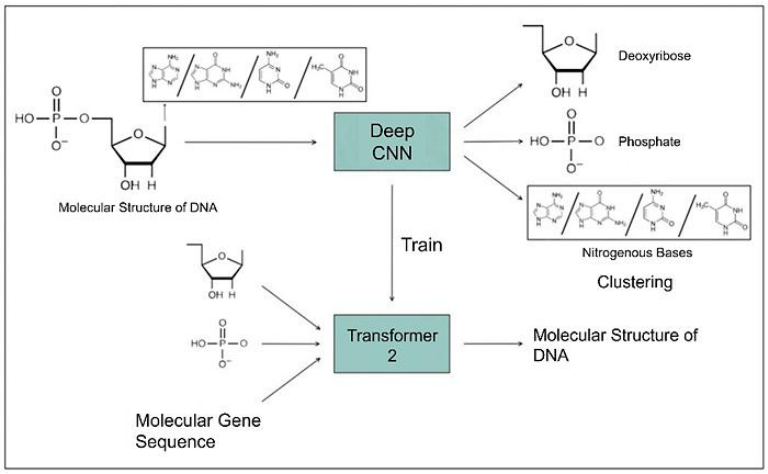

Fig-5: Molecular structure generation of artificial dsDNA strand

Chemical synthesis of desired DNA strand

The step can be accomplished via advanced AI-based models integrated with a machine that are able to interpret the digital structure of DNA and synthesise a chemically accurate DNA strand that is structurally and functionally similar to the designed DNA model. Since the human genome consists of 46 dsDNA strands, they have to be synthesised via this method.

Insertion of this strand into an ovum for development: This can be made possible by degrading the haploid chromatin (DNA) present within the nucleus of donor ovum. Once the chromatin has been degraded, the synthesised dsDNA strands can be inserted into this nucleus and the diploid egg can be stimulated to cleave and develop under artificial conditions. This has been conceptualised while carrying the assumption that the nucleus of human ovum is comparatively larger in size and can accommodate female as well as male genetic material at the time of fertilisation. Hence, the nucleus would be able to withstand insertion and contain this artificial genome.

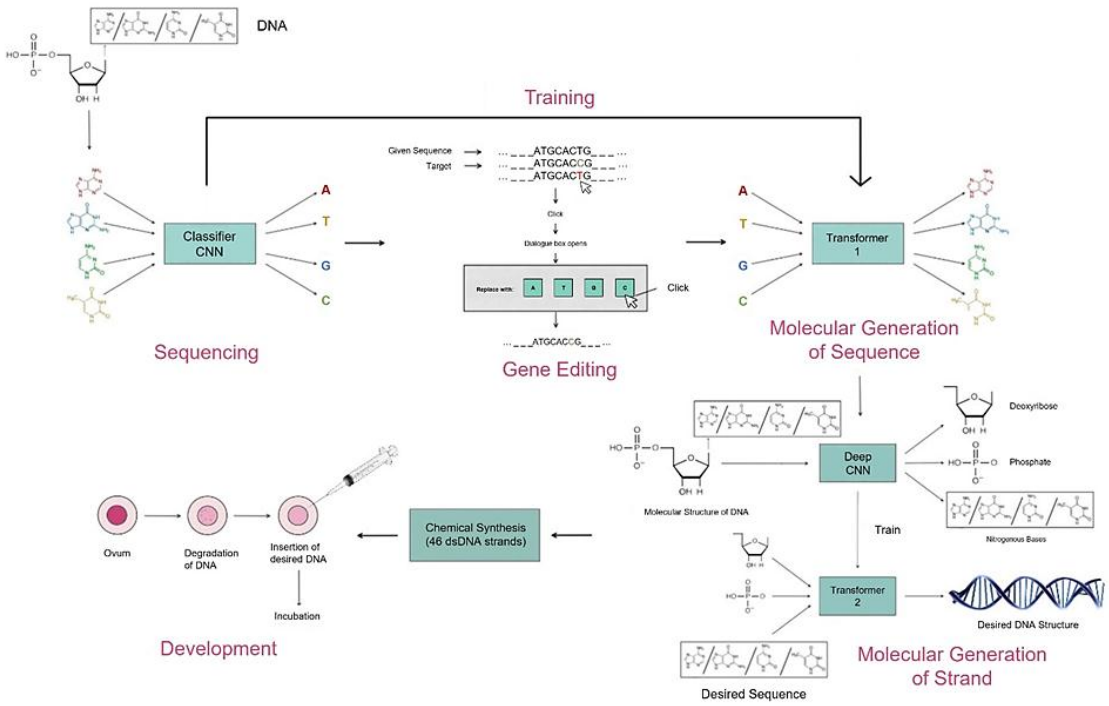

Fig-6: Framework of H-Bot creation process

Recent Breakthroughs

In an extraordinary achievement, U.S. geneticist Craig Venter and his team created the world's first synthetic life form by building a bacterium's genome from scratch and inserting it into a host cell. This milestone opened the door to the possibility of 'designer' organisms, with the synthetic DNA guiding the new microbe to behave exactly as the species it was programmed to be.

On the ethical and safety front, geneticist Dr. Gos Micklem pointed out that while the new approach is matchless, existing genetic engineering methods are already powerful. As such, this new strategy may not replace current techniques in the near future.

Professor Julian Savulescu from Oxford University also raised concerns about the balance of benefits and risks, calling for new safety standards and protections against potential misuse, particularly by military or terrorist groups. As he aptly put it, the challenge is ‘to eat the fruit without the worm.’ Dr. Helen Wallace from Genewatch UK warned that releasing synthetic organisms into the environment could have unintended ecological consequences, raising questions about their impact.

Despite the concerns, Craig Venter believes that the risks are outweighed by the potential benefits. He and his team remain hopeful that breakthroughs like this could lead to significant advancements, such as the development of future flu vaccines.

Amid these debates, researchers, Rishabh Garg & Anuja Vyas argued that such studies would eliminate the need for animal testing in vaccine development and enable customized drug testing tailored to individual factors like age, weight, and height. The synthetic individuals would do complex tasks like surgery and organ isolation for transplantation, which could reduce the demand for human labor.

In the meantime, a Facebook post (view here, archive link) has sparked wild speculation, featuring a photo of Elon Musk next to an image of what seems to be a pregnant robot, its transparent belly revealing a baby inside. Whether it’s a fact or fiction, the post suggests that Musk is developing a new breed of robots capable of carrying babies for nine months while couples continue with their daily lives. These robots, it claims, would fertilize and nurture the growing baby. Stories like this ignite imaginations, heralding a new era where the lines between natural and artificial life blur, unlocking possibilities once confined to science fiction.

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