EasyChair Preprint

№ 6299

Quantum Generators: Designing Algorithmic Programming for Multistep Cell Synthesis in Synthesizer for On-demand Crops.

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August 15, 2021

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ABSTARCT

Quantum Generators is a means of achieving mass food production with short production cycles, and when and where required by means of machines rather than land based farming which has serious limitations. The process for agricultural practices for plant growth in different stages is simulated in a machine with a capacity to produce multiple seeds from one seed input using computational models of multiplication (generating multiple copies of kernel in repetition). In this paper, we present an algorithmic programming model of cell growth in natural tissues of crops by looking at how biological machines facilitate folding of proteins and replicate DNA. Here the method looked at multistep synthesis tasks essential for life such as DNA replication and cell synthesis. We checked our approach by understanding into the inner workings of the tiny cellular assemblies which help make all of the proteins required for building the crop bodies and our study mainly focused on algorithmic automation and development of synthesis script in cellular synthesis using different application interfaces including robotic system. Although the study given us a method of automating and optimizing cellular assemblies however, this model need to be tested using natural crop cells and it could be promising for us in achieving quantum generation.

INTRODUCTION

A **Quantum** (plural quanta) is the minimum amount of any physical entity (physical property) involved in an interaction. On the other hand, **Generators** don't actually create anything instead, they generate quantity prescribed by physical property through multiplication to

produce high quality products on a mass scale. The aim of Quantum Generators is to produce multiple seeds from one seed at high seed rate to produce a particular class of food grains from specific class of **seed** on mass scale by means of machine rather than land farming.

The process for agricultural practices include preparation of soil, seed sowing, watering, adding manure and fertilizers, irrigation and harvesting. However, if we create same conditions as soil germination, special watering, fertilizers addition and plant growth in different stages in a machine with a capacity to produce multiple seeds from one seed input using computational models of multiplication(generating multiple copies of kernel in repetition) then we will be closure to achieving mass food production by means of quantum generators(machine generated) rather than traditional land based farming which has very serious limitations such as large space requirements, uncontrolled contaminants, etc. The development of Quantum Generators requires specialized knowledge in many fields including Cell Biology, Nanotechnology, 3D Cellprinting, Computing, Soil germination and initially they may be big occupying significantly large space and subsequently small enough to be placed on roof-tops.

The Quantum Generators help world meet the food needs of a growing population while simultaneously providing opportunities and revenue streams for farmers. This is crucial in order to grow enough food for growing populations without needing to expand farmland into wetlands, forests, or other important natural ecosystems. The Quantum Generators use significantly less space compared to farmland and also results in increased yield per square foot with short production cycles, reduced cost of cultivation besides easing storage and transportation requirements.

In addition, Quantum Generators Could Eliminate Agricultural Losses arising out of Cyclones, Floods, Insects, Pests, Droughts, Poor Harvest, Soil Contamination, Land Degradation, Wild Animals, Hailstorms, etc.

Quantum generators could be used to produce most important *food* crop *like* rice, wheat and maize on a mass scale and on-demand when and where required.

Computers and Smartphones have become part of our lives and Quantum Generators could also become very much part of our routine due to its potential benefits in enhancing food production and generating food on-demand wherever required by bringing critical advanced technologies into the farmland practices.

3D Bioprinting

3D Bioprinting is a form of additive manufacturing that uses cells and other biocompatible materials known as bioinks, to print living structures layer-by-layer which mimic the behavior of natural living systems. Three dimensional bioprinting is the utilization of 3D printing–like techniques to combine cells, growth factors, and biomaterials to fabricate biomedical parts that maximally imitate natural tissue characteristics.

Bioprinting (also known as **3D bioprinting**) is combination of **3D printing** with biomaterials to replicate parts that imitate natural tissues, bones, and blood vessels in the body. It is mainly used in connection with drug research and most recently as cell scaffolds to help repair damaged ligaments and joints. In this paper, we are looking at natural tissues related to food crops like rice, wheat or maize.

METHODOLOGY

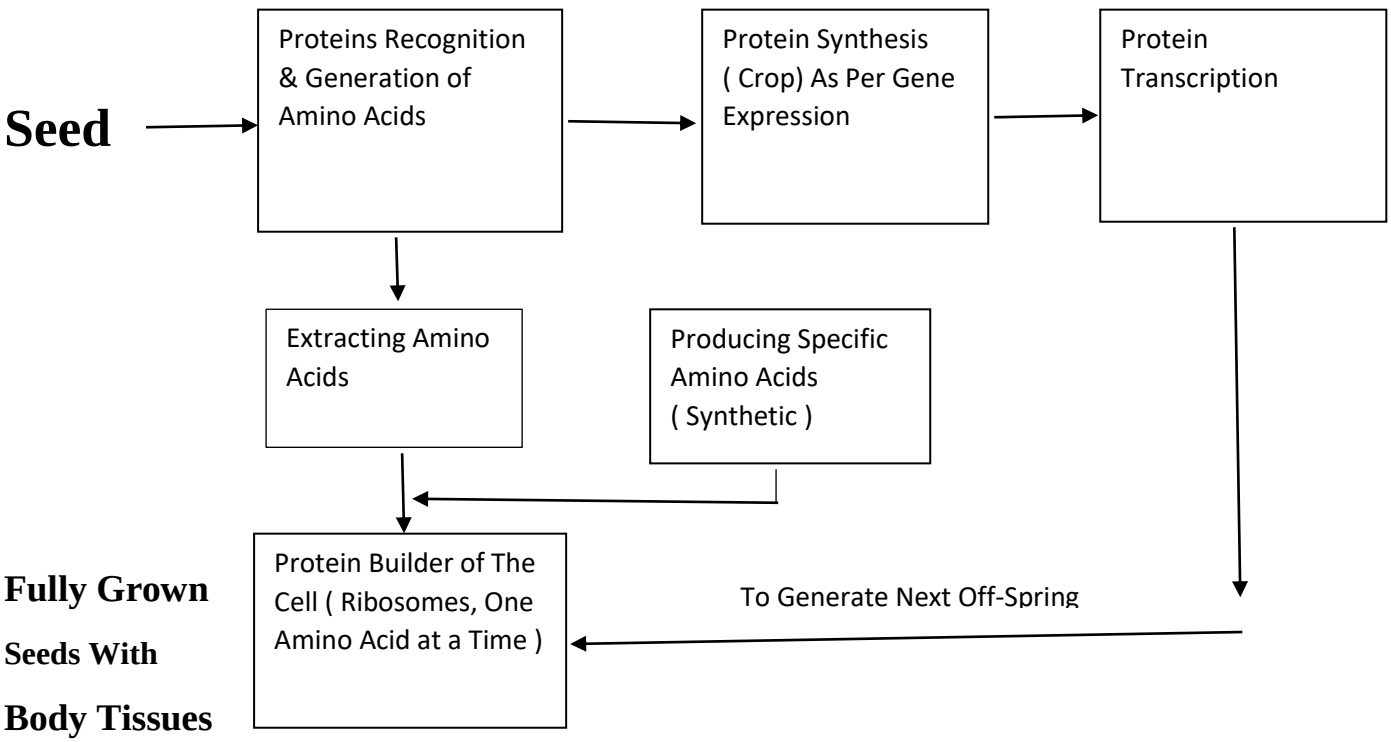

Fig 1. Process Flow Diagram of Seed Builder

Protein from input seeds is broken down into individual amino acids which are reassembled by Quantum Generating ribosomes into proteins that Crop cells need to be generated. The information to produce a protein is encoded in the **cell's** DNA. When a protein is produced, a copy of the DNA is made (called mRNA) and this copy is transported to a ribosome.

Protein **synthesis** is the process used by the QG(Quantum Generator) to make proteins. The first step of protein **synthesis** is called Transcription. It occurs in the nucleus. During transcription, mRNA transcribes (copies) DNA.

Body tissues **grow** by increasing the number of cells that make them up. Every **cell** in the crop body contains protein. The basic structure of protein is a chain of amino acids. We need protein in our diet to help human body repair cells and make new ones. Protein is also important for growth and development in children, teens, and pregnant women.

The major steps in protein synthesis are:

- DNA unzips in the nucleus.
- mRNA nucleotides transcribe the complementary DNA message.
- mRNA leaves nucleus and goes to ribosome.
- mRNA attaches to ribosome and first codon is read.
- tRNA brings in proper amino acid from cytoplasm.
- a second tRNA brings in new amino acid.

The journey from gene to **protein** is complex and tightly controlled within each cell. It consists of two major **steps**: transcription and translation. Together, transcription and translation are known as gene expression.

Protein synthesis is the process in which **cells make proteins**. It occurs in two stages: transcription and translation. Transcription is the transfer of genetic instructions in DNA to mRNA in the nucleus. Translation occurs at the ribosome, which consists of rRNA and proteins**.**

Ribosomes are the protein builders or the protein synthesizers of the cell. They are like construction guys who connect one amino acid at a

time and build long chains. Ribosomes are special because they are found in both prokaryotes and eukaryotes.

Ribosomes, large complexes of **protein** and ribonucleic acid (RNA), are the cellular organelles responsible for protein synthesis. They receive their “orders” for protein synthesis from the nucleus where the DNA is transcribed into messenger RNA (mRNA).

During the **process** of transcription, the information stored in a gene's DNA is passed to a similar molecule called RNA (ribonucleic acid) in the cell nucleus. A type of RNA called transfer RNA (tRNA) assembles the protein, one amino acid at a time.

Ribosomes are the sites in a **cell** in which **protein** synthesis takes place. Cells have many ribosomes, and the exact number depends on how active a particular cell is in synthesizing proteins. For example, rapidly growing cells usually have a large number of ribosomes.

Amino acids can be produced by breaking down proteins, known as the extraction method. However, the amount of amino acids in the source protein limits the amount of amino acids made. Extraction is not good for making mass quantities of specific amino acids**.** So Synthetic Methods of making amino acids is necessary in protein synthesis.

The Quantum Generator contains pre-programmed Protein Synthesizer relevant to specific Crop/Tissue which essentially reassembles ribosomes (Sites in a Cell) into proteins that your crop cells need. The sequence and information to produce a protein is encoded in the synthesizer of Quantum Generator.

ARCHITECTURE

Robotics for Automation and Optimization in Cell Synthesis

We believe that the potential of rapidly developing technologies (e.g., machine learning and robotics) are more fully realized by operating seamlessly with the way that synthetic biologists currently work. To reproduce this fundamental mode of operation, a new approach to the automated exploration of biological space is needed that combines an abstraction of biological synthesis with robotic hardware and closed-loop programming.

As there is a growing drive to exploit rapidly growing robotic technologies along with artificial intelligence-based approaches and applying this to biology requires a holistic approach to cell synthesis design and execution. Here, we outline an approach to this problem beginning with an abstract representation of the practice of cell synthesis that then informs the programming and automation required for its practical realization. Using this foundation to construct closed-loop robotic synthesis engine, we can generate new synthesises that may be optimized, and repeated entirely automatically. These robots can perform synthesis reactions and analyses much faster than that can be done by other means. As such, this leads to a road map whereby molecules can be synthesized, optimized, and made on demand from a digital code.

The ability to make small molecules autonomously and automatically will be fundamental to many applications, including quantum generators. Additionally, automated synthesis requires (in many cases) optimization of reaction yields; following optimization, the best conditions can be fed to the synthesis robot to increase the overall yield. There are different approaches to automated yield optimization, and as optimization of reaction conditions requires live feedback from the robotic system, many different detectors are required to monitor progress of the reactions, including benchtop nuclear magnetic resonance spectroscopy, Raman spectroscopy, UV-Vis spectroscopy, etc. Harvested data are then fed to optimization algorithms to explore often the multidimensional parameter space. The platform could be easily reconfigured to the desired task in a plug-and-play fashion, by attaching different modules to the platform core and Robotic approaches also promise to speed up biological space exploration and realization.

Machine Learning towards Biological Space Exploration

Machine learning approaches are fundamental to scientific investigation in many disciplines. In biological studies, many of these methods are widely applicable, we explore how robotics/automation are helping to progress cell synthesis through exploring biological space and beyond. Scientists have begun to embrace the power of machine learning coupled with statistically driven design in their research to predict the performance of synthetic reactions. For our study, the yield of a synthetic reaction can be predicted using **random forest (machine learning algorithm)** in the multidimensional space obtained from robotic automation to map the yield landscape of intricate synthesis following synthesis code allowing improved prediction of high-yielding conditions

and replication mechanisms. Meanwhile, our emphasis is on automation of synthesis, which is controlled by robots/computers rather than by humans. Synthesis through automation offers far better efficiency and accuracy. In addition, the machine learning algorithm explored a wider range of biological space that would need to be performed purely automated random search and it is observed that self-driven laboratories/robots lead the way forward to fast-track synthesis, and collaboration between smart robotics and humans may be sometimes even more efficient than either alone. This brings the development of automation, optimization, and molecular synthesis very close.

In general, this approach allows for faster and more efficient retrosynthetic analysis than any other well-known method. Figure 2 shows a graphical representation of workflow for joining automated retrosynthesis with a synthesis robot and reaction optimization. The retrosynthetic module will generate a valid synthesis of the target that can then be transferred into synthesis code that can be executed in a robotic platform. The optimization module can optimize the whole sequence, getting the feedback from the robot.

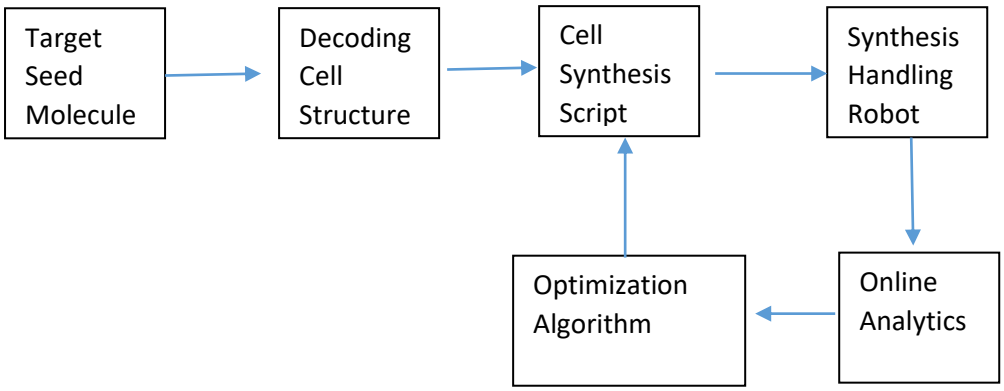

Fig. 2 Architecture of Robotic Synthesis of Crop Cells in a Quantum Generator

The Random Forest is a machine learning algorithm and as the name suggests, "**Random Forest** is a classifier that contains a number of **decision** trees on various subsets of the given dataset and takes the average to improve the predictive accuracy of that dataset. Instead of relying on one **decision tree**, the **random forest** takes the prediction from each decision **tree** and merges them together to get a more accurate and stable prediction.

Protein Synthesis – Synthesis Script

Protein synthesis can be divided broadly into two phases - transcription and translation. During transcription, a section of DNA encoding a protein, known as a gene, is converted into a template molecule called messenger RNA (mRNA). This conversion is carried out by enzymes in the nucleus of the cell and the mRNA, so converted, is initially produced in a premature form (pre-mRNA) which undergoes post-transcriptional modifications to produce mature mRNA. The mature mRNA is exported from the cell nucleus for translation to occur. During translation, the mRNA is read by ribosomes which use the nucleotide sequence of the mRNA to determine the sequence of amino acids and the specific protein factors required for protein synthesis. The ribosomes catalyze the formation of peptide bonds between the encoded amino acids to form a polypeptide chain.

Following translation the polypeptide chain must fold to form a functional protein; for example, to function as an enzyme the polypeptide chain must fold correctly to produce a functional active site. In order to adopt a functional three-dimensional (3D) shape, the polypeptide chain must first form a series of smaller underlying structures called secondary structures and the polypeptide chain in these secondary structures then folds to produce the overall 3D structure. Once correctly folded, the protein can undergo further maturation through different post-translational modifications which can alter the protein's ability to function, and the protein's ability to interact with other proteins.

A synthesis reaction occurs when two or more reactants combine to form a single product. This type of reaction is represented by the general equation: **A + B** → **AB**. An example of a synthesis reaction is the combination of sodium (Na) and chlorine (Cl) to produce sodium chloride (NaCl). The approach for improving protein synthesis using the potential of various species i.e. natural and synthetic extract lies in the mixing of various extracts inside the same reaction platform creating a new cell system with original features. Such hybrid cell systems have been generated by mixing various commonly used extracts together or adding classically used extract for adoption in cell synthesis platforms. The idea supporting such systems lies on each individual cell extract might present specific potentials but also specific drawbacks, mixing two different extracts in a rational way could help compensate individual limitations and combine to achieve the advantages of each system.

In Protein Synthesis, the Script essentially involves:-

1. Each amino acid is attached to a tRNA molecule specific to that amino acid by a high-energy bond and the tRNA is said to be “charged” when the amino acid is attached:
2. The energy of the charged tRNA is converted into a peptide bond linking the amino acid to another one on the ribosome.
3. New amino acids are linked by means of a peptide bond to the growing chain:
4. This process continues until the final amino acid is added. The whole thing works only in the presence of mRNA, ribosomes, several additional protein factors and enzymes.

Genetic Algorithm – Algorithmic Predictions

The efficacy of cell systems i.e. assessing parameters for improving cell synthesis reactions could rely on a considerable number of variables and the amount of work required for exploring variables toward transcription or translation elements in cell systems can be reduced by using Computational Design approaches. Therefore, there is a need to use a learning loop oriented by models generated from Computational Design approaches for optimising cell protein synthesis reactions and achieving good accuracy in the combinatorial space calculation to be tested. And this requires testing of (i) a combination of genetic designs of few constructs by varying spacers around RBS(Ribosome Binding Sites) and sequences, and (ii) other reaction components (amino acids, glucose, etc.) to an incomplete cell synthesis reaction buffer. By optimising one variable at a time with a learning algorithm, the designs could managed to reach higher than that of normal increase in protein production in different iterations of execution.

The strategy can be applied for a library of synthetic promoters, Untranslated Regions (UTR) and Ribosome Binding Sites (RBS), at the level of Coding sequence (CDS) and even Translation machinery can be supplemented or adjusted to improve protein synthesis. Further, Reaction buffers can be optimised to infer what composition needs better adjustment per cell preparation and once established a cell protein synthesis protocol, reactions can be optimised for better protein function and desired output.

Mathematical models either stochastic or deterministic can be digitally be evolved to generate optimal synthesis designs that satisfy a particular objective and genetic algorithm is suitable for use to design gene regulatory platforms that exhibit ideal cell synthesis. A genetic algorithm is a metaheuristic inspired by the process of natural selection that belongs to the larger class of biological evolutionary algorithms. This algorithm reflects the process of natural selection where the fittest individuals are selected for reproduction in order to produce offspring of the next generation. Initially a pool of unique gene designs were required to be generated from basic reactions that satisfy design goal. These design courses were subsequently evolved using numerical simulations to obtain a desired output by repeated rounds of digital mutations and functional screening. These designs could serve as alternatives to consider, model or test during the cell synthesis cycle.

Protein Synthesis Workflow

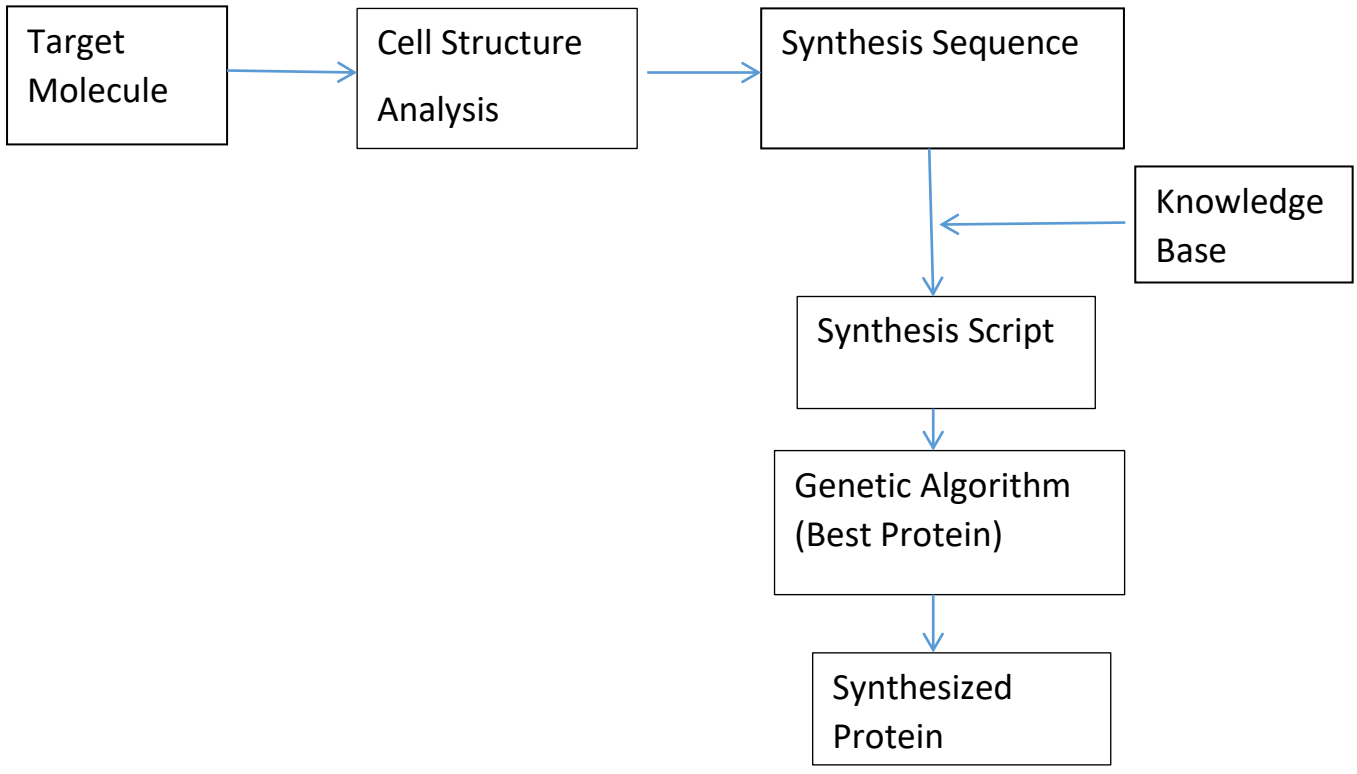

Fig. 3 Graphical representation of Protein Synthesis Workflow

An approach to the problem of biological synthesis design and execution, beginning with an abstract representation of the practice of biological synthesis that then gets executed as per the required synthesis programming for its practical realization. Using this foundation to construct closed-loop synthetic procedure in a synthesizer with an abstraction of biological synthesis, we can generate new crop proteins that may be verified, optimized, and repeated entirely automatically. However, this leads us to test the reactions with different synthetic parameters and conditions.

The synthesis script can be developed using any high-level programming language with automation in combination with machine learning and AI. Additionally, automated synthesis requires(in many cases) optimization of reaction yields, the best conditions can be programmed in a synthesizer to increase the overall yield.

It may be seen that how closed-loop synthesizer with programmed synthetic procedure can be synergistically combined with automation to ensure high quality conclusions are formed. Additionally, Software (abstraction representing biological synthesis) control over cell synthesizer units including sequence flow allowed for combination of individual unit operations into multistep organic synthesis.

TEST RESULTS

The synthesis of crop molecules/proteins can be successfully scripted and performed automatically with yields comparable to manual by adopting algorithmic programming models. We presented a flow system for navigating a network of biological reactions/sequences utilizing on the sensor for data feedback and the system will be able to select the most-reactive conditions autonomously on the basis of change in the sensor data between starting materials and the end products.

CONCLUSION

Quantum Generators (QG) creates new seeds iteratively using the single input seed and the process leads to a phenomenon of generating multiple copies of kernels in repetition. We presented an algorithmic programming model of cell growth in living natural tissues by understanding cell assembly tasks such as DNA replication and cell

synthesis. We checked our approach by developing algorithms and synthesis scripts for the inner workings of the tiny cellular assemblies and our study mainly focused on development of synthesis code interfacing other applications including robotic automation in cellular synthesis. Although the study given us a method of automating and optimizing cellular assemblies however, this need to be tested using natural crop tissues and it could be promising in quantum generation.

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