

mRNA SYNTHESIS IN REAL WORLD USING AR

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Abstract

Augmented Reality provides an interactive experience of a real-world environment where the objects that reside in real world are superimposed by computer-generated perceptual information. This can provide an engaging, immersive experience for students of all ages, and allows them to view and understand subjects and topics through personal experience. Concepts such as nucleotide sequence, genome analysis, protein synthesis are pretty complex to understand and the minute details of the concepts are just left to the student's imagination. Objective of the work is to use Augmented Reality to create an interface in such a way that when the device's camera is pointed at a picture of DNA molecule the recognition of the human DNA molecule happens, and projection of known and unknown DNA nucleotide sequence will appear where in identification of the mRNA sequence and genome analysis is done. This environment works on marker-based Augmented Reality where the Target 2D image will be uploaded to Vuforia. The 3D models required in the project are imported as assets and are organized on the scene in Unity. The nucleotide sequence is collected from NCBI (National Center of Biotechnology Information), The EMBOSS tools is used for sequence analysis where it uses Needleman-Wunsch algorithm to align protein or nucleotide sequences. The expected outcome is an AR driven learning model along with identification of the mRNA sequence, demonstrate transcription translation and also protein synthesis.

Keywords: Augmented Reality, Genome Analysis, Unity, Vuforia, Education

I. INTRODUCTION

The seminar is about to show the AR model for mRNA Synthesis showing translation, transcription Process where the marker is scanned to get the 3D model of gene and its process. The project considers nucleotide sequence of Homo sapiens as the basic gene or the known gene sequence. Other two genes are Acinetobacteria calcoaceticus and Azotobacteria vinelandii. Homo sapiens gene sequence is compared with other gene sequence to find the best match. The best match nucleotide is used for further processing of protein synthesis which involves processes such as translation and transcription and then finally the protein formation.

Home screen consists of two buttons to start and to quit. Start button takes to the next scene and quit will quit the application from running. Introduction scene gives information about genome Analysis. Continue and back button will go to next scene and back button will go to home page. The 3D model shown here is of 423 characters. Buttons to move back and next are present. Next to show the binding of homo sapiens gene with Acinetobacteria calcoaceticus when clicked on GA1 button, binding of homo sapiens gene with Azotobacteria vinelandii when clicked on GA2, binding of homo sapiens gene with Acinetobacter baumannii when clicked on GA3 and , binding of homo sapiens gene with Azotobacter chroococcum when clicked on GA4 . The binding is shown when marker is scanned and with 3D model of binding is shown. Transcription process is shown next, DNA strand go through promoter site of polymerase, Nucleotide binds with RNA polymerase and in the output new mRNA sequence in produced. This also has the button to go next and before scene. In translation process in tRNA, amino acids along with mRNA plays important role in protein synthesis. 3D model protein synthesized with the translation process is shown at last.

The best match is decided based on the results of the Emboss Tool. Emboss is open source free analysis software developed for the needs of the molecular biology and bioinformatics user community. Emboss Needle takes the sequence of both the gene and provides the detailed results of the match and other results needed. The emboss needle reads two input sequences and writes their optimal global sequence alignment to file. It uses the Needleman-Wunsch alignment algorithm to find the optimum alignment (including gaps) of two sequences along their entire length. The algorithm uses a dynamic programming method to ensure the alignment is optimum, by exploring all possible alignments and choosing the best. A scoring matrix is read that contains values for every possible residue or nucleotide match. Needle finds the alignment with the maximum possible score where the score of an alignment is equal to the sum of the matches taken from the scoring matrix, minus penalties arising from opening and extending gaps in the aligned sequences. The substitution matrix and gap opening and extension penalties are user-specified. Swissmodel is another site which is used to get the 3D model of protein. After the

translation process when protein sequence is generated, that sequence is given in Swissmodel site which gives the 3D model of protein. That model is imported into the unity scene to show the 3D model generated protein. The 3D model animation and button working is done through C# code, the detection of the 3D model happens via Vuforia engine. This needs to include AR camera and also the target image as marker, that is when image is scanned the 3D model is displayed. Application is converted to App once the execution is done completely. App asks the permission for the camera and once the marker is scanned then all the 3D models and its working are shown.

Augmented reality (AR) adds digital elements onto a camera, creating an illusion that holographic content in a part of the physical world around. To show the relevant content to the user AR uses computer vision, simultaneously localization and depth tracking (sensor data calculating the distance to the objects.) this allows cameras to collect, send and process data in order to show digital content. Computer vision processes the objects (from the book) captured by the camera and recognizes it. Then, the program executes and the process happens every time the user holds a camera in front of the target image and so as the output is seen. Augmented reality (AR) has recently received a lot of attention in education. Multiple AR systems for learning have been developed and tested through empirical studies often conducted in lab settings. While lab studies can be insightful, they leave out the complexity of a classroom environment. Physical objects and virtual information are used as teaching aids in classrooms everywhere, and until recently, merging these two worlds has been difficult at best. Augmented reality offers the combination of physical and virtual, drawing on the strengths of each. AR creates possibilities for collaborative learning around virtual content and in non-traditional environments, ultimately facilitating personally meaningful experience

II. EXISTING AND THE PROPOSED SYSTEM

In the existing system they are trying to develop many biological applications using AR to make the study exciting and interesting. The AR application shows like heart skull and many more are already developed, that makes understanding easy and fast learning.

The proposed system develops an AR based application related to biological study taking a deeper look into the cell. mRNA identification and protein synthesis are macromolecules. This application shows step wise scene to synthesis protein from mRNA which in turn comes from DNA or Nucleotide. The proposed model makes easy the understanding of protein synthesis from the nucleotide. This shows the steps that include binding with sequence, finding best match and then using this best match to generate protein using the transcription and translation process.

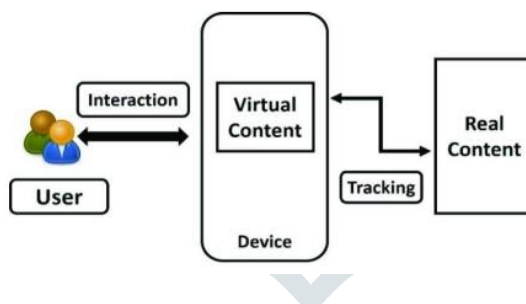


Fig 1: Context Diagram

III. TOOLS AND TECHNOLOGIES

Technology used in this work is the marker based Augmented Reality which is developed using Unity tool and components inside it is Microsoft Visual Code and Vuforia.

Marker based augmented reality - Marker-based augmented reality requires a static image also referred to as marker/target image that a user can scan using their mobile device via an augmented reality app. The scan will further trigger the additional content (3D model, animation etc.) prepared in advance to appear on top of the marker. The target image(marker) has to be unique. Marker recognition can be local or cloud-based, it means that marker databases can be stored on devices and recognition also happen on device. The databases can also be stored on a cloud and recognition happened on a server.

Unity is a cross-platform game engine developed by Unity Technologies used to develop video games for PC, consoles, mobile devices and websites. It was first announced and released in June 2005 at Apple Inc.'s Worldwide Developers Conference as a Mac OS X-exclusive game engine. Unity comes with powerful animation tools that make it simple to create your own 3D cut scenes or build 2D animations from scratch. Unity has played important role in developing 3D applications and gave exited experience of VR and AR.

Visual Studio Code is a free source-code editor made by Microsoft for Windows, Linux and macOS. Visual Studio Code combines the simplicity of a source code editor with powerful developer tooling, like IntelliSense code completion and debugging. Unity uses visual studio as tool to write code and make the components working.

Vuforia is an augmented reality software development kit for mobile devices that enables the creation of augmented reality applications. It uses computer vision technology to recognize and track planar images and 3D objects in real time. This image registration capability enables developers to position and orient virtual objects, such as 3D models and other media. To use Vuforia we have to use license and target image. To do this we should register to Vuforia and get the development key and upload the target image then download that image put it in unity.

IV. SYSTEM DESIGN

The following are the modules in the current work

1. To show the known sequence – In this the homo sapiens DNA or nucleotide is shown in 3D model
2. To show binding with unknown sequence – 3D model of the binding with unknown sequence is shown. Unknown sequence is of Acinetobacteria calcoaceticus, Azotobacteria vinelandii. And its match results are shown
3. To show transcription process – 3D model of transcription process, which shows old gene and formed mRNA, which is further used for translation.
4. To show translation process – 3D model of translation is shown, which includes tRNA and another macromolecule.
5. To show 3D model of myoglobin – 3D model of the protein or myoglobin synthesized is shown.

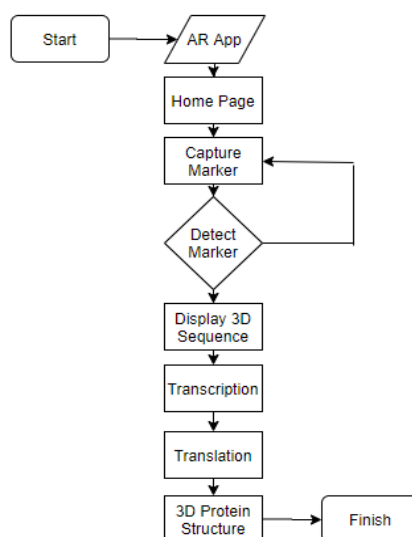


Fig 2: Block Diagram

V. RESULT SET

The result sets of this system describe about the results which are derived after the project is tested. Result set shows how each and every module runs and what its result is. The result set are as follows:

1. The home page

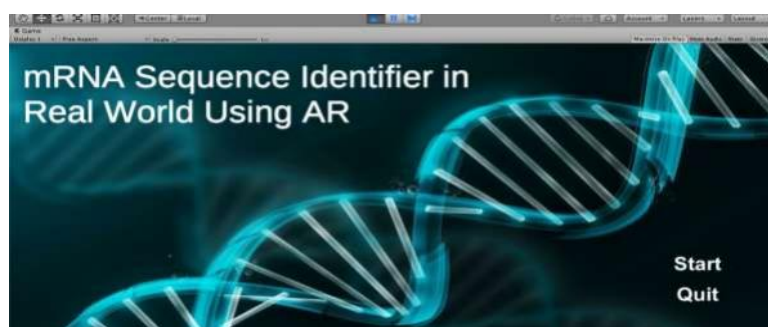


Fig 3: Home page

The home page is a basic designed home page which first appears to the user when they open the application. The start button will further guide the user to the info page which explains the genome analysis.

2. Genome Analysis

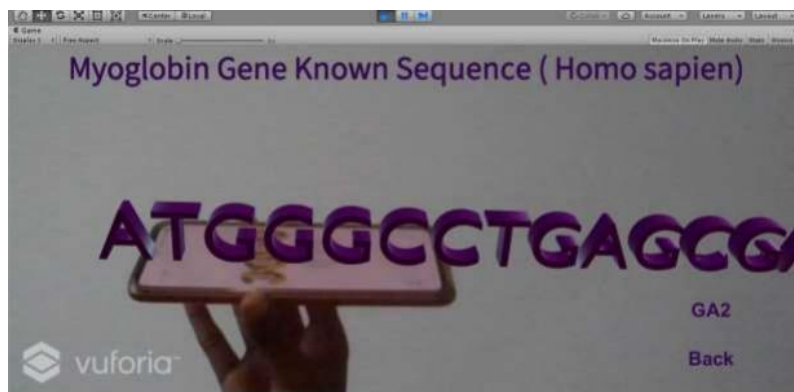


Fig 4: Know Sequence

Genomic analysis is the identification, measurement or comparison of genomic features such as DNA sequence, structural variation, gene expression, or regulatory and functional element annotation at a genomic scale. The 3D model of the known sequence (Homo Sapiens) is displayed.

3. GA1

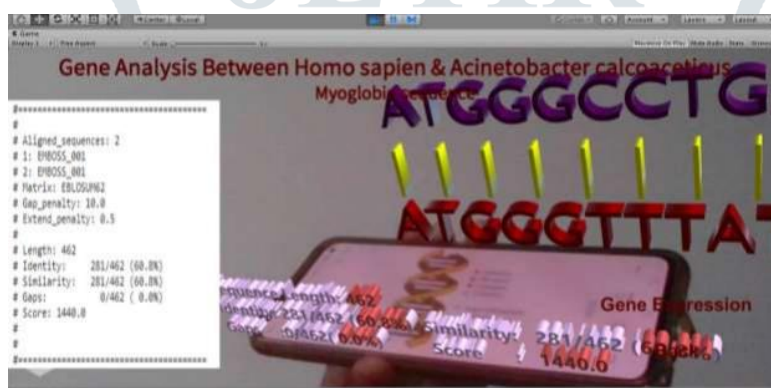


Fig 5: GA1

Further the genome analysis between the know sequence (Homo Sapiens) and the unknown Sequence (Acinetobacteria calcoaceticus) is depicted. The match, gap etc., are checked using the emboss tool.

4. GA2

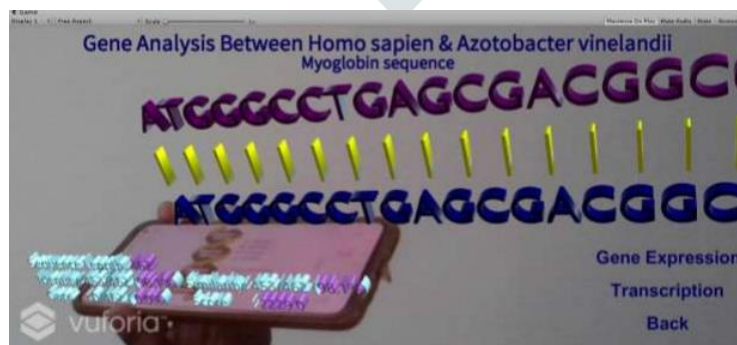


Fig 6: GA2

Further the genome analysis between the know sequence (Homo Sapiens) and the unknown Sequence (Azotobacteria vinelandii) is depicted. The match, gap etc., are checked using the emboss tool.

5. Transcription

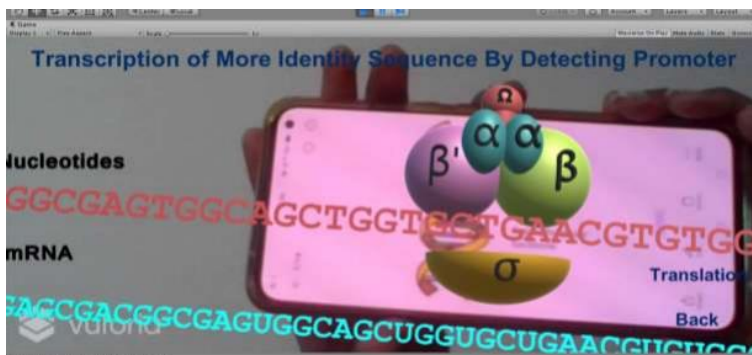


Fig 7: Transcription

Transcription is the process of making an RNA copy of a gene sequence. This copy, called a messenger RNA (mRNA) molecule, leaves the cell nucleus and enters the cytoplasm, where it directs the synthesis of the protein, which it encodes.

6. Translation



Fig 8: Translation

Translation is the process of translating the sequence of a messenger RNA (mRNA) molecule to a sequence of amino acids during protein synthesis. The genetic code describes the relationship between the sequence of base pairs in a gene and the corresponding amino acid sequence that it encodes.

VI. MATHEMATICAL MODULE

A mathematical model is a description of a system using mathematical concepts and language. The process of developing a mathematical model is termed mathematical modeling. Mathematical models are used not only in the natural sciences and engineering disciplines but also in the social sciences. Physicists, engineers, statisticians, operations research analysts and economists use mathematical models most extensively. A model may help to explain a system and to study the effects of different components, and to make predictions about behavior. Mathematical models can take many forms, including but not limited to dynamical system, statistical systems, differential equations or game theoretic models.

Set Theory: Set theory is the branch of mathematical model that studies sets, which are collections of objects. Although any type of object can be collected into a set, set theory is applied most often to objects that are relevant to mathematics. A set is a collection of objects which are called the members or elements of that set. If we have a set we say that some objects belong (or do not belong) to this set, are (or are not) in the set. We say also that sets consist of their elements. Set $S = I, R, O$ Where, I is set of all inputs giving to system. R is set of rules that drives your input set. O is set of output expected from system.

Venn Diagram: A Venn diagram or set diagram is a diagram that shows all possible logical relations between a finite collection of sets. They are used to teach elementary set theory, as well as illustrate simple set relationships in probability, logic, statistics, and linguistics and computer science. A Venn diagram is an illustration of the relationships between and among sets, groups of objects that share something in common. This type of diagram is used in scientific and engineering presentations, in theoretical mathematics, in computer applications, and in statistics.

Mathematical Model of the proposed system: -

1. Design and Implementation Constraints (OOD) Mathematical Model • Problem Description:

Let us S be the technique set to transform an image into 3d model

Such that $S = \{I, F, O\}$ where,

$I = \{I1\}$

$I1 =$ Input images ($N \times M$) to be transformed

Where, $N =$ Number of Images

$M =$ User

And F is the set of Function:

$F = \{F1, F2, F3, F4, F5, F6\}$

$F1 =$ Set Marker

$F2 =$ Import Packages

$F3 =$ Track Marker

$F4 =$ Object Recognition

$F5 =$ Mount 3D Model

$F6 =$ Display 3D Model

And O is the set of Outputs:

$O = \{O1\}$

$O1 =$ 3D Model

2. Set Theory and Venn Diagram:

Here relations between the inputs, functions and outputs are shown. Venn diagram describes the graphical representations of all sets. From the Venn diagram we can say that, $O < I$.

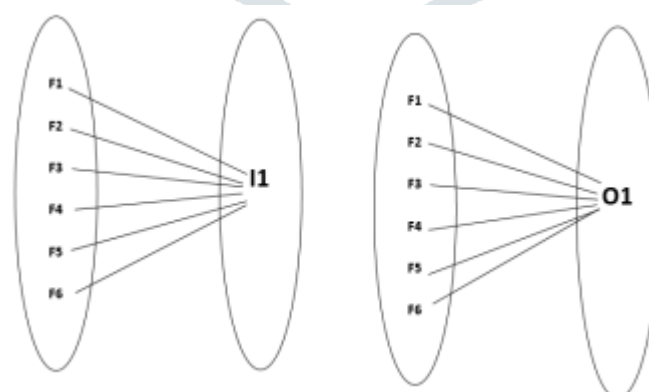


Fig 9: Relations between inputs, function and outputs

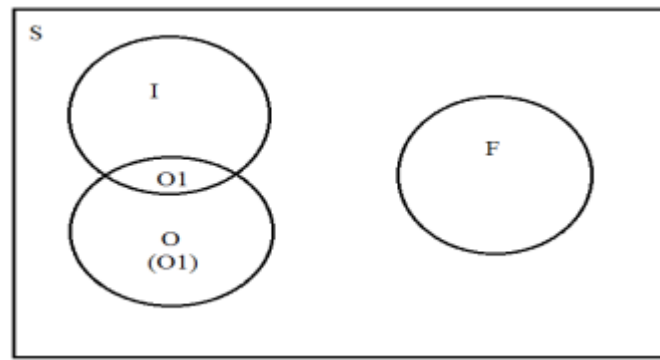


Fig 10: Venn Diagram

VII. CONCLUSION

Biotechnology is a science that combines technology and networks to meet human needs. The development of learning media based on augmented reality is able to increase interest in participating in learning. When interest is achieved the criteria for learning objectives are easy to achieve. This learning media is packaged based on technology so that it is able to synchronize the domains it wants to achieve in learning. The next goal in this research process is to develop content that is packaged in biotechnology learning modules so that it becomes a learning medium that is compatible with learning for elementary schools.

The proposed paper gives idea of only one gene synthesis and shows direct implementation of translation and transcription. This project can be enhanced to show matches of more than one gene. The proposed system only shows the protein synthesis process. The next enhancement can be showing where this gene is present in the cell, how actually it takes place inside the living cell making the 3D model still more enhanced and attractive. Showing the 3D model of cell and components inside it where the protein synthesis takes place makes the application more enhanced.

VIII. REFERENCES

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