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Abstract. Mobile Augmented Reality (MAR) is considered to be a promising tool in science classes to foster kids' imagination. In this paper, a parametric simulation method of DNA three-dimensional structure is proposed for middle school biology class. Affine transformation was used to stack and spiral complementary paired nucleotides in three-dimensional space according to the structural parameters of different DNA conformations. The process of vector construction was dynamically simulated by the recognition technologies (i.e., image characteristics and collision detection). The prototype system was developed using mobile technologies, which combines multiple interactive methods (i.e., viewing, listening, touching, and physical objects) to provide users with an appropriate learning and cognitive way. The system is useful for learners (especially K-12 students) to utilize the fragments of spare time outside the class to promote the cognition of DNA. In the future, such technology-assisted education would be a popular open learning form.

Keywords: Mobile Augmented Reality, DNA conformations, Parametrization, Affine transformation, Mobile technologies.

1 Introduction

It is difficult to imagine the three-dimensional morphology and the spatial layout of helix and twisted double chains of DNA, especially for those teenaged students who first learn it in the classroom. In biology classes, pictures, texts, videos and so on are commonly shown for demonstration with limited form and effect [1-2]. Thus, teachers attempt to use some physical objects (e.g., paper clips, foam, etc.) or 3D-printed objects as the DNA components, and stitch them together one by one in the classroom to show the three-dimensional schematic model of DNA molecular to help students understand the knowledge [3]. Those actions usually occupy much time but having poorly visual effects, which affect the effect of teaching and learning. Moreover, the limitations of these material-combined models prevent them from dynamically showing DNA-related microscopic biological processes (i.e., base complementation, vector construction and so on). With the advantages (i.e., imagination, interactivity and im-

mersion), the technology of virtual reality and augmented reality can be used to present phenomena that cannot be observed or manipulated in the real (e.g., the process changes too fast or too slow). Integrated with professional knowledge, augmented reality (AR) builds immersive 3D visualization scenes by accurately overlaying virtual scenes and real scenes to enhance the user's perception experience in real environments [4]. It is a new method and a supporting technology to promote teaching [5-6], and has been adopted widely in STEM courses [7-8], physics classes [9], biochemistry teaching [10-11] and other aspects. As the popularization of mobile learning in daily life, AR has drawn more and more attention and becomes a positive trend [12-14]. The mobile AR cognitive tools can overcome the time & space constraints of classrooms or laboratories, and enable students to autonomously learn anytime and anywhere, thus triggering students' deeper thinking and inquiry-based learning [15-17].

There are two types of MAR technology in scientific education (i.e., location-based and image-based) [18]. Location-based AR usually combines with geographic locations requiring real-time data and large space, and is more suitable for scientific query-based learning [18]. Image-based AR (including marked and unmarked technology) provides real-time interactive experiments to improve students' spatial ability, practical skills and understanding of concepts [19]. A number of AR tools have promoted the development of biochemistry teaching [20-21]. Several software packages can simulate the relationship between the structure and function of biological macromolecules, such as BioChemAR [22], Augment [23], ArBioLab [24], Palantir [25] and so on. However, most existing tools were dedicated for university students and scientific research. They are not suitable for biology teaching in middle school because of its complex and lack of dynamical simulation of micro-process-like phenomena and poorly interactive experience.

In this paper, the dynamic processes of vector construction and three-dimensional shape of DNA were simulated with parametric and an interactive real time AR-based app was implemented. Adopting the interactive technologies of mobile device, learning on microscopic phenomena of DNA is full of fun with finger touches, voice controls and real things' interactions, which are recognized and tracked by image-based natural feature detection. Some mobile experience tests are conducted among middle school students.

2 Simulation of Three-Dimensional DNA Structure

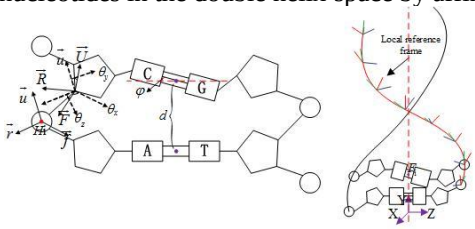
2.1 Double Helix Structure of DNA

DNA is a molecule composed of a phosphate group, deoxyribose and one of four nitrogen-containing nucleobases (i.e., adenine (A), thymine (T), guanine (G) and cytosine (C)). The three-dimensional (3D) structure of DNA has the following characteristics [26-27]: (1) Deoxyribose and phosphate groups are alternately connected by phosphodiester bonds to form the two DNA strands in a reverse parallel way; (2) The nitrogenous bases of the two separate polynucleotide strands are bound together by hydrogen bonds, according to base pairing rules (A-T, C-G).

Modeling DNA Strands. Since the two DNA strands are located on the reference cylindrical surface of the double helix space, a local reference coordinate system is established at the center of bottom so that y-axis is aligned with the central axis. The affine transformation matrix (i.e., M) is gained according to parameters about different DNA (i.e., pitch (d), twist angle (φ), diameter and so on). The affine transformation matrix is used to move the paired nucleotides along the y-axis by a distance (i.e., d) and rotate around the y-axis by an angle (i.e., rotation angle (θ)). The point (i.e., H_0) on the cylinder repeatedly performs a series of transformations to obtain the local reference frame (i.e., H_i) of phosphate groups, which is connected to become the two DNA strands based on curve. The local reference frame of deoxyribose on each paired nucleotide can be calculated using orthogonality. The direction information of phosphodiester bond can be calculated by the local reference frame of phosphate groups and adjacent deoxyribose. Assuming that the direction vector of the local frame on deoxyribose of adjacent paired nucleotide in world coordinates (i.e., $\left(\vec{F},\vec{U},\vec{R}\right)$) and the direction vector of the local frame of phosphate group (i.e., $\left(\vec{f},\vec{u},\vec{r}\right)$) are shown in Figure 1(a). The orientation information of the phosphodiester bond in the world coordinate system (i.e., $\left(\theta_X,\theta_y,\theta_z\right)$) can be calculated by formula (1). Similarly, the information of the phosphodiester bond (i.e., spatial position, length, scale factor and so on) can be obtained. Finally, all the above elements were instantiated and rendered at their corresponding spatial positions.

$$\left[\theta_X \quad \theta_y \quad \theta_z\right]^T = \begin{bmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \end{bmatrix} \begin{bmatrix} COS^{-1}\left(\vec{f},\vec{F}\right) \\ COS^{-1}\left(\vec{u},\vec{U}\right) \\ COS^{-1}\left(\vec{r},\vec{R}\right) \end{bmatrix} \tag{1}$$

Stacking Base Pairs. The dynamic stacking of paired nucleotides in the DNA double helix space is shown in the figure 1(b). First, the local reference frame (i.e., F_i) of paired nucleotides is calculated by matrix multiplication, which is located on the central axis of the double helix column space. The local reference frame of phosphoric acid on each paired nucleotide can be calculated based on the three-dimensional structure parameters of DNA (i.e., pitch (d), rotation angle (θ), etc.).The origin of phosphate groups' local reference frame on the same side is connected by a curve to form a target region for moving paired nucleotides freely. Interpolation is performed according to the set random moving step sequence and time. The dynamic process of gradually stacking paired nucleotides in the double helix space by affine transformation.



(a)Direction vector of the local frame in the world coordinate system

(b)Stack to generate DNA double helix structure

Fig. 1. Structure of DNA double helix

2.2 Common Structure

Linear DNA is a common DNA structure, which mainly includes B-DNA and A-DNA. The parametric interactive modeling method was used to simulate the 3D shape of different DNA conformations. The aim is to improve students' cognition of the true structure of DNA and promote students' spatial imagination.

Summarized the rules of common DNA structure from bird's-eye views, the parameters of the double helix DNA structure in different patterns can be calculated as shown in Figure 2. Assuming that the y-axis was set as the direction of the helix axis, and the local coordinate frame of base pair (e.g., F_i) can be calculated by formula (2) and formula (3).

$$\begin{bmatrix} x_i & y_i & z_i & 1 \end{bmatrix} = \begin{bmatrix} x & y & z & 1 \end{bmatrix} T \tag{2}$$

$$\begin{bmatrix} \theta_i & 1 \end{bmatrix} = \begin{bmatrix} \theta & 1 \end{bmatrix} \begin{bmatrix} 1 & 0 \\ \sum_{0}^{i-1} \varphi & 1 \end{bmatrix} \tag{3}$$

Among them, (x_i, y_i, z_i) is the three-dimensional coordinate of i-th paired nucleotide's center point. (x, y, z) is the three-dimensional coordinate of the first paired nucleotide's center point in the bottom of the double helix space. T is the affine transformation matrix (B-DNA takes T_B. A-DNA takes T_A). θ_i is the i-th paired nucleotide's rotation angle. θ is the initial offset angle of paired nucleotide in the reference double helix space. The twist angle of the helix is described as φ (B-DNA takes 36°, A-DNA takes 33.6°).

The paired nucleotides of B-DNA molecular structure took D_B as the interval in y-axis and rotated at the angle φ (that is 36°) to change T_B as shown in formula (4):

$$T_B = \begin{bmatrix} 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 \\ 0 & \sum_{0}^{i-1} D_B & 0 & 1 \end{bmatrix} \tag{4}$$

The inclination of paired nucleotides is 13°, which causes the base plane no longer be perpendicular to the spiral axis. The effect of force causes the paired nucleotides to be extrapolated, forming a wider and deeper groove [28]. There is a "hollow" phenomenon in A-DNA from the top view, as shown in the shaded part of Figure 2. The center of the paired nucleotides (B_i) pass through the spiral axis and then are pushed a distance (d) to the opposite side (A_i). In the meantime, the rotation transformation is performed at φ (i.e., $33.6°$). According to formula (5), the rotation transformation matrix (T_A) of A-DNA can be obtained.

$$T_A = \begin{bmatrix} 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 \\ d \cdot \cos(\varphi \cdot i) & \sum_{0}^{i-1} D_A & d \cdot \sin(\varphi \cdot i) & 1 \end{bmatrix} \tag{5}$$

Users can interactively select the type of common DNA, and then change the structural parameters of DNA to obtain different three-dimensional DNA conformation. All paired nucleotides in the axis direction did not completely fill the double helix room, showing the phenomenon of "major groove" and "minor groove".

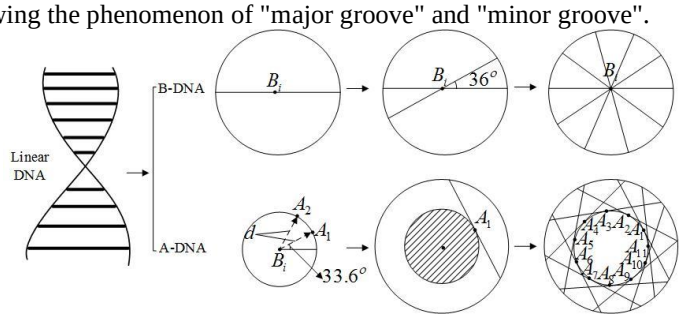


Fig. 2. Comparison of Structure of DNA molecular

3 Interactive Simulation for Mobile-Learning

3.1 Interactive Design for Mobile Device

Mobile-Learning is different from traditional teaching, emphasizing that students are the main participants. There are different requirements for learning content, learning methods, learning environment and evaluation. With its advantages (i.e., flexible, convenient, personalization and so on), mobile-learning can better satisfy the needs of learners for learning in spare time. Based on the analysis of the needs about learning, the above-mentioned contents of DNA-related were reorganized in accordance with the principles (i.e., layout, moderate content and convenient operation). Those existing teaching resources (i.e., videos, problems, pictures, text, etc.) were fully used by optimally combining the technology of voice interaction and touch interaction, which can stimulate the senses of learners and improve the acceptance rate of Knowledge. Virtual button designed by UI can simplify the interactive operation process and control the switching of different modules. A number of microscopic phenomena were dynamically reproduced by combining AR technology with DNA. Several portable cards with more information of features were designed as interactive tools in order to get rid of the dependence on traditional operating tools.

3.2 Marker-Based Interactive simulation

Vector construction is a microscopic process of changing the gene sequence according to human intentions as shown in Figure 3. Restriction enzyme (e.g., the recognition site of EcoRI is GAATTC/CTTAAG) and ligase are required for vector construction. Vector construction requires restriction enzyme, ligase and genes of interest. In this paper, three pictures were designed as markers (i.e., Mark1 is restriction enzyme, Mark2 is genes of interest, Mark3 is ligase). With the help of camera from mobile, students can interactively manipulate the process of vector construction by moving the marker.

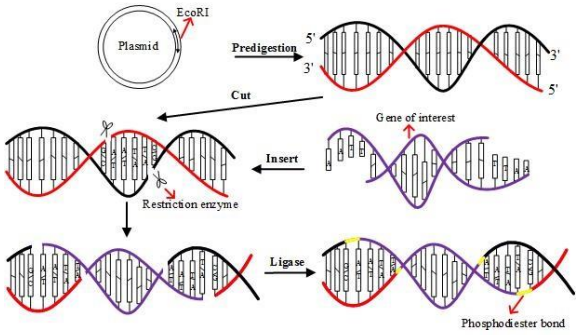


Fig. 3. Principle of vector construction

This paper mainly used the image-based AR technology (i.e., it was used to detect and track related objects.) and the collision detection technology (i.e., it was used to achieve event response.). The interactive simulation of vector construction process is shown in Figure 4. The main steps are as follows:

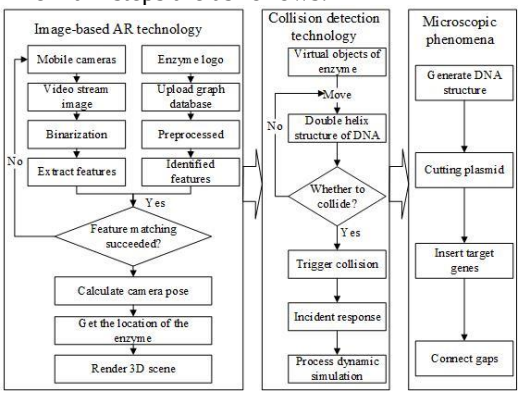


Fig. 4. Implementation process of Enzyme marker detection and tracking

(1)The target picture is preprocessed to obtain feature information.

(2)The current frame of the video captured by the camera is converted to binary data and extracts feature information.

(3)The feature matching method is used to match the feature information of the target image and the captured image. If the matching is successful, the camera's current pose information will be calculated according to formula (6).

$$s\begin{bmatrix} x \\ y \\ 1 \end{bmatrix} = \begin{bmatrix} f_x & 0 & b_x \\ 0 & f_y & b_y \\ 0 & 0 & 1 \end{bmatrix} \begin{bmatrix} r_{3\times3} & T_{3\times1} \end{bmatrix} \begin{bmatrix} X \\ Y \\ Z \\ 1 \end{bmatrix} = N \begin{bmatrix} X \\ Y \\ Z \\ 1 \end{bmatrix} \tag{6}$$

Among them, (x, y) is the point's two-dimensional coordinates in the image coordinate system. (X, Y, Z) is the point's three-dimensional coordinates in the world coordinate

system. f_x and f_y are the camera's focal length in the x and y directions. (b_x, b_y) is the pixel coordinate vector of the principal point in the image space. $r_{3\times3}$ and $T_{3\times3}$ are the camera's transformation matrix. N is the homography matrix.

(4)Using the camera's pose information, virtual objects are rendered at the appropriate position by affine transformation to achieve the effect of Virtual-Actual combination.

(5)The marker is moved in order to cause the collision detection of virtual objects containing hierarchical bounding volumes, so that the function of OnTriggerEnter() is triggered in Unity3D. If the collision detection is successful, it will respond to the effect of cutting plasmid, inserting target genes and so on.

4 Prototype Development

4.1 System Structure and Function

In this Study, Unity3D and augmented reality application development engine (e.g., Vuforia SDK) were integrated in the Visual Studio2017 development environment. The development process of DNA mobile AR system was shown in Figure 5. Autodesk 3ds Max software was used to establish the DNA model of each components, (i.e., deoxynucleotides, enzymes, bases, etc.). The software of Unity3D integrated Vuforia SDK to develop the detection and tracking of AR tags and dynamically simulated microscopic phenomena (i.e., the three-dimensional structure of DNA, replication and vector construction). A variety of interactions (i.e., single-touch/multi-touch, voice assistance and physical interaction) have been realized. The content designed includes pre-class guidance, in-class demonstration and after-class review to guide and motivate students to study independently. The method by using funny games to expand the standard knowledge points of the course is suitable for the exploratory learning of students with different knowledge levels.

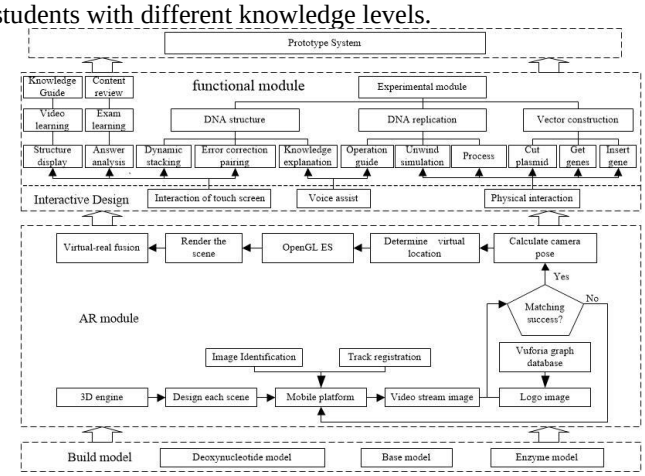


Fig. 5. Flow of system implementation

The system consisted of three modules (i.e., knowledge guide module, experiment operation module and content review module). The knowledge guide function module included the video learning, which guides students to learn relevant knowledge (i.e., the discovery of DNA double helix structure, the concept of DNA structure, DNA replication process and characteristics, etc.). The experimental operation module included three contents (i.e., the structure of DNA, the replication of DNA and vector construction) was be prepared by videos and audios preview. Among them, simulation of the structure of DNA was described paired nucleotides dynamically stacking in the three-dimensional space. Some contents about replication and vector construction (i.e., plasmid cutting, target gene acquisition, target gene insertion, etc.) were simulated to reproduce the micro process. The module of content review included knowledge review and exercise of question bank (i.e., common question type, error-prone question type and so on). After students completed the solution, the system will explain the question.

4.2 Result

Users can purposefully make the selection of experimental module through the user interface as shown in Figure 6(a). The dynamic simulation of vector construction is conducive to improve students' interest as shown in Figure 6(b). Figure 6(c) showed the microscopic phenomena of DNA replication process improving users' spatial imagination and reducing cognitive difficulties.

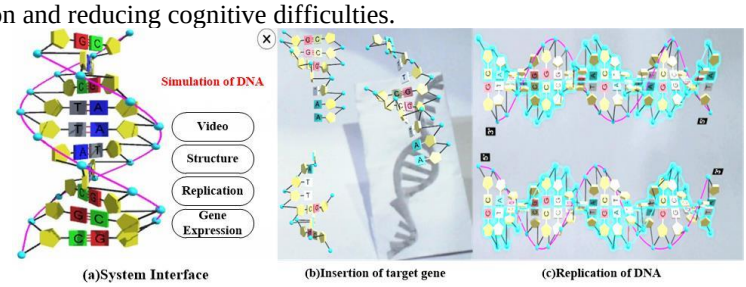


Fig. 6. Screenshots of virtual experiment system

5 Discussion and Conclusions

5.1 Testing and Discussion

Some students in junior high school or senior high school were chosen for testing about this mobile experience. During the modeling process of DNA three-dimensional shape, the change of students' learning attitude was recorded. At the end of all tests, participants were asked to give feedback and analyze the collected experimental results.

To evaluate whether the system was useful for teaching the knowledge of DNA in middle school, the prototype system would be released as an "APK" file and installed on students' mobile phones. Meanwhile, the feedback of all users participating in the mobile test is shown in Table 1.

Table 1. Part data contrast of system simulation

Items of test	Good	Average	poor
Fluency	90%	6%	4%
Simple Operation	92%	3%	5%
Extensity	97%	3%	0
Attraction	90%	7%	3%
Fun	95%	3%	2%

The experimental results showed that the prototype system has realized a variety of interactive ways (e.g., view, hearing, touch and object), which has been widely welcomed by students in middle school. This research method can intuitively represent the three-dimensional structure of DNA, simulate the dynamic process of paired nucleotides superimposing helix, and display the process of vector construction in real time. Since an interactive learning tool is popular among students in middle school, it can effectively improve students' cognition of DNA structure.

Students who used AR-assisted learning thought that this system can help them to increase interest in learning and enhance the spatial perception. What's more, the methods adapt to the transformation of learning in the new era.

5.2 Conclusion

We have set the hierarchical relationships and a variety of interactive ways in order to show components of double helix DNA model clearly. We have released a mobile AR app based on Unity3D for teaching the knowledge of DNA in middle schools, which can dynamically simulate the process of vector construction. A reasonable combination of touch screen interaction, voice control and physical interaction can achieve a better users' experience by using collision detection technology and image-based natural feature detection technology. With the help of this app, students can watch those videos about background story and manipulate double helix DNA structure interactively in a variety of ways to master key conceptions, which contain the experiments' contents, steps and so on. Furthermore, they can gain a better understanding and deeper thinking of the structure-function spatial pattern by comparing the 3D shape of common DNA (e.g., A-DNA and B-DNA).

Some students from different middle schools, as volunteer, joined our test expressing their experience to run the mobile AR app. Then the collected information of the test was analyzed. The results show that our tool is committed help students understand the structure of DNA and cultivate their spatial visualization by realistically simulation. After the tests, these students show a greater will of learning new things independently and effectively anywhere and anytime by gamification.

It’s clear that AR-based mobile-learning tools can take advantages of mobile-learning (i.e., flexible and convenient) to overcome the time & space limitation of traditional learning methods. Simplified prototype of the interactive operations make it easy for students to use. They can enable learners to study autonomously anytime and anywhere. AR-based mobile learning tools can expand students' imagination and give them appropriate cognition. It would be a promising tools for the experience of K-12 courses and open learning environments in the future.

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