AN INTERACTIVE SEQUENCE EDITOR APPLICATION IN ANDROID PLATFORM

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ABSTRACT
Nucleic acid is an organic substance found in chromosomes of living cell that plays an important role in the storage of hereditary information and can be expressed through protein synthesis. Nucleic acid can be classified into two which is deoxyribonucleic acid (DNA) and ribonucleic acid (RNA). DNA serves as a template for the transcription of RNA to occur. RNA is then sent to a ribosome to be translated into protein. No doubt that there are many available online tools and standalone software in personal computer provides this mechanism, however it is very limited in mobile platform. Thus, SeqEditor is a proposed mobile application build in android platform that perform several function which manipulate DNA or RNA sequences based on the input by the user. Several function such as reverse, complement, reverse complement, transcription, translation, calculate total occurrences of bases, calculate the length of the sequence and provide amino acid table which visualize the properties of amino acid. The application will only show translation result for one standard protein code and reading frame. Furthermore, the application also does not provide save function. Therefore, future enhancement is focused on solving the limitation of the application.

KEYWORDS: Nucleic acid Thus, SeqEditor, reverse, limitation of the application.

1. INTRODUCTION
Nucleic acid is a group of organic substances found in the chromosomes of living cells and viruses that plays a central role in the storage and replication of hereditary information which can be expressed through protein synthesis. In short, nucleic acids are biomolecules that
store hereditary information in the form of deoxyribonucleic acid (DNA) and ribonucleic acid (RNA). The central dogma of molecular biology is that the information in DNA is transferred to mRNA and then to protein itself.\textsuperscript{[2]} Proteins are the workhorse molecules of life, performing much of the active biochemistry in an organism. Although there are many online web tools that provide the manipulation of genetic information, however it is very limited in mobile platform. Healthcare professionals are using their mobile devices in an increasingly varied and creative way.\textsuperscript{[3]} Since the mobile application development landscape has substantially changed over the past several years, mobile development platforms have become more integrated and generally play the role of application portal, device manufacturer, or even both. Application portals tend to become more centralized, facilitating the link between developers and consumers. Thus to fully utilize the advantages of mobile application, a sequence editor application is built to serve biological community with interactive functions provided. seqEditor is a mobile application that is developed for fast and less cost processing in android platform since Android is designed to be fast, powerful and easy to develop.\textsuperscript{[4]} Besides that, seqEditor is an interactive sequence editor application for manipulation and synthesizing of nucleic acid sequence in Android 4.2 platform. It enables the inserted nucleic acid sequence to be converted into its respective functions; reverse, complementary, reverse complementary, transcription and translation as well as the amino acid table at the user’s convenience.

2. METHODS
The main programming language used is Hyper Text Markup Language 5.0 (HTML) while Cascading Style Sheets 2.1 (CSS) is used to style the application and Javascript is used for the execution of actions and functions. As for developing the application, the environment used is Adobe Dreamweaver CS5.5. Moreover, Android SDK has to be installed in order to compile, package and sign the application specifically for Android platform. In addition, Android Virtual Device is used for testing and debugging.

2.1. Input
seqEditor application system is an application system that allows user to choose the process they intend to do such as central dogma process, sequence manipulation process and properties process. For central dogma process, seqEditor accepts DNA sequence up to 2000 base long as input. As for sequence manipulation process and properties process, a short DNA or RNA sequence is entered as an input.
3. RESULTS

In central dogma process, seqEditor will display the result immediately after user clicks the ‘convert’ button. The DNA sequence will be transcribed to produce mRNA sequence and translated into protein sequence of 1 letter code and 3 letter codes. There is also a link to view the amino acid table.

In sequence manipulation process, seqEditor will display the results of the given sequence. Results shown will be the reverse, complementary and reverse complementary of input sequence.

Properties process in seqEditor will display the results when ‘properties’ button is clicked. Here, the length, base, amino acid and codon occurrence of the given sequence are counted. The occurrences are displayed in two forms which are: whole number and percentage.

4.0. DISCUSSION

Figure 1 For central dogma process, (a) input sequence query, (b) results, (c) Amino Acid table; For sequence manipulation process, (d) Sequence option, (e) DNA sequence query, (f) results; For properties process, (g) RNA sequence query, (h) and (i) results

Several problems are left unsolved. This is due to time restriction. The problems include only one reading frame for translation process, the input sequence query limited to one source which is direct input and the work or result obtained cannot be save.
Some of the future enhancement is to address all the stated limitations completely. Apart from that, seqEditor will also add features such as provide statistical analysis of the query sequence. Properties process allows user to view result in table form, so the future enhancement may include the representation of result in the form of graph or chart. In addition, seqEditor will also be implemented in different mobile platforms such as iOS and blackberry.

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5.0 REFERENCE