User's Manual

Team: UESTC

iGEM 2013

Contents

1. Team introduction

Hi! We are team UESTC (University of Electronic Science and Technology of China) for iGEM 2013. There are 7 student members, 2 advisors and 3 instructors in our team. We spent this iGEM summer and finally made it.

For more information about 2013 iGEM UESTC team, please visit our wiki: http://2013.igem.org/Team:UESTC

2. Projects tutorial
2.1 Nebula
2.1.1 Introduction

Nebula (Network of Elaborated Biobricks based on User Locating and Automation) is a biological circuit design tool composed of Auto Mode & Manual Mode. It is freely available for devices powered by IOS. We classified the parts released in 2013 and constructed a database for users to choose what they want. We use AHP (Analytic Hierarchy Process) to score parts and edges (passage linking two parts) according to parts quality including availability, usefulness, sample status, part status and sequencing. According to weight of edges, we present "Index of stability" to users. Users can save the circuits designed in Nebula in case they want to check or change it later.

2.1.2 Begin first launch

Download Nebula in Apple App Store:
https://itunes.apple.com/cn/app/nebula-igem/id701400025?mt=8,
and install it on your iPhone or iPad following the instructions.

2.1.3 Let's go!

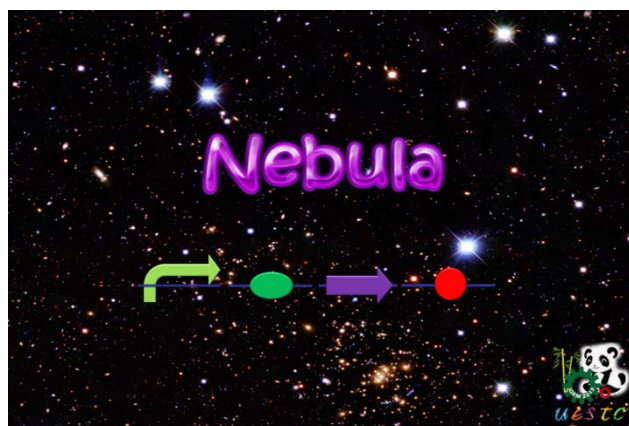Click the app, and you will see the loading page. (Figure 1)

Figure 1 Loading page

After the loading is done, you come to Nebula's main page. (Figure 2)

Figure 2 Main page

There are two modes for users to choose: Auto Mode and Manual Mode. They can share results with friends via Twitter as soon as the design is done. By clicking "History" button, you can see the designs saved on your device before. (Figure 3)
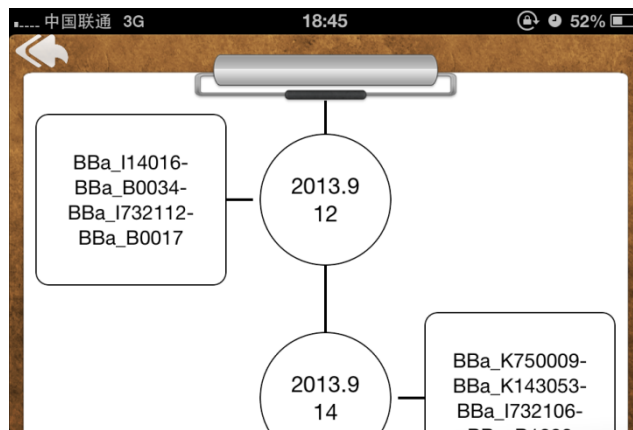

Figure 3 History

① **Manual Mode**

Click "Manual Mode" and you will come to the interactive part. (Figure 4)

Figure 4 Auto mode

Click "Add" to add the parts you want. You can choose the part you want according to our categories to design your device.
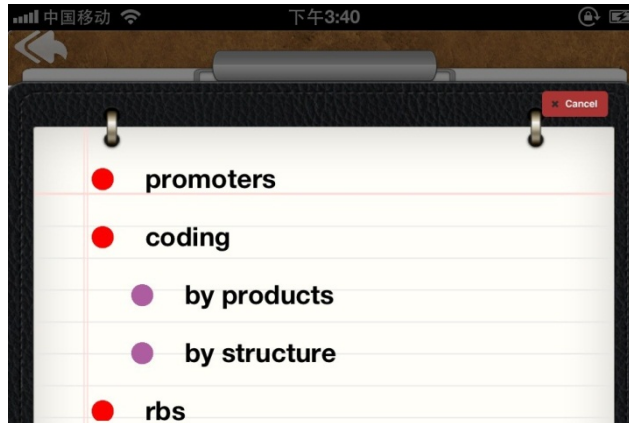
Figure 5 Categories
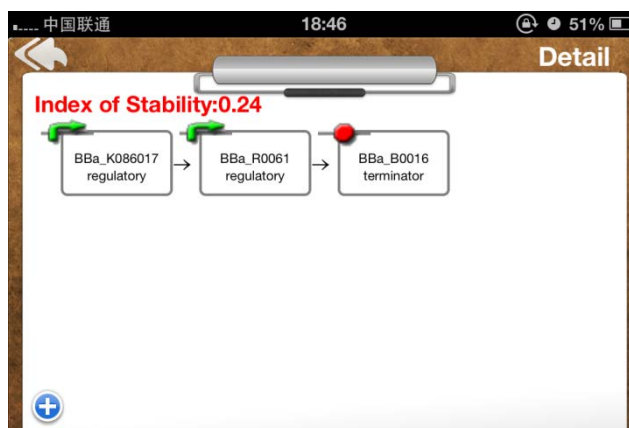
Then click "Done" to get your design.

Figure 6 Device

At the same time, Nebula will calculate "Index of Stability" of your device. Click the blue icon below, you can save your design or share it with your friends.

Figure 7 Sharing page

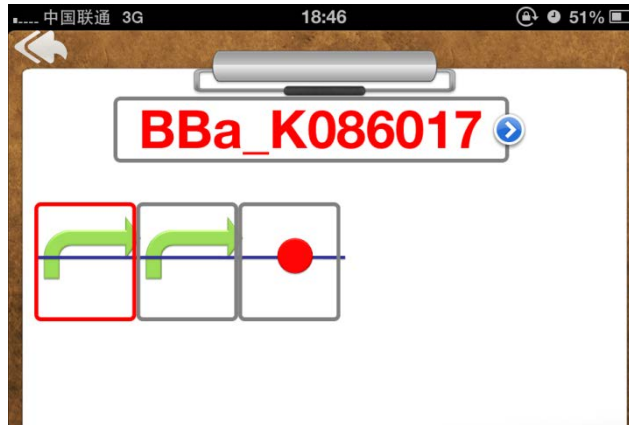You can click "Detail" to see more details.

Figure 8 Detailed information

Click each part and you can see the part ID. Then click the part ID to see more information. If you want to come to iGEM parts registry to inquire more details, just click the blue arrow.
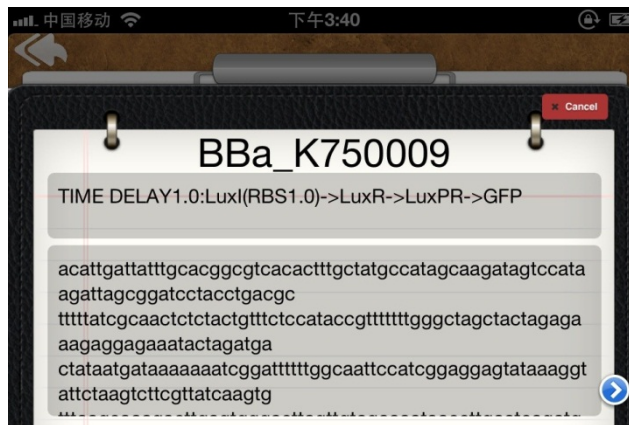

Figure 9 Part information

② **Auto Mode**

To be more convenient, you can try our auto mode. Just give your input and output, and then Nebula will show several devices with different scores of stability. You can choose whatever you like according to your experiment requirement.
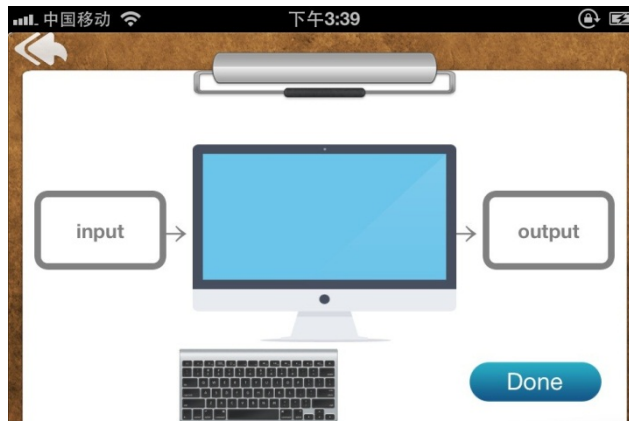
Figure 10 Auto mode

Once you have made your choices of input and output, click "Done" to see the results. You have to choose a terminator before you see the detailed information. Slide the page to see different results, and you can click "Detail" to see more information, the same function as manual mode. (Figure 11-14)
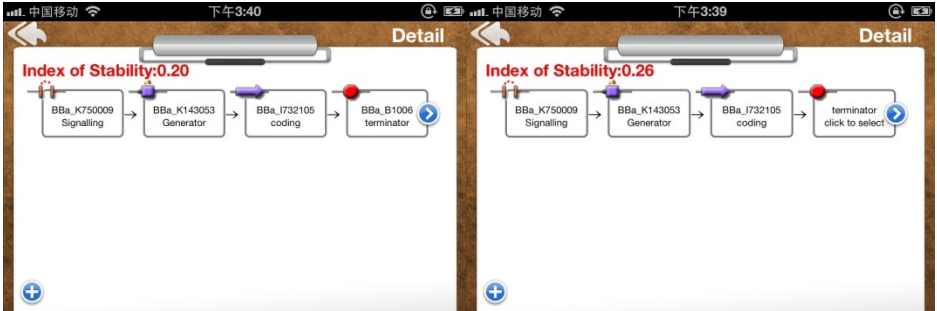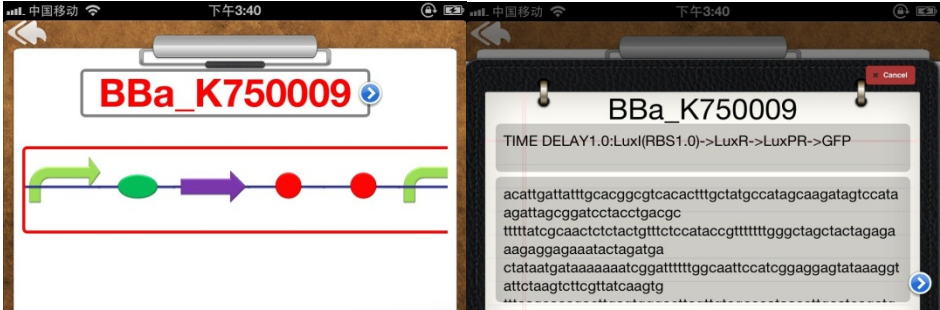

Figure 11 Result page

Figure 12 Result page

Figure 13 Device page

Figure 14 Part information
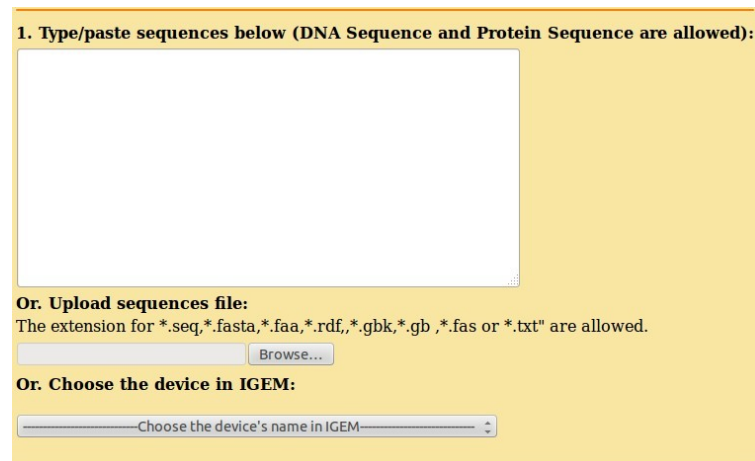
2.2 Transspeeder

2.2.1 Introduction

Transspeeder is a tool for designing devices with different translation speed via mutating gene sequence based on alignment against SD sequence of host (*e.g.* in *E.coli*).It has reported that codon choice will avoid the homology of ribosome binding sites (RBS) sequence in order to improve the translation speed. (doi: 10.1038/nature10965.). Transspeeder can help users to control the translation speed in ways of synonymous mutation. We have verified Transspeeder with experimental method.

Stand-alone version of Transspeeder is written in Java. And we also provide it online on http://cefg.cn/transpeeder.

2.2.2 Web interface

①   Input sequence

First, users have to type a sequence or upload a sequence or choose the device in the parts registry (Figure 15). Note that users can only choose one of the three formats to input the sequence. Otherwise, the program will prompt an error.

Figure 15 Input page

②   Select the sequences format

When the sequence is input, its format should be chosen (Figure 16A). Transspeeder supports three types of formats: FASTA format, GenBank format and Synthetic Biology Open Language (SBOL). The examples of the formats are provided (Figure 16B-16D).

A

B

C

D

Figure 16 Format selection and examples

③ **Select the Shine-Dalgarno sequence**

After that, users should choose the host. In the current version, only *E.coli* is available. (Figure 17)

Figure 17 The selection of SD sequence

④ **Result page**

Click 'Submit' and the program will run on the server before returning the result to the result page (Figure 18).The page shows the mutated fast and slow sequence. And the nucleic components of the two sequences are presented, respectively.

The sequence is lack of initiation codon and termination codon ,a initiation codon and a termination codon have been added to the head and tail of the sequence respectively.
WARNING:There is(are) a termination codon(s) in the sequence.
The fast sequence is:(G+C%: 0.433526011561 ;A+G%: 0.485549132948)

```
>fast_sequence
ATGAACAAAACCCATATCAAAAACGATTTCACCCGCAAAAAATATCTCAAAAACGTCCGCGACCAACAAG
AATGCCTGCCGTCCCGCTCCGGCCGCTGGCAATCCTAAGGCGAAGAACAGTGCTCTGCCGGCCAGGGCCA
GGGCTGCTGCTGCTGTTCATGGTCATTCCGCGCCACCGGCGGCAAAGAATATATCGGCTGCGGCTCCGGC
CGCTGCTGACTCCGCGAGGGCCAAGACCGCCCGGAACAGGTTGCCATCCGCGTGAATTTTGGCTCTTATA
ACTTCCCTTTTCTCATTAACTGCTGGGATTTTCAAATCAAATTTGGCTCTCACAATTAATTCTCCTATTC
CTCTTATCTTCTGCTTTTTCTTGTTCTTTAATGTTTTAACGTCTCTTCCCCTTTTCGCTGCACCACCTTT
GGCACCCTGTCACTGATCAACAAAATCTAATTTAAATTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAATAA
```

The slow sequence is:(G+C%: 0.42774566474 ;A+G%: 0.631984585742)

```
>slow_sequence
ATGAATAAGACGCACATTAAGAATGACTTTACGAGGAAGAAGTACTTGAAGAATGTAAGGGACCAGCAGG
AATGTCTACCCAGTAGGAGTGGGAGGTGGCAAAGTTGAGGTGAGGAGCAATGTTCAGCTGGGCAGGGGCA
GGGATGTTGTTGCTGTAGTTGGAGTTTTAGGGCTACGGGAGGTAAGGAGTACATAGGATGTGGAAGTGGT
AGGTGCTAGCTTAGGGAAGGTCAGGACAGGCCTGAGCAGGTAGCTATTAGGGTAAACTTCGGAAGTTACA
ATTTCCCGTTCTTGATAAATTGTTGGGACTTTCAGATTAAGTTCGGAAGTCACAACTAGTTTAGTTATAG
TAGTTACTTGCTATTGTTCTTGGTACTGTAGTGTTTCAATGTAAGTAGTCCGTTCAGGTGCACGACGTTC
GGAACGTTGAGCTTGATAAACAAGATATAGTTTAAGTTCTAGAAGAAGAAGAAGAAGAAGAAGAAGAAGA
AGAAGAAGAAGAAGAAGAAGAAGTAG
```

Figure 18 Result page

2.2.3 Desktop version

The desktop version of Transpeeder is able to run on your computer even if there is no JRE. We use Eclipse to export runnable jar file and free software named JavaLauncher to generate exe file. The source code and exe file including clustalw2.exe can be downloaded from http://cefg.cn/transpeeder/download. Double-click the file transpeeder.exe, you'll see this page:

Figure 19 Loading page

After launching our software, you will see the main page is shown as follows:

Figure 20 Main page

① **Input sequence**

Users can type/paste sequence, upload files or choose the device in part registry after DNA/Protein is chosen (Figure 21). Note that users can only choose one of the three formats to input the sequence. Otherwise, the program will prompt an error.

Figure 21 Sequence input

② **Select format**

Our app supports three types of formats: FASTA, GenBank and Synthetic Biology Open Language (SBOL). Examples are provided so you can click the buttons below then it'll be shown in the input area (Figure 22)

Figure 22 Format selection

③   **Select the Shine-Dalgarno sequence**

After that, users should choose the host. In this version, it only collects the SD sequences of *E.coli*. (Figure 23)
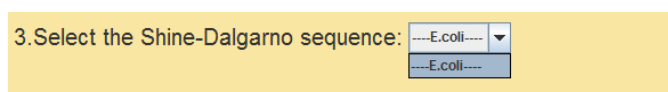

Figure 23 The selection of SD sequence

④   **Output section**

Press "Submit" and the program will run for a moment before returning the result to output text area (Figure 24). The result shows users the fast and slow sequence.
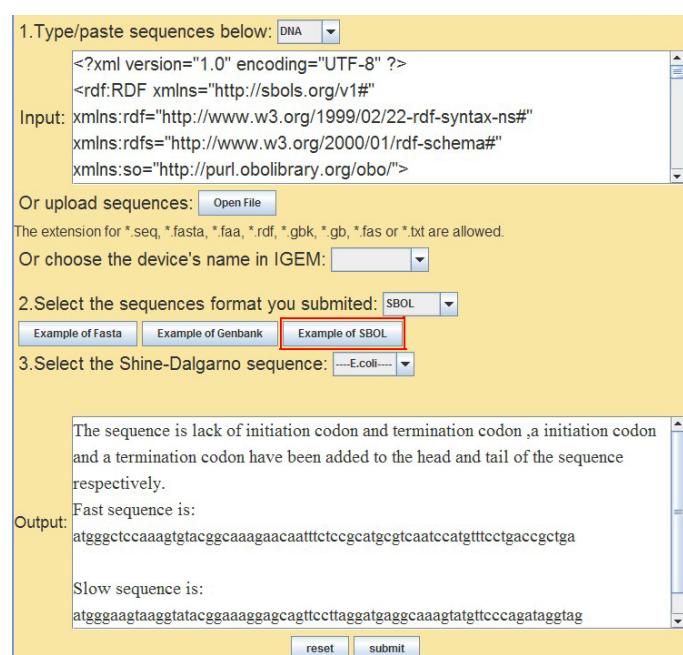

Figure 24 Results

2.2.4 Input data

①   **Format**

It supports three types of formats: FASTA format, GenBank format and Synthetic Biology Open Language (SBOL).

FASTA format: http://www.ncbi.nlm.nih.gov/BLAST/blastcgihelp.shtml

GenBank format: http://www.ncbi.nlm.nih.gov/Sitemap/samplerecord.html

SBOL: http://www.sbolstandard.org/

②   **Built-in data**

For parts in iGEM, we chose some sequences which were annotated with "only CDS". Due to the length of some sequences is not 3N, we found that the sequences have tail motifs (see below). We moved the motifs to backend.

③   **Tail motifs**

agtcgcttaa

tctataaagc

tgtagatcac

tgtagatccc

tgtagatcgc
tgtagatctc

2.3 iBricks

2.3.1 Introduction

IBricks is a video game concerning synthetic biology on iPhone. In this game, what you need to do is to synthesize protein to protect a cell. At first, you are provided with several basic parts to combine the circuit. Once you accomplish combining these parts into a circuit, you will enter into translation process, during which phage will continuously attack your circuit. To protect it, you can press on these phages to kill them. You can also utilize several tools to eliminate phages with higher efficiency. After successfully synthesizing the protein, you can get new parts that increase the possibility of successfully synthesizing proteins.

All parts are classified into 4 categories: promoter, RBS, CDS and terminator, meanwhile each part has 3 attributions: stability which indicates that how many times your circuit can withstand the attack from phages, transcription speed, which implies the time you need to synthesize the protein, and probability of gaining tools that can eliminate phages during process of synthesis. The value of attributions varies from parts. You need to combine 4 different kinds of parts to gain the most stable, low time consuming circuits with higher possibility of gaining tools.

This game aims to popularize the concept of synthetic biology among the public. Users with no biology background can learn basic information of synthetic biology and meanwhile have great fun.

To download iBricks, please visit the page:

https://itunes.apple.com/cn/app/ibricks-uestc/id702877975?mt=8

2.3.2 Game interface

① **Start Game**

On this page, users can click on "play" button to start the game.

Figure 25 Main page

② **Choose Level**

Users can choose the level of game they want to play. Phage in white is the first level. Phage in blue is the second level. Phage in green is the third level. Phage in yellow is the fourth level. Phage in red is the fifth level. User can only start from the first level. If they have passed all levels, they can freely choose the level they want to play.

Figure 26 Level choice

③ **Splice Parts**

Users can assemble the device they want to translate. The devices are composed of 4 parts. All parts are classified into 4 categories: promoter, RBS, CDS and terminator, meanwhile each part has 3 attributions: stability which indicates that how many times your circuit can withstand the attack from phages, transcription speed, which implies the time you need to synthesize the protein, and probability of gaining tool that can eliminate phages during process of synthesis. The value of attributions varies from parts. Users need to combine 4 different kinds of parts to gain the most stable, low time consuming circuits with high possibility of gaining tools.

Figure 27 The choices of parts

④   **Protect Your Cell**

Finally, the users come to the process of translation. In this process, phage will continuously attack your circuit and thus destroy the process of translation. To protect it, you can press on these phages to kill them. You can also utilize several tools to eliminate phages with higher efficiency. After successfully synthesizing the protein, you can get new parts that increase the possibility of successfully synthesizing proteins and meanwhile enter into the next level where the phage will be faster and stronger.
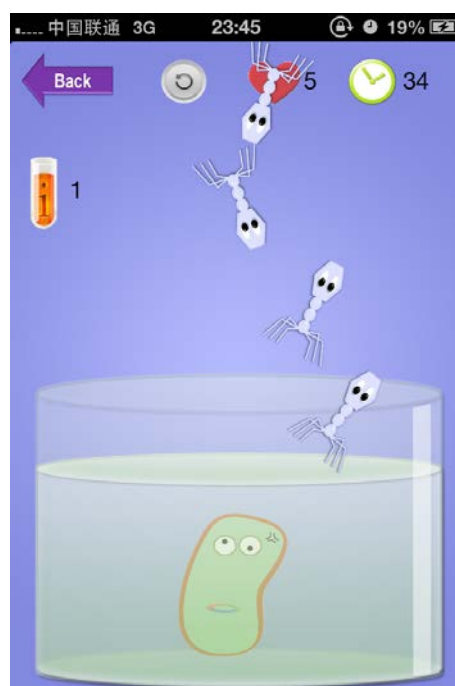

Figure 28 Game page

3. Source code

To download our software and source code, please visit team UESTC of iGEM 2013 on GitHub: https://github.com/igemsoftware/UESTC2013

4. Acknowledgements