Second Version

Overall

The first version of ***BiArkit*** is now completed and released. The second version, ***BiArkit 2.0***, has been proposed and designed to be more competent to fulfill the needs of synthetic biology researchers. ***BiArkit 2.0*** will still concentrate on how to deeply exploit bio-information for researchers to design and execute their further experiments. First, every kit will be optimized functionally and ameliorated to be more user-friendly. Second, the explosion of second generation sequencing motivates us to involve the next generation sequencing data to ***BiArkit 2.0***. Third, for more information coming from biological systems, including reconstruction networks, molecular interactions, and artificial networks, we will make standards and integrate them into one section to provide the comprehensive prospects for researchers to employ. Fourth, as ***BiArkit*** was coden by ***JAVA***, we plan to make this software run not only on ***Win*** but also on the platform of ***Mac*** and ***Linux***.

GenomeBrowser

The updated GenoneBrowser will incorporate bio-information out of RNA-Seq, ChIP-Seq and tiling-array to illustrate the genome expression level under given conditions and locate molecular that

interact with the genomes. With the known annotation, the genomes can be divided according to the products they transcribed. Besides, for make this kit more user friendly, we are going to refine it and allow researchers to screen their interested genomes graphically only by pasting the relevant web links to the interface. After pasting the links, this kit will download the xml or fasta from the original web automatically.

Biobrick

The updated Biobrick section will focus on three parts to be optimized. First, we will specifically classify the known biobricks. As lots of accomplishments by using biobricks have come out, some bricks have been tested to be adjustable to the specific kinds of researches. For example, a kind of biobricks are always used to implement the cell signals transportation and another kind are always applied to the cell colony communication etc. This ***research-oriented*** classification facilitate researchers get the useful information they need conveniently and efficiently. Second, we will refine the codes to make this kit updated immediately according to the official website. Third, we will try to improve the ways of restoring the data by documenting more graph and credit identification information for each biobricks.

Regulator Designer

Apart from Riboswitch and SiRNA, some other kinds of regulator will also be considered in the next version of the kit. One of the most common used in synthetic biology is transcriptional factors (TFs). We will develop a TFs matcher for researchers to find their desired TFs according to the experimental requirements. The selection process is executed based on the existent TFs database and previous common used TFs in synthetic biology. And our ultimate goal is to add the regulator designer, including riboswitch, siRNA, TFs and others to the ***Clotho*** frame for sharing among all the researchers.

Simulator

The advanced version of Simulator will be improved from three prospects.

(1) One focuses on ameliorating the Algorithms of the original one. The next version of Simulator, other methods for simulating will combined into this part according to the completeness of the information necessary for certain kind of analysis provided by the SBML files. In the first version, we use the constraint-based FBA but in the next version algorithm with both constraint and kinetic approaches will be applied to enhance the reliability and sensitivity of simulation. For program code To realize FBA analysis, the

original version is realized based on Package ‘abcdeFBA’ of R. While in the second version of this part, programming will be supported directly by JAVA or C++, which will not only reduce the size of the software but also accelerate computation.

(2) One focuses on improving the user experiencing. Firstly, for model used in simulation, users will not only use SBML files documented in released database like Biomodels but also can edit and save the SBML in a user-friendly way. Information necessary for FBA including reactions and metabolites will be showed clearly and in the interface where user can revise model . The new model can be saved in a revised SBML file. Secondly, the metabolic network can be visualized in the interface. Users can drag the pathways joint to a right place in the screen like playing the building block game, which can add to the fun of this simulation.

(3) Inspired by the recent whole-cell model in predicting phenotype and giving insights in some undiscovered cellular behaviors, we plan to expand our models and simulation not only concentrating on metabolome information but also should involve genome annotation, transcriptome , proteome and molecular interaction into consideration. As cell processes have been divided into 28 submodels and synthetic biology have developed many typical artificial systems recent years, we hope to give out a new

standard for documenting these cellular process and relevant bioinformation mentioned above in one file. Thus, researchers just need to edit such kinds of files, such as adding metabolites or deleting one interaction between two molecular, to simulate their designed systems before experiments. And the mentioned comprehensive bio-information can be applied to offset the difference between prediction and experiments, which often motivate the discovery of unobserved cellular process.

Trans-platform Realization

As the first version of BiArkit is written by JAVA completely, it facilitate us to make the whole software transferable. BiArkit 2.0 will be available on both of Mac and Linux and researchers can use it conveniently in terms of their own equipments.