README

1.Description

BiArkit is a versatile toolkit that integrates different modules together and helps researchers approach information on synthetic biology. The first kit is **GenomeBrowser**, which visualizes the genomes of some model microorganisms, locates the genes on the genome and makes it easy to study the genomes. Secondly, **Biobrick** from the registry are transformed into the localized search tool. Thirdly, **Riboswitch** and **SiRNA** assist the design of regulatory elements. Fourthly, we have developed **MetaNetwork** to optimize the methods of scanning and output of the existing database of pathways. Fifthly, to analyze the dynamic change in various metabolic networks, we present the **Simulator** that help researchers analyze the network in silico. Sixthly, **G-Circle** is designed to illustrate the expression level of different genomes under the given environment. And it has been added to the Clotho. Further, to make it more convenient, the software is localized; that is to say, all functions mentioned above can be achieved without linkage to Internet.

2.Directory Structure

src - including source code of BiArkit, including the seven application and rjava package.

BiArkit Project .rar - including open source code of BiArkit, which is provided for the advanced development and improvement by other programmers. It can be opened by Netbeans. Notice: you should open the folder " BiArkit\ Rjava" by eclipse and make sure your R's path is set correctly.

install . **txt** - including the guides for users to install BiArkit.

BiArkit_windows_1_00.exe - including Setup of BiArkit.

Tutorial - including the guides for using BiArkit.

3.Compiling the code

Announcement: You just need to click on the Setup to install BiArkit and if you want to refine the codes, you can open BiArkit Project . rar by Netbeans.