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Home

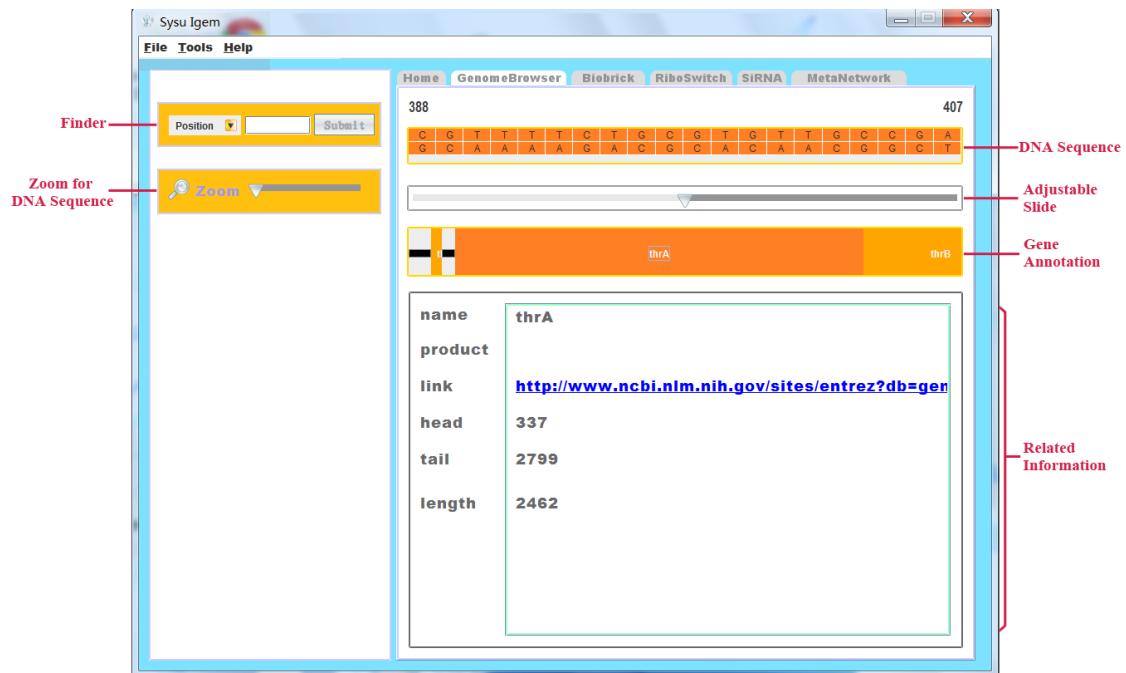


On the left is the logo of **BiArkit** which is created by 2012 SYSU-software igem team. In the main display window, there are seven buttons, G-Circle, Network Illustrator, RiboSwitch, Genome Browser, SiRNA, Biobrick, and Simulator, which will take you to corresponding parts once clicking.

Genome Browser

Procedure:





In the main display window, the first ribbon is the sequence that the user has inputted, and the third ribbon shows the corresponding gene annotation. You can click any annotation that you want, and then the sequence site will automatically jump to the fragment related to it. Between those ribbons is an adjustable slider, which can adjust your view location by sliding to the left or to the right. Above the sequence are the head and tail of the location that you are viewing while the head and tail of the whole sequence are displayed in the bottom textbox. What's more, the textbox contains the length, product, tag of the sequence, and links of related papers are also included sometimes.

On the left, there are two useful tools: you can search the fragment that you want by position, product or name (Position represents the position of its head, Product and Name stand for products and names of related genes, both of them support fuzzy search), besides, whether you choose product or name, a dialog box that contains names of related genes will appear; the slider of Zoom is designed for regulating the display frame rate of the sequence.

Biobrick

Procedure:

Open your biobrick file (in xml format)

The figure consists of two screenshots of the Sysu Igem software interface.

Top Screenshot:

- Finder:** A search bar labeled "FIND BIOBRICK" with a "GO!" button.
- Biobrick List:** A tree view showing categories like "Composite parts" and specific files such as BBa_B1101.xml through BBa_B1210.xml.
- Component Biobrick:** A schematic diagram showing the structure of the biobrick, consisting of several colored arrows (red, green, blue) connected by lines.
- Related Information:** A detailed table of properties for the biobrick, including part_id (8050), part_name (BBa_B1103), part_short_name (B1103), part_short_desc (B1003 I13507), part_type (Composite), part_status (Available), part_results, partNickname, part_rating, part_entered (2007-01-29), part_author (Haiyao Huang), best_quality (None), and twins.

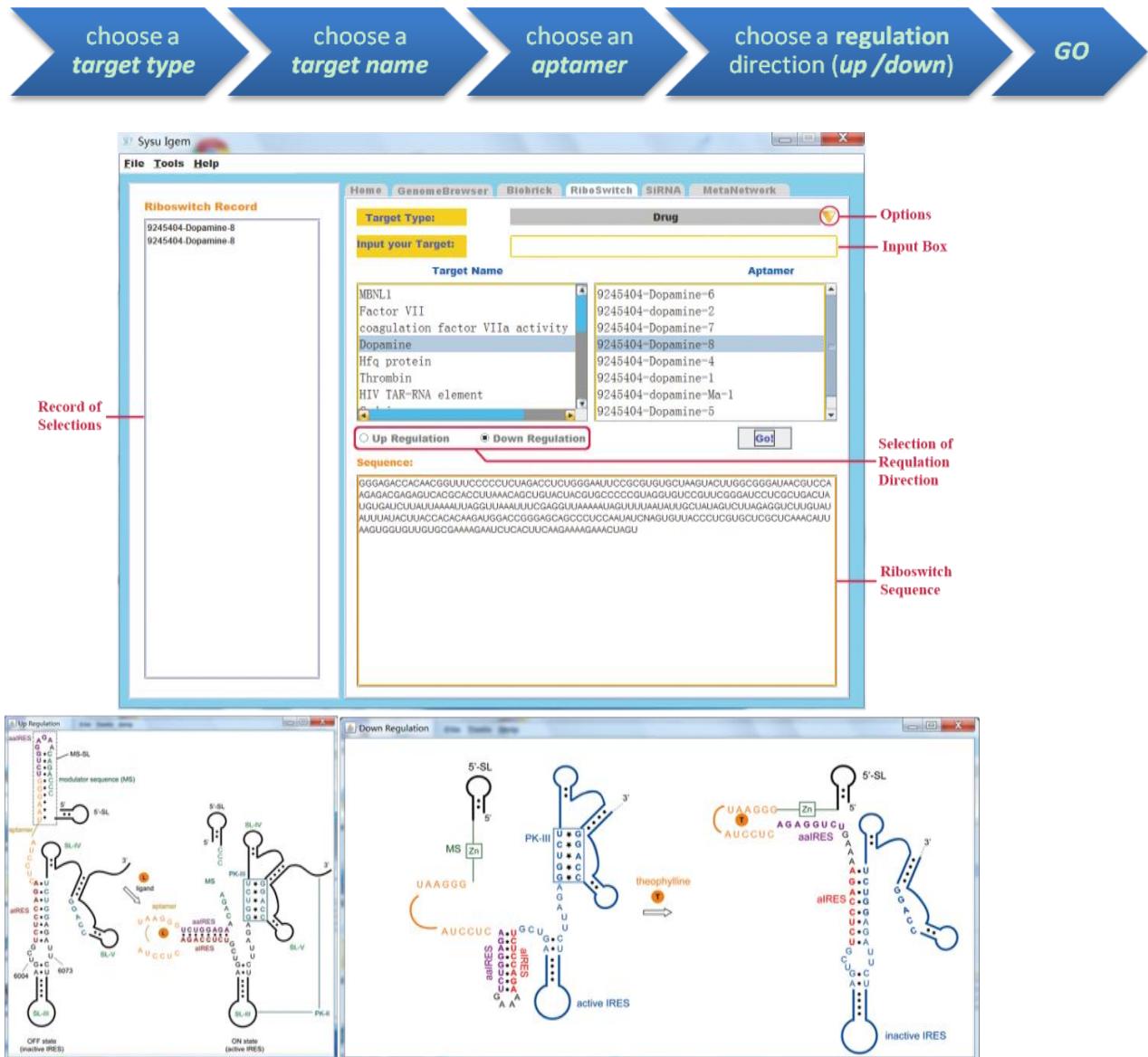
Bottom Screenshot:

- Finder:** A search bar with "0034" entered.
- Biobrick List:** A tree view showing categories like "biobrick", "Composite parts", "DNA", etc., with "BBa_BO034.xml" selected.
- Show Biobrick search result:** A pop-up window titled "Show Biobrick search result" containing a list of XML files: BBa_B0034.xml, BBa_B1101.xml, BBa_B1102.xml, BBa_B1103.xml, BBa_B1104.xml, BBa_B1105.xml, BBa_B1106.xml, BBa_B1107.xml, BBa_B1108.xml, BBa_B1109.xml, BBa_B1110.xml, BBa_B1201.xml, BBa_B1202.xml, BBa_B1203.xml, BBa_B1204.xml, BBa_B1205.xml, BBa_B1206.xml, BBa_B1207.xml, BBa_B1208.xml, BBa_B1209.xml, and BBa_B1210.xml.
- Properties:** Below the search result window, there are fields for part_author, best_quality, and twins.

Notice that there is a finder on the left; you can search biobricks by key words and then a window showing the search result will pop up. Below it is a list of biobrick. Turning to the right, a schematic diagram that shows components of the biobrick is on the top. And related information about the biobrick is below it.

RiboSwitch

Procedure:

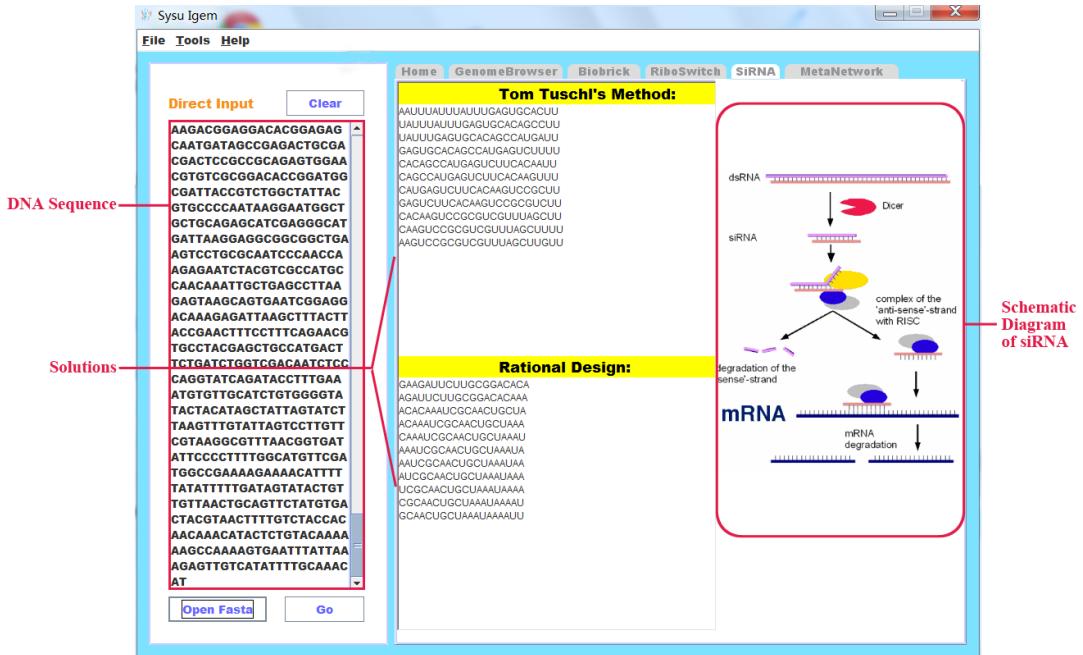


On the right is the main operating area and you can choose your target type (your experimental object) and corresponding target name, aptamer and regulation direction. Attention should be paid to the input box named Input your Target. You can search your target name by key words or even several letters of it. It should be useful to you. Click GO and you will see a picture. The designed riboswitch is in the dotted box on the top left corner. Below it is a diagram to show how the riboswitch works. Besides, there is a list on the left box. It records your choices that you have made in created riboswitch project, and you need only click GO next time.

SiRNA

Procedure:

Input your DNA sequence

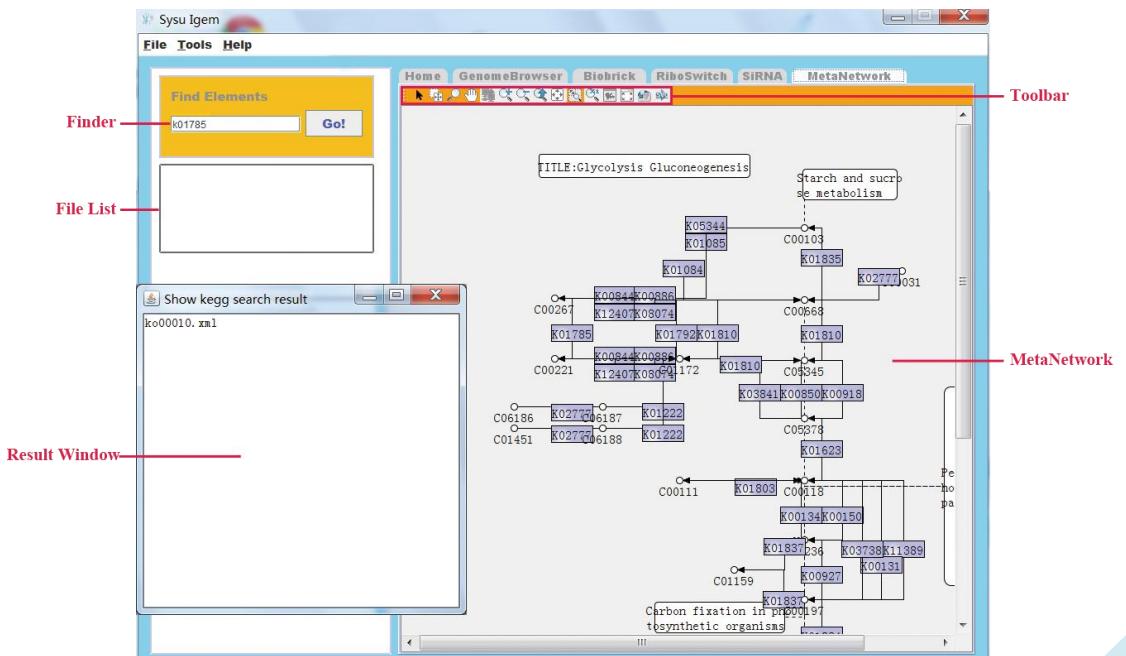


The left textbox is for you to input DNA sequence. There are two ways to input that: you can either input the sequence directly or open a file in FASTA format. If you choose the former, click **Direct Input**, then input your sequence, and click **Go**. If you choose the latter, you need only click **Open Fasta** and choose your FASTA file to open. Two solutions are provided on the right— one is solved by Tom Tuschl's method and the other is by rational design.

Network Illustrator

Procedure:

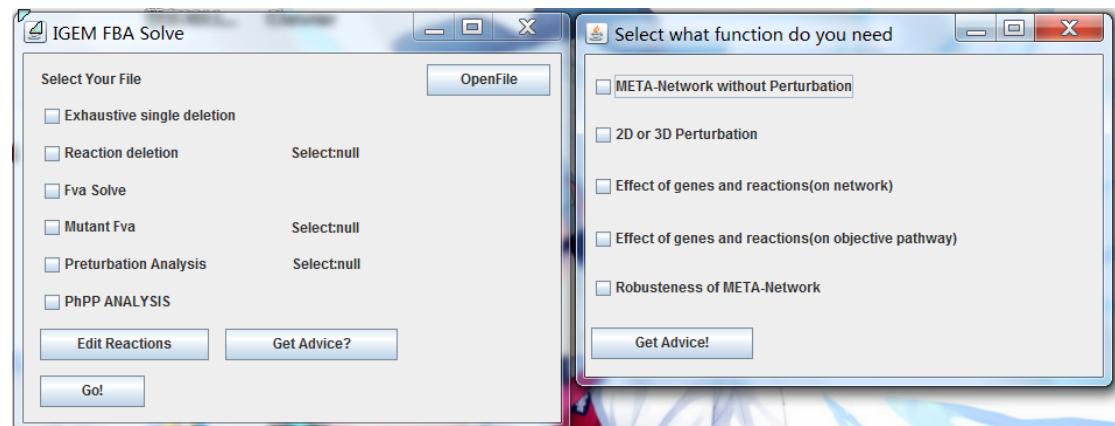
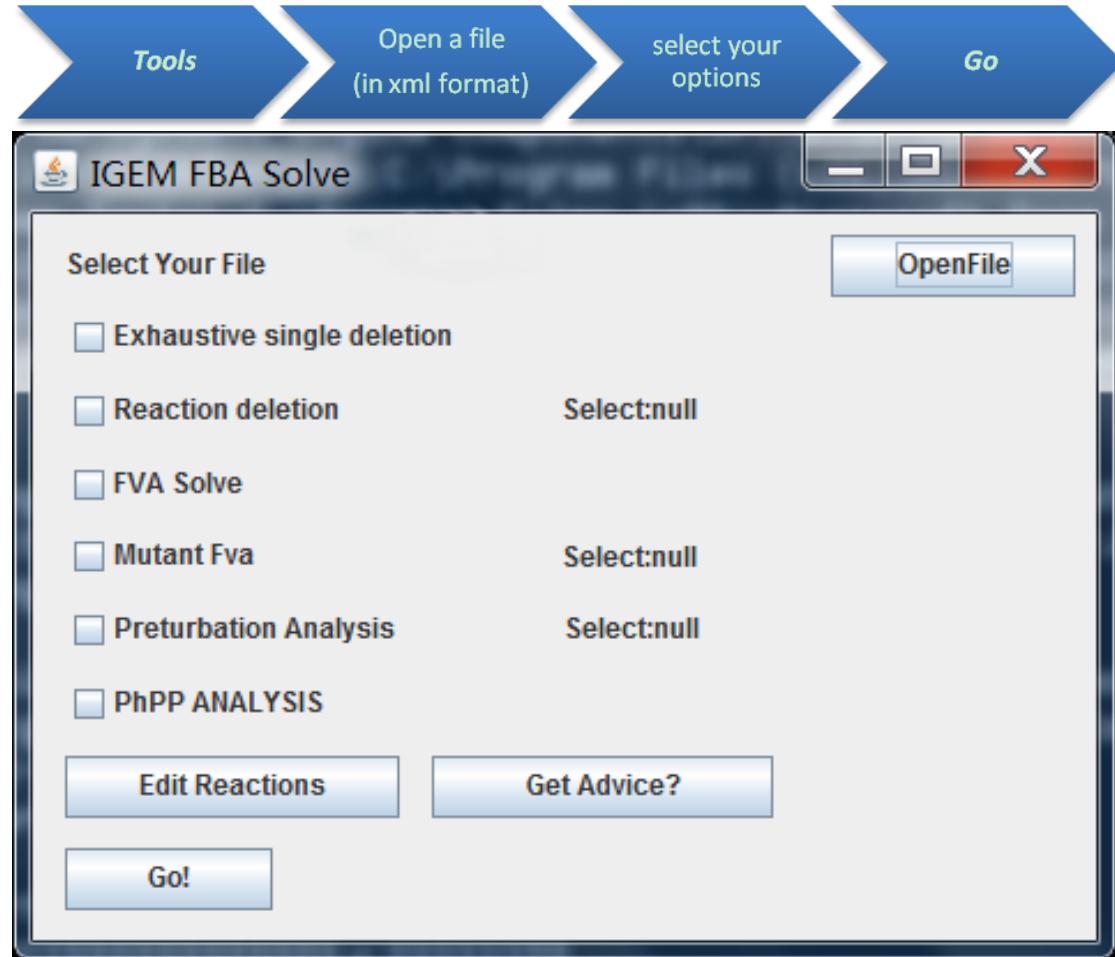
open a file (in xml format)

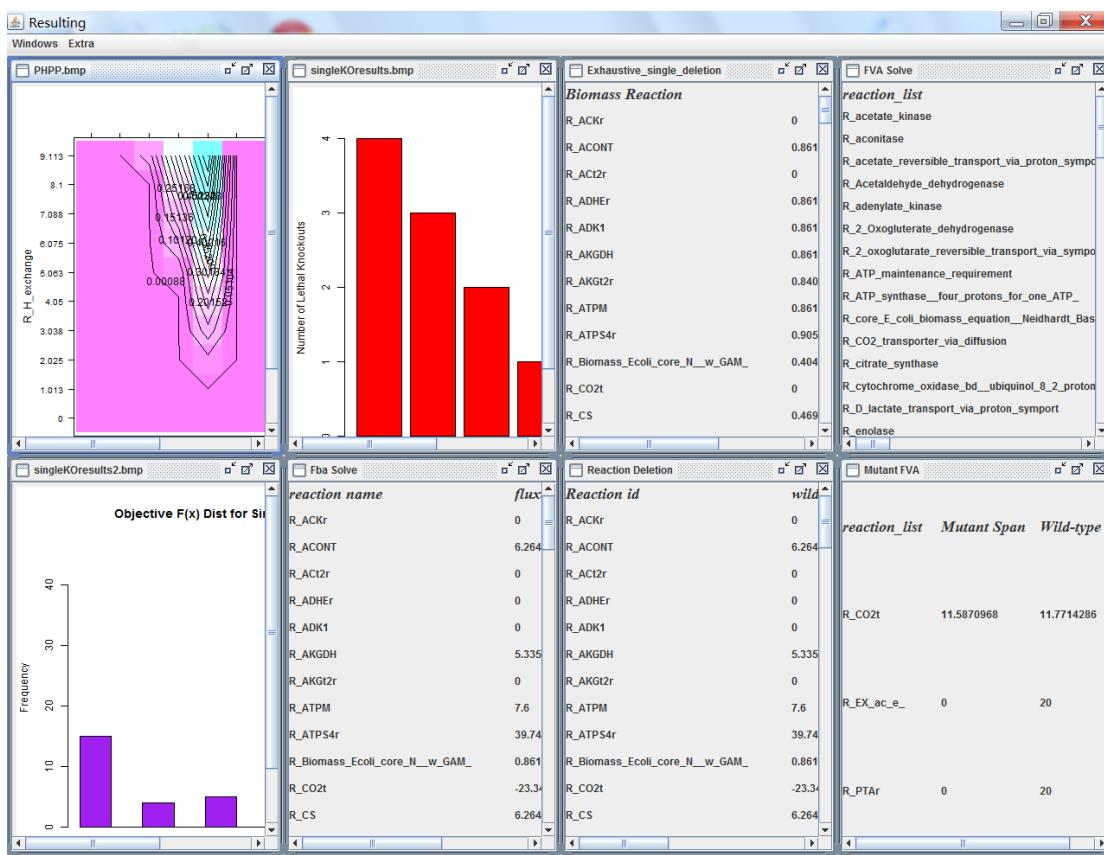
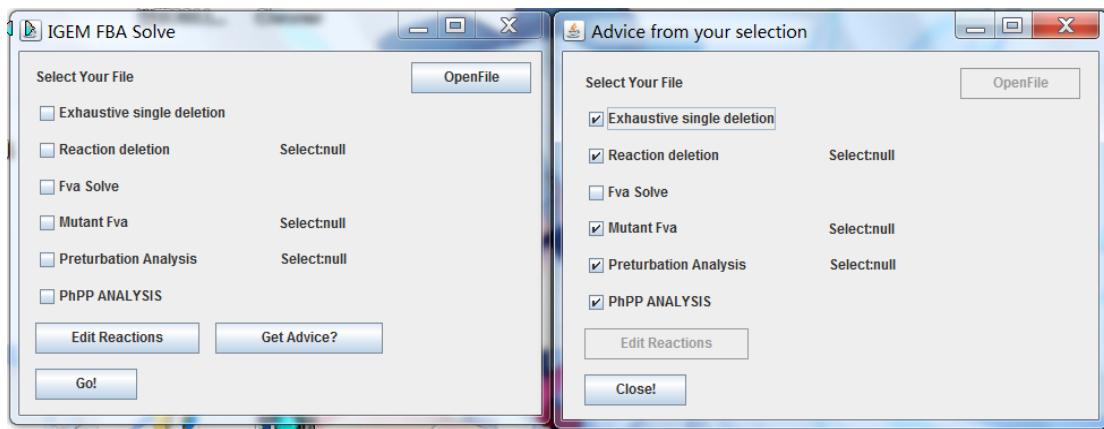


In the main display window, you will see a network from KEGG website. On the left, there is a finder; you can search elements in the network and a window that shows the search result will pop up. Below it is a box containing a list of files that you have opened. Pay attention that you can right click the main display window to open another KEGG xml file or to search any element in the network (choose **find element**).

Simulator

Procedure:





There are 5 options for you to select: exhaustive single deletion, reaction deletion, Fva analysis, Perturbation analysis and PhPP analysis. They with FBA solve will be introduced in detail. You can select all of them or part of them, or even nothing, then click **Go!**. If you select none of them, you will see a table showed basic information of each reaction. If you select several of them, the corresponding windows will tiled in the resulting window. If you select reaction deletion option, a selection of the reaction you want to wipe off is required, and if there is any change, it will be highlighted in red font.

1.FBA_solve

reaction name	fluxes
R_ACKr	0
R_ACONT	6.264896
R_ACT2r	0
R_ADHr	0
R_ADK1	0
R_AKGDH	5.335524
R_AKGt2r	0
R_ATPM	7.6
R_ATPS4r	39.747017
R_Biomass_Ecoli_core_N_w_GAM	0.861407
R_CO2t	-23.342377
R_CS	6.264896
R_CYTBD	44.693007
R_D_LACt2	0
R_ENO	14.84908
R_ETOHt2r	0
R_EX_ac_e_	0
R_EX_akg_e_	0
R_EX_co2_e_	23.342377
R_EX_etoah_e_	0
R_EX_for_e_	0
R_EX_fum_e_	0
R_EX_glc_e_	-10
R_EX_h2o_e_	24.920131
R_EX_h_e_	9.112915
R_FUM_e_	0

Left column displays names of the reactions while the right one displays the flux amount of each reaction

2. exanstive single deletion

Calculate the flux amount of the objective reaction when each other reaction is deleted one by one.

<i>Reaction name</i>	<i>Objective fluxes</i>
R_ACKr	0.861407
R_ACONT	0
R_ACT2r	0.861407
R_ADHER	0.861407
R_ADK1	0.861407
R_AKGDH	0.840372
R_AKG12r	0.861407
R_ATPM	0.905523
R_ATPS4r	0.404474
R_Biomass_Ecoli_core_N_w_GAM_	0
R_CO2t	0.469464
R_CS	0
R_CYTBD	0.240825
R_D_LACI2	0.861407
R_ENO	0
R_ETOH12r	0.861407
R_EX_ac_e_	0.861407
R_EX_akg_e_	0.861407
R_EX_co2_e_	0.469464
R_EX_etoh_e_	0.861407
R_EX_for_e_	0.861407
R_EX_fum_e_	0.861407
R_EX_glc_e_	0
R_EX_h2o_e_	0.450957
R_EX_h_e_	0

Left column display names of the reactions

The right one displays the flux amount of objective reaction the user has chosen, when each other reaction is deleted one by one.

Lethal Deletions

R_ACONT
R_Biomass_Ecoli_core_N_w_GAM_
R_CS
R_ENO
R_EX_h_e_
R_EX_pi_e_
R_GAPD
R_ICDHyr

Sub Optimal Dels

R_AKGDH

R_ATPS4r

R_CO2t

R_CYTBD

R_EX_co2_e_

R_EX_h2o_e_

R_EX_o2_e_

R_FBA

R_FUM

R_G6PDH2r

R_GND

R_H2Ot

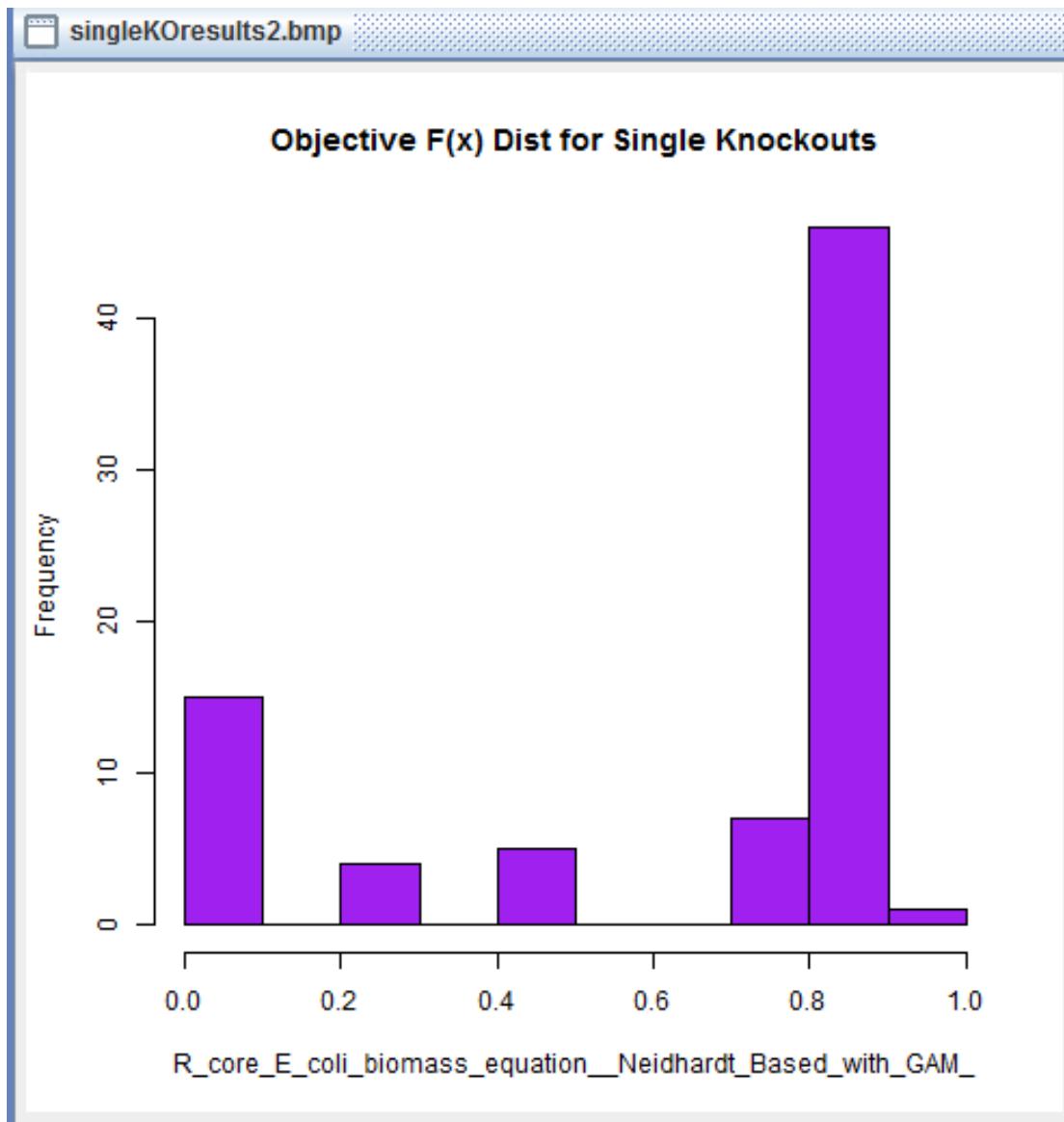
Super Optimal Dels

R_ATPM

when rolling down the screen, you can see the reaction-names related to lethal deletions, sub optimal deletions and super optimaldeletions.



This graph shows how many lethal knockouts in each reaction subsystem. The information of the reaction subsystem can be attained in SBML



This hist graph shows the frequency of reaction which has different quantified effect showed in the X-axis opon objective reaction.

3. reaction deletion

Resulting

Reaction Deletion

<i>Reaction id</i>	<i>wildtype fluxes</i>	<i>mutant fluxes</i>
R_ACKr	0	-0.76
R_ACONT	6.264896	0
R_ACI2r	0	-0.76
R_ADHER	0	0
R_ADK1	0	0
R_AKGDH	5.335524	0
R_AKG12r	0	0
R_ATPM	7.6	7.6
R_ATPS4r	39.747017	6.08
R_Biomass_Ecoli_core_N_w_GAM_	0.861407	0
R_CO2t	-23.342377	-3.04
R_CS	6.264896	0
R_CYTBD	44.693007	6.08
R_D_LACt2	0	0
R_ENO	14.84908	0.76
R_ETOHt2r	0	0
R_EX_ac_e_	0	0.76
R_EX_akg_e_	0	0
R_EX_co2_e_	23.342377	3.04
R_EX_etoh_e_	0	0
R_EX_for_e_	0	0
R_EX_fum_e_	0	0
R_EX_glc_e_	-10	-0.76
R_EX_h2o_e_	24.920131	3.04
R_EX_h_e_	9.112915	0.76

Middle column displays the flux amount of the wild type while the right column displays the mutant type, which is calculated based on the deletion of one chosen reaction.

4. FVA analysis

Resulting

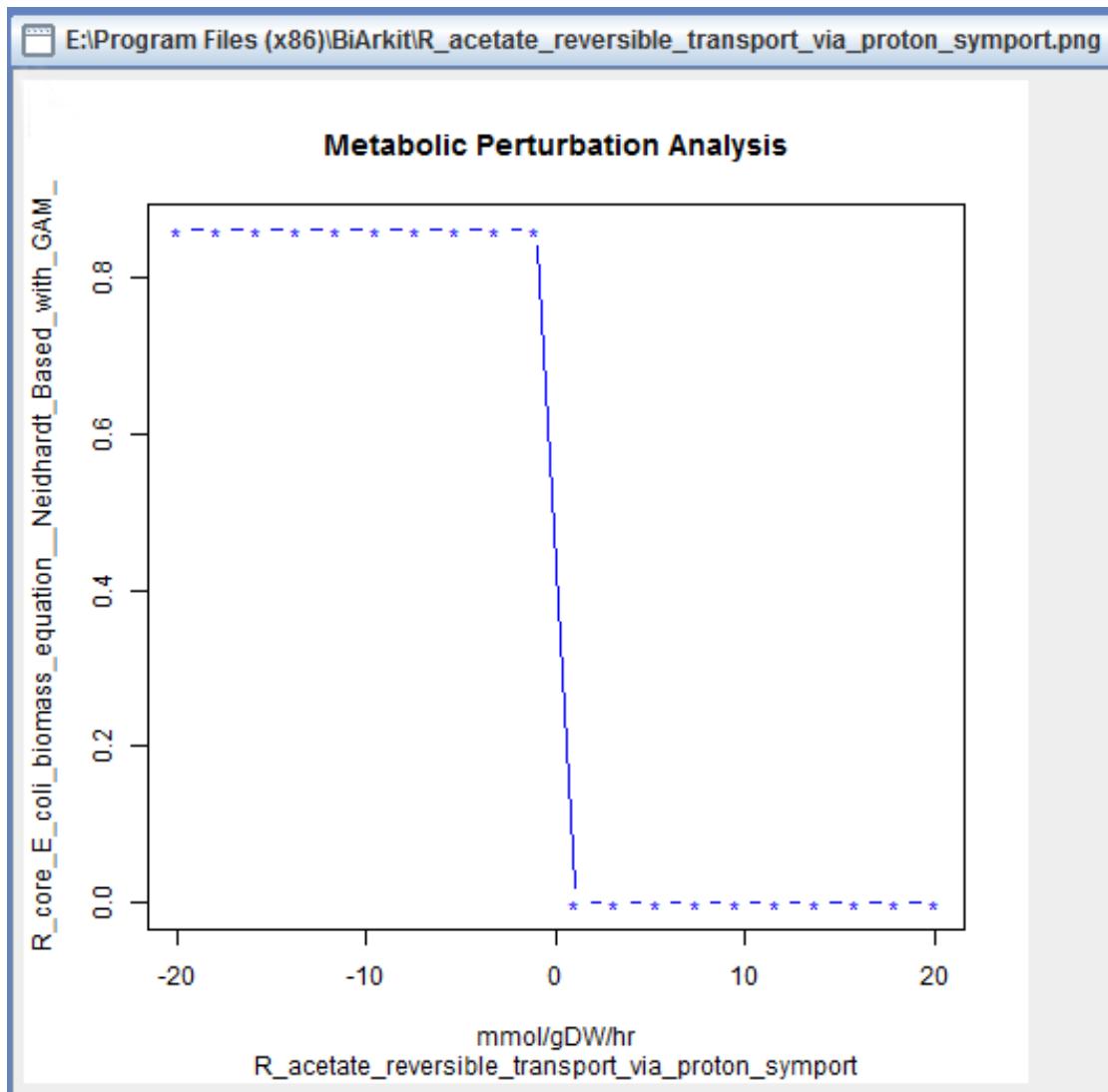
Windows Extra

FVA Solve

reaction_list	lower flux limit	wild-type flux	upper flux limit
R_acetate_kinase	-20	0	0
R_aconitase	0	6.2648963	20
R_acetate_reversible_transport_via_proton_symport	-20	0	0
R_Acetaldehyde_dehydrogenase	0	0	20
R_adenylate_kinase	0	0	142.4
R_2_Oxoglutarate_dehydrogenase	0	5.3355238	20
R_2_oxoglutarate_reversible_transport_via_symport	-10	0	0
R_ATP_maintenance_requirement	7.6	7.6	7.6
R_ATP_synthase__four_protons_for_one_ATP_	-32.4	39.470168	120
R_core_E_coli_biomass_equation_Neidhardt_Based_with_GAM_0		0.8614074	0.8614074
R_CO2_transporter_via_diffusion	-60	-23.3423769	11.7714286
R_citrate_synthase	0	6.2648963	20
R_cytochrome_oxidase_bd_ubiquinol_8_2_protons_	0	44.6930075	120
R_D_lactate_transport_via_proton_symport	-20	0	0
R_enolase	0	14.8490795	20
R_ethanol_reversible_transport_via_proton_symport	-20	0	0
R_Acetate_exchange	0	0	20
R_2_Oxoglutarate_exchange	0	0	10
R_CO2_exchange	-11.7714286	23.3423769	60
R_Ethanol_exchange	0	0	20
R_Formate_exchange	0	0	40
R_Fumarate_exchange	0	0	0
R_D_Glucose_exchange	-10	-10	-0.5066667
R_H2O_exchange	-10	24.9201307	60
R_H_exchange	0	9.1129152	40
R_D_lactate_exchange	0	0	20
R_O2_exchange	-60	-22.3465037	0
R_Phosphate_exchange	-3.1688594	-3.1688594	0
R_Pyruvate_exchange	0	0	20
R_Succinate_exchange	0	0	16.8195122
R_fructose_bisphosphate_aldolase	-10	7.5707824	10
R_fructose_bisphosphatase	0	0	142.4
D_formate_transport_via_diffusion	-40	0	0

This analysis exams the robustness of the whole metabolic network by calculating flux value which can be reached in reality. In other words, this function works out the upper and lower limit of the flux of each reaction, as you can see in the column name ‘lower flux limit’ and ‘upper flux limit’.

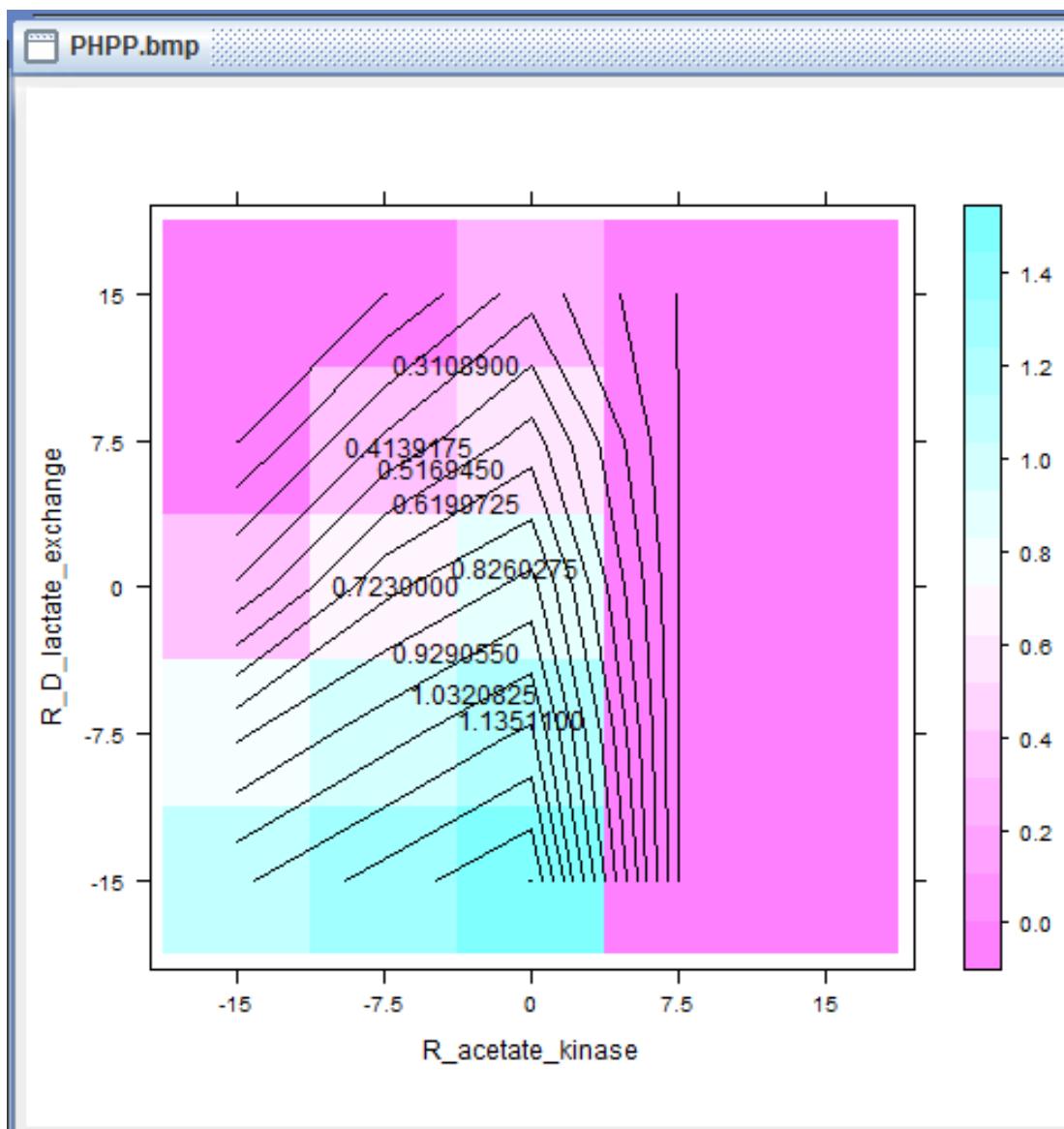
5.Perturbation analysis:



X-axis refers to the continuously increasing flux value of the chosen reaction.

Y-axis refers to the flux value of the objective reaction according to the variation of the flux value of chosen reaction in the X-axis

6.PhPP analysis

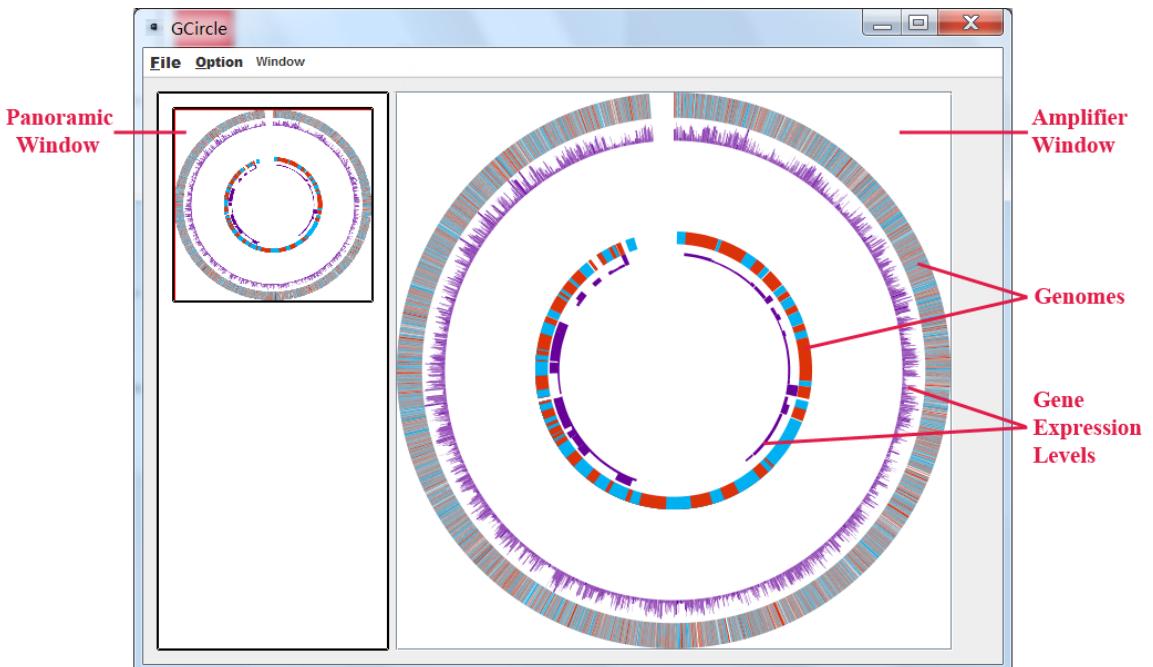


The value marked on the contour represents the flux value of the objective reaction based on the variation of two chosen reactions. The color of the graph changes according to the altitude, namely, the objective flux value.

G-Circle

Procedure:



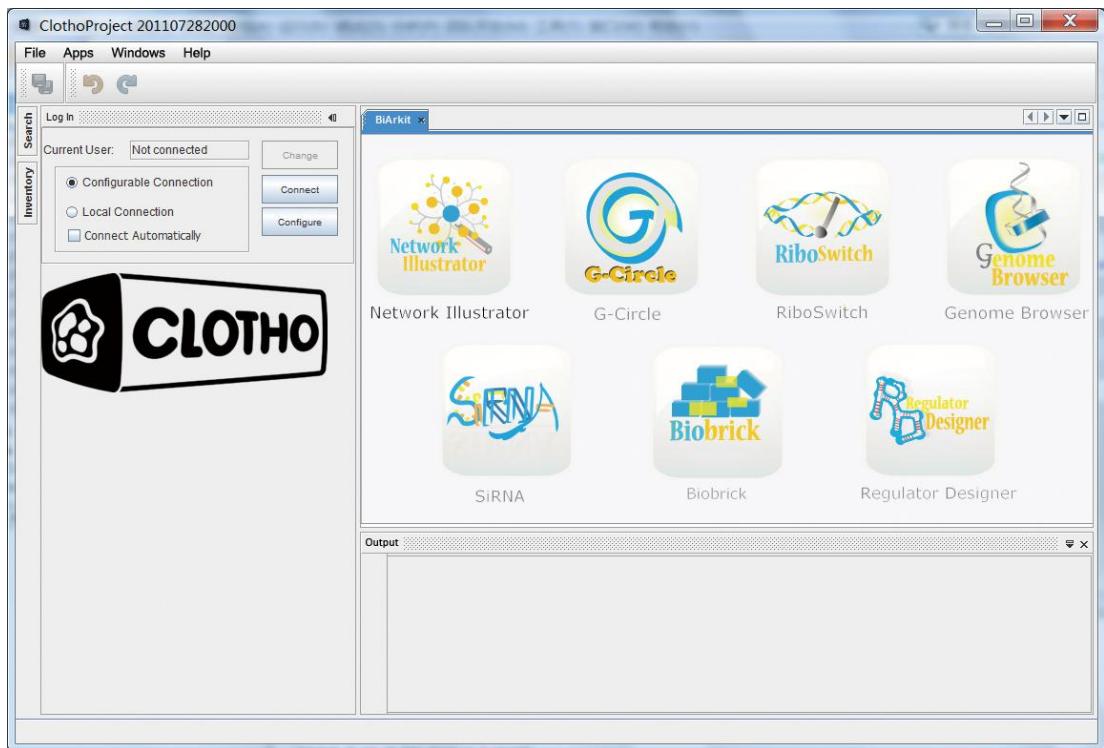


You can open several file so that you can compare the difference of these genomes. Each genome have 2 circles in the picture: the outer one is the genes of the genome, the inner is the expression level of corresponding genes. By the way, right click different sites in the small panoramic window or left click and drag the picture in the zoom window, you can move to anywhere you want to enlarge and see more details in the amplifier window.

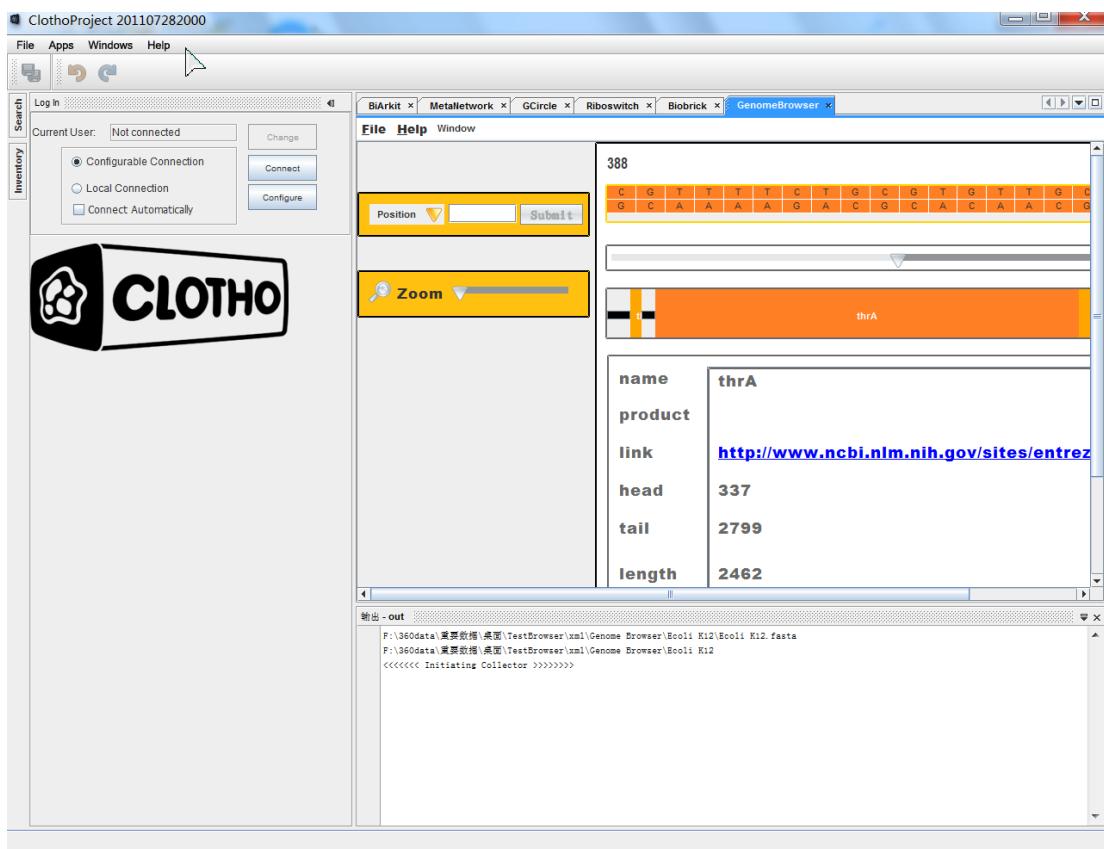
Clotho

All above seven parts have been developed into ***Clotho*** apps and have been updated into ***Clotho***, which has met the requirements for gold medal of IGEM.

- Home



● Genome Browser



The screenshot shows the Genome Browser interface. On the left, there's a search bar with 'Position' and 'Submit' buttons, and a 'Zoom' button. The main area displays a DNA sequence from position 760 to 779. Below the sequence is a schematic representation of the gene structure, showing exons (orange) and introns (grey). To the right of the schematic is a detailed gene record:

name	A
product	DNA packaging protein
link	http://www.ncbi.nlm.nih.gov/sites/entrez?db=gen
head	711
tail	2636
length	1925

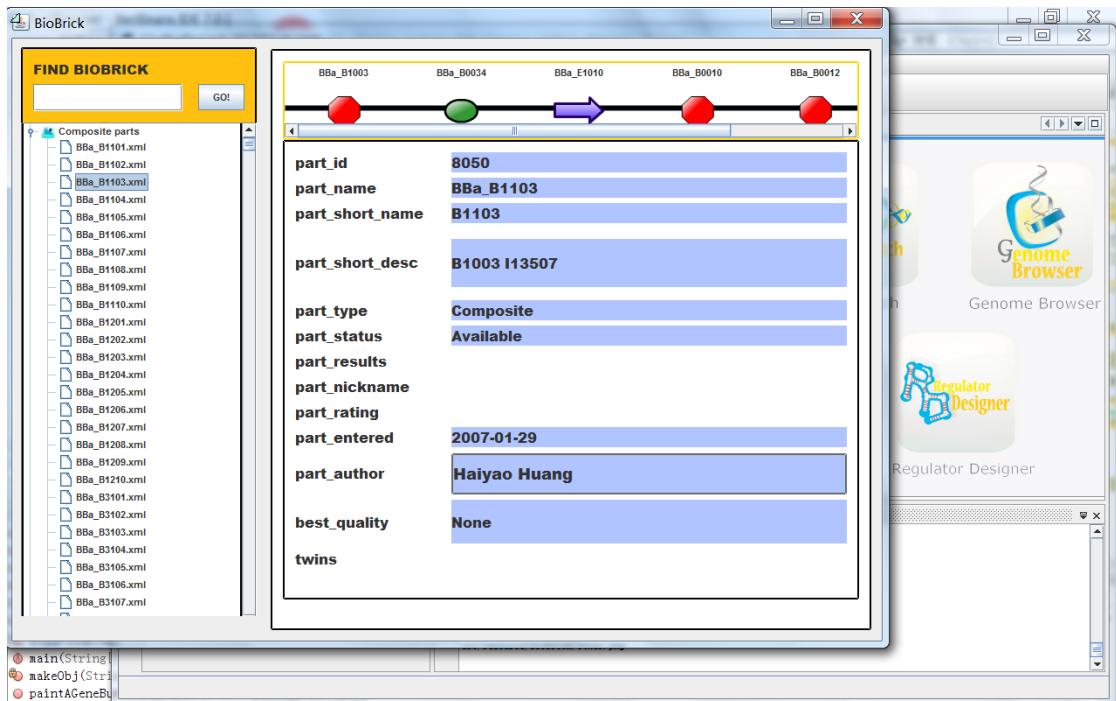
At the bottom left, there are some command-line entries: `makeObj(Str)` and `paintAGeneBu`.

● Biobrick

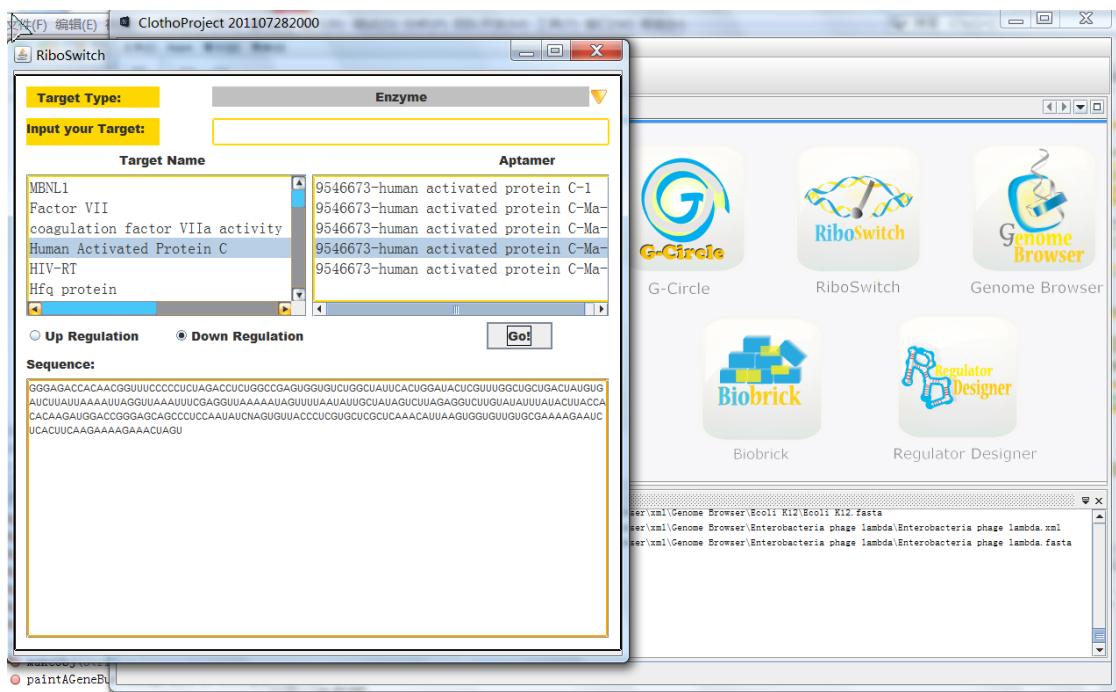
The screenshot shows the ClothoProject software interface. On the left, there's a 'Search' bar and a 'Log In' section. The main area has tabs for BiArkit, MetallNetwork, GCircle, Riboswitch, and Biobrick. The Biobrick tab is active, showing a search interface with a 'FIND BIOBRICK' button and a list of composite parts. To the right, a detailed view of a specific biobrick is shown:

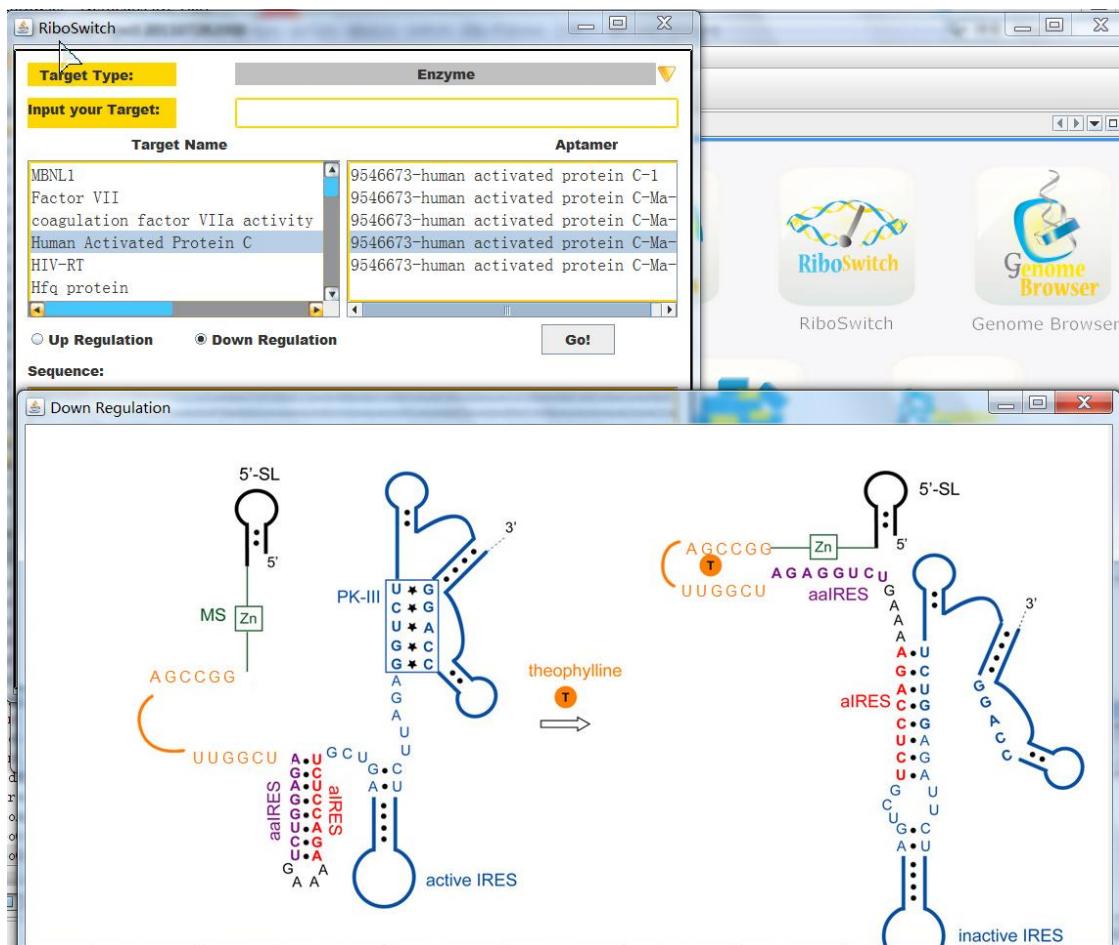
part_id	8050
part_name	BBa_B1103
part_short_name	B1103
part_short_desc	B1003 I13507
part_type	Composite
part_status	Available
part_results	
part_nickname	
part_rating	
part_entered	2007-01-29
part_author	Haiyao Huang

Below the details, there's a '输出 -out' panel showing file paths for various biobrick components.



● RiboSwitch

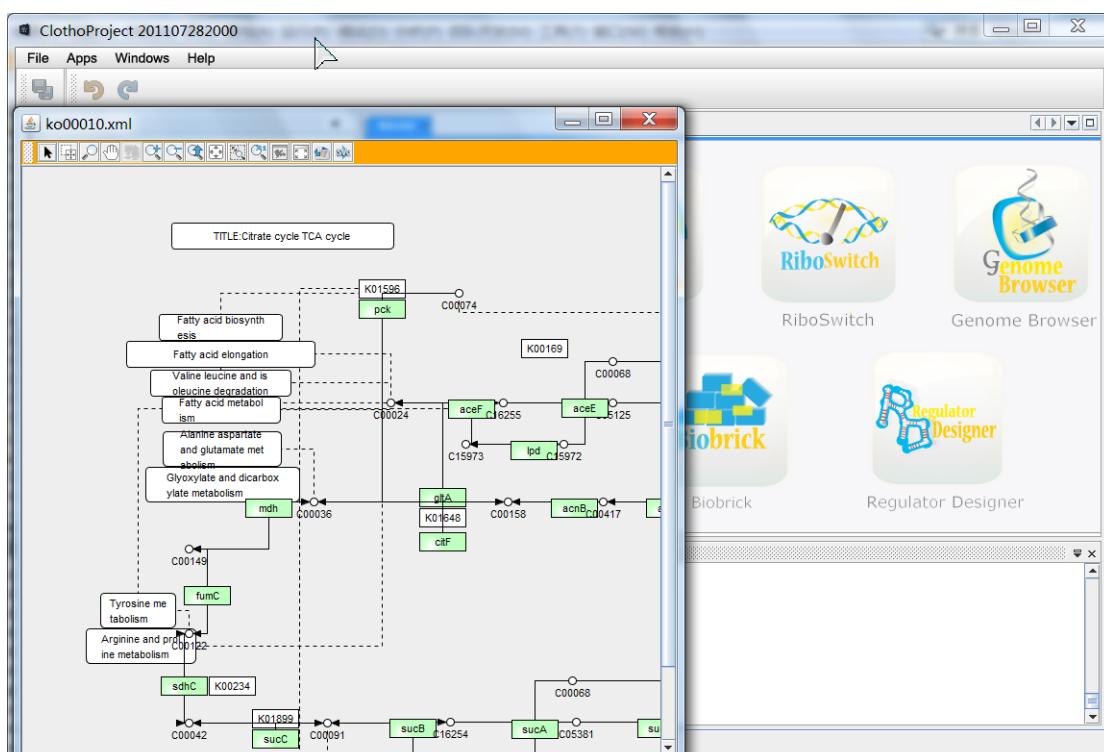
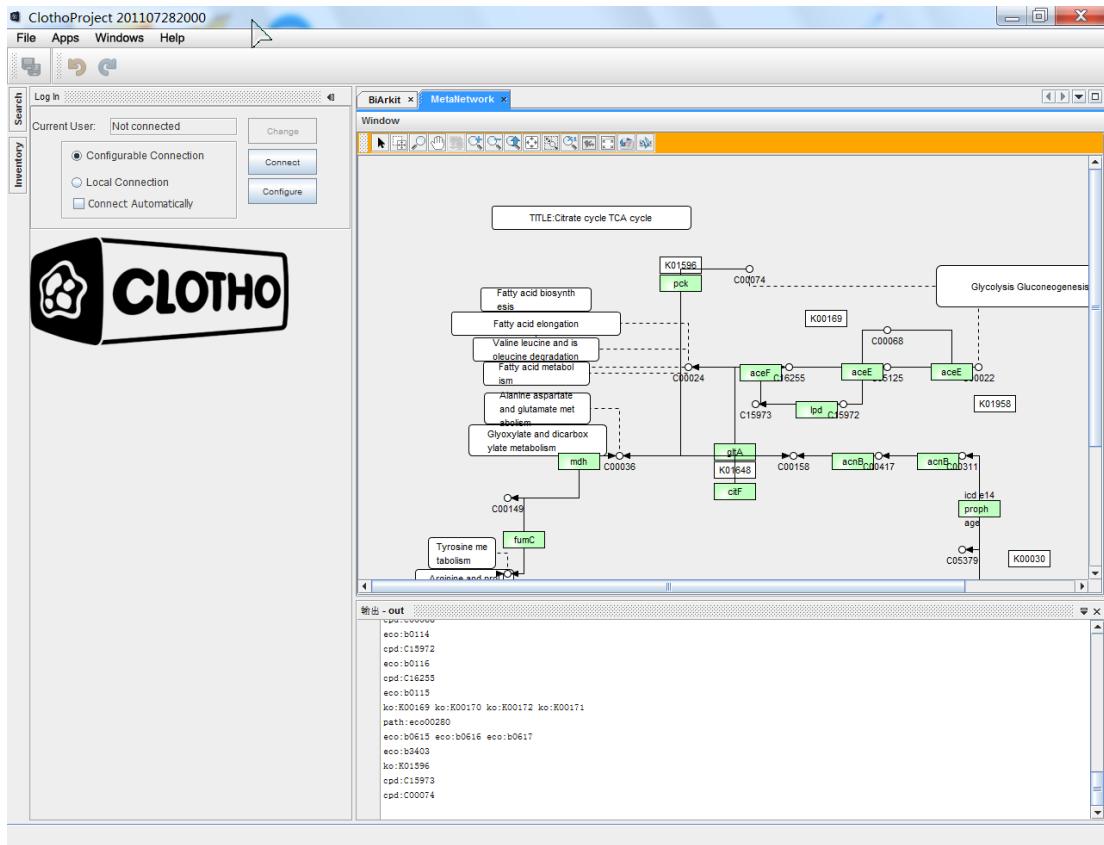




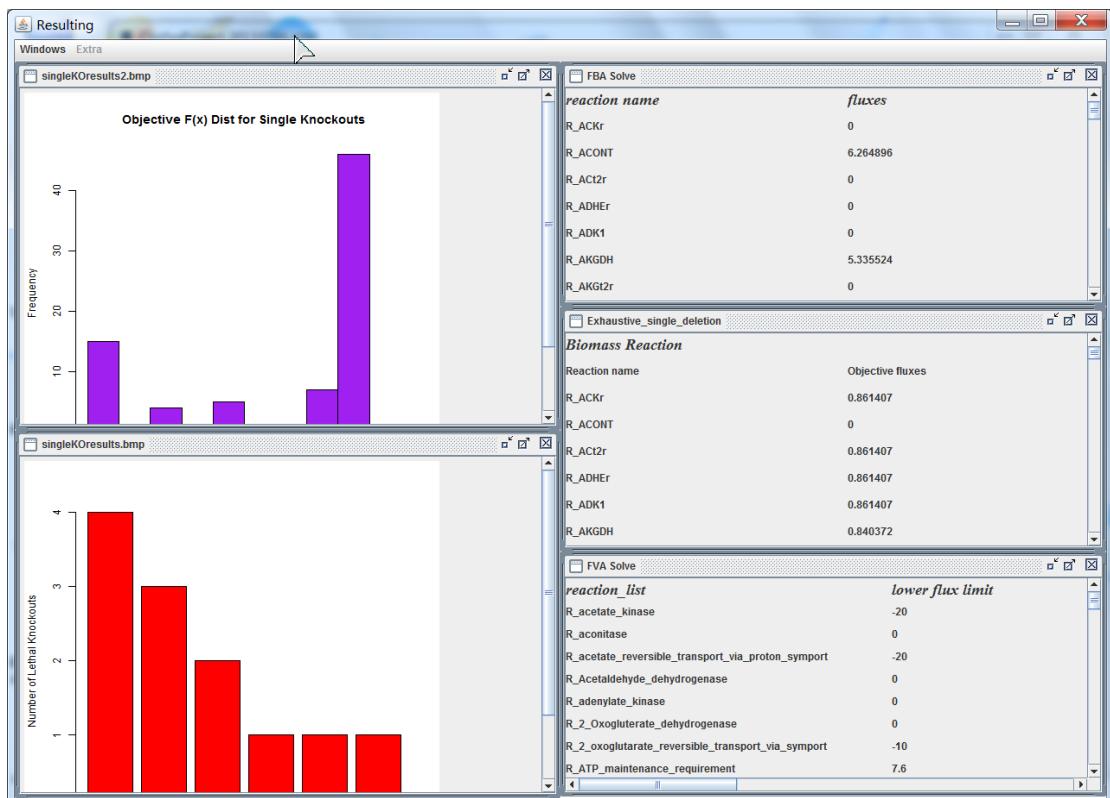
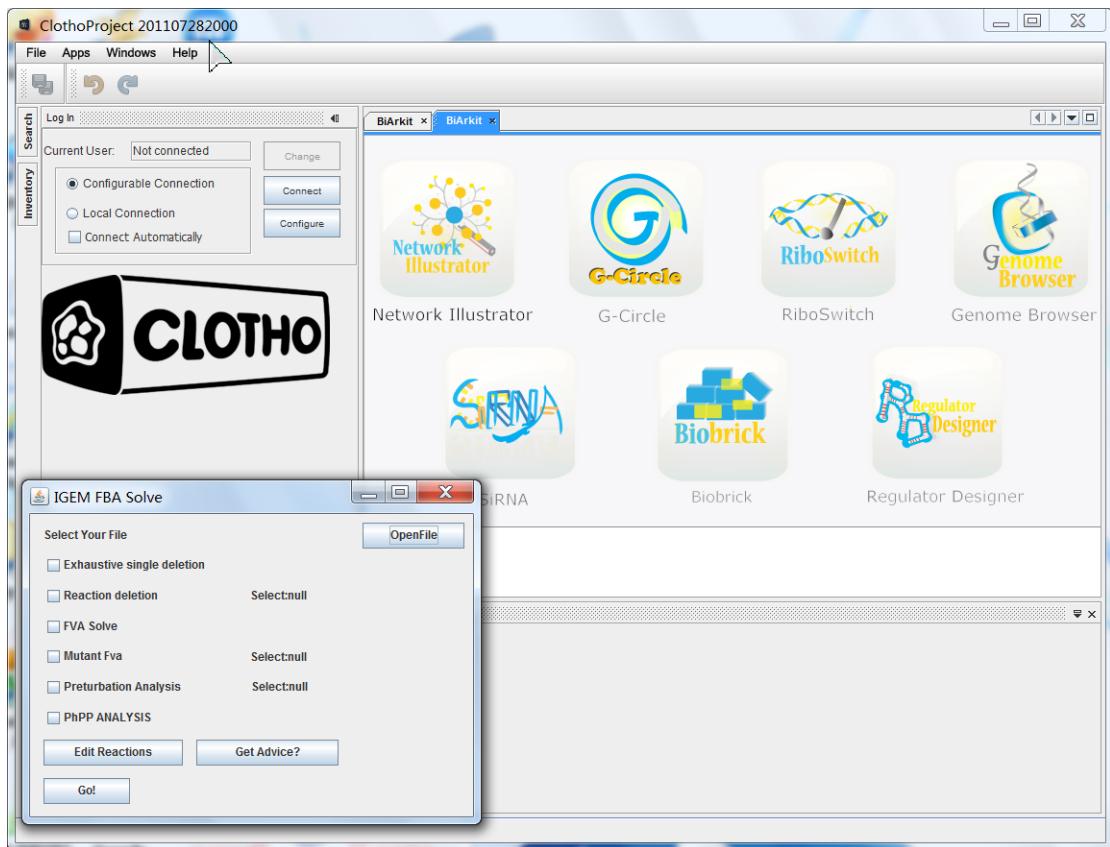
● SiRNA

The screenshot shows the ClohoProject software interface for siRNA design. On the left, a "Direct Input" window displays a long DNA sequence (dsRNA) consisting of multiple lines of nucleotide pairs. On the right, a central panel titled "Tom Tuschl's Method:" provides a schematic of the siRNA processing pathway. It shows dsRNA being cleaved by Dicer into siRNA strands. These siRNA strands then form a complex with the RISC (RNA-induced silencing complex). One strand of the complex degrades the sense strand of mRNA, while the other strand remains associated with the RISC complex. This leads to the degradation of the mRNA. The right side of the interface also features icons for "Genome Browser" and "Regulator Designer".

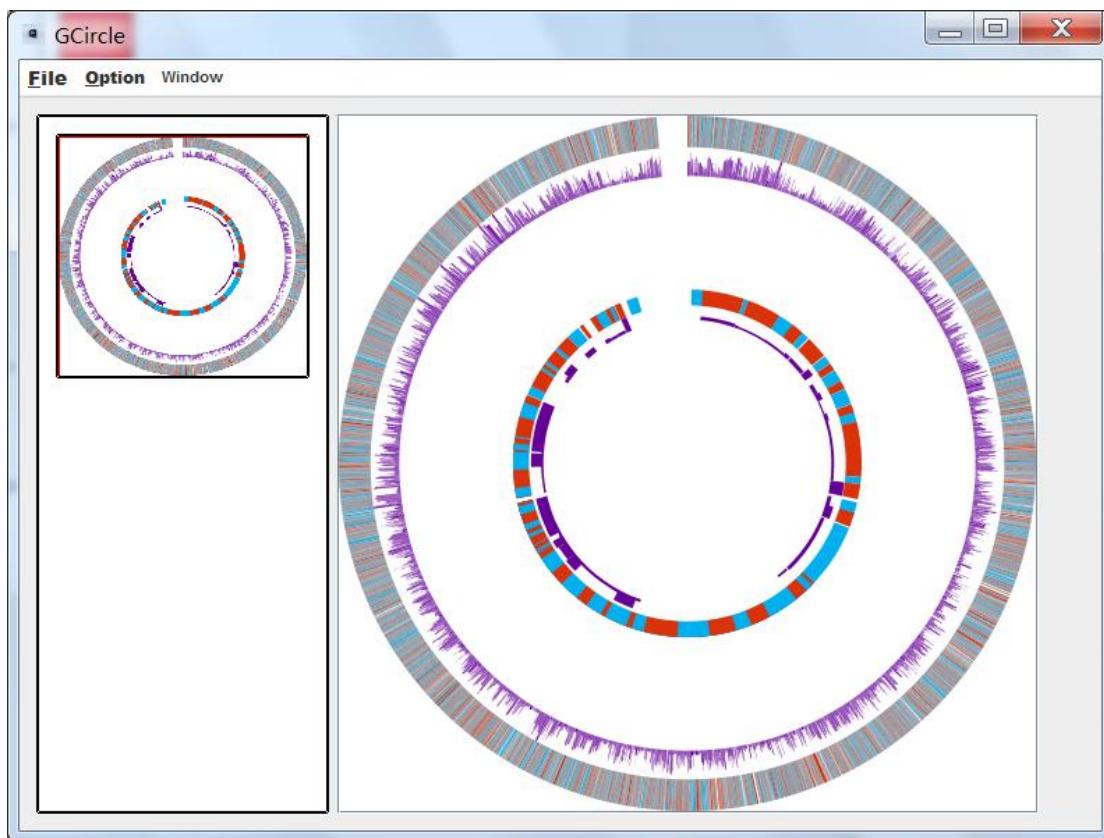
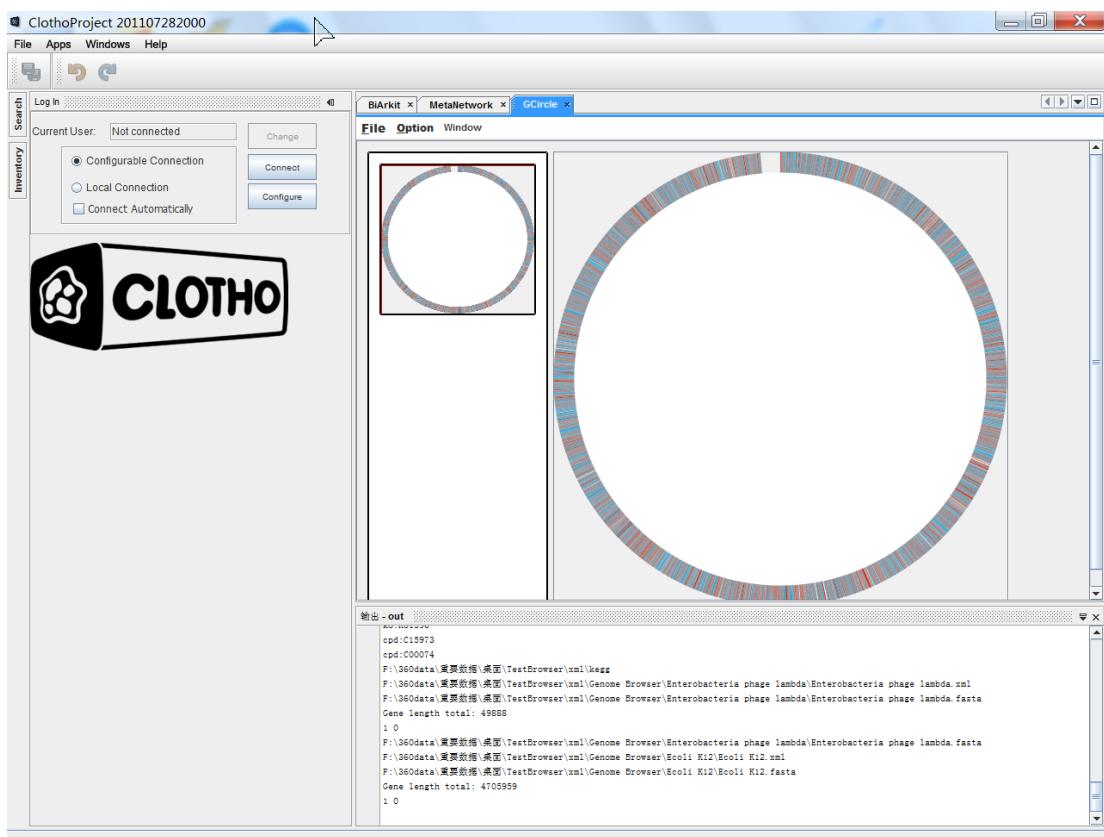
● Network Illustrator



- Simulator



● G-Circle



Contant us:

Download our software:

https://github.com/igemsoftware/SYSU_Software_2012

<https://github.com/sysu-software/BiArkit>

Our wiki:<http://2012.igem.org/Team:SYSU-Software>

Team leader's e-mail:jiang2@mail2.sysu.edu.cn or shanjiang-2008@163.com

Any question about our software: 1036479561@qq.com or whenjonny@gmail.com

You can speak Chinese if you can.