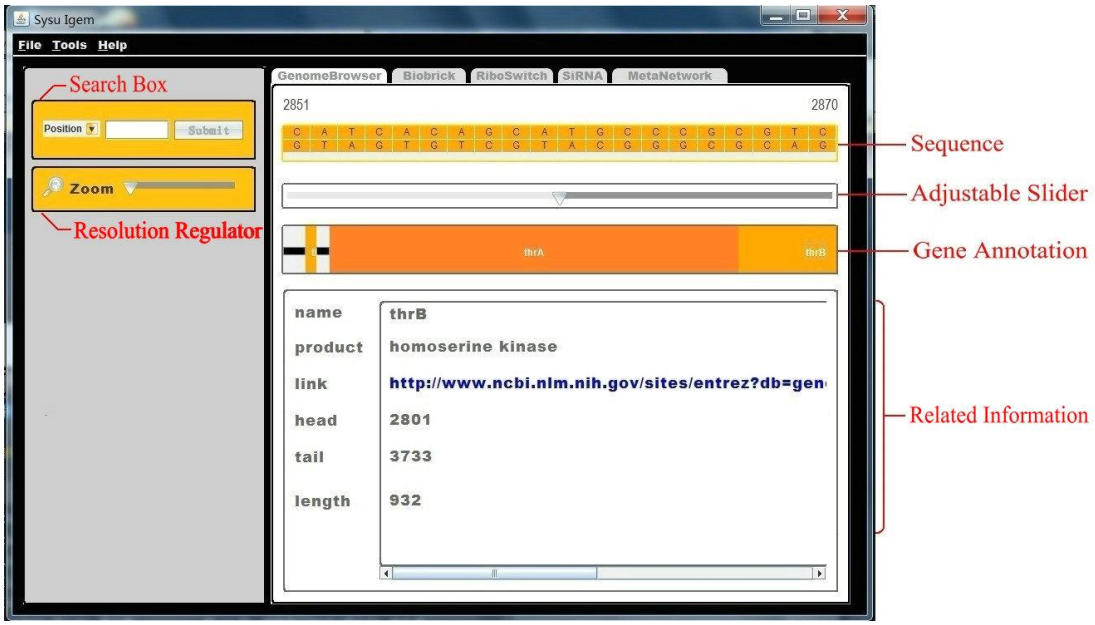
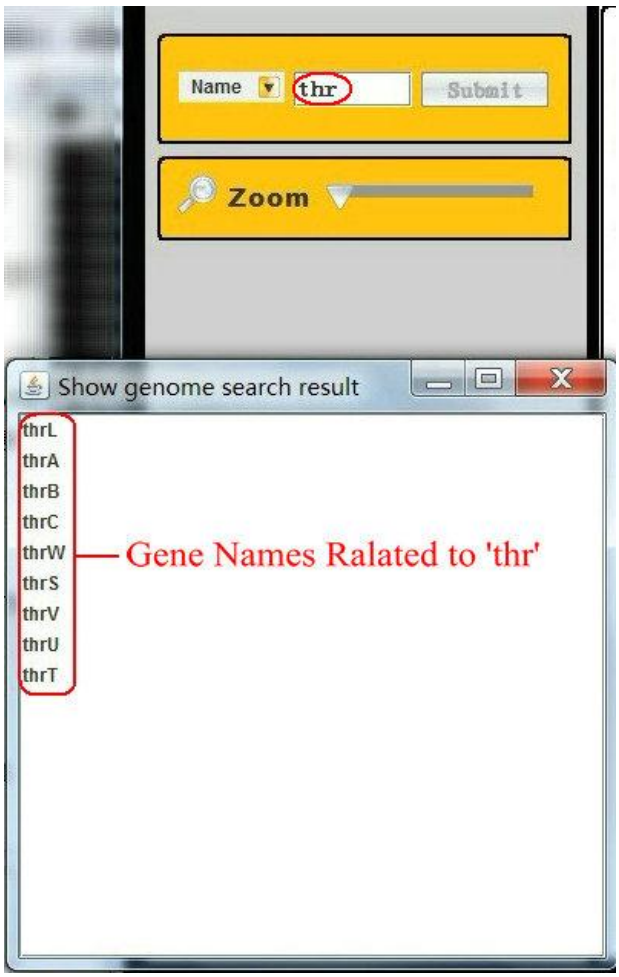
Contents

GenomeBrowser

Procedure:

File → Open Fasta





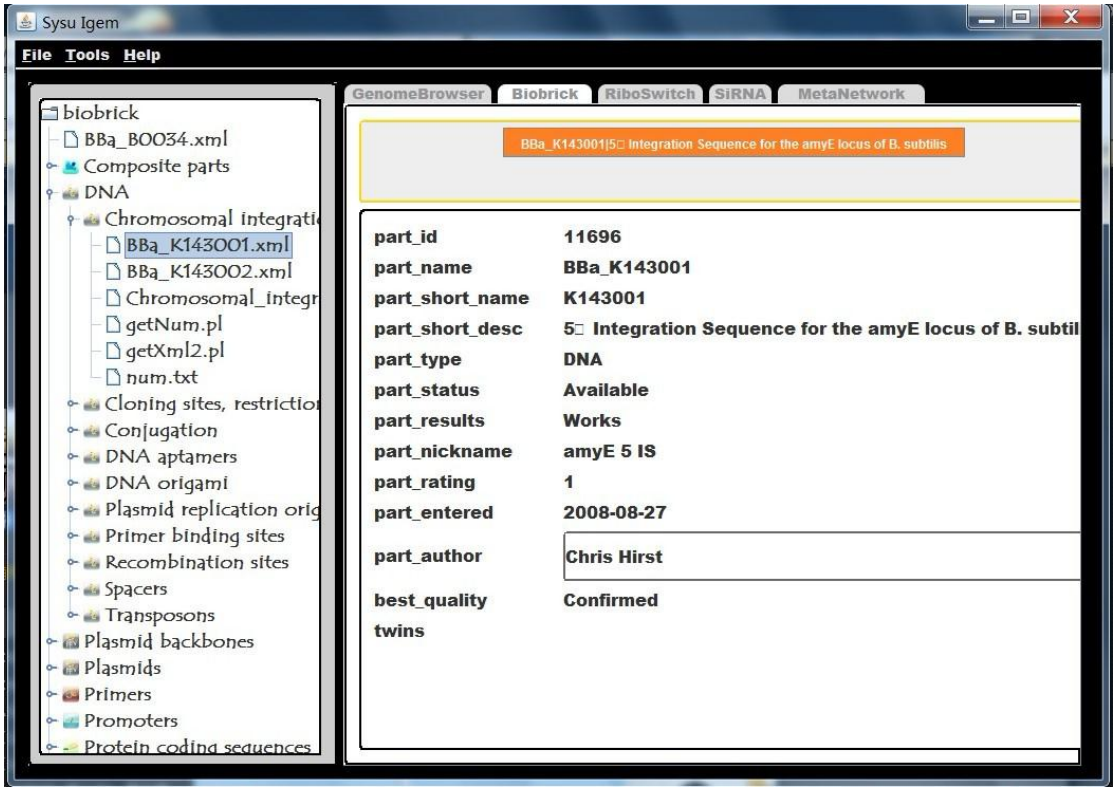
In the main display window, the first ribbon is the sequence that the user has inputted, and the third ribbon shows the corresponding gene annotation. You can click any annotation that you want, and then the sequence site will automatically jump to the fragment related to it. Between those ribbons is 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)

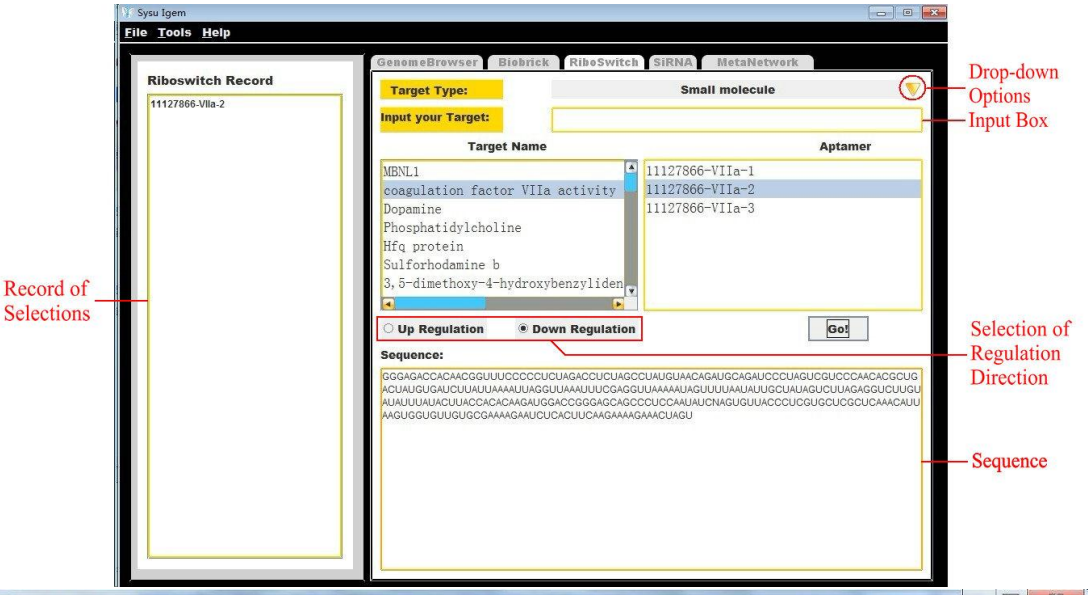


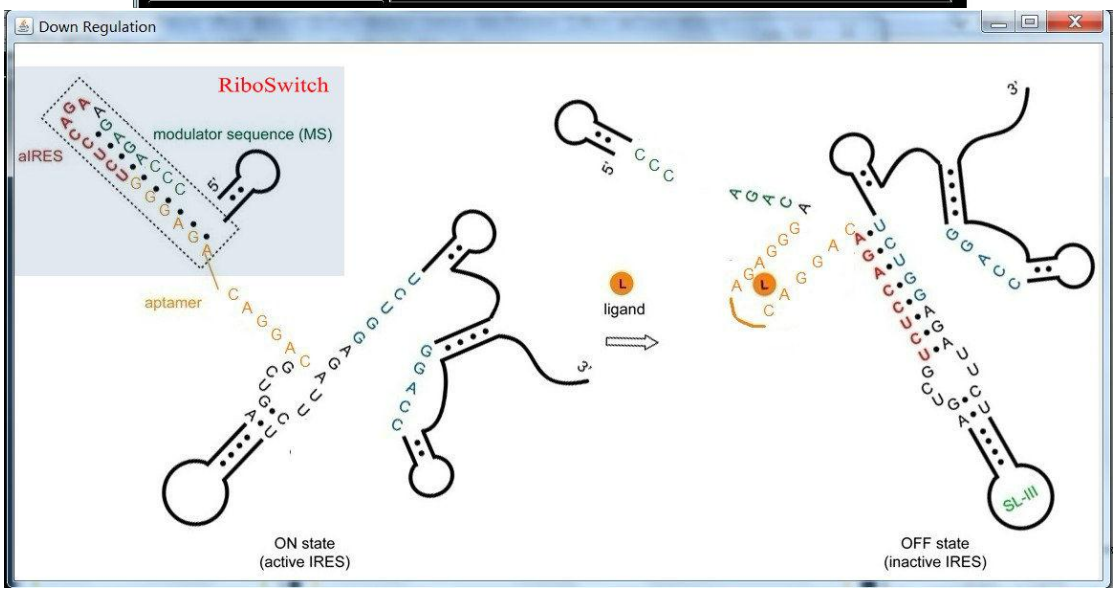
In the main display window, you can view the information of existing biobricks, which are all localized and enable you to get rid of loading when you are studying a biobrick. On the left is the list of the files that you have opened.

Riboswitch

Procedure:

choose a ***target type*** → choose a ***target name*** → choose an ***aptamer*** → choose a **regulation** direction (***up /down***) → ***GO***



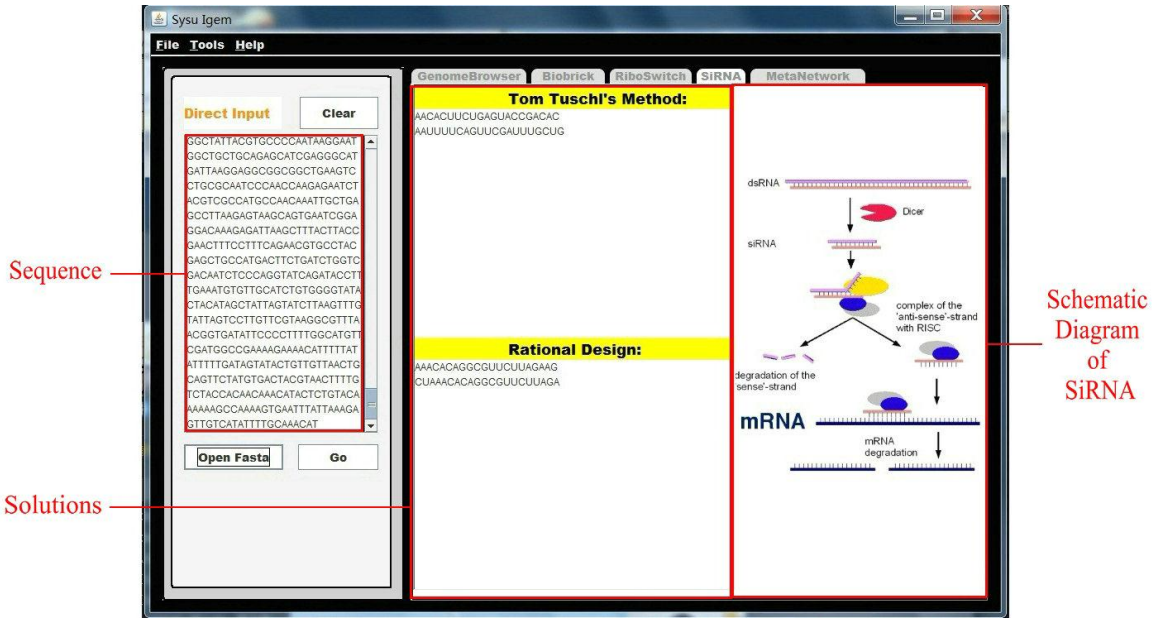


On the right is the main operating area and you can choose your target type (your experimental object) and corresponding target name, aptamer and regulation direction. Attention should be paid to the input box named Input your Target. You can search your target name by key words or even several letters 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 riboswich project, and you need only click **GO** next time.

SiRNA

Procedure:

Input your DNA sequence

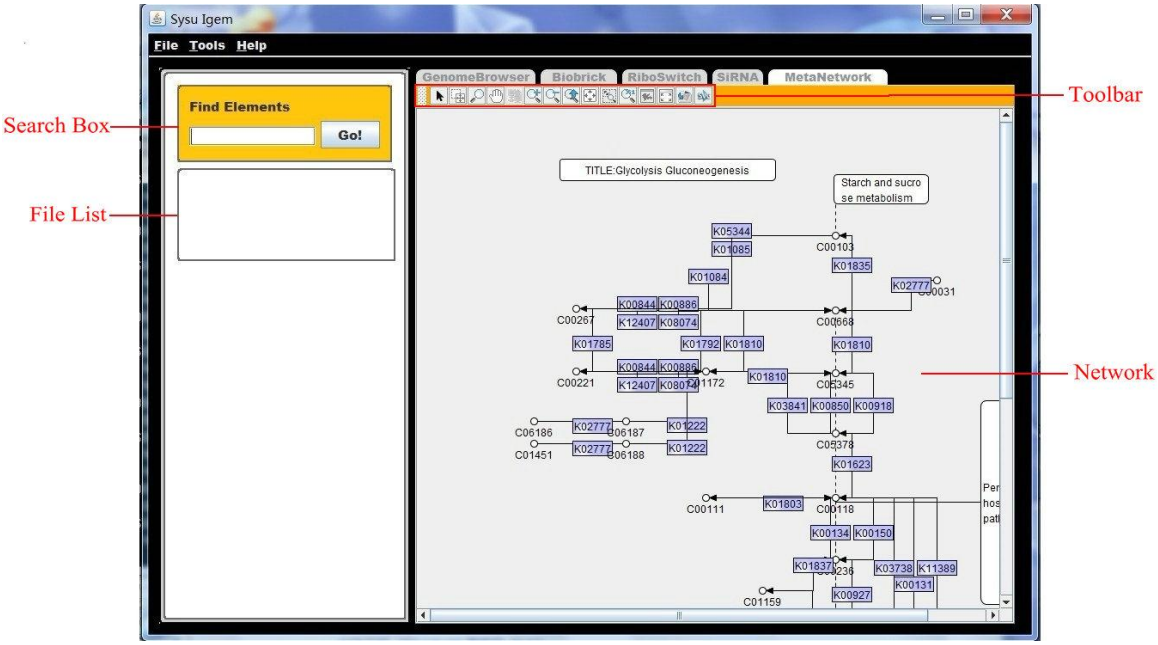


The left textbox is for you to input DNA sequence. There are two ways to input that: you can either input the sequence directly or open a file in FASTA format. If you choose the former, click **Direct Input**, then input your sequence, and click **Go**. If you choose the latter, you need only click **Open 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.

MetaNetwork

Procedure:

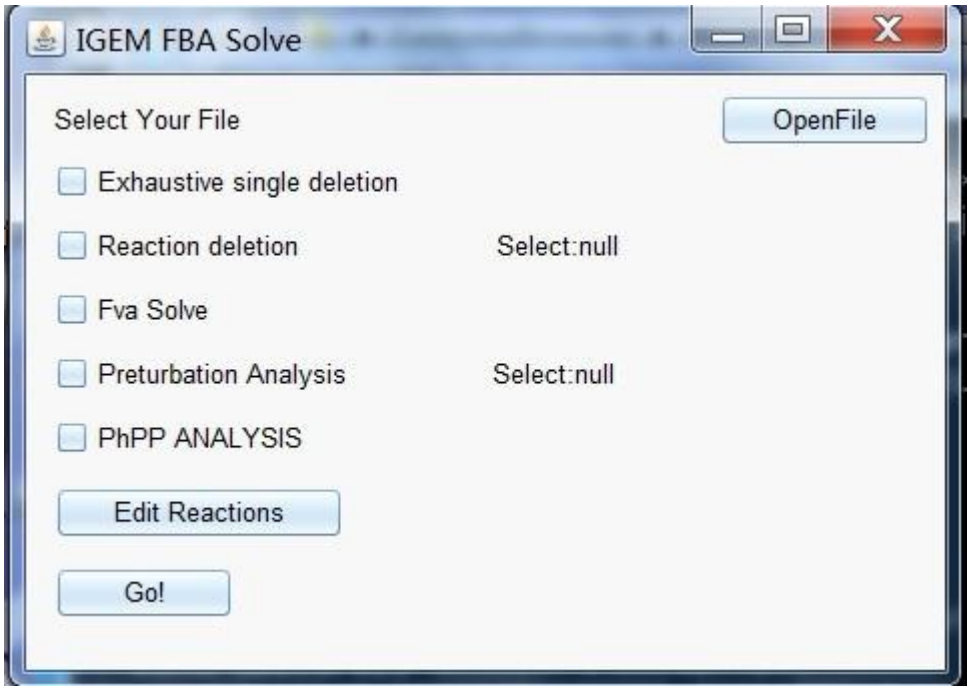
open a file (in xml format)

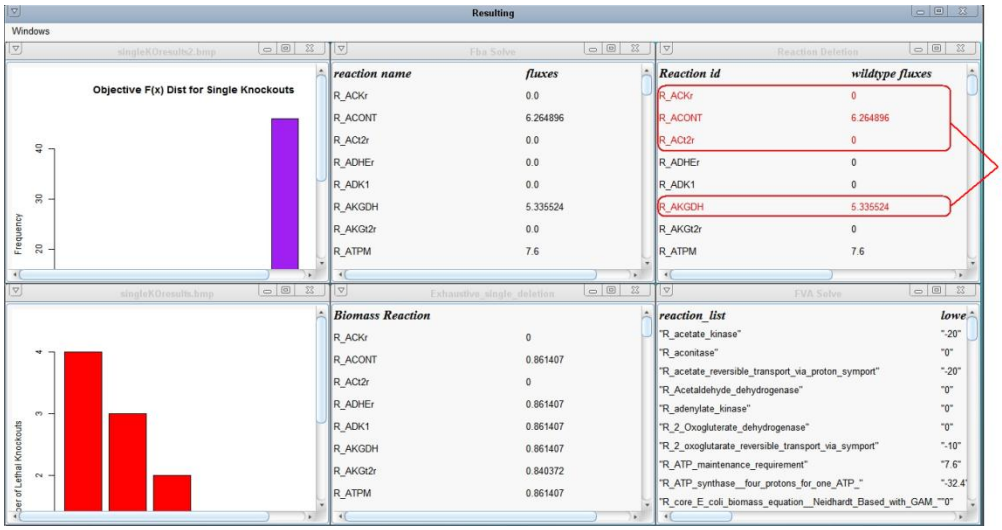


In the main display window, you will see a network from KEGG website. On the left box displays a list of the files you have opened. Pay attention that you can right click the main display window to open another KEGG xml file or to search any element in the network (choose **find element**).

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_ADHEr	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

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.

Biomass Reaction	
R_ACKr	0
R_ACONT	0.861407
R_ACt2r	0
R_ADHEr	0.861407
R_ADK1	0.861407
R_AKGDH	0.861407
R_AKGt2r	0.840372
R_ATPM	0.861407
R_ATPS4r	0.905523
R_Biomass_Ecoli_core_N__w_GAM_	0.404474
R_CO2t	0
R_CS	0.469464
R_CYTBD	0
R_D_LACt2	0.240825
R_ENO	0.861407
R_ETOHt2r	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

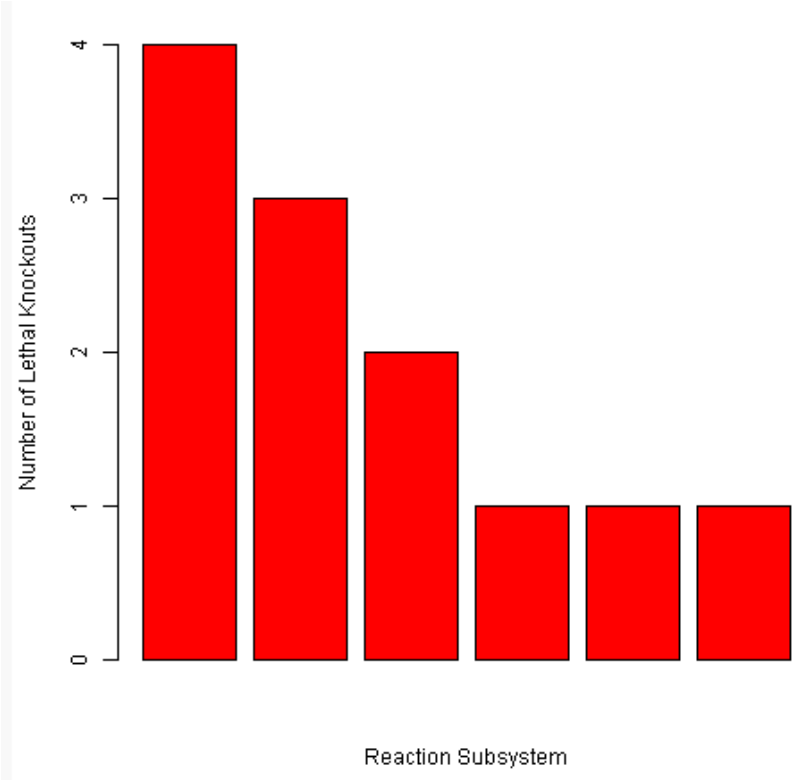
R_GND

R_H2Ot

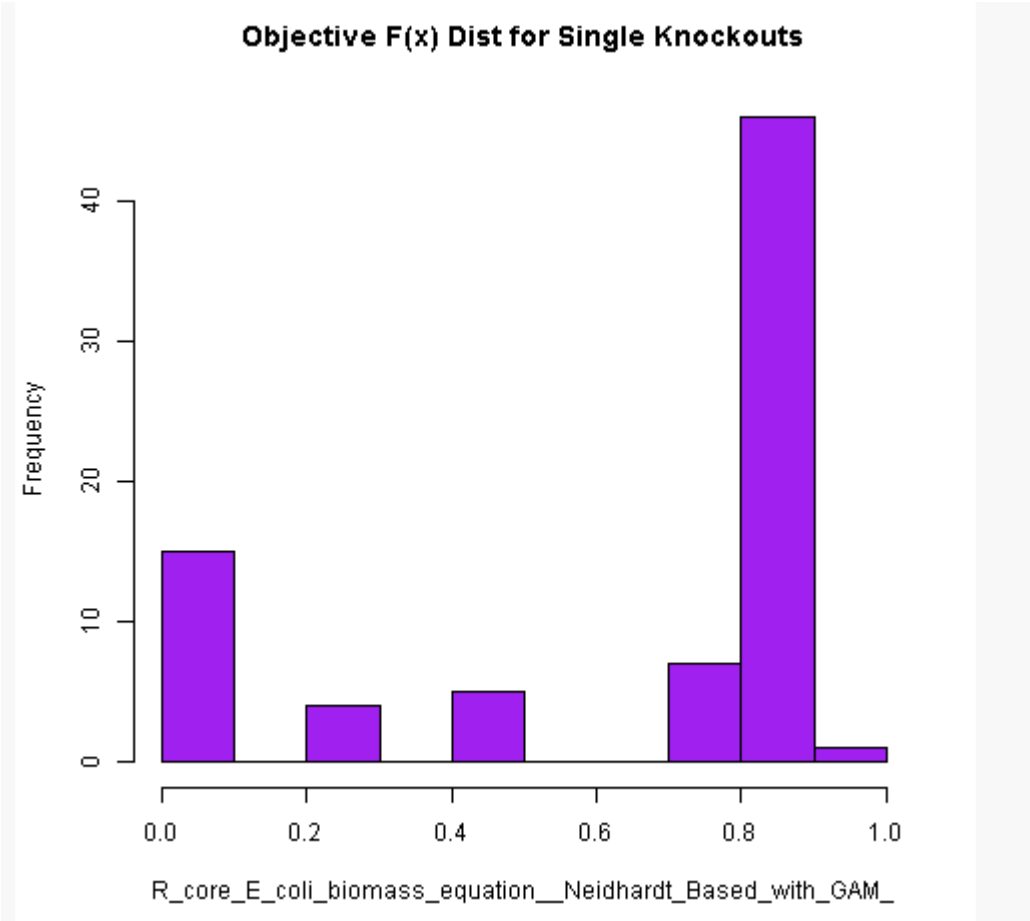
Super Optimal Dels

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

Reaction id	*wildtype fluxes*	*mutant fluxes*
R_ACKr	0	0
R_ACONT	6.264896	6.216358
R_ACt2r	0	0
R_ADHEr	0	0
R_ADK1	0	0
R_AKGDH	5.335524	0
R_AKGt2r	0	0
R_ATPM	7.6	7.6
R_ATPS4r	39.747017	41.654587
R_Biomass_Ecoli_core_N__w_GAM_	0.861407	0.840372
R_CO2t	-23.342377	-24.237565
R_CS	6.264896	6.216358
R_CYTBD	44.693007	46.532022
R_D_LACt2	0	0
R_ENO	14.84908	14.590913
R_ETOHt2r	0	0
R_EX_ac_e_	0	0

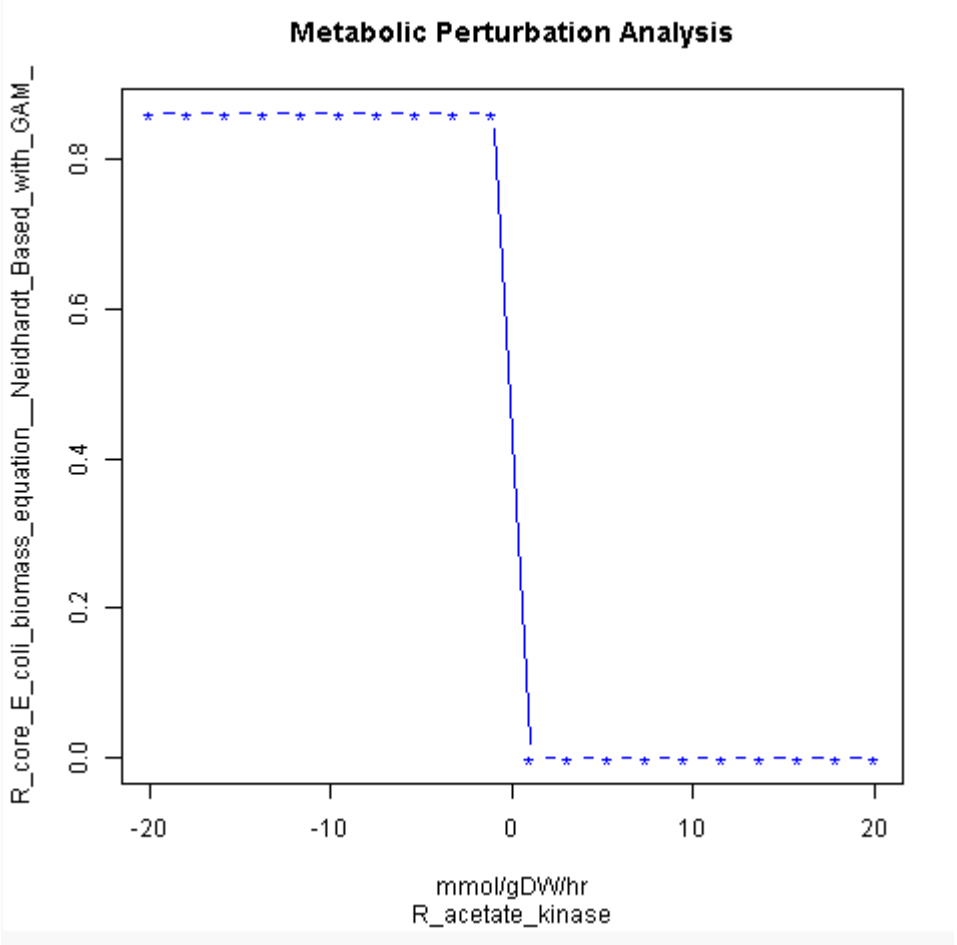
Middle column displays the flux amount of the wild type while the right column displays the mutant type, which is calculated based on the deletion of one chosen reaction.

4. FVA analysis

reaction_list	*lower flux limit*	*wild-type flux*	*upper flux limit*	*flux span*
"R_acetate_kinase"	"-20"	"0"	"0"	"20"
"R_aconitase"	"0"	"6.2648963"	"20"	"20"
"R_acetate_reversible_transport_via_proton_symport"	"-20"	"0"	"0"	"20"
"R_Acetaldehyde_dehydrogenase"	"0"	"0"	"20"	"20"
"R_adenylate_kinase"	"0"	"0"	"142.4"	"142.4"
"R_2_Oxogluterate_dehydrogenase"	"0"	"5.3355238"	"20"	"20"
"R_2_oxoglutarate_reversible_transport_via_symport"	"-10"	"0"	"0"	"10"
"R_ATP_maintenance_requirement"	"7.6"	"7.6"	"7.6"	"15.2"
"R_ATP_synthase__four_protons_for_one_ATP_"	"-32.4"	"39.7470168"	"120"	"152.4"
"R_core_E_coli_biomass_equation__Neidhardt_Based_with_GAM_"	"0"	"0.8614074"	"0.8614074"	"0.8614074"

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’.

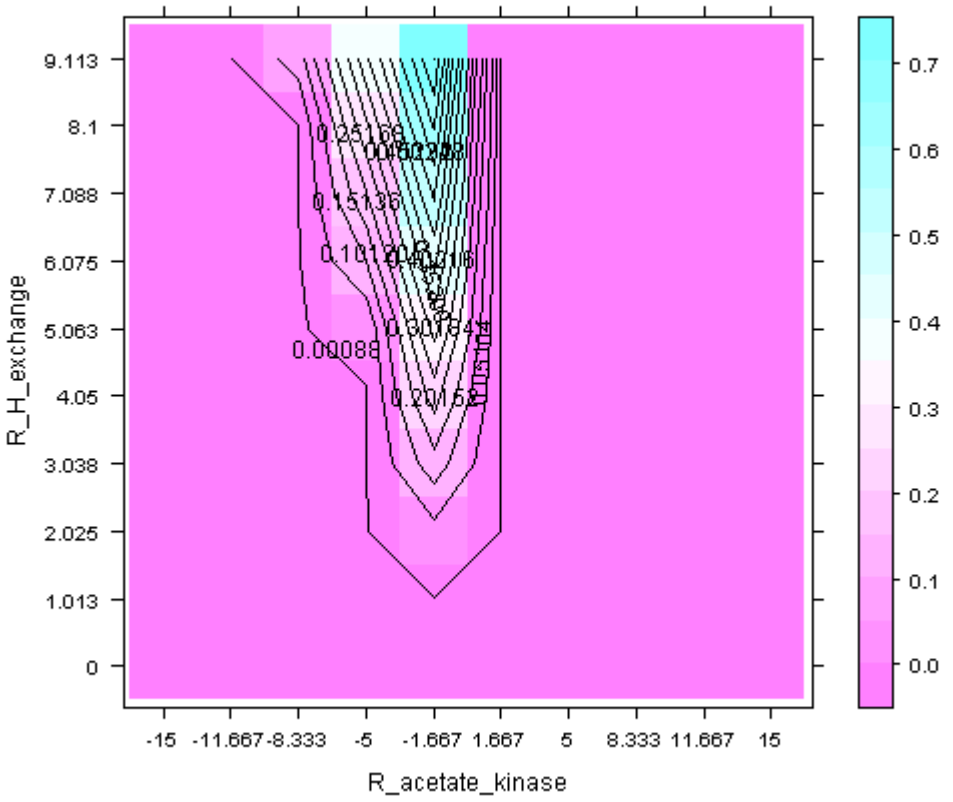
5.Perturbation analysis:



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

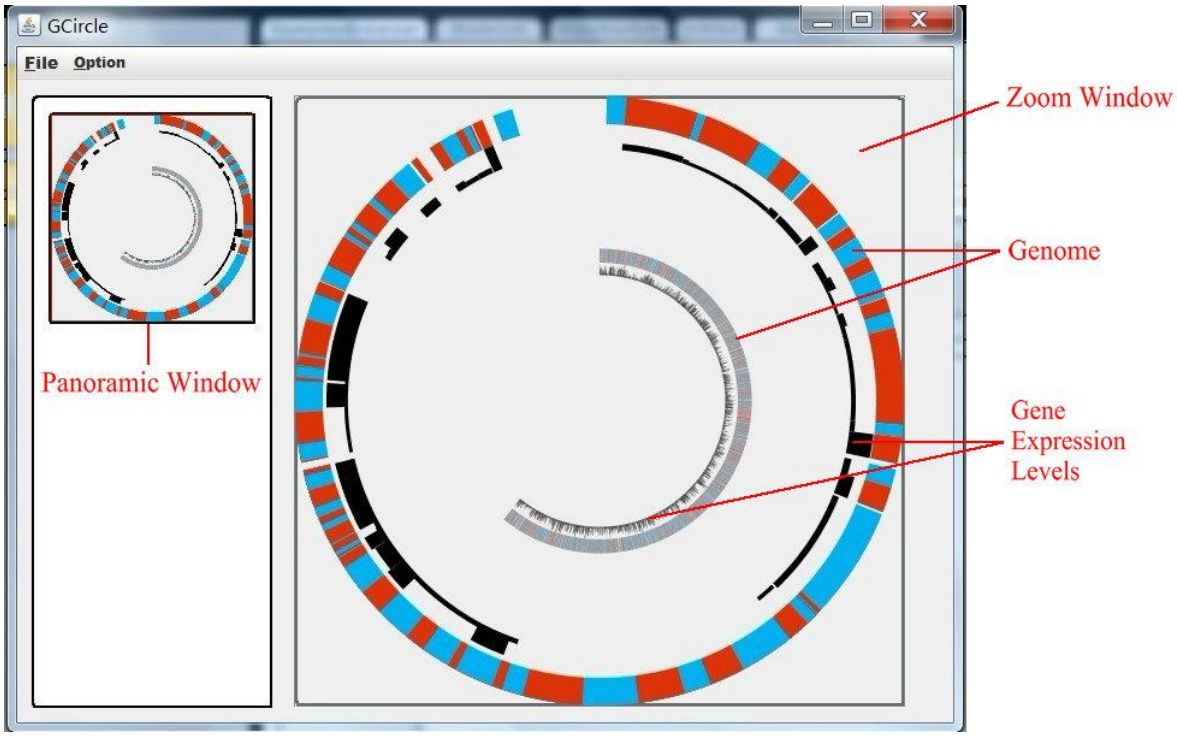


The value marked on the contour represents the flux value of the objective reaction based on the variation of two chosen reactions The color of the graph changes according to the altitude, namely, the objective flux value.

G-Circle

Procedure:

Tools → Circos → Open a file



You can open several file so that you can compare the difference of these genomes. Each genome have 2 circles in this picture: the outer one is the genes of the genome, the inner is the expression level of corresponding genes under two different conditions. 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 zoom window.