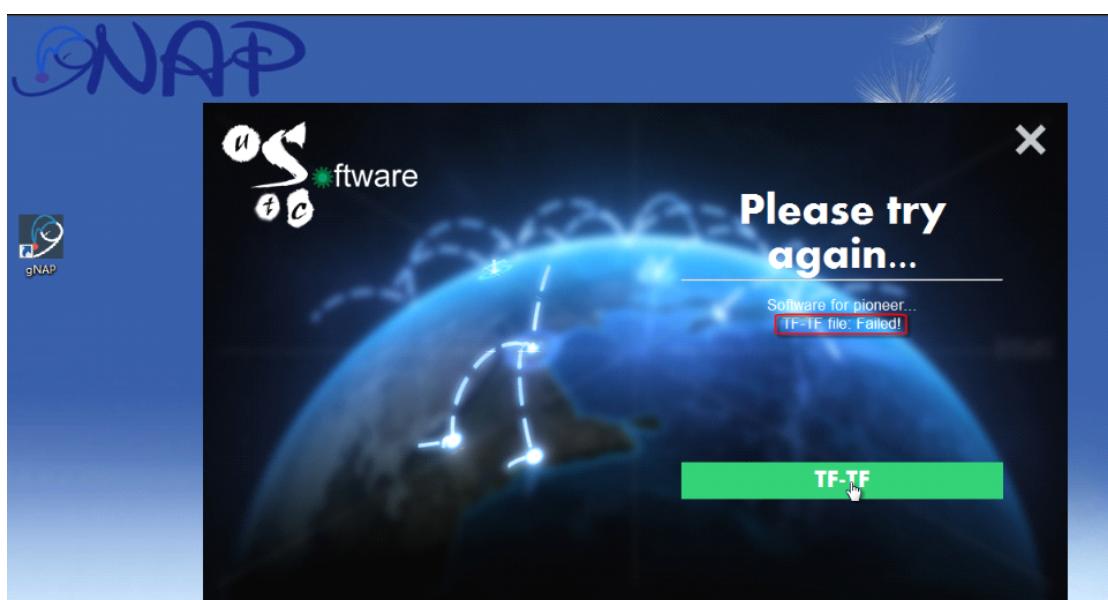
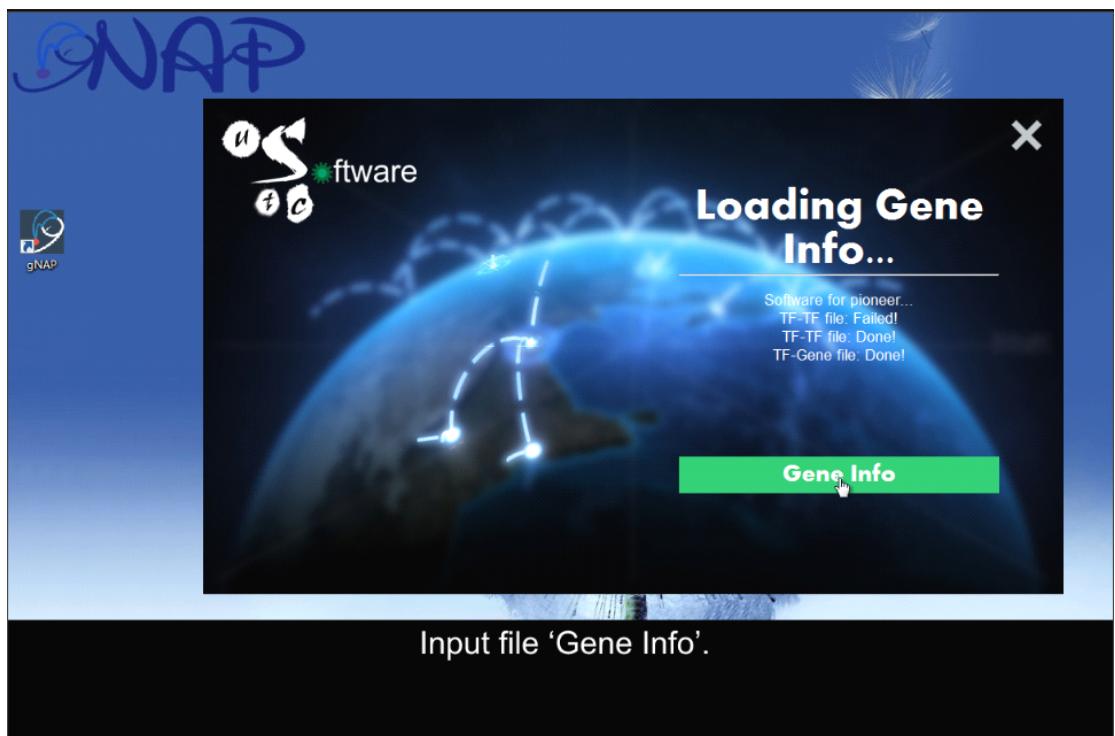
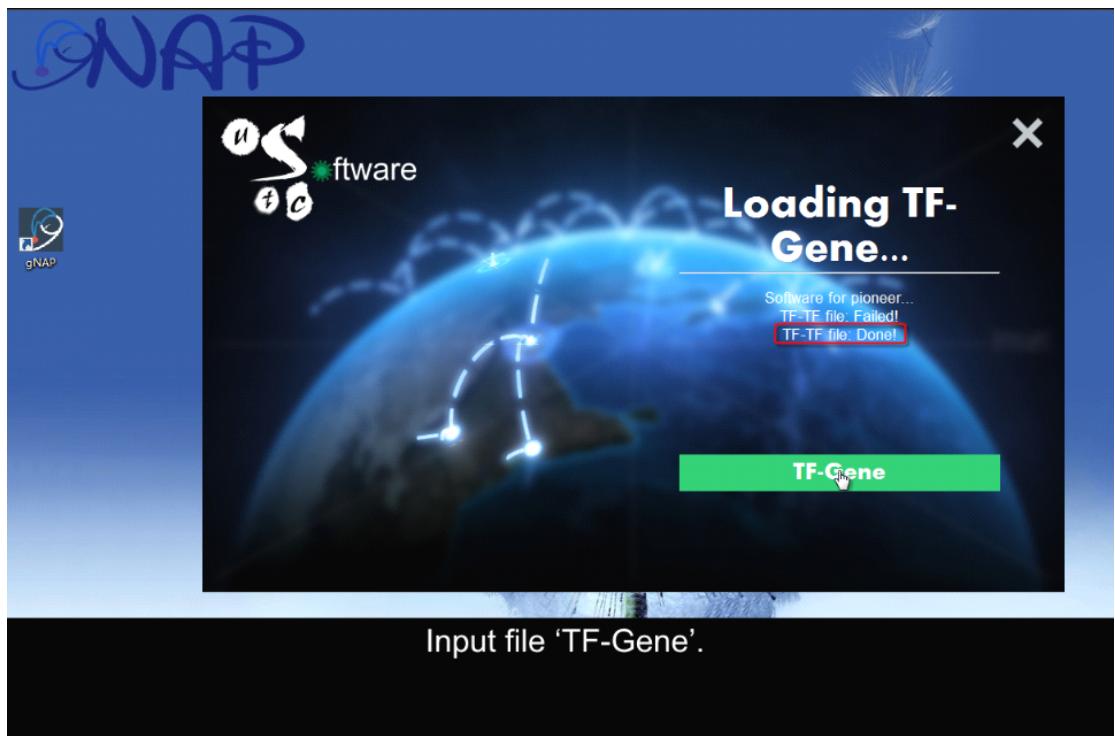
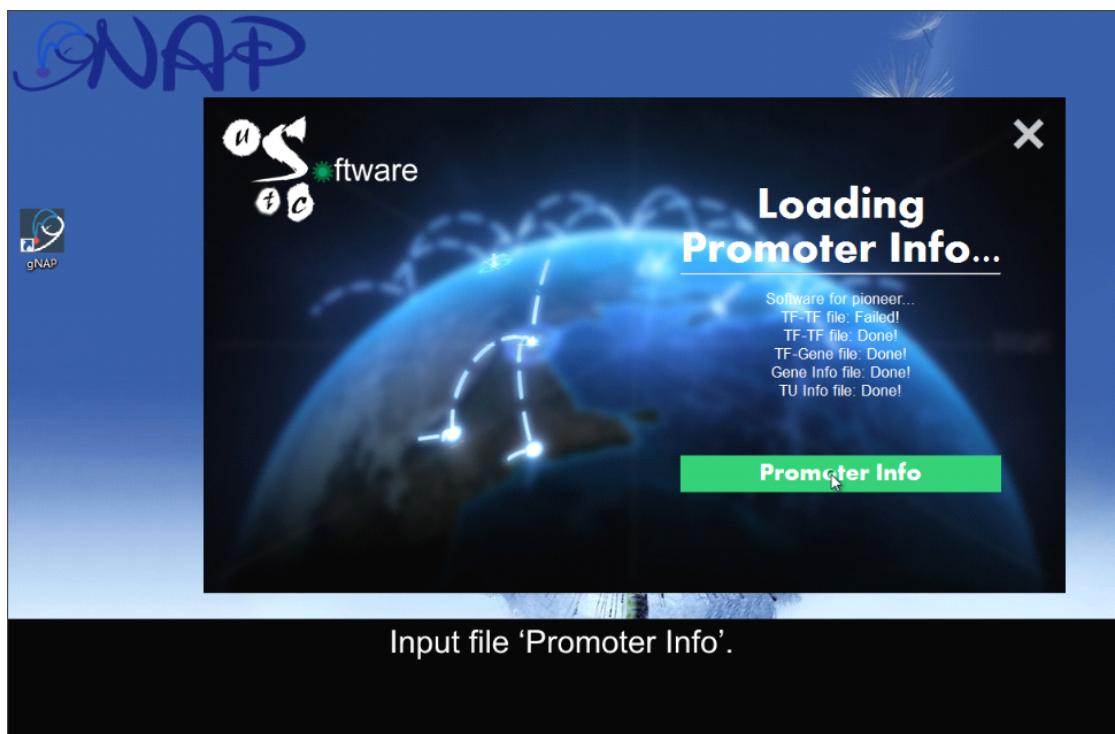
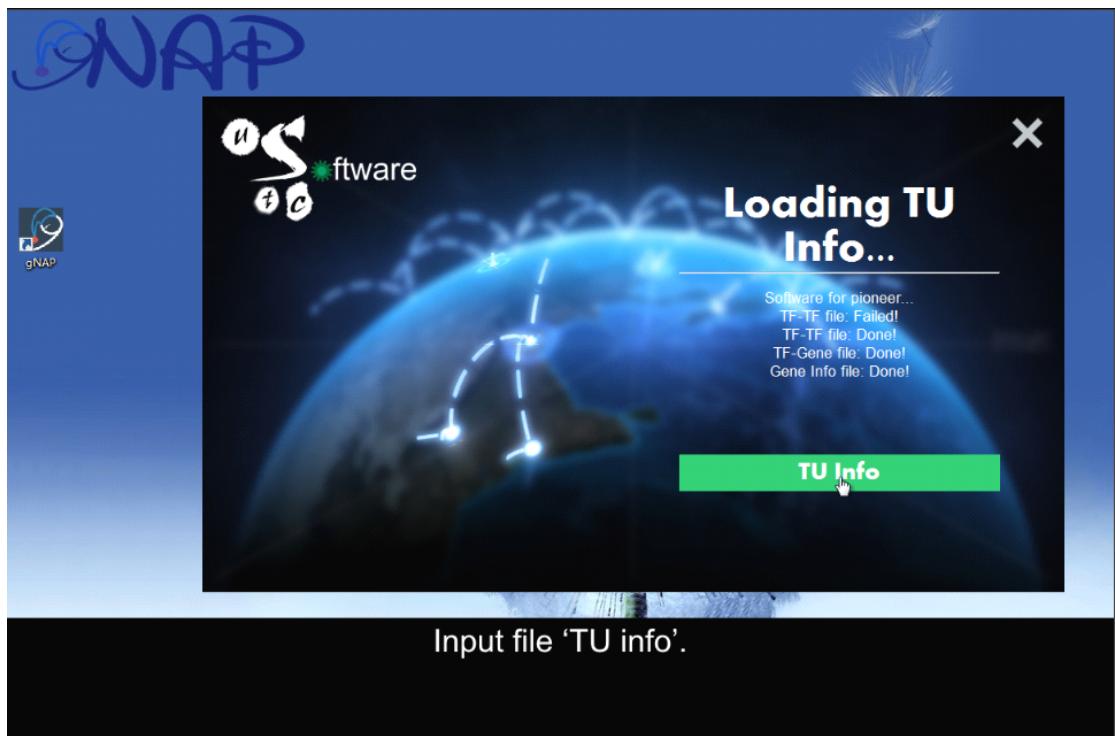


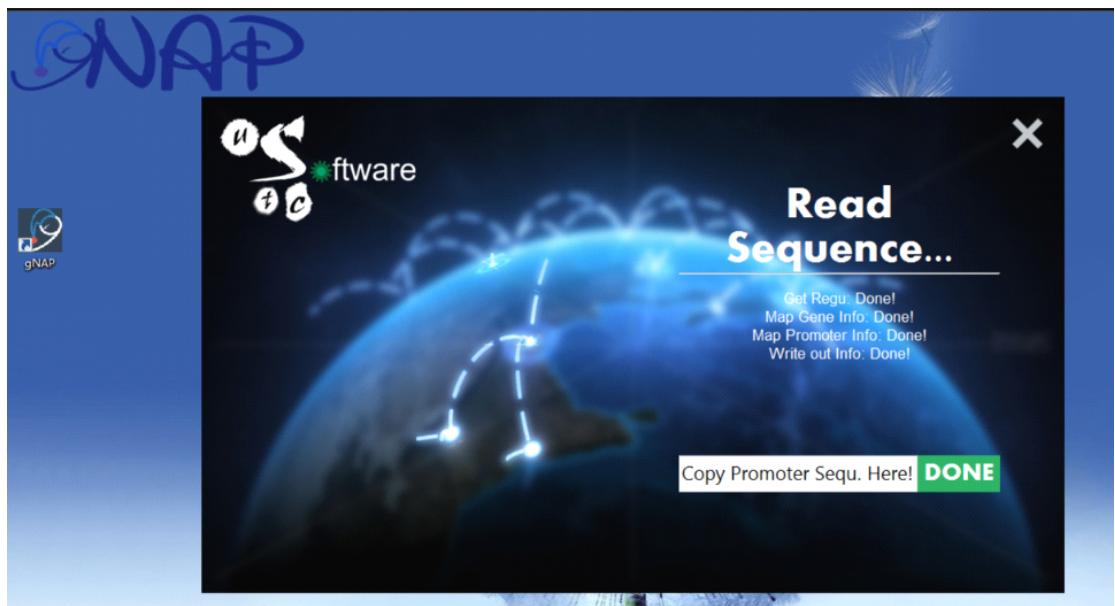
Now please input a file exactly named 'TF-TF'. If the file not named properly,



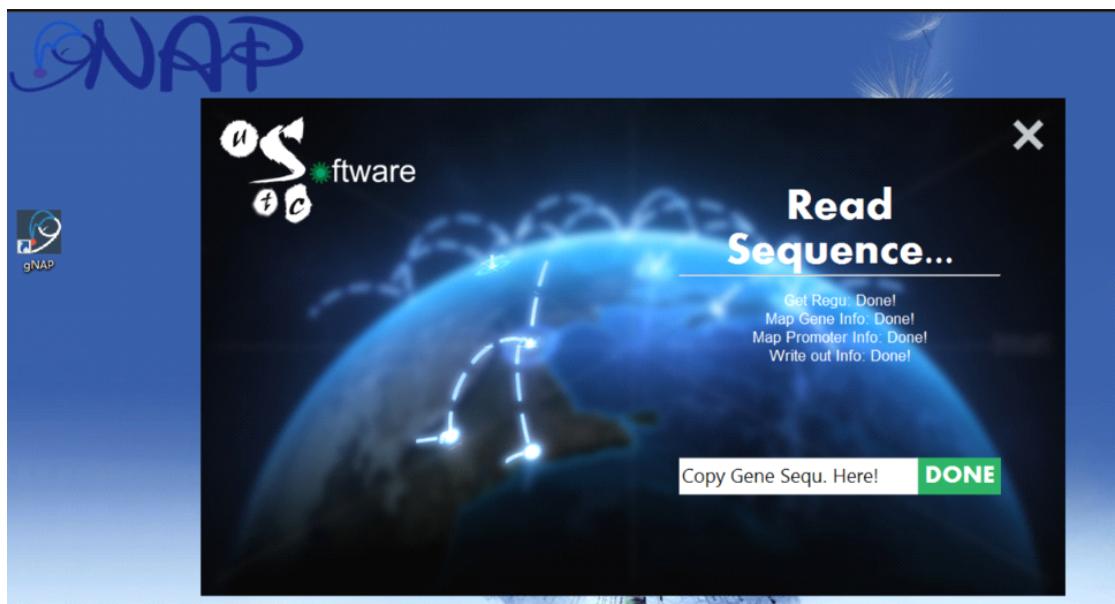
the system would report the mistake and you need to input a correct file again.



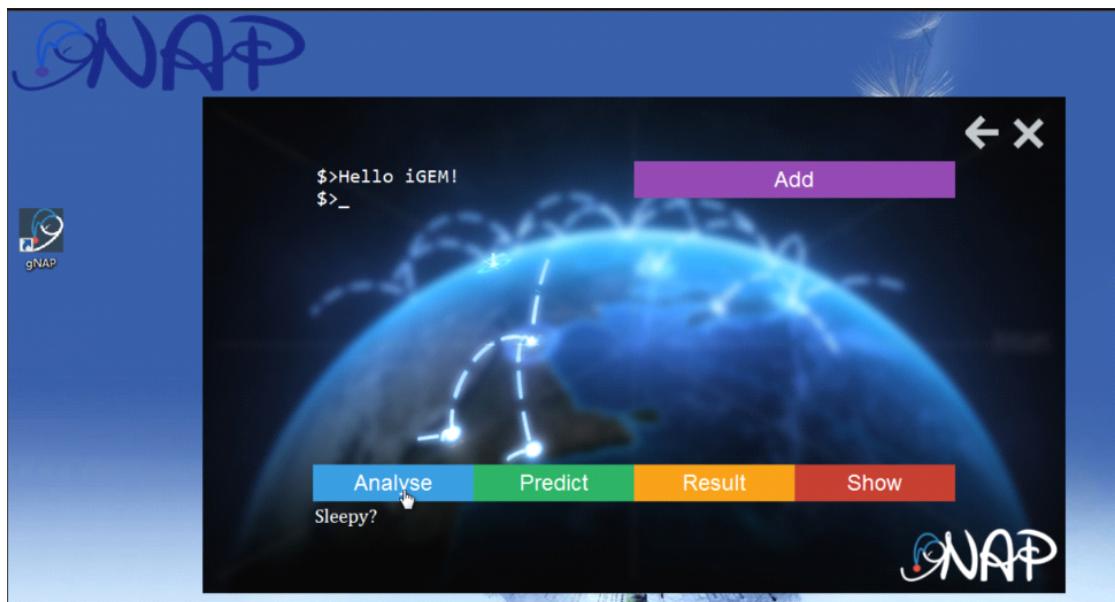




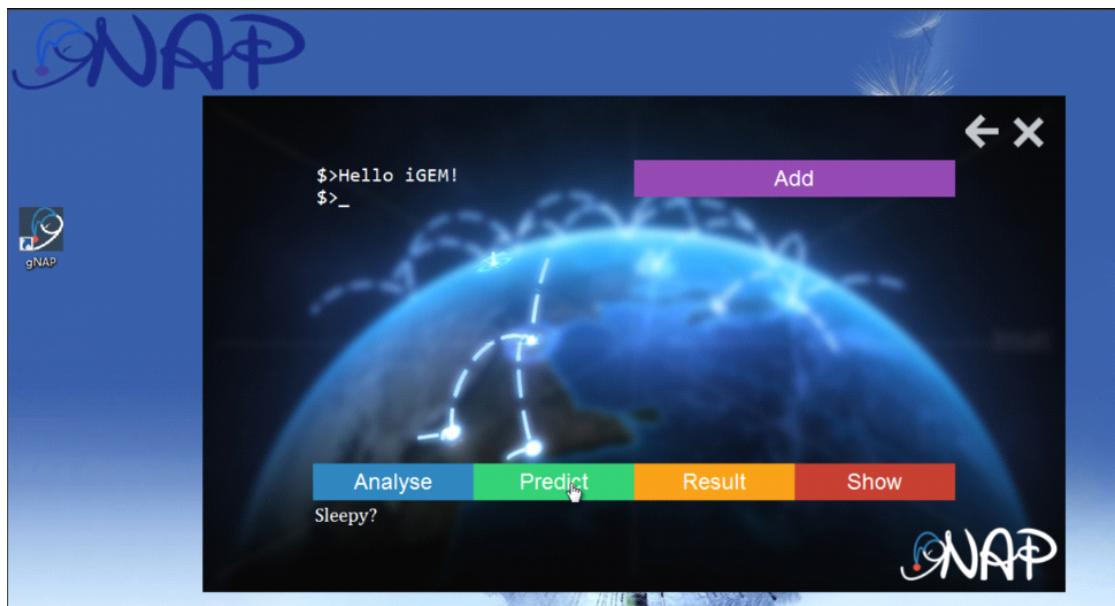
Please enter a promoter sequence.



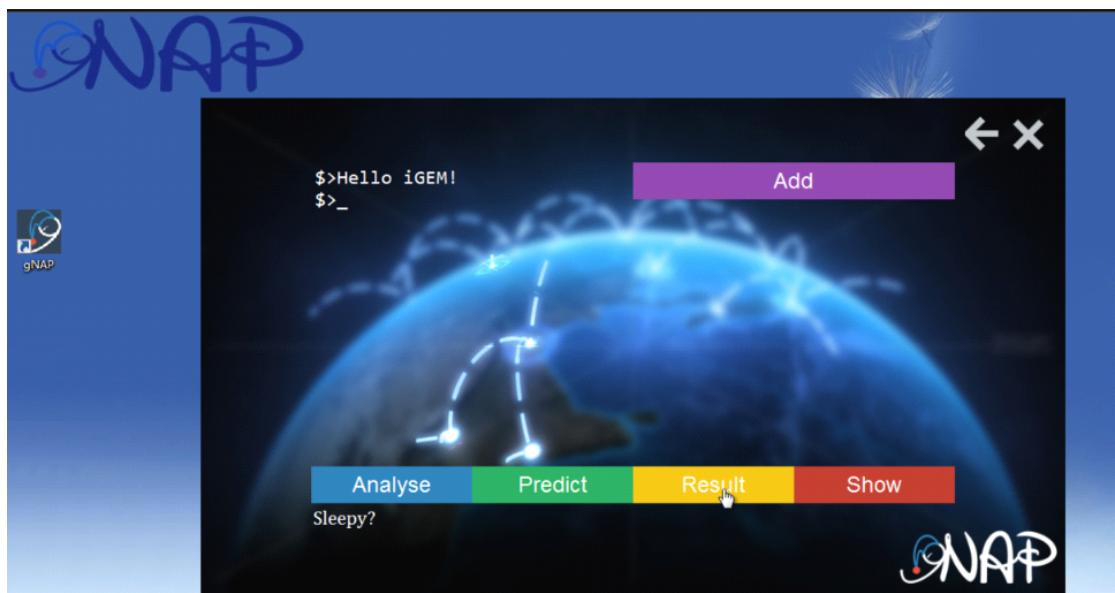
Please enter a Gene sequence.



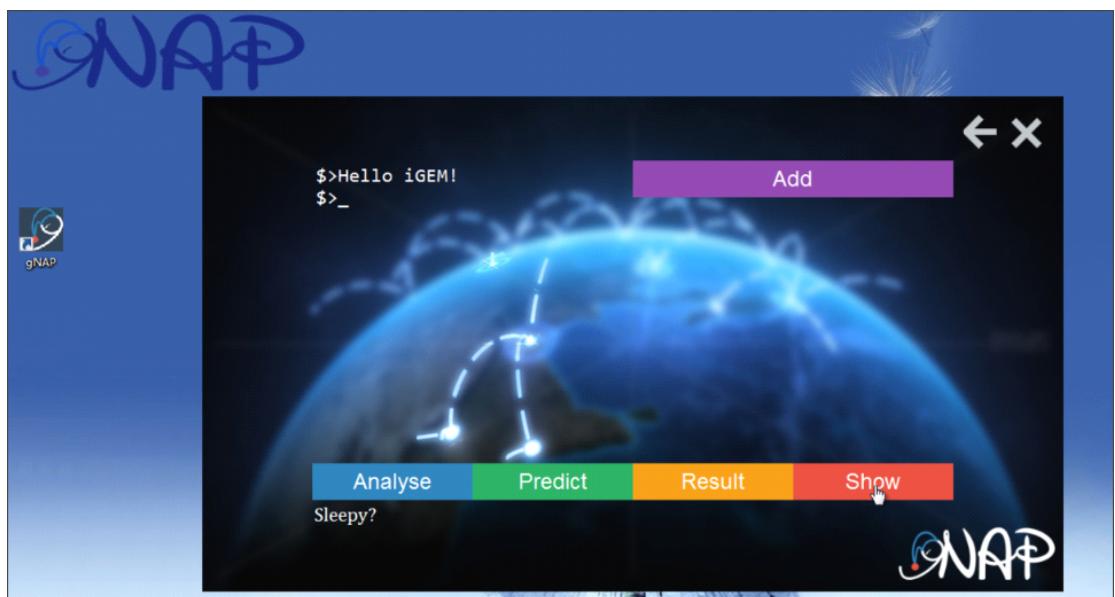
"Analyse" panel analyses the change pattern of the network



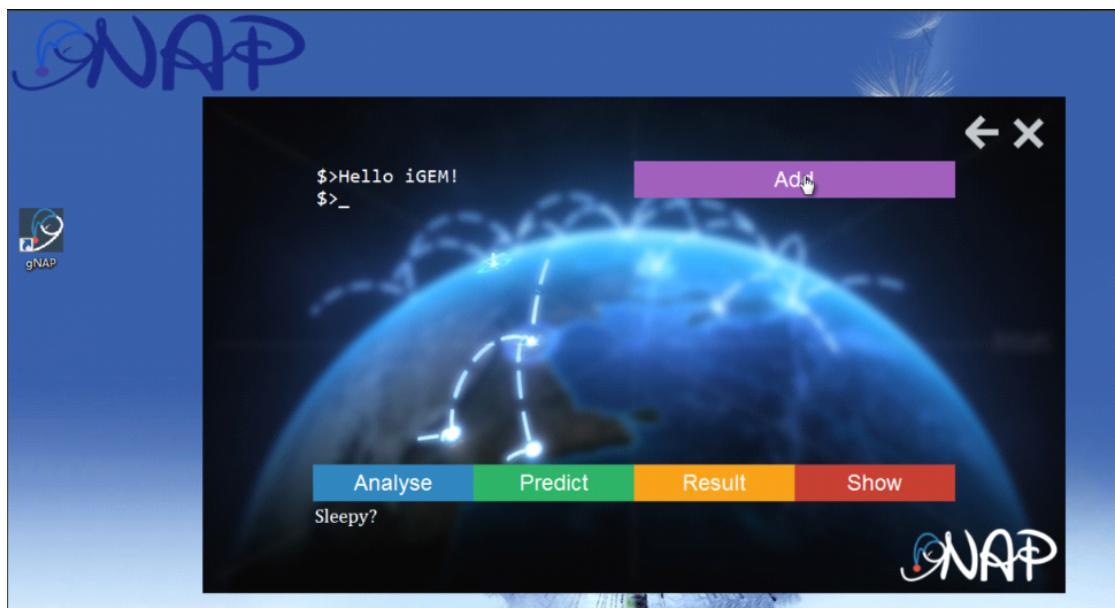
"Predict" panel predicts the new gene's regulation relationship with the network



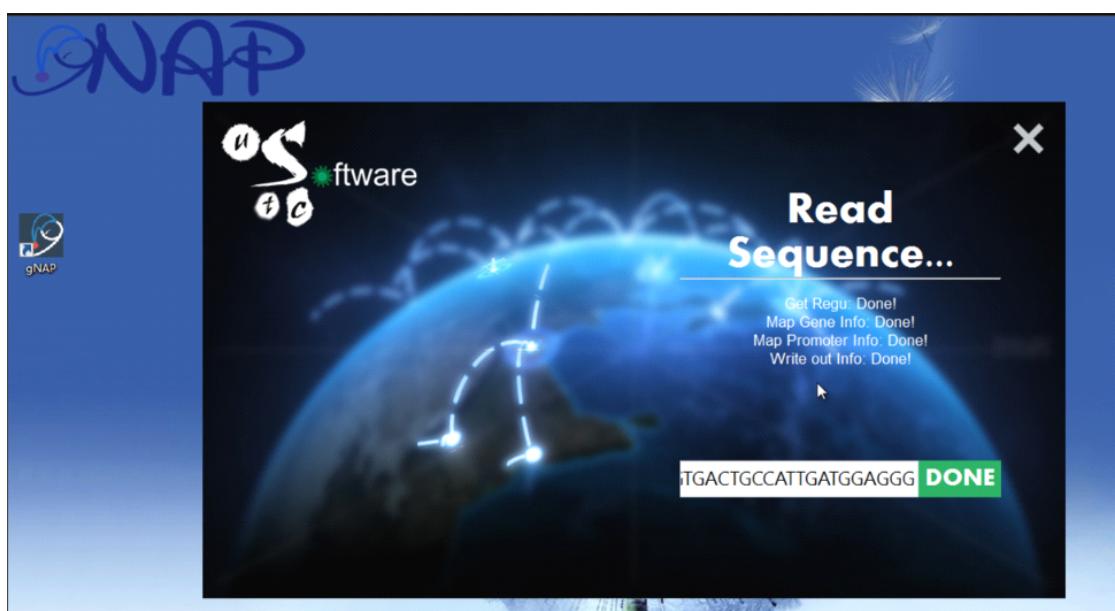
In result panel you can check the output



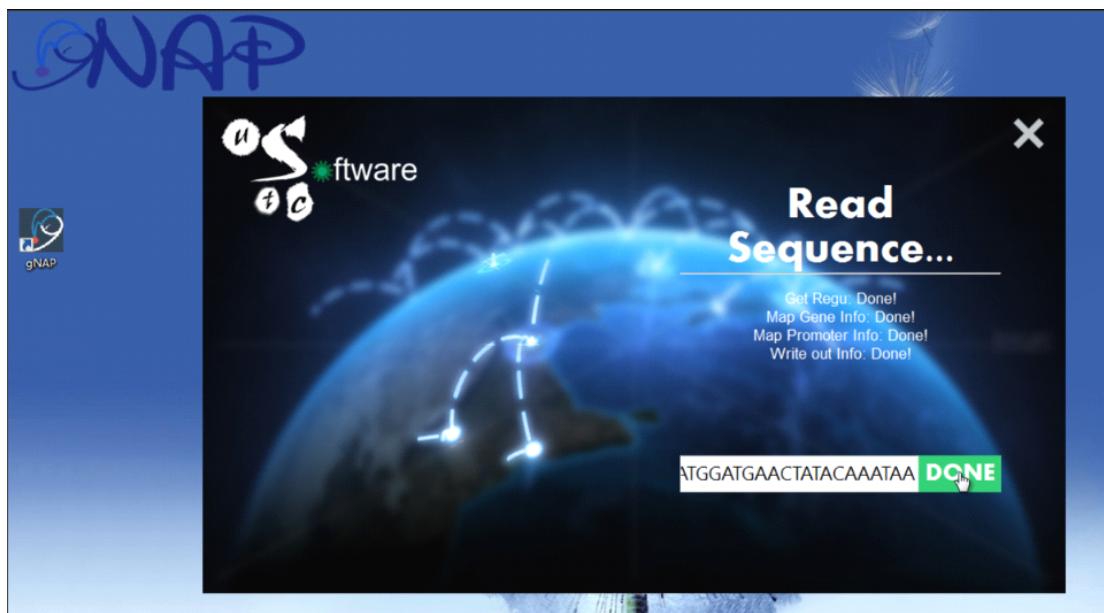
"Show" function provides visual output.



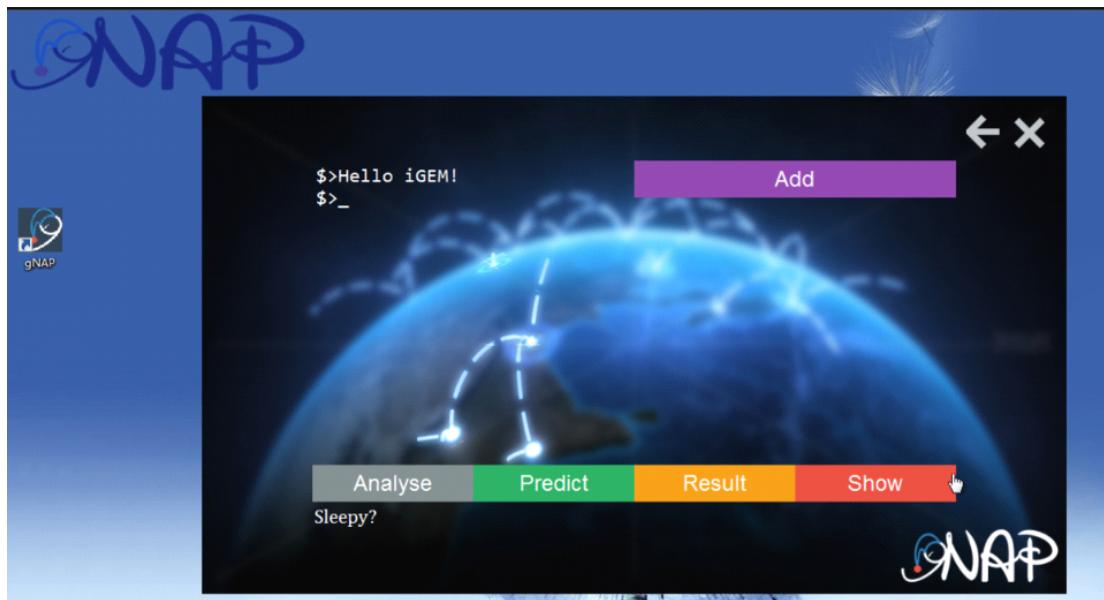
Click "Add" to input the expected express level of the original gene.



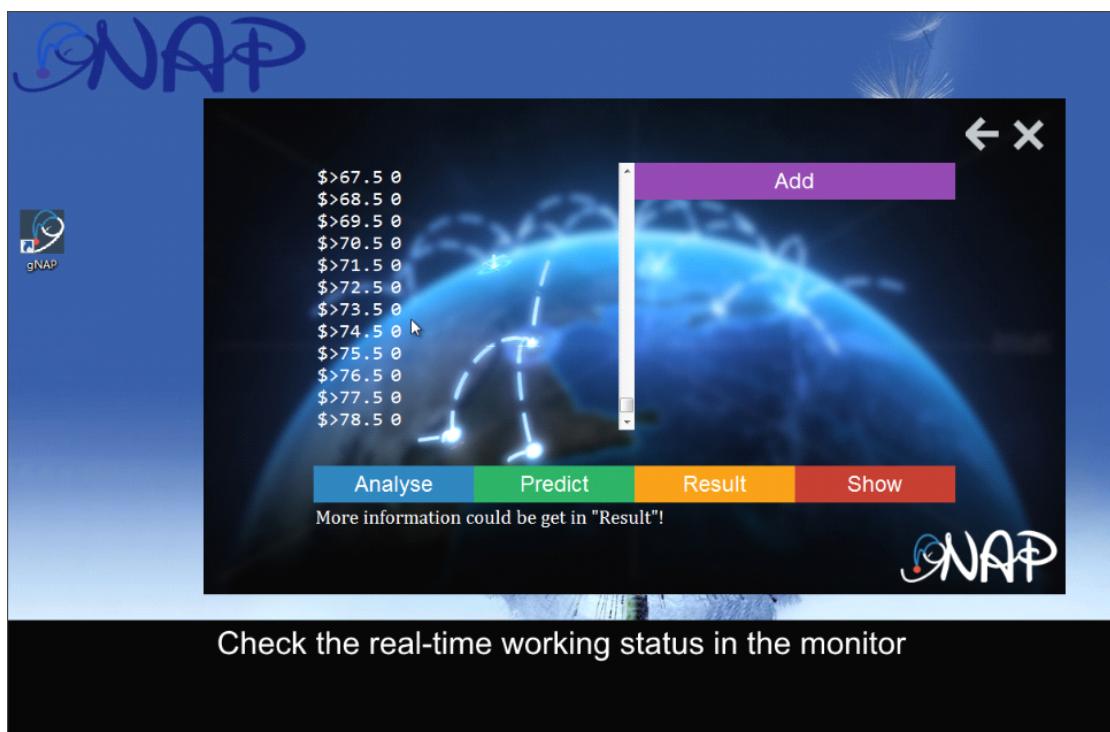
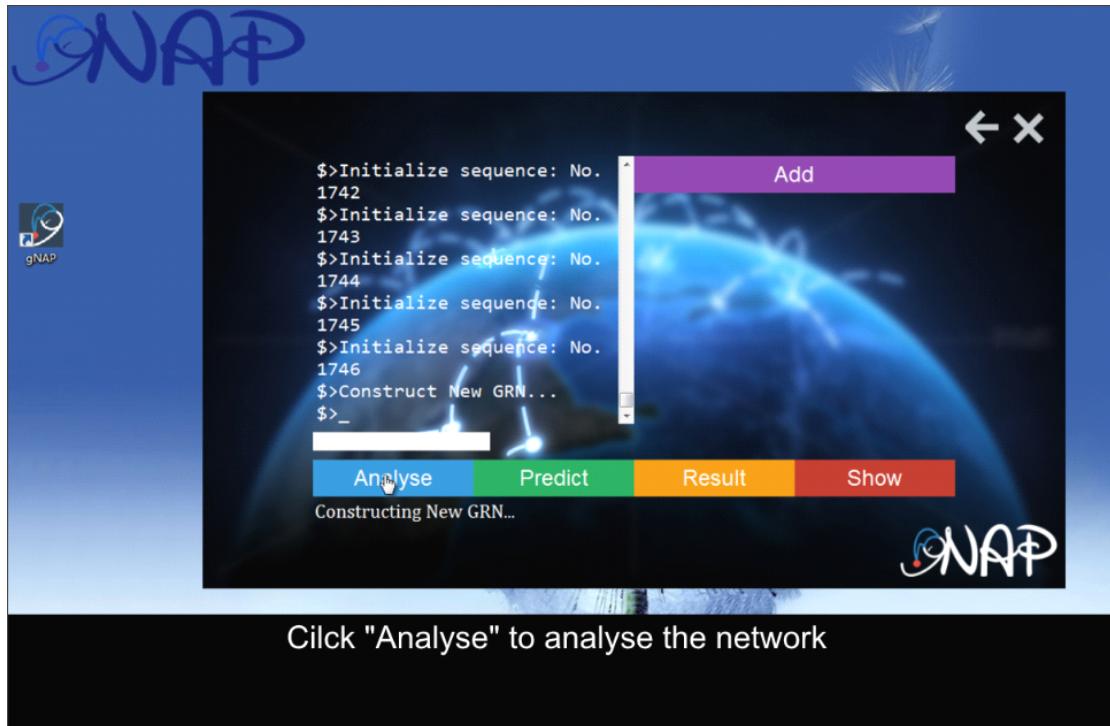
If no promoter sequence or gene sequence were entered,

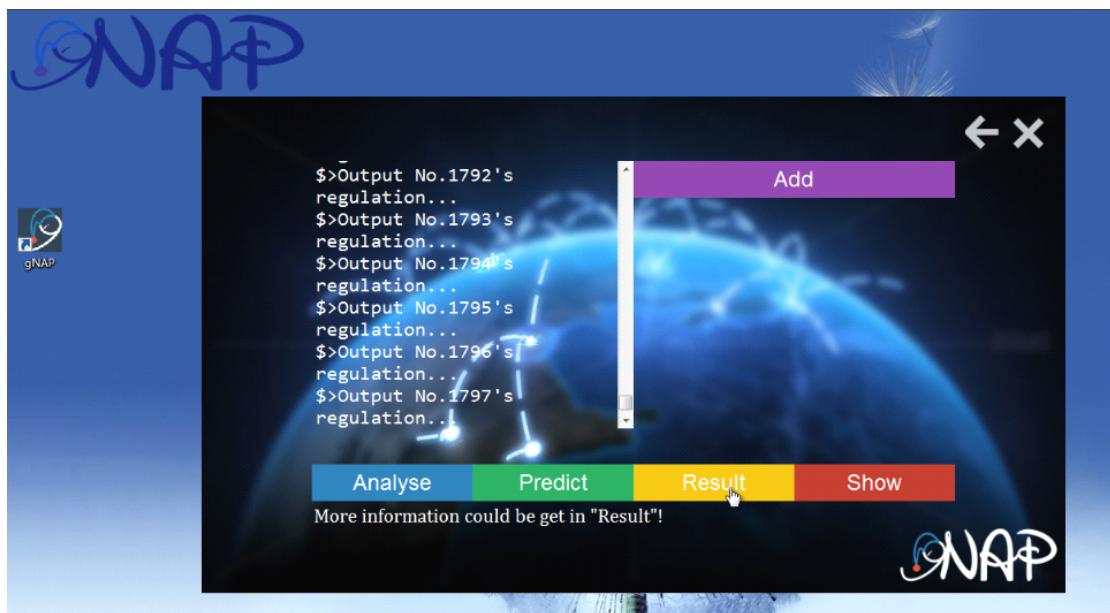


then the analyse function would be unavailable while predict function still functions normally.

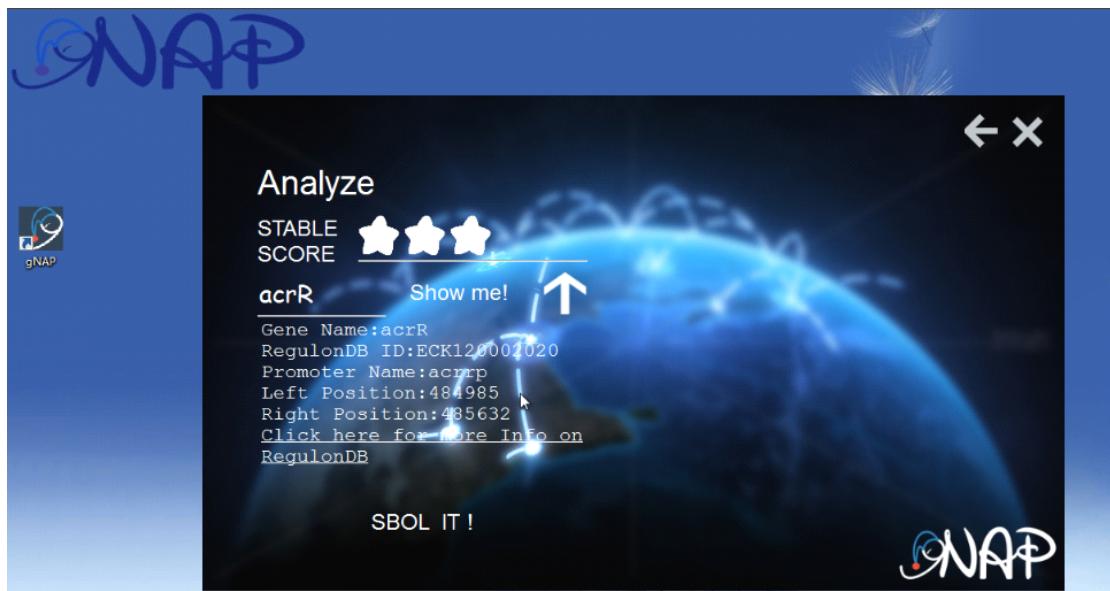


then the analyse function would be unavailable while predict function still functions normally.

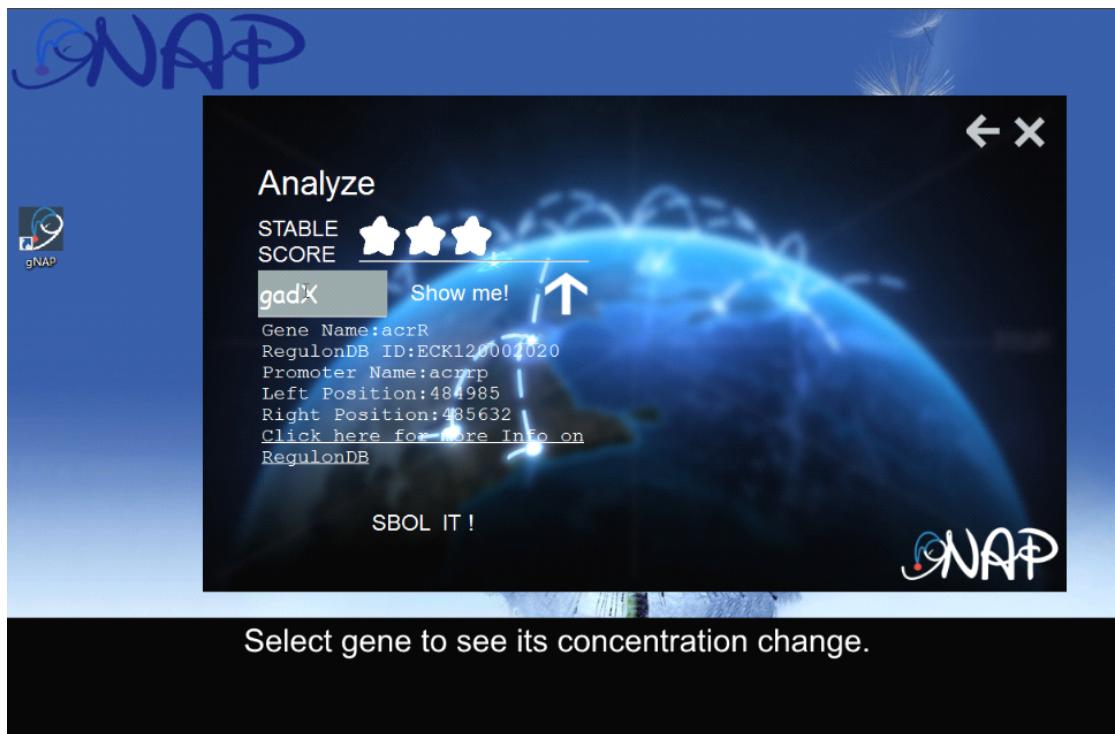




Click "Result" for the analysis output



Stable ability indicates the stable points of the network.



Promoter Name:acrrp
Left Position:484985
Right Position:485632
[Click here for more Info on RegulonDB](#)

SBOL IT !

Click here to check the introduction of the gene in "RegulonDB".

 gNAP

Analyze

STABLE SCORE  

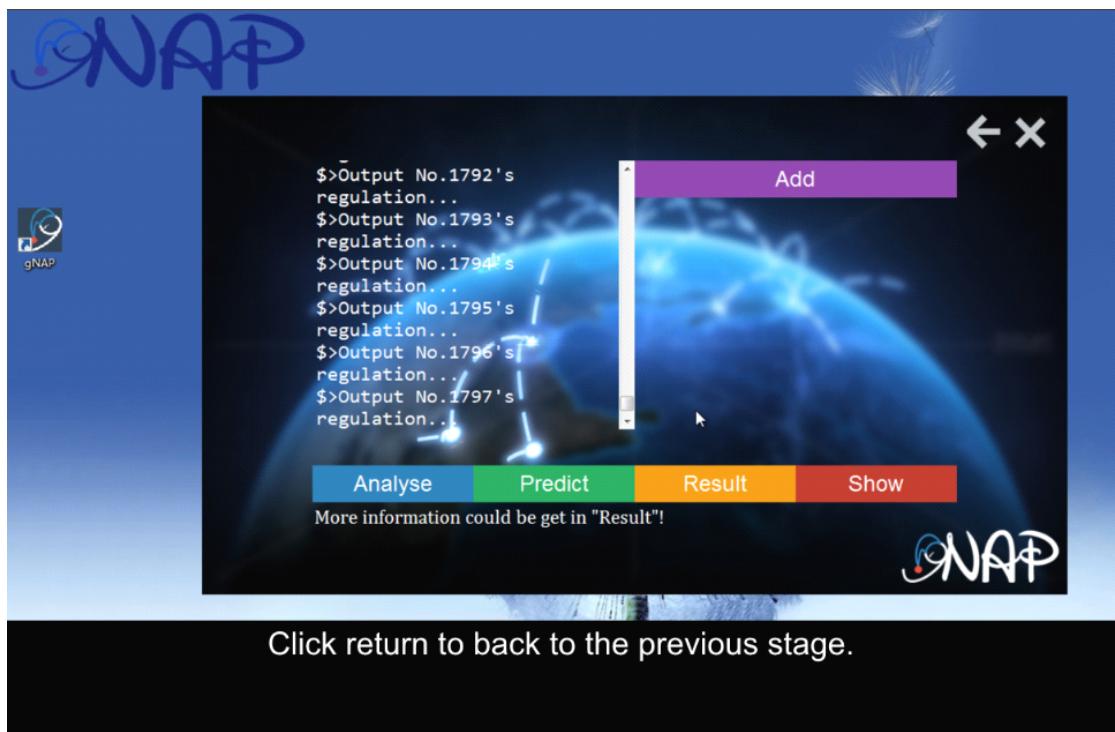
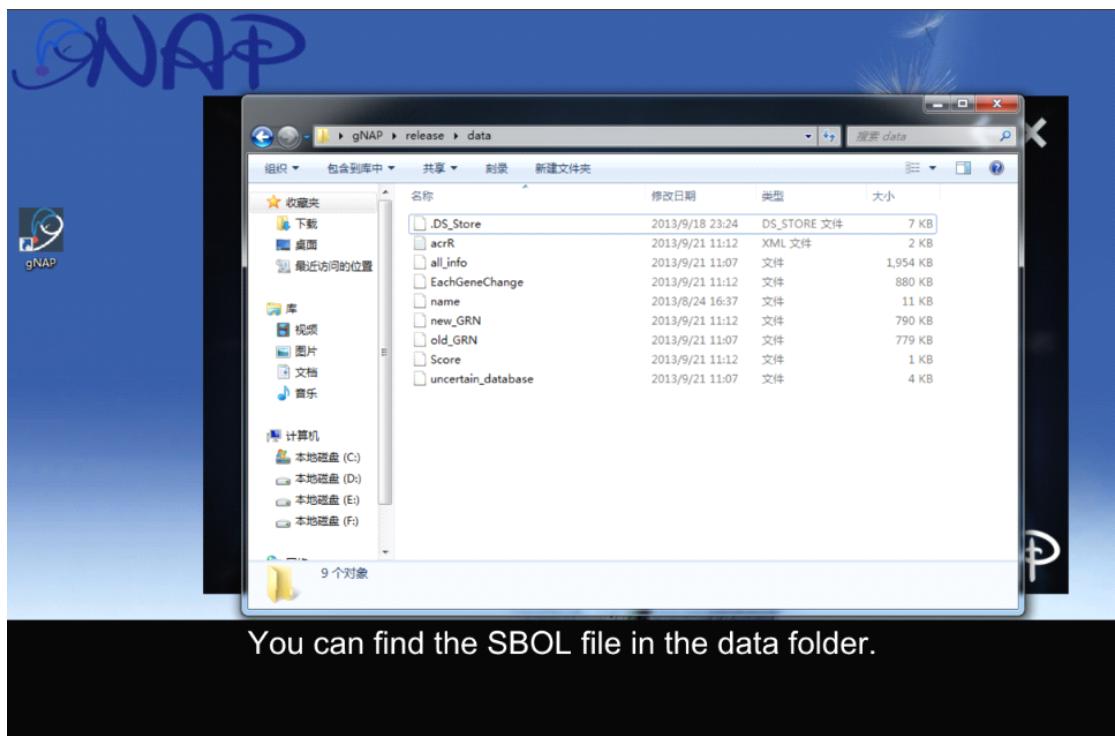
acrR [Show me!](#) 

Gene Name:acrR
RegulonDB ID:ECK120002020
Promoter Name:acrrp
Left Position:484985
Right Position:485632
[Click here for more Info on RegulonDB](#)

 SBOL IT !

 gNAP

Output a SBOL file.



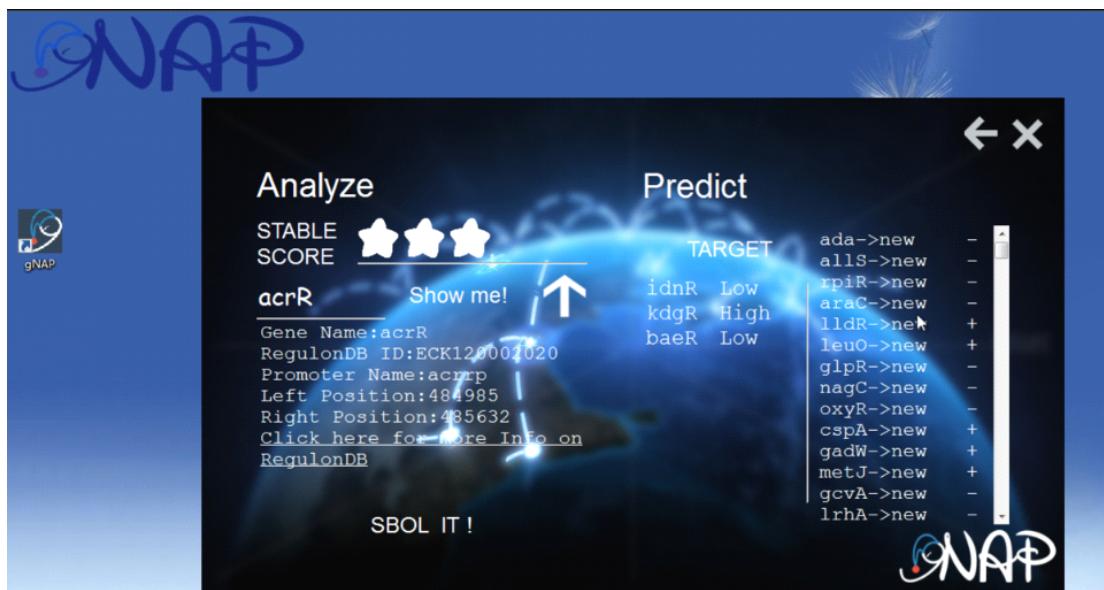
The gNAP interface shows a list of genes under the heading "Output No.1792's regulation...". The list includes: \$>Output No.1792's regulation..., \$>Output No.1793's regulation..., \$>Output No.1794's regulation..., \$>Output No.1795's regulation..., \$>Output No.1796's regulation..., \$>Output No.1797's regulation.... Below this is a placeholder text "Please add TARGET gene above!" and a button labeled "Add". At the bottom are four buttons: Analyse (blue), Predict (green, currently selected), Result (orange), and Show (red).

Add gene and adjust the expression pattern of the gene.

The gNAP interface displays two main sections: "Analyze" and "Predict".
In the "Analyze" section, there is a "STABLE SCORE" with three stars, a gene name "acrR", a "Show me!" button, and a "SBOL IT!" button.
In the "Predict" section, there is a "TARGET" dropdown menu containing the following entries:

ada->new	-
allS->new	-
rpiR->new	-
araC->new	-
lldR->new	+
leuO->new	+
glpR->new	-
naqC->new	-
oxyR->new	-
cspA->new	+
gadW->new	+
metJ->new	+
gcvA->new	-
lrhA->new	-

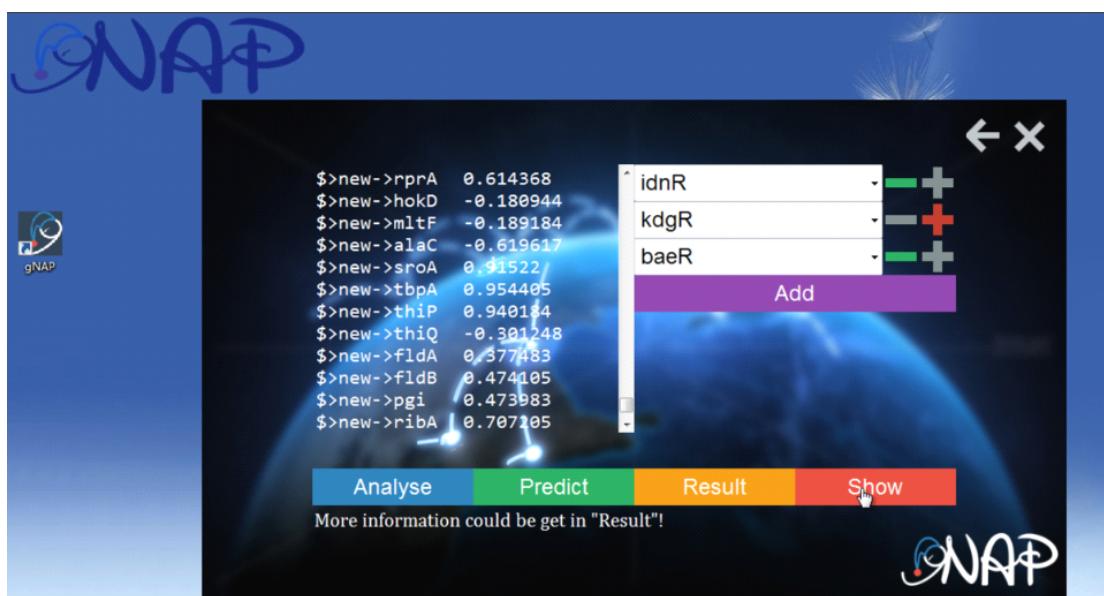
Here is the goal you want .



The screenshot shows the gNAP web interface. On the left, under 'Analyze', there is a 'STABLE SCORE' section with three stars and a link to 'RegulonDB'. Below it, detailed information about the gene 'acrR' is provided: Gene Name: acrR, RegulonDB ID: ECK120001020, Promoter Name: acrrp, Left Position: 484985, Right Position: 485632, and a link to 'Click here for more Info on RegulonDB'. A blue arrow points from this section towards the right. On the right, under 'Predict', there is a 'TARGET' section showing regulatory interactions. The table lists targets like idnR, kdgR, and baeR with their respective scores (Low or High). A blue arrow points from the 'Predict' section back towards the 'Analyze' section.

TARGET	
idnR	Low
kdgR	High
baeR	Low
ada->new	-
allS->new	-
rpiR->new	-
araC->new	-
lldR->new	+
leuO->new	+
glpR->new	-
nagC->new	-
oxyR->new	-
cspA->new	+
gadW->new	+
metJ->new	+
gcvA->new	-
lrhA->new	-

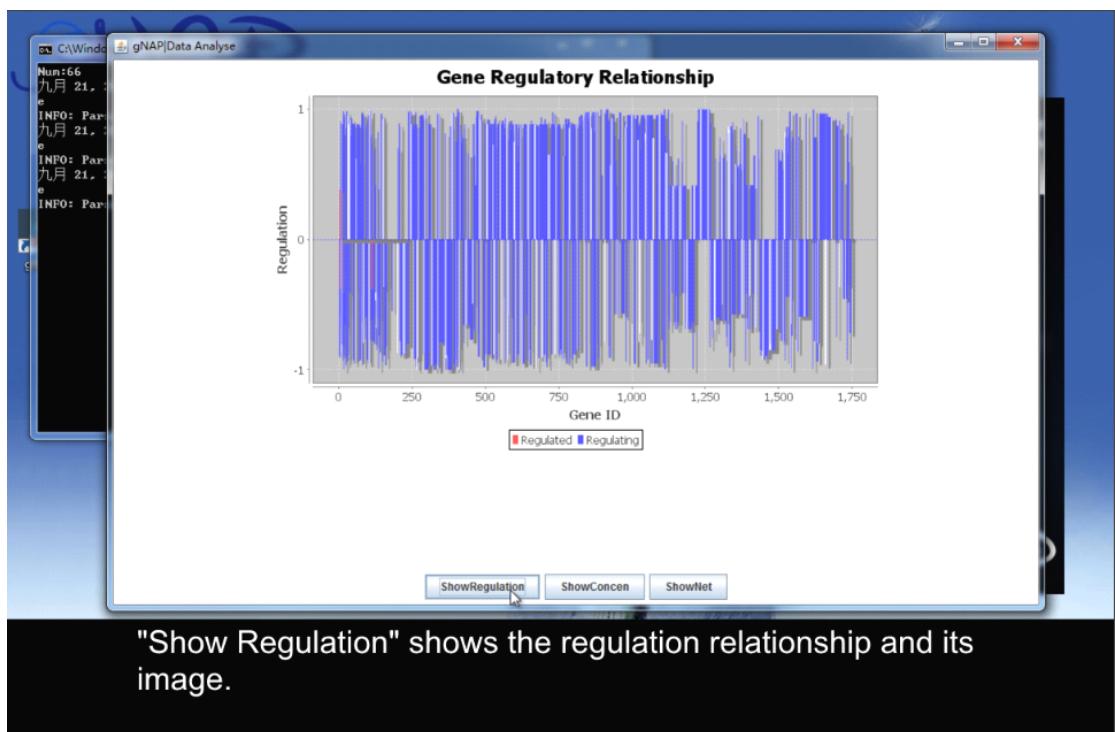
Here shows the prediction result.



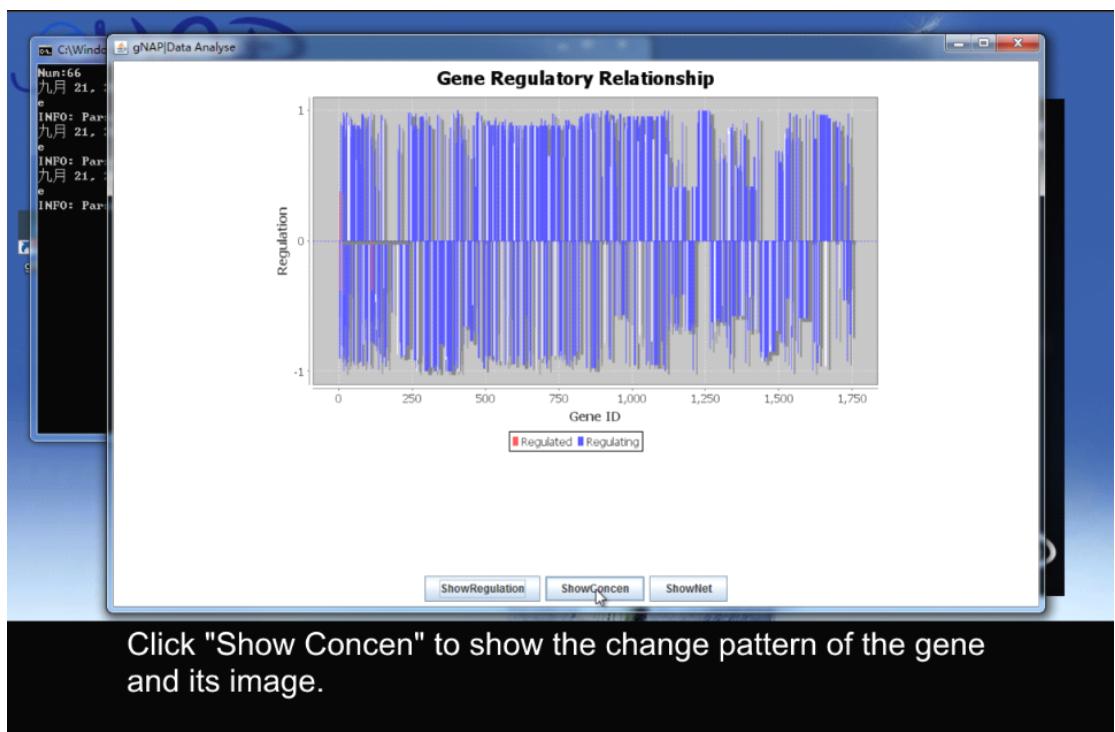
The screenshot shows the gNAP web interface. On the left, a list of regulatory interactions with their scores is shown: \$>new->rprA 0.614368, \$>new->hokD -0.180944, \$>new->m1tF -0.189184, \$>new->alaC -0.619617, \$>new->sroA 0.915221, \$>new->tbpA 0.954405, \$>new->thiP 0.940164, \$>new->thiQ -0.301248, \$>new->fldA 0.377483, \$>new->fldB 0.474105, \$>new->pgl 0.473983, and \$>new->ribA 0.707105. A blue arrow points from this list towards the right. On the right, there is a 'Result' section with a table showing target genes idnR, kdgR, and baeR, each with a green plus sign icon. Below the table is a purple button labeled 'Add'. At the bottom, there are four buttons: 'Analyse' (blue), 'Predict' (green), 'Result' (orange), and 'Show' (red). A blue arrow points from the 'Result' section towards the 'Show' button. A message at the bottom says 'More information could be get in "Result"!'. A blue arrow points from the 'Result' message towards the 'Show' button.

target	
idnR	+
kdgR	+
baeR	+

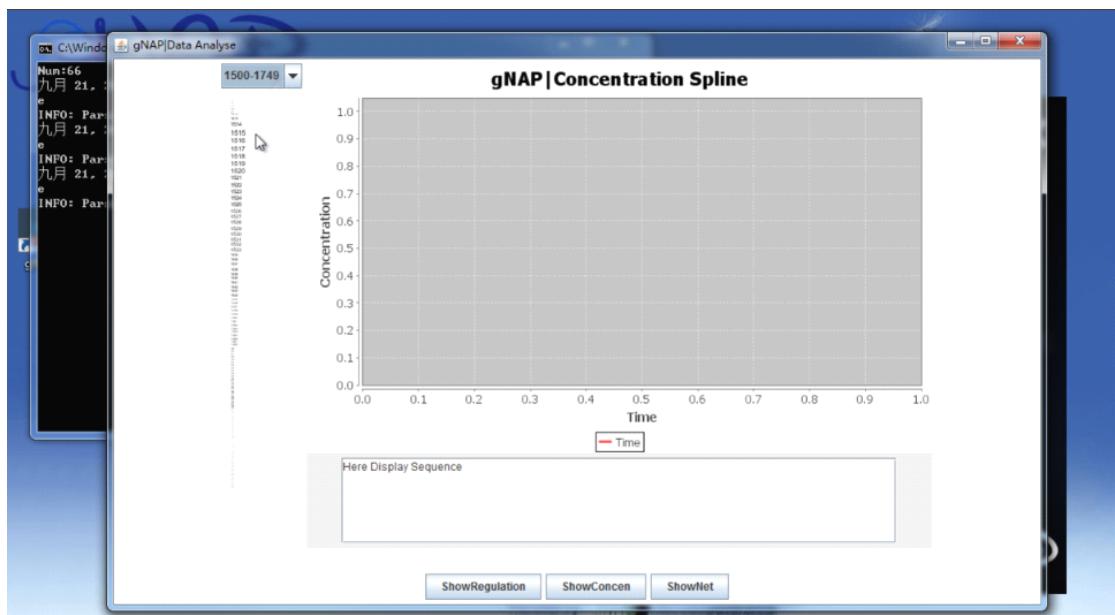
Click "Show" to the visual data platform.



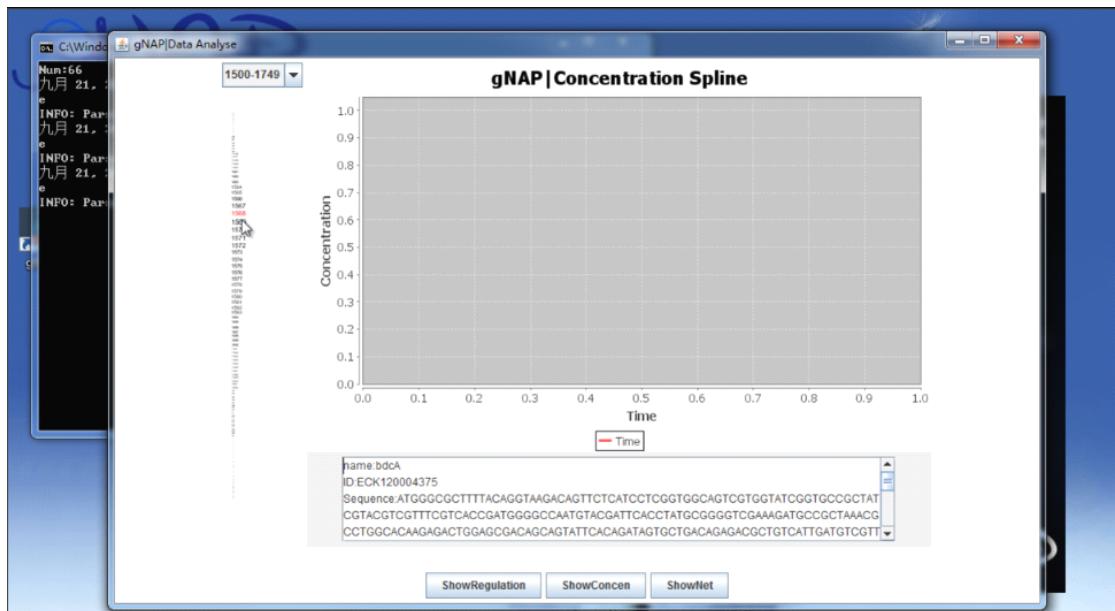
"Show Regulation" shows the regulation relationship and its image.



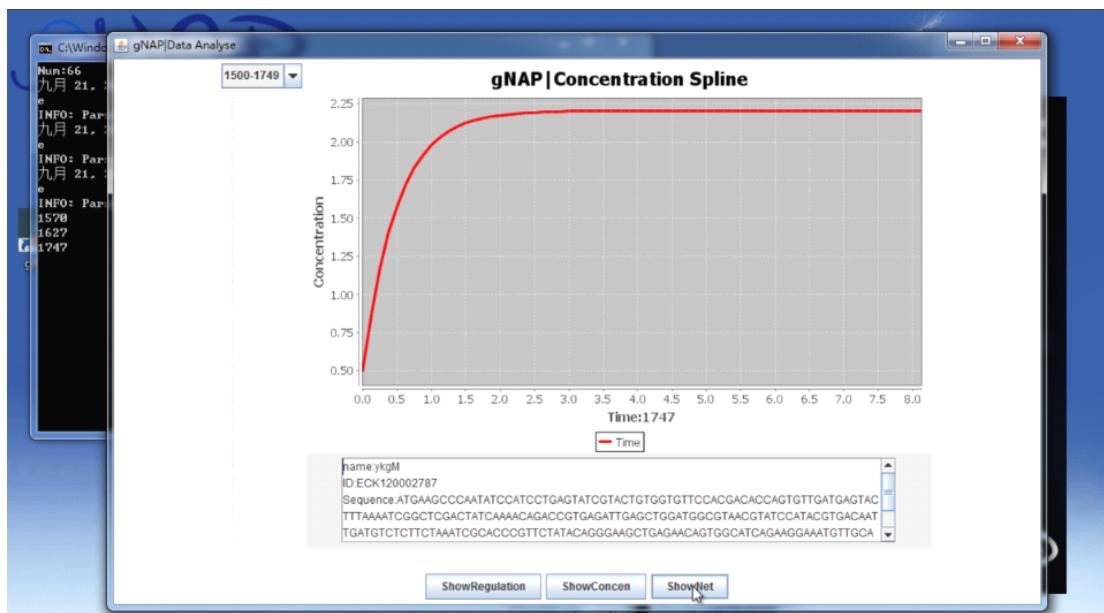
Click "Show Concen" to show the change pattern of the gene and its image.



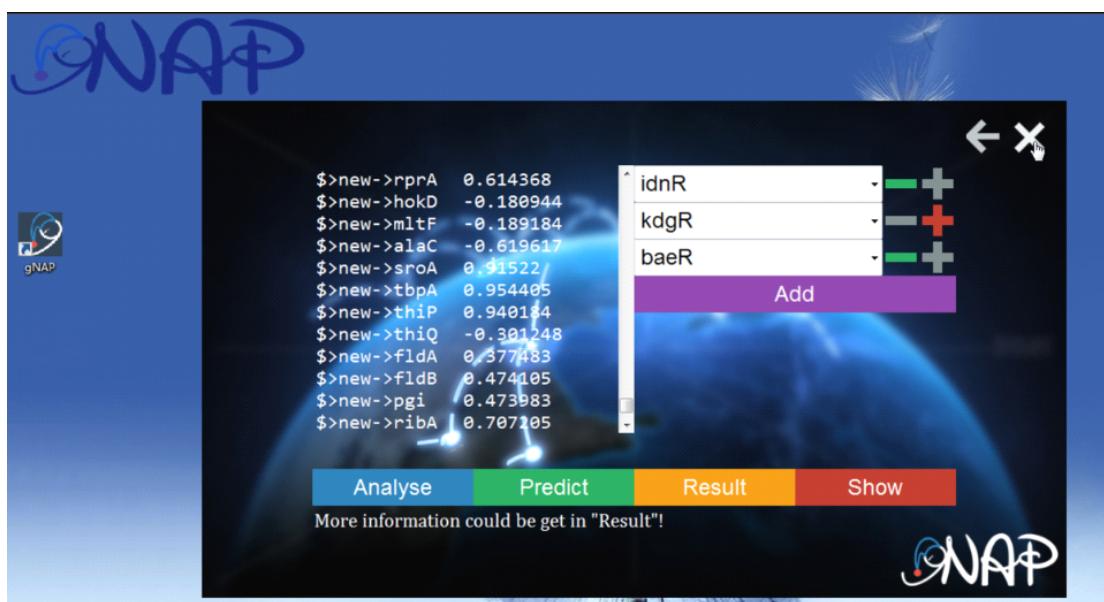
Select the gene's position and number, its properties will be shown below.



Then click to view its change pattern.



Click "Show Net" to show the image of the gene network's relationship.



Thank you.