Gene Network Analyze and Predict Tool

Version 2.1.5

Tutorial

iGEM USTC-Software

Preface

Welcome to use our software — gNAP. We hope it will bring you a pleasant experience in you academic life.

About this Document

This document is version 2.1.5.

The latest version of this document will always be available on gNAP's wiki website.

Welcome to gNAP

Welcome to gNAP, an easy-to-use analysis tool for DNA-Network.

With gNAP, you will be able to:

*choose database

*rapidly prepare and analyses your network

*output in SBOL

*generate files for further analyzing

*store results in specific folder

*get the gene expression rate you want

*get the property of the extraneous genes which satisfy users' needs

gNAP aims at getting analysis done easily and quickly, and it's user interface is extremely simple and clean. You can simply click on different buttons to use varies functions.

gNAP is an analysis tool providing powerful bioinformatics calculation for synthetic biology, especially for extraneous genes. This powerful tool makes complex and daunting analysis work a light and relaxing one. It can also liberate synthetic biologist and experimenters from complex algorithm realizing, time-consuming coding and endless debugging.

gNAP is also user-friendly: there are some brief descriptions in the interface of the application which will let you know what you are doing and what you have done. These will make it much easier to spot mistakes and bring you up to speed on using this tool.

gNAP is an open-source software and it is available on Windows(32bit/64bit), Linux and Mac OS X. All output files, whether in SBOL or other formats, can be read on any platforms with a text reader.

Credits

Designed and coded by USTC-Software.

Thanks to all sponsors and the other contributors to this application.

Contact

The gNAP home page is at: http://2013.igem.org/Team:USTC-Software

For help with gNAP, further developing cooperation or report bugs,

please mail us: ustckun@gmail.com (Chenkun Wang, the Captain of the USTC-Software2013)

Installation

This topic describes how to install gNAP.

The user just needs to download a copy of the application to their computer disregard of your operating system.

Release notes

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What's new

Version 1.0

*Code generation improvements, including better interface and display part.

*First public release.

Version 2.1.5
*Change the interface style
*Add data visual platform

Platform differences

Although every effort has been made to make gNAP work (in) the same way on both Windows and Linux, some small differences are inevitable.

*Under the IOS the progress bar can't be seen.

Interface

Please click on a topic to learn about the individual gNAP windows.

Data input

What you need to do is just simply importing correct database files.

To make users choose correct files, the status board will tell if you have chosen correct files in every step. If the user has chosen a correct file, the status board will refresh itself and be added a new line: *Step-Name:Done* show. If not, it will remind the user with displaying *Step-Name:failed* as a new line in the status board.

If you successfully completes the choosing part, a new button displays instead of path input bar and button. You can click on it and do what it tells. Just take a gNAP, data loading will take only a short time.

Completing this process, you can enter another interface. Please refer to the next section

Read sequence

You need to input the promoter sequence and protein coding sequence according to the prompt messages.

Core panel

In this section we will talk about a new interface. This interface integrated all the main algorithm trigger buttons and a running status visual division. We name trigger buttons as *Analysis, Predict, Result, Show* according to their functions. And the running visual division will show the user much more details about the program when it is running. What's more, you will find a transparent message bar beneath the trigger button, which will help you a lot when you make mistakes or leave something behind.

Analysis

Simply click the orange button. If it is gray, it means the user has missed something. Then the user should follow the tip bar until the analysis bottom turns blue.

*By the way, you won't need to restart the application or import database files again if you just want to try another gene sequence. The the arrow at the right-top corner will help you back to the previous phase, where you can input gene sequence which will cover the gene sequence you input before.

Tips: Using copy and paste properly will make your work more effective.

Predict

You should input the changes you want to take place in the network which you save in the data base files by clicking the Add button. Then choose a specific DNA name and select the change in express level by clicking the plus button or the minus button.

After preparation, you can just click the *Predict* button and have a gnap when you are waiting for the computer calculating results.

Result

This is the third trigger button leading the user to another interface which shows the predict results vividly and briefly in a special style.

The more stars you see, the better its stability is. In the next line, you can search a specific gene by typing the name on the underline and click the Show me button to get its changes and basic information.

SBOL

This is the second function designed in the application, a simple but convenient function for users. Instead of writing all the information by hands, troubling with spelling mistakes and wrong grammar, a single click on the SBOL button can get everything done instantly.

Predict Division

After clicked on the Predict button, the result platform will be shown on the right of the screen.

Show

This trigger button will bring you to another interface where the calculating results are well displayed in a proper style -- the visual data platform. It protrudes the data property and make it can be easy to know, brief to describe, beauty to understand.

Show Regulation

This part of the application will show the regulation relationship and its image.

Show Concen

The dynamic state graph will show the concentration of the specific gene selected. It will help the user to know the details of dynamic state of the network and give the user some inspiration when they want to build a module to describe or simulate the real network, in mathematics on in silicon. And you will know gene information in the interface.

Show Net

This part of the application will show the image of the gene network's relationship and give you a general feeling about the network a visible way.

Reference

This section describes provides further reference information.

A brief guide to some related databases

RegulonDB Download

http://regulondb.ccg.unam.mx/menu/download/datasets/index.jsp

RegulonDB Doc&Help

http://regulondb.ccg.unam.mx/central_panel_menu/doc_and_help_menu.jsp

A brief introduce for the developing process and philosophy

Wiki: http://2013.igem.org/Team:USTC-Software