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MEDUSA is an interaction graph viewer and editor. A Graph is composed of nodes and edges, where edges indicate an interaction between two nodes. Medusa is a front end (interface) to the STRING protein interaction database. It is also a general graph visualization tool. The STRING web interface, while extensive, is static. It does not allow users to create their own networks, enhanced with STRING interactions. Medusa gives you much greater freedom in manipulating STRING data. As a general tool, Medusa is very easy to use and flexible. Users can load their own data or interactively add or delete nodes and edges. It is also free for academic use and easy to install. Medusa was originally a house tool at EMBL and has been used in a number of successful scientific projects. We hope that others too can benefit from Medusa. Protein-protein interactions (PPI) are considered to be fundamental to the functioning of living organisms. The availability of genomes has made it possible to analyse PPI networks in greater depth than ever before, and to study the properties of these networks in greater detail than was possible before. In this chapter, we first discuss the kinds of interactions that are being identified in molecular biology, and then describe how PPI networks may be constructed from the available biological data. We then describe the methods for determining the reliability of interactions in the network, before discussing some of the statistical properties of networks. Finally, we review the questions that can be addressed through PPI network analysis. Protein-protein interactions (PPI) are considered to be fundamental to the functioning of living organisms. The availability of genomes has made it possible to analyse PPI networks in greater depth than ever before, and to study the properties of these networks in greater detail than was possible before. In this chapter, we first discuss the kinds of interactions that are being identified in molecular biology, and then describe how PPI networks may be constructed from the available biological data. We then describe the methods for determining the reliability of interactions in the network, before discussing some of the statistical properties of networks. Finally, we review the questions that can be addressed through PPI network analysis. Interacting molecules have a functional role in a living cell. They are present in a specific cellular compartment and in a certain order. This is known as a 'protein complex' or 'protein assembly'. In this chapter, we show you how to detect protein interactions within a protein complex. Protein-protein interactions (PPI

SH Medusa Crack For Windows

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SH Medusa (LifeTime) Activation Code PC/Windows

Medusa is a general tool for manipulating, visualizing and analyzing STRING network data. Medusa has two main capabilities: 1. Graph manipulation A user can create a node or edge and change its attributes, e.g. the type of interaction. 2. Graph visualization Users can view graphs. They can also play with the nodes and edges to create new networks. Major Features: Medusa is a generic network viewer and editor. It provides a set of toolbox functions for manipulating STRING network data. Biology - OReCab 1.1.5 ORECab is a software system for mapping and annotation of data from mass spectrometry experiments of proteins in Oryctolagus cuniculus. ORECab can read the results of a mass spectrometry analysis of samples such as serum, plasma, sperm or liver. The software offers multiple annotation methods for single-protein identifications and for protein groups. ORECab can be used as a standalone application. The BioShark workflow, however, offers much more possibilities for integrating ORECab into an analysis workbench. ORECab offers multiple import formats, including Mascot score files, Mascot XML files, mgf-files and Filemaker files. Biological - TyteArray v1.0 TyteArray v1.0 is a program to control and visualize UTA. UTA is an autonomous expression system for GFP and other fluorescent proteins based on the Tn10 tetracycline-controlled transactivator system. To use TyteArray, you only need an RT-PCR product of the GFP gene (Ty1::GFP or other reporter), a PCR fragment of the DNA sequence of your choice for the target of the PCR product, and the TyteArray sequence. You can also use TyteArray for cloning of RNAi constructs, reporter constructs, or to analyze promoter sequences. TyteArray v1.0 can be used for digital RT-PCR, GFP-tagging of proteins, transcriptional activity analysis, promoter analysis, and monitoring the binding of transcription factors. TyteArray - Biominator 1.1.2 Biominator is an interactive visualizer and model builder for statistical data. The application facilitates the connection and manipulation of a wide variety of data sources. Each data set can be represented as a simple graphical model

What's New In SH Medusa?

SH Medusa is a front end (interface) to the STRING protein interaction database. It is also a general graph visualization tool. Medusa is a front end (interface) to the STRING protein interaction database. It is also a general graph visualization tool. It gives you much greater freedom in manipulating STRING data. As a general tool, Medusa is very easy to use and flexible. Users can load their own data or interactively add or delete nodes and edges. It is also free for academic use and easy to install. Since the starting point was to develop a graph visualization tool to help analyze and explore STRING data, Medusa quickly evolved into being an interesting tool in its own right. Today, it is one of the most used tools for analyzing and exploring STRING data. Properly representing biological data can be difficult. Proteins interact with other proteins in various ways (co-expression, binding, phosphorylation, etc.). In addition to the problems of normalization across samples, data is often ambiguous, and researchers often don't know the true relationship between proteins. The STRING database serves to be a useful tool to help overcome these problems and make protein interaction data more understandable and interpretable. However, since the STRING database is just a database, it is not enough to visualize the interactions; one needs to manipulate the data in order to make the correct conclusions about the data. Medusa allows one to do exactly that. Medusa is a Python library. You can load a STRING database from a local directory, or you can upload it from a server over HTTP. You can then explore the data using the interactive front end, or you can import your own data. You can save the view as a set of image files. You can also export the data as a set of text files, or graph files. You can also use these files in other applications (e.g., Jmol, Cytoscape, Fireworks, and AmiGO). Medusa is a simple application that allows you to interactively add or delete nodes and edges. Each node can be associated with a string representing the protein. Edges can be added between two nodes, and the strength of the interaction is indicated by the weight of the edge. The program outputs a set of files that represent the graph. It also allows users to export their graph as image files for visualization in other applications. This includes PNG, JPEG, JPG, and BMP files. This project contains the following files: Medusa source code. A detailed description of the software can be found in the Source Code section. Medusa documentation. This

System Requirements:

General Recommended PC: Windows 7, 8, 10 (64-bit version only) Processor: Intel Core 2 Duo E2140 (2.4 GHz), AMD Athlon II X4 640 (2.7 GHz) Memory: 4 GB RAM Storage: 30 GB available space DirectX: Version 9.0 Video Card: Intel GMA 4500, Radeon HD 4850, NVIDIA GeForce 8600, ATI Mobility Radeon HD 5670 Resolution: 1280x1024 Sound Card: DirectX 9

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