GeneGo Pathways Software Guide

About GeneGo MetaCore

MetaCore is an integrated “knowledge-based” platform for pathway analysis of OMICs data and gene lists. Easy to use, intuitive tools for data visualization and analysis plus workflows with reports.

- Manually annotated database of protein interactions verified by “small experiment” data and gene-disease associations
- Human, mouse and rat species-specific interactions, pathways and protein complexes
- High quality manually created pathway maps and networks for cell processes, diseases, toxic categories and more...
- Easy search for genes, proteins, compounds, pathway maps and diseases
- A toolkit for ontology enrichment, interactome, topology and network analysis
- Automated workflows with Word and Excel reports

Technical requirements for MetaCore

The Galter Library license for MetaCore is a web portal access to the software, with 5 concurrent user positions available. The web portal works with Internet Explorer, Firefox, Chrome and Safari.

To use the software on the MetaCore web portal, you will need:

- PC or Mac with (recommended) Internet Explorer 9.0, Mozilla Firefox 17, or Safari 6 or Chrome 33
- Macromedia Flash Player 8 or higher
- JRE (Java Runtime Environment) 1.5.0
- P4 equivalent CPU or better and 1 GB of RAM
- Web portal access is protected by Verisign

Terms of use

You must adhere to these requirements for the use of MetaCore pathways analysis package:

- You may not charge a fee to any third party for analysis that you have done using this software
- You must acknowledge and properly cite MetaCore in any publication that utilizes analysis done with this software
- You must remember to sign out when you are done
- You must be a member of the Northwestern research community (faculty, staff or student)
- You must use an email account from Northwestern University (northwestern.edu), Northwestern Memorial Hospital (nmh.org), Ann & Robert H. Lurie Children’s Hospital of Chicago (luriechildrens.org), Northwestern Medical Faculty Foundation (nmff.org) or Rehabilitation Institute of Chicago (ric.org) to register and access MetaCore. You may NOT use a gmail, Yahoo or other e-mail address
- If you fail to comply with the above requirements, the Galter Health Sciences Library reserves the right to restrict,
suspend or revoke your individual access to MetaCore and in extreme cases revoke access to the library and all its services.

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### How to Cite MetaCore

MetaCore is owned by Clarivate Analytics. The company requests: Please state that you have used “MetaCore from Clarivate Analytics” in the abstract and main body of the text. You can also use the specific version of MetaCore if you think that is required. Using a version number is highly recommended, to provide the greatest information available to readers of your manuscripts, so they can duplicate your experimental conditions.

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### Accessing MetaCore

Galter Health Sciences Library has purchased a site license with two (5) simultaneous user spaces for MetaCore.

- You must be a member of the Northwestern University research community to use this software
  - Even if your lab is on the Evanston campus, you may use MetaCore if you engage in bioscience research and are approved by the Galter Library administrator for the software
- You must login to your Galter Library profile to register for the software. If you do not have a Galter Library account, please [create an account](#) at our user login page (click on the “Create an account” link on the right side of the page).

In order to use this software, **you must register**. Once your registration status is verified, you will be sent log-in instructions from GeneGo directly.

**Register for MetaCore**

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### User help from Clarivate and Galter Library

- [MetaCore general information page](#)
- MetaCore has help pages available from within the application. After you log in to MetaCore, you can [access these help pages](#).
- Contact Biosciences & Bioinformatics Librarian, [Pamela Shaw](#), for assistance with using MetaCore.

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Printed: Tuesday, June 5, 2018 3:16 PM