

Molecular Analysis Tools Knowledge Center

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 Dear Molecular Analysis Tools Knowledge Center community,

As of May 11, 2012 the Molecular Analysis Tools Knowledge Center, as with all caBIG@ Knowledge Centers, will no longer be operated by dedicated Knowledge Center staff. The online resources associated with the Knowledge Center, such as forums and wikis, will remain operational; however, new content on them from this date will be 100% community-provided, rather than provided by individuals and groups that are funded by NCI to do so. The Knowledge Center sites are open and free for all to use, and we encourage your continued active participation, so that users may continue to ask, and obtain answers to, pertinent questions relating to these informatics capabilities. Furthermore, please note that the former Knowledge Center personnel are free to continue to post to the Knowledge Center online resources as community members; they are simply no longer paid to do so.

In addition to the peer support made possible by the online resources of the Knowledge Centers, triaged direct support remains available from NCI Application Support which, as always, can be contacted by e-mail at ncicb@pop.nci.nih.gov or by telephone at 301-451-4384 (toll free: 888-478-4423). Support is available Monday to Friday, 9 a.m. to 5 p.m. US Eastern Time, excluding government holidays.

NCI's Center for Biomedical Informatics and Information Technology (CBIIT) expects to continue the provision of informatics support currently provided by the Knowledge Centers, in a manner consistent with such feedback as we obtain from the NCAB ad hoc Informatics Oversight Committee, soon after the launch of the new National Cancer Informatics Program (NCIP). NCIP is not a renaming of the caBIG@ program, but rather an opportunity to reevaluate and reshape how NCI supports the informatics needs of the cancer community. If you would like to voice concerns, questions or suggestions beyond immediate requests for support, please contact Anthony Kerlavage (anthony.kerlavage@nih.gov).

About the MAT Knowledge Center

The Molecular Analysis Tools (MAT) Knowledge Center provides a centralized, authoritative repository of knowledge, information, and web-based support to facilitate the deployment and ongoing development of tools, standards, and infrastructure in the MAT domain. The Knowledge Center provides a platform for fostering open source development of MAT tools.

For First-time Visitors

If you want to post in the forum or add entries into the defect tracking/feature request system, please create a free account at [KC signup](#).

Upon receiving your account credentials, you can post messages to the forums. To receive email notification when responses to your posts are made, simply click the "subscribe forum" or "subscribe topic" link at the bottom of the page.

If you have been using various email lists for the tools below, please be advised that forums hosted by this Knowledge Center will gradually become the main vehicle for your comments and questions on the tools. The email lists will be used mainly for announcements in the near future. Thank you for your understanding and support. Please let us know your thoughts and experience with this new channel of communication so that we can make it better.

What's New

Most recent Software Releases

- [caArray 2.4.1](#) was released on 10/3/2011
- [geWorkbench 2.3.0](#) was released on 3/16/2012
- [calIntegrator 1.3.1](#) was released on 12/2/2011
- [GenePattern 3.3.3](#) was released in 10/2011
- [caGWAS 1.1.0](#) was released on 11/6/2009

For more news, visit [What's New](#).

Tools Supported by the MAT KC

The following software tools are currently supported by the Molecular Analysis Tools Knowledge Center. Links are provided to the tool summary page for each tool, which provides an overview of the tool with links to resources including the knowledge base, forum, bug tracker, feature request system, and the developer's code repository.

caArray

caArray is an open-source microarray data management system which is accessible both via the web and programmatically. caArray guides the annotation and exchange of array data using a federated model of local installations whose results are shareable across the cancer Biomedical Informatics Grid (caBIG®). Visit the [caArray](#) page for more information.

calIntegrator

calIntegrator is a web-based software application that allows researchers to set up custom, caBIG®-compatible web portals to conduct integrative research, without requiring programming experience. These portals bring together heterogeneous clinical, microarray and medical imaging data to enrich multidisciplinary research. Visit the [calIntegrator](#) page for more information.

geWorkbench

geWorkbench (genomics Workbench) is a Java-based open-source platform for integrated genomics. Using a component architecture it allows individually developed plug-ins to be configured into complex bioinformatic applications. At present there are more than 50 available plug-ins supporting the visualization and analysis of gene expression and sequence data. Visit the [geWorkbench](#) page for more information.

GenePattern

GenePattern combines a powerful scientific workflow platform with more than 150 computational and visualization tools for the analysis of genomic data. Visit the [GenePattern](#) page for more information.

Tool Adoption Case Studies

Many academic institutes and research/commercial organizations have adopted various caBIG tools in the past. In this section we link to a few key documents where caBIG tool adopters have created materials about their experience for the benefit of those considering an adoption project of their own.

From the Jackson Laboratory:

[ICR Tools Aoption Project Outcome Presentation](#)

[Lessons Learned Presentation](#)

Integration of Tools

There is extensive integration among caArray, caIntegrator2, caIntegrator, geWorkbench, and GenePattern. For example, geWorkbench and caIntegrator2 can retrieve microarray data directly from caArray hosted at NCI or on a local server. GenePattern is also connected to caArray for data retrieval. caIntegrator2 and caIntegrator use GenePattern as one of its data analysis services.

Instead of developing all data analysis modules independently, geWorkbench and GenePattern each can invoke several modules of the other party to provide a comprehensive data analysis platform. To learn how to use these tools together, please check out corresponding tool's wiki pages as well as the forums (End Users forum and Developers forum) dedicated to the integration of these tools.

Visit MAT Knowledge Center Forum

The [Molecular Analysis Tools Domain Forum](#) is for visitors to submit questions and comments that are beyond the scope of any specific tool, but that are within the domain addressed by the Knowledge Center. What questions or comments do you have that extend beyond the coverage of the existing tool set? Write your thoughts in this forum.

Related Links

- [ICR Workspace](#) (On caBIG® Community Website)
- [Support Service Provider Listing](#)
- [caBIG® Community Website](#)