

Core 1: Computer and Information Science core is developing a computing architecture that permits the harnessing of diverse data sources and algorithms into a single cohesive framework for problem solving by biomedical scientists.

Core 2: Bioinformatics and Knowledge Acquisition core, is building an integrated information store for molecular biology and software tools for information retrieval, bioinformatics analysis, model construction and model testing.

Core 3: Researchers from the Driving Biological Problems (DBP) are solving problems including gene fusions in cancer, complication of diabetes and bipolar disorder comorbidities.

Core 4: Infrastructure core provides the computational infrastructure for NCIBI including hardware management, user authentication, and network communications.

Core 5: Education core is establishing innovative education and training programs, including a new Certificate in Integrative Biomedical Informatics that will leverage the Center's integrated information and computational resources.

Core 6: Outreach and Dissemination core is aiding in developing problem solving techniques in the collaborative study of complex biological systems.

Core 7: Administration core provides the administrative management of the Center including an External Scientific Advisory Committee. The Executive Committee oversees the Center, management of the cores and interactions outside the Center.

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National Center for Integrative Biomedical Informatics

University of Michigan

Mission

The mission of the National Center for Integrative Biomedical Informatics (NCIBI), is to create targeted knowledge environments for molecular biomedical research that help guide experiments and enable new insights from the analysis of complex diseases. Founded in October 2005, NCIBI develops efficient software tools, data integration methods, and systems modeling environments. The resulting NCIBI "Suite of Tools and Data" facilitates rapid construction of context-appropriate molecular biology information schemas from experimental data, biomedical databases, and the published literature.

<http://www.ncibi.org>



MiMI

<http://mimi.ncibi.org/>

The Michigan Molecular Interactions Index provides a rich data set of molecular interactions. Through a combination of interfaces MiMI allows external tools and users to integrate with its extensive molecule gene and pathways database.

SNP Functional Portal

<http://brainarray.mbni.med.umich.edu/Brainarray/>

[Database/SearchSNP/snpfunc.aspx](#)

The SNP Function Portal is designed to be a clearing house for all public domain SNP functional annotation data, as well as in-house functional annotations derived from different data sources.

MarkerInfoFinder

<http://brainarray.mbni.med.umich.edu/brainarray/datamining/MarkerInfoFinder/>

The development of highly efficient SNP genotyping methods provides the opportunity of performing genome-wide scanning for various diseases.

Biological Concept Diagram Editor (BCDE)

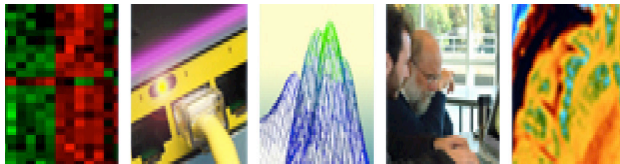
<http://arrayanalysis.mbni.med.umich.edu/draw/>

The BCDE is a conceptual relationship diagramming tool specifically designed for biomedical researchers.

Oncomine

<http://www.oncomine.org>

Oncomine is a resource for examining gene expression in cancer. Oncomine pre-computes cancer profiles, clusters, and gene set modules so you can focus on discovery. Oncomine contains data from nearly 100 human tumor microarray studies, 18 different tumor types, and 75 million microarray measurements.



Cytoscape Plugin for MiMI

<http://mimiplugin.ncibi.org/>

Cytoscape is a widely used open source software tool for the analysis of biomolecular interaction networks. The MiMI Cytoscape plugin retrieves molecular interactions from MiMI and allows these interaction networks to be visualized using Cytoscape.

SAGA

<http://saga.ncibi.org>

SAGA implements an efficient approximate subgraph matching algorithm. SAGA currently supports matching pathways in the KEGG pathways dataset.

MiSearch

<http://msearch.ncibi.org>

MiSearch is an adaptive literature search tool designed to facilitate the identification of relevant citations in the PubMed database.

BioSearch2D

<http://biosearch2d.ncibi.org>

BioSearch-2D renders the contents of large biomedical document collections into a single, dynamic map, allowing users to generate a summary map of genes vs. ontology.

Gene2MeSH

<http://gene2mesh.ncibi.org>

Gene2MeSH is an automated annotation tool that associates Medical Subject Heading (MeSH) terms with genes using the National Library of Medicine's PubMed literature database.

Bayesian Network Tools

miniTUBA

<http://www.minituba.org>

MiniTUBA is a web-based modeling system that allows researchers to perform complex medical/clinical inference and prediction using dynamic Bayesian network (DBN) analysis with temporal datasets.

MARIMBA

<http://marimba.hegroup.org>

MARIMBA is a web-based environment for modeling biological pathways using Bayesian networks.

Bubble

<http://bubble.engin.umich.edu>

Bubble is a web-based resource for performing several Bayesian Network learning tasks on biological data.

NLP Tools

Clairlib

<http://www.clairlib.org>

The Clair library is intended to simplify a number of generic tasks in Natural Language Processing (NLP), Information Retrieval (IR), and Network Analysis (NA).

Gene Interaction Network (GIN)

<http://gin.ncibi.org>

GIN is a system for browsing articles and molecule interaction information.

