

NIH Roadmap's National Centers for Biomedical Computing Initiative: A Programmatic Overview

Peter Lyster, Ph.D.

**The Human Brain Project: Linking
Within and Beyond**

Monday April 24, 2006

Brief Journey Through the Seven Centers

NIH Roadmap National Centers for Biomedical Computing (NCBC)

Physics-Based Simulation of Biological Structures (SIMBIOS)
Russ Altman, PI

National Center for Integrative Biomedical Informatics (NCIBI)
Brian D. Athey, PI

Informatics for Integrating Biology and the Bedside (i2b2)
Isaac Kohane, PI



The National Center For Biomedical Ontology (NCBO)
Mark Musen, PI

National Alliance for Medical Imaging Computing (NA-MIC)
Ron Kikinis, PI

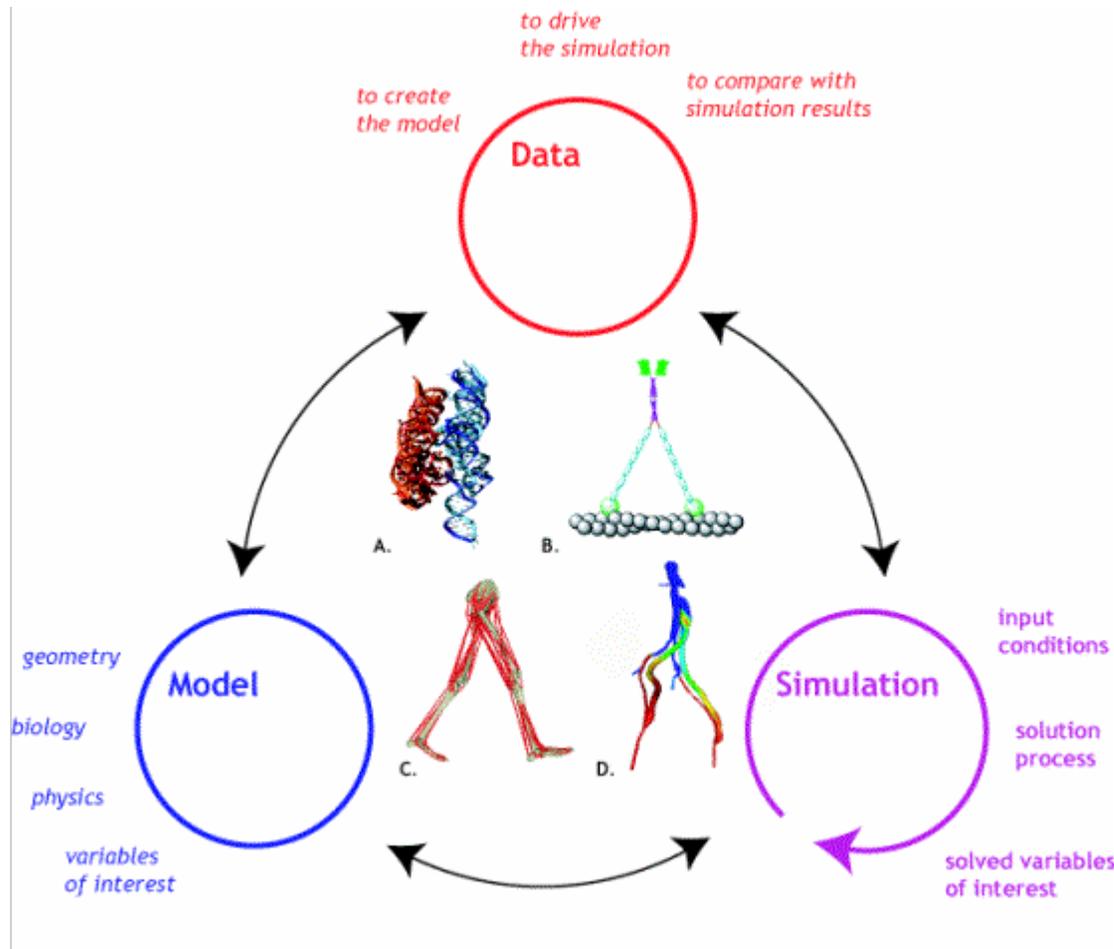
Center for Computational Biology (CCB)
Arthur Toga, PI

Multiscale Analysis of Genomic and Cellular Networks (MAGNet)
Andrea Califano, PI

Physics-based Simulation of Biological Structures (SIMBIOS)

PI: Russ Altman, M.D., Ph.D.

PI Institution: Stanford University

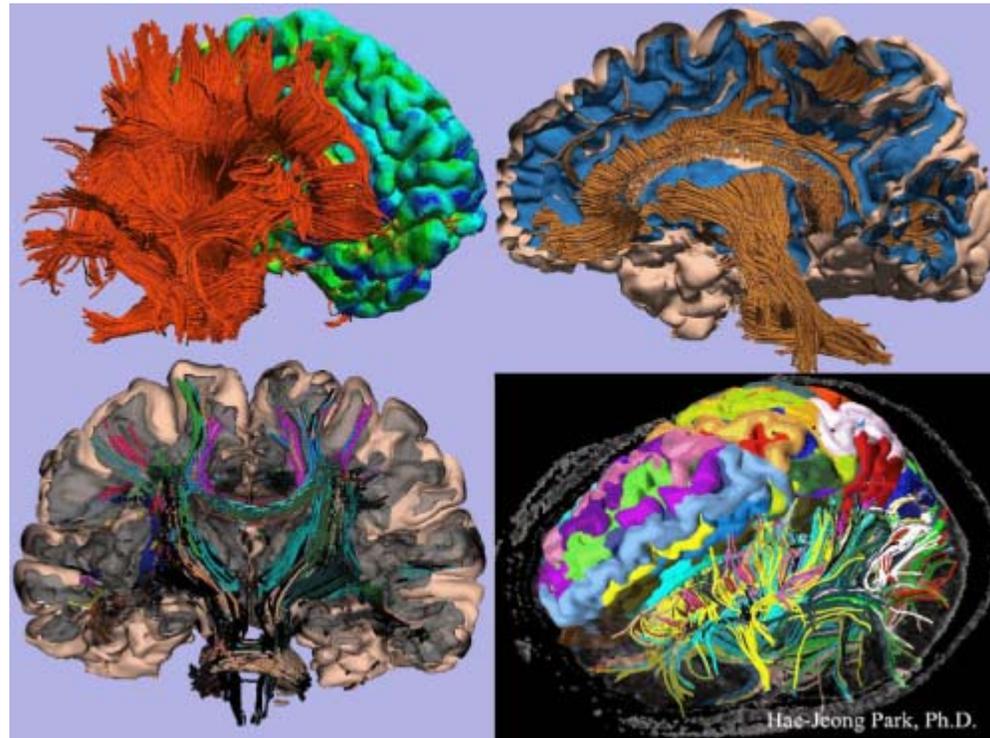


This Center will develop, disseminate, and support a simulation tool kit (SimTK) that will enable biomedical scientists to develop and share accurate models and simulations of biological structures from atoms to organisms. SimTK will be an open-source, extensible, object-oriented framework for manipulating data, models, and simulations. The software will include advanced capabilities for modeling the geometry and physics of biological systems, generating the governing differential equations of these systems, integrating the equations to simulate the system dynamics, and interpreting the simulation results through comparison with experimental data.

National Alliance for Medical Imaging Computing (NAMIC)

PI: Ron Kikinis, M.D.

PI Institution: Brigham and Women's Hospital



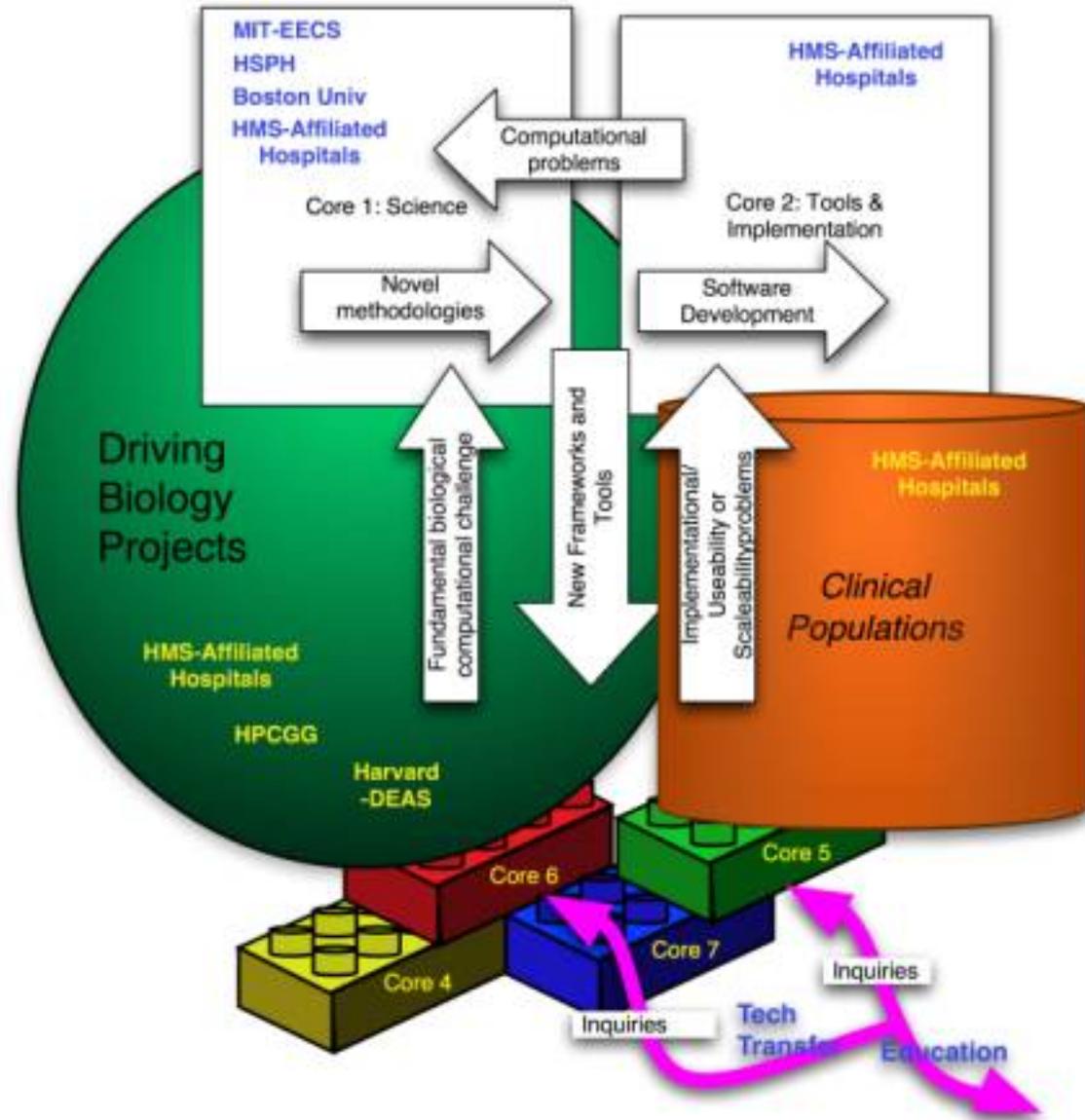
The National Alliance for Medical Image Computing (NAMIC), proposed here, will integrate the efforts of leading researchers with a shared vision for development and distribution of the tools required to advance the power of imaging as a methodology for quantifying and analyzing biomedical data. This shared vision is based on a thorough composition of computational methods, from image acquisition to analysis, that builds on the best available practices in algorithm development, software engineering, and application of medical image computing for understanding and mitigating the effects of disease and disability. NAMIC's goal is to develop, integrate, and deploy computational image analysis systems that are applicable to multiple diseases, in different organs. To provide focus for these efforts, a set of key problems in schizophrenia research has been selected as the initial Driving Biological Projects (DBPs) for NAMIC.

Informatics for Integrating Biology and the Bedside (I2B2)

PI: Isaac Kohane, M.D., Ph.D.

PI Institution: Brigham and Women's Hospital

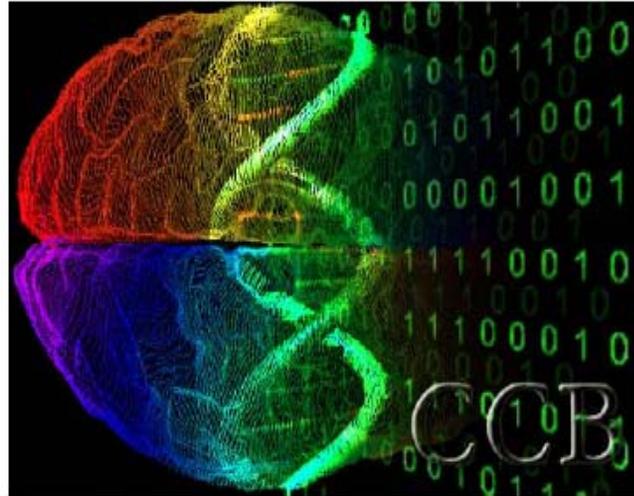
I2B2 (Informatics for Integrating Biology and the Bedside) is an NIH-funded National Center for Biomedical Computing based at Partners HealthCare System. The I2B2 Center is developing a scalable informatics framework that will bridge clinical research data and the vast data banks arising from basic science research in order to better understand the genetic bases of complex diseases. This knowledge will facilitate the design of targeted therapies for individual patients with diseases having genetic origins.



Center for Computational Biology (CCB)

PI: Arthur Toga, Ph.D.

PI Institution: University of California at Los Angeles



The Center for Computational Biology (CCB) was established to develop, implement and test computational biology methods that are applicable across spatial scales and biological systems. Our objective is to help elucidate characteristics and relationships that would otherwise be impossible to detect and measure. The CCB employs an integrative approach, both in terms of the biology and the participating disciplines. The Center focuses on the brain, specifically on neuroimaging, and involves research in mathematics, computational methods and informatics. It also is involved in the development of a new form of software infrastructure – the *computational atlas* – to manage multidimensional data spanning many scales and modalities. This will be specifically applied to the study of brain structure and function in health and disease, but will have much broader applicability to both biomedical computing and computational biology.

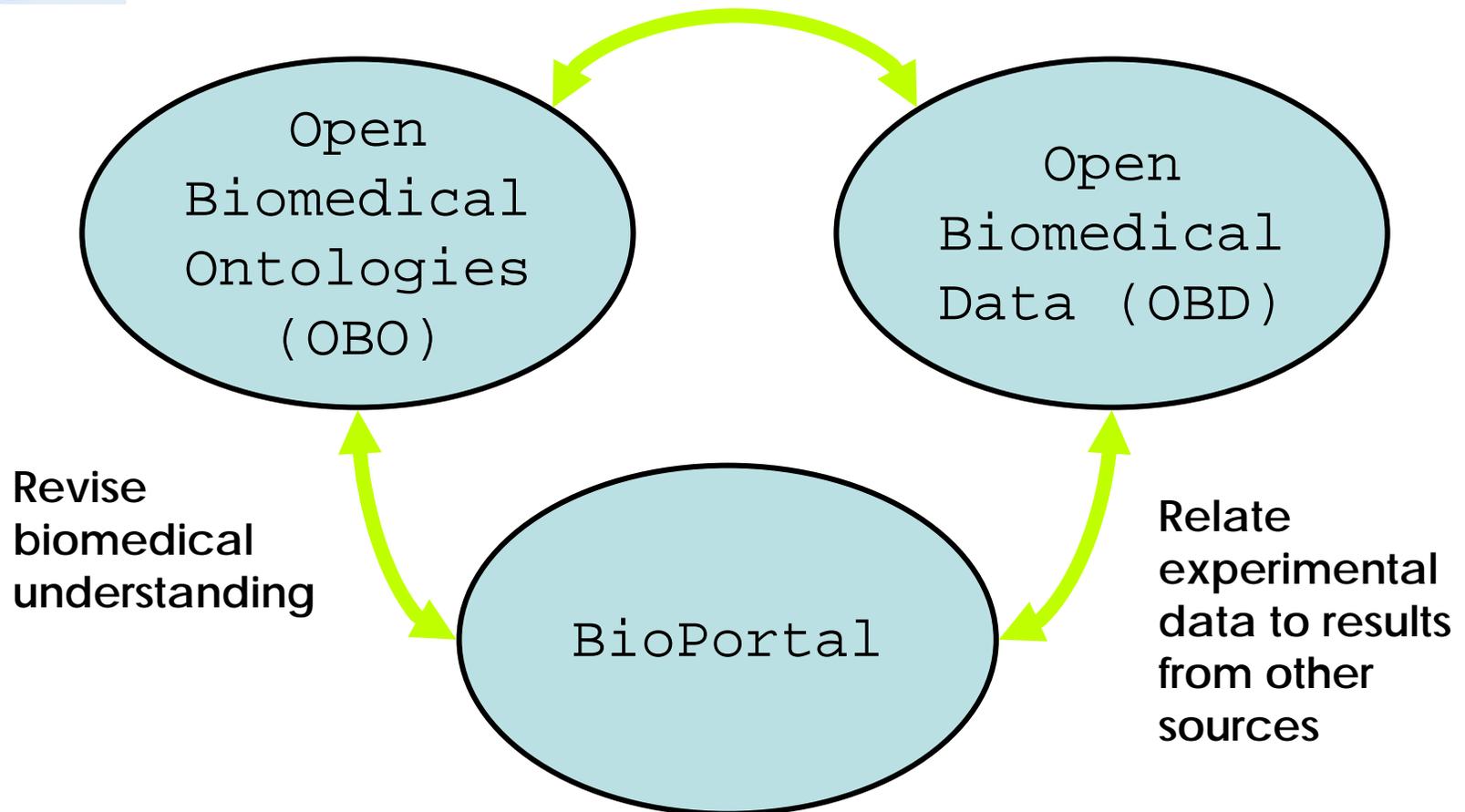
National Center for Biomedical Ontology (NCBO)

PI: Mark A. Musen M.D., Ph.D.

PI Institution: Stanford University



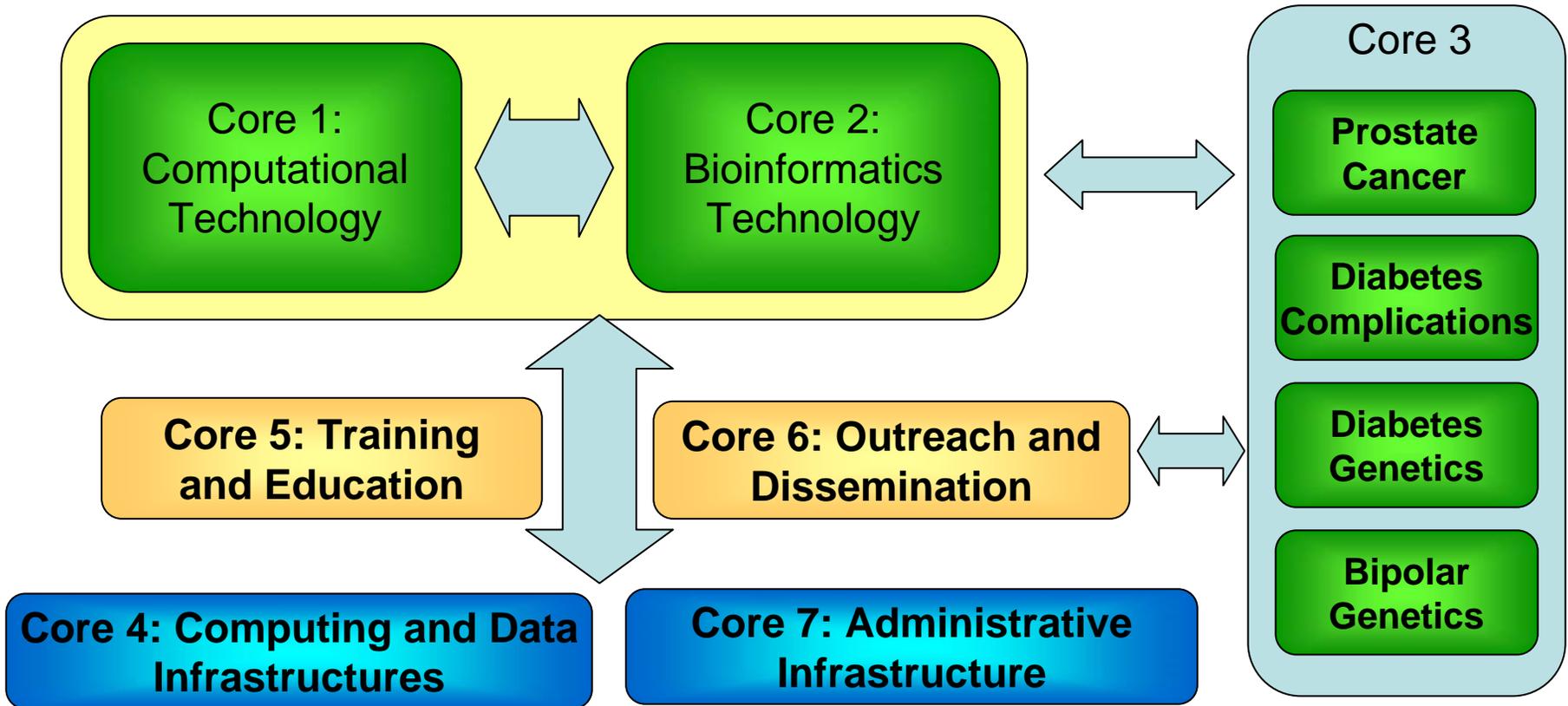
Capture and index experimental results



National Center for Integrative Biomedical Informatics (NCIBI)

PI: Brian D. Athey Ph.D

PI Institution: University Of Michigan



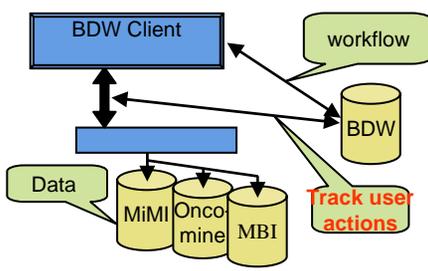
Granular Overview of NCIBI Activities Underway: Cores 1-3

First User Environment

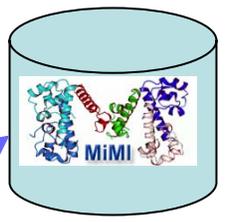
User Environment Analyses:
Mirel, Ackerman labs



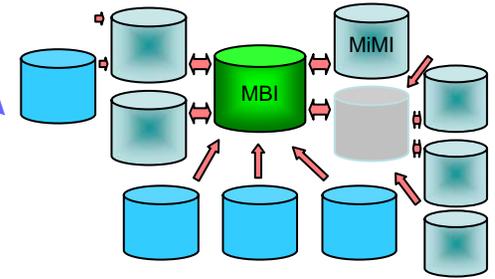
BDW: Biomedical Data Workbench prototype: Weymouth



Database Technologies for Deep Integration of Biological Information



MiMI: Michigan Molecular Interactions DB: Jagadish lab, Tarcea



MBI: Molecular Biology Integration DB: States lab, Phillips

Tools for large-Scale analysis

- SAGA: Patel Lab**
- Bayesian Nets: Woolf Lab**
- Workflows: Weymouth, McEachin, & Programming team**
- Natural Language Processing: States, Meng, Radev Labs**
- Concept Mapper: Rhodes, Patel, Woolf**

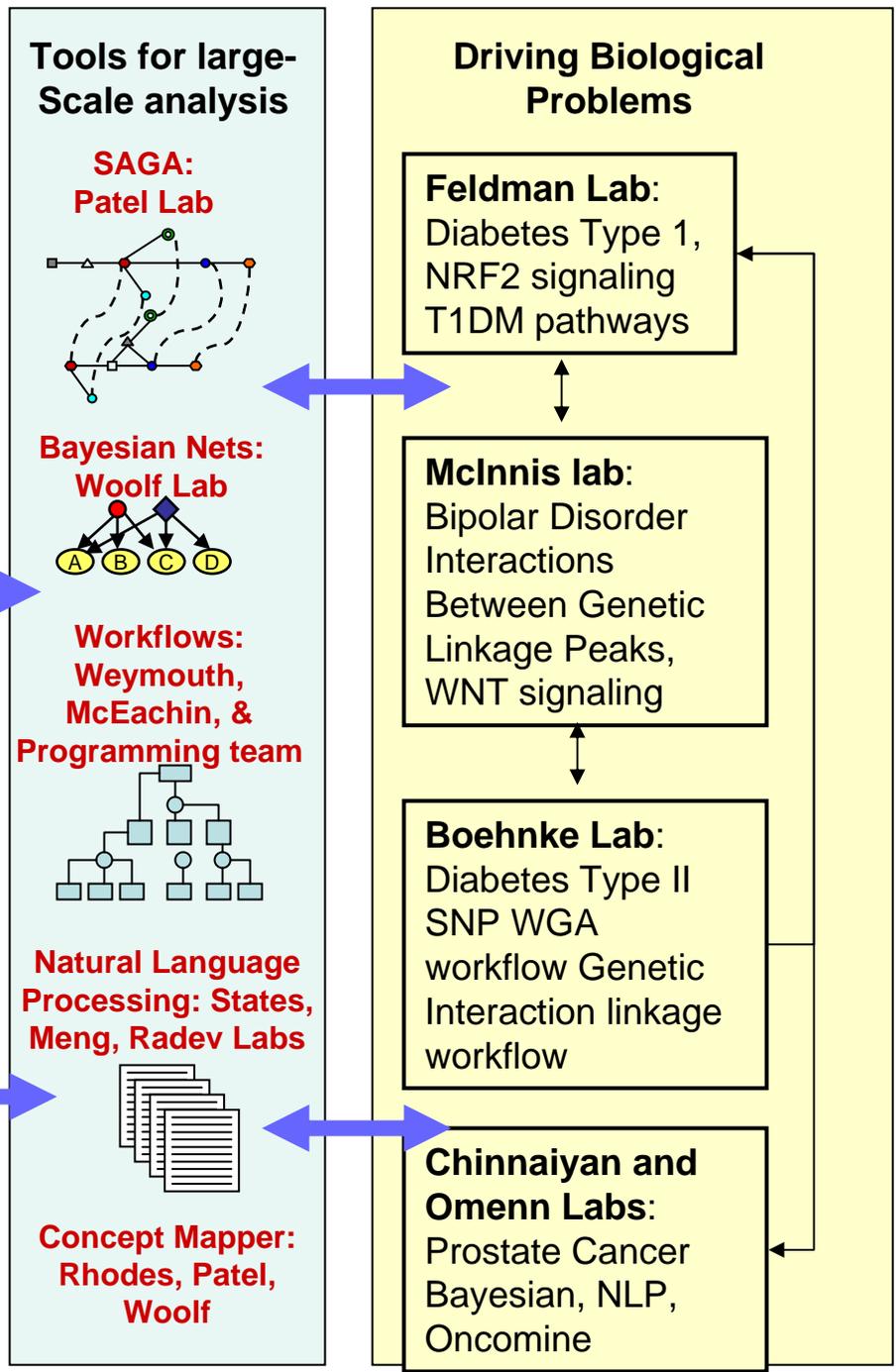
Driving Biological Problems

Feldman Lab:
Diabetes Type 1, NRF2 signaling T1DM pathways

McInnis lab:
Bipolar Disorder Interactions Between Genetic Linkage Peaks, WNT signaling

Boehnke Lab:
Diabetes Type II SNP WGA workflow Genetic Interaction linkage workflow

Chinnaiyan and Omenn Labs:
Prostate Cancer Bayesian, NLP, Oncomine



Multiscale Analysis of Genomic and Cellular Networks (MAGNet)

PI: Andrea Califano Ph.D.

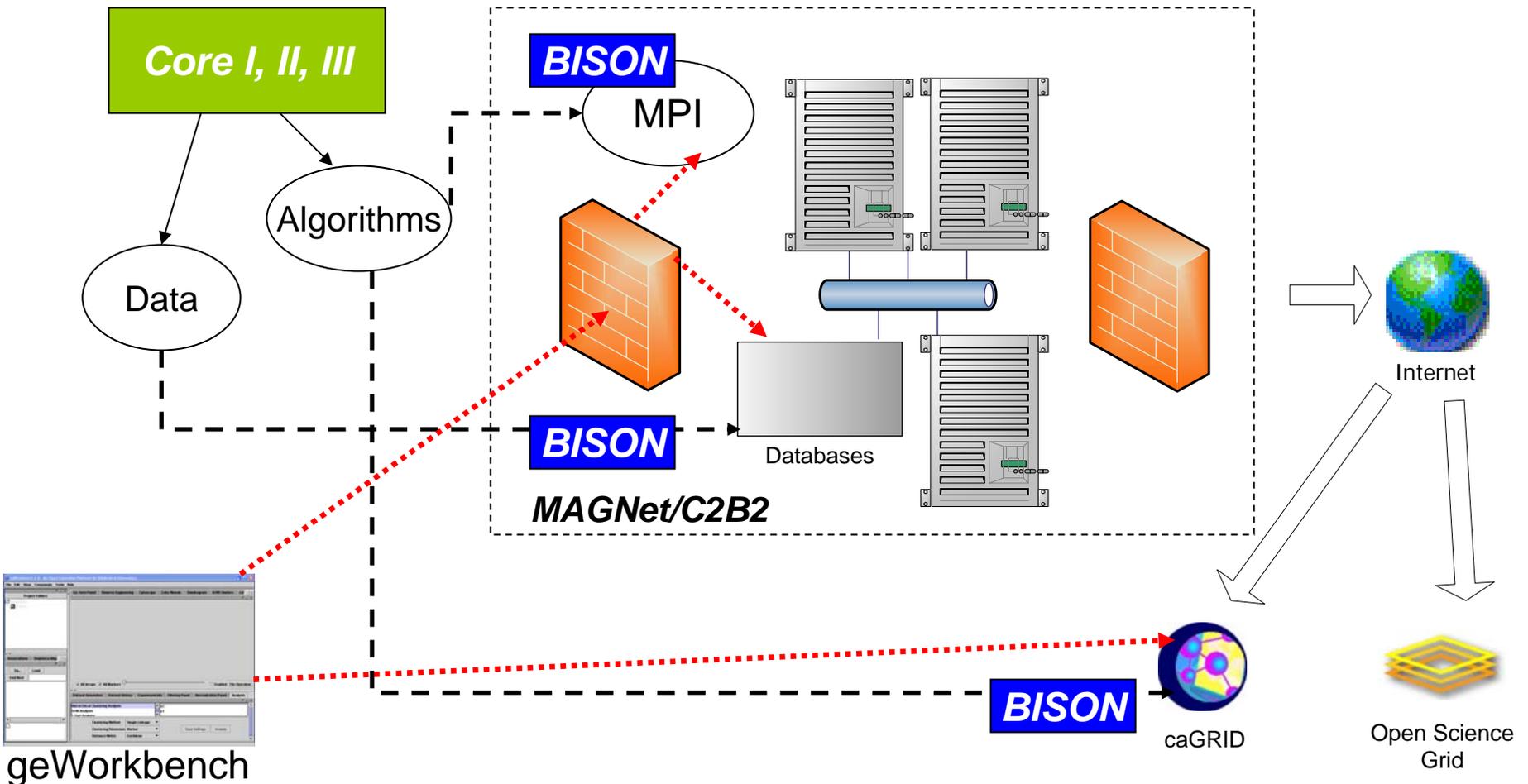
PI Institution: Columbia University

- *To study the organization of the complex networks of biochemical interactions whose concerted activity determines cellular processes at increasing levels of granularity.*
- *To provide an integrative computational framework to organize molecular interactions in the cell into manageable context dependent components.*
- *To develop interoperable computational models and tools that can leverage such cellular interaction maps to elucidate key biological processes and to dissect complex diseases.*

Core 1: Computational Sciences

Core 2: Bioinformatics

Core 3: Cadherin binding; Cancer; Genetic determinants of common heritable disorders (Alzheimer's, Autism)



The RFA states the goal of creating “the networked national effort to build the computational infrastructure for biomedical computing for the nation”:

What would you do?

Building Bridges and the Hub and Spoke Model

NIH Project Team

- John Whitmarsh (Chair), Michael Ackerman, Carol Bean, Milt Corn, Gregory Farber, Valerie Florence, Valentina di Francesco, Charles Friedman, Dan Gallahan, Peter Good, John Haller, Peter Highnam, Michael Huerta, Don Jenkins, Jennie Larkin, Peter Lyster, James Onken, Grace Peng, Salvatori Sechi, Karen Skinner, Jennifer Villani

NIH Science Officer Team

- Cadre of NIH Program Staff who help make connections

Collaborations with National Centers for Biomedical Computing

Regular grants (R01) **PAR05-063**, and smaller grants involving innovate, high-risk/high-impact research that does not require preliminary data (R21) **PAR06-223**. **These announcements require open source software.**

These collaborations are meant to expand the scope of biological problems currently being addressed by the NIH NCBCs and to offer a mechanism to bring the computational expertise of the NIH NCBCs to these new areas of biomedical and behavioral science.

Building Bridges: Software and Data Integration Working Group (SDIWG)

Mission: to further the networked national effort:

1. To advance the domain sciences, and promote software interoperability and data exchange.
2. To capture the collective knowledge of software engineering and practices among the Centers and publish this knowledge widely.

NCBC Staff serving on SDIWG

- Bill Lorensen (NA-MIC)
- Mike Sherman (Simbios)
- Henry Chueh (I2B2)
- Ivo Dinov (CCB)
- Aris Floratos (MAGNet)
- Daniel Rubin (NCBO)
- Brian Athey (NCIBI)
- Many others—Suzi Lewis, David States, Steve Pieper, Tina Kapur, Shawn Murphy, Center Pls...

NIH Staff serving on SDIWG

Peter Lyster (NIGMS, Chair)

Michael Ackerman (NLM)

Carol Bean (NCRR)

Art Castle (NIDDK)

German Cavelier (NIMH)

Larry Clarke (NCI)

Zohara Cohen (NIBIB)

Elaine Collier (NCRR)

Jennifer Couch (NCI)

Peter Covitz (NCI)

Valentina Di Francesco (NIAID)

Dan Gallahan (NCI)

Peter Good (NHGRI)

John Haller (NIBIB)

Donald Harrington (NIBIB)

Peter Highnam (NCRR)

Michael Huerta (NIMH)

Donald Jenkins (NLM)

Jennie Larkin (NHLBI)

Yuan Liu (NINDS)

Michael Marron (NCRR)

Richard Morris (NIAID)

Bret Peterson (NCRR)

Salvatore Sechi (NIDDK)

Karen Skinner (NIDA)

Michael Twery (NHLBI)

Terry Yoo (NLM)

Web 2: Wiki

Allows communities of scientists to collaborate, communicate, and maintain records of the threads, and upload documents with guaranteed provenance.

The wiki technology has emerged as a powerful tool for collaborative research.

Discussions in the First Year

- Demonstration projects
- Collaborative software development environment (yellow pages, knowledge environment, full development environment or Framework)
- NIH-forge
- Emerging efforts in the community (Neuroscience Information Framework, Clearinghouse)
- Intangibles—pairwise interactions, consciousness raising
- Example—SimTK<->ITK

1. Resourceome and semantic web for software

Why?

- Improved access and awareness about tools, e.g., IATR
- Use of semantic web as enabling technology for composition of applications whose components were developed in heterogeneous software and hardware environments



Internet Analysis Tools Registry



supported by The Human Brain Project

153 tools registered

Not signed in

Home

About IATR

Introduction to IATR

About tool reviews

About auto-updates

Proposed tool description vocabulary

Access the database

Search

Display all tools

User accounts

Sign in

Forget your password?

Create an account

Other IATR resources

Languages

Developer resources

Image

databases

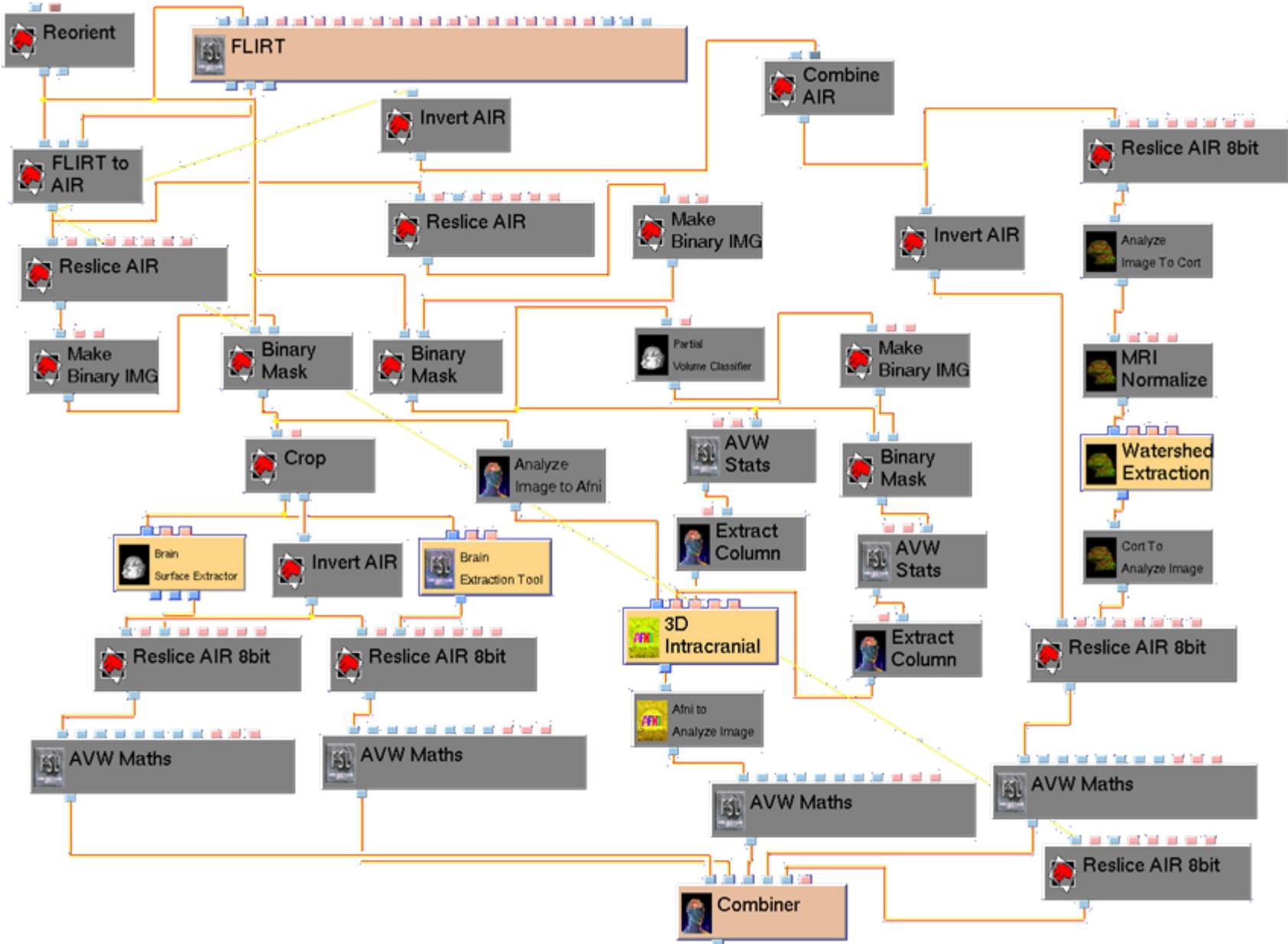
Home

Welcome to the Internet Analysis Tools Registry.

There have been 227 display requests from 52 unique hosts in the past 24 hours, 1390 display requests from 347 unique hosts in the past week, and 5353 display requests from 1315 unique hosts in the past month.

[IATR now supports user reviews of listed tools.](#)

Example of a CCB/LONI Pipeline



2. Scientific Ontologies

1. What does each NCBC need by way of ontologies?
2. What is each NCBC currently doing in this regard?
 - What ontologies are being used with no regrets?
 - What ontologies are being used, but with reservations?
 - What ontologies are being used because there is no credible alternative?
3. What content areas need to be better defined with standard ontologies?
4. Work with OBO Foundry and 'seed the system' to achieve de facto integration of data

There are a number of similar efforts to SDIWG at NIH

- Integrated Cancer Biology Program (ICBP)
- NIAID (Allergy/Infectious Diseases) Bioinformatics Resource Centers (BRC)
- Clinical Research Networks (NECTAR)
- Chronic Disease Outcomes (PROMIS)
- BIRN/caBIG/Sysbiol/Glue/PSI/TCNP/P41/PGA/GAIN/GEI...

Is there a big picture?

- This is a multi-decadal effort.
- Efforts at infrastructure and enabling technologies are difficult to evaluate—the big picture seems to evolve slowly, while individual researchers make gains.

Contact:

Peter Lyster Ph.D.