

# **Cores 5 and 6**

## **Evaluation, Training, Education, Outreach and Dissemination**

Barbara Mirel, Core 5 Director

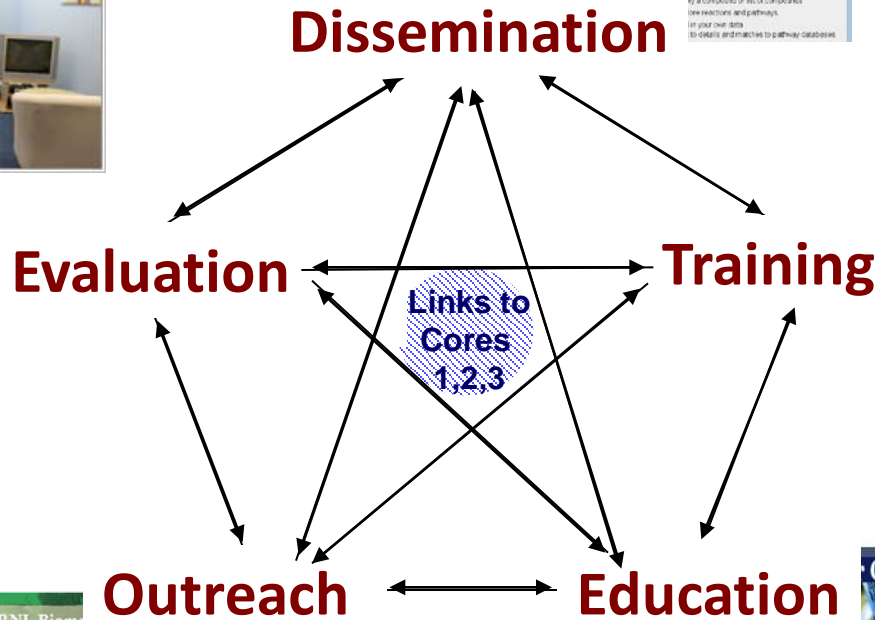
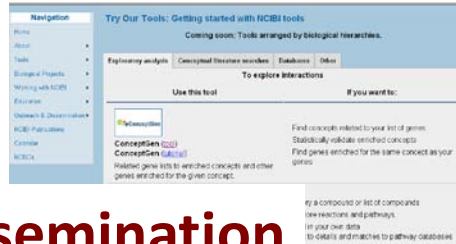
Brian Athey, Core 6 Director

Alex Ade, Jyoti Athanikar, Aaron Bookvich, Jim  
Cavalcoli, Beth Kirschner, Jean Song,  
Glenn Tarcea, Alex Terzian, Paul Trombley,  
Terry Weymouth, Zach Wright

Annual Research Meeting, April 28, 2009



# Integrated Bioinformatics: The Public Face



**AMIA** American Medical Informatics Association  
Summit on Translational Medicine  
March 15-17, 2009  
summit2009.amia.org

**BSEC** First Annual ORNL Biomolecular Science & Engineering Conference

8:00 – 8:30 **Welcome and Administrative Comments**  
Barbara Becker, Director, Center for Computational Biology  
Jeff Nichols, PI, Computational Biology  
Thomas Zachar, Director, Computational Biology

**BIO SITEMAPS**  
Home -> Biositemaps

8:30 – 9:15 **Keynote Spe**  
Keeping up with Biomedicine

9:15 – 9:45 **Plenary Spe**  
Imaging in the 21st Century

NCBC Resource Working Group: developed technologies to address

**Computational Medicine and Bioinformatics**

**Bioinformatics Graduate Program**

The Bioinformatics Graduate Program (BGP) was established as an interdepartmental program in 1998 at the University of Michigan, and enrolled its first matriculating class in 2001. The BGP is the academic component of CCMB, led by Dr. Margit Burmeister, Professor of Human Genetics. Currently there are Ph.D. and M.S. students. This Program is highly interdisciplinary in nature and involves many different schools and departments across campus. [MORE]

NAVIGATION  
Home  
Graduate Program  
Research/Faculty  
Events  
Contact



# Evaluation and Training

# Distinct NCIBI Focus on Optimal Tool-Scientist Fit

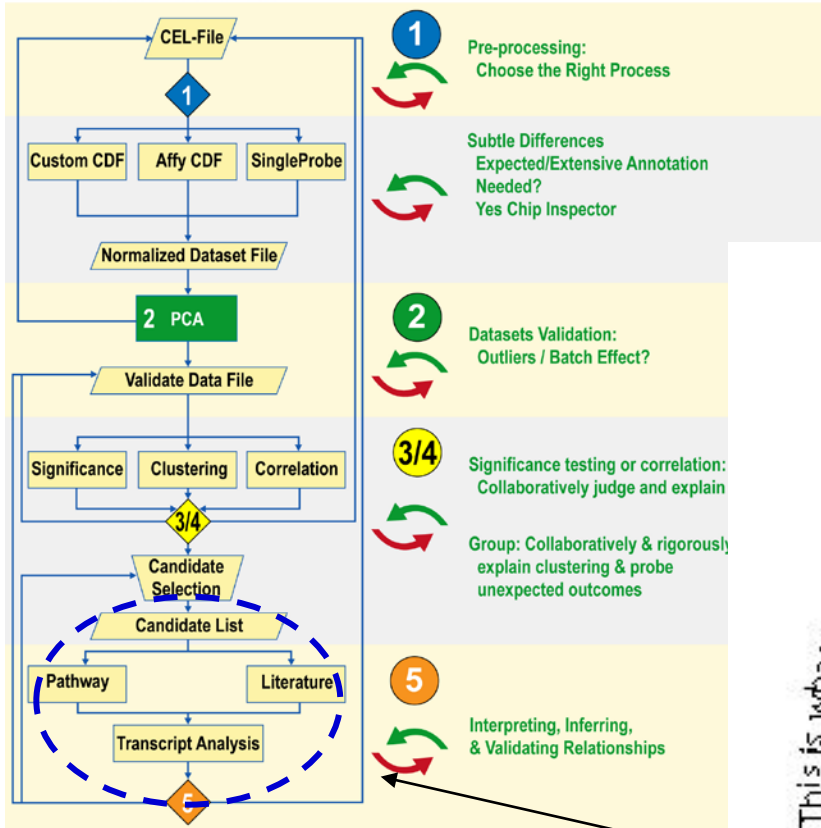
Integrated resources for integrated analysis

1. Useful to scientists' actual analyses
2. Usable based on established UI principles
3. Easy to use and effective for tasks
4. Aids for learning
5. Ease of access to tools and tutorials

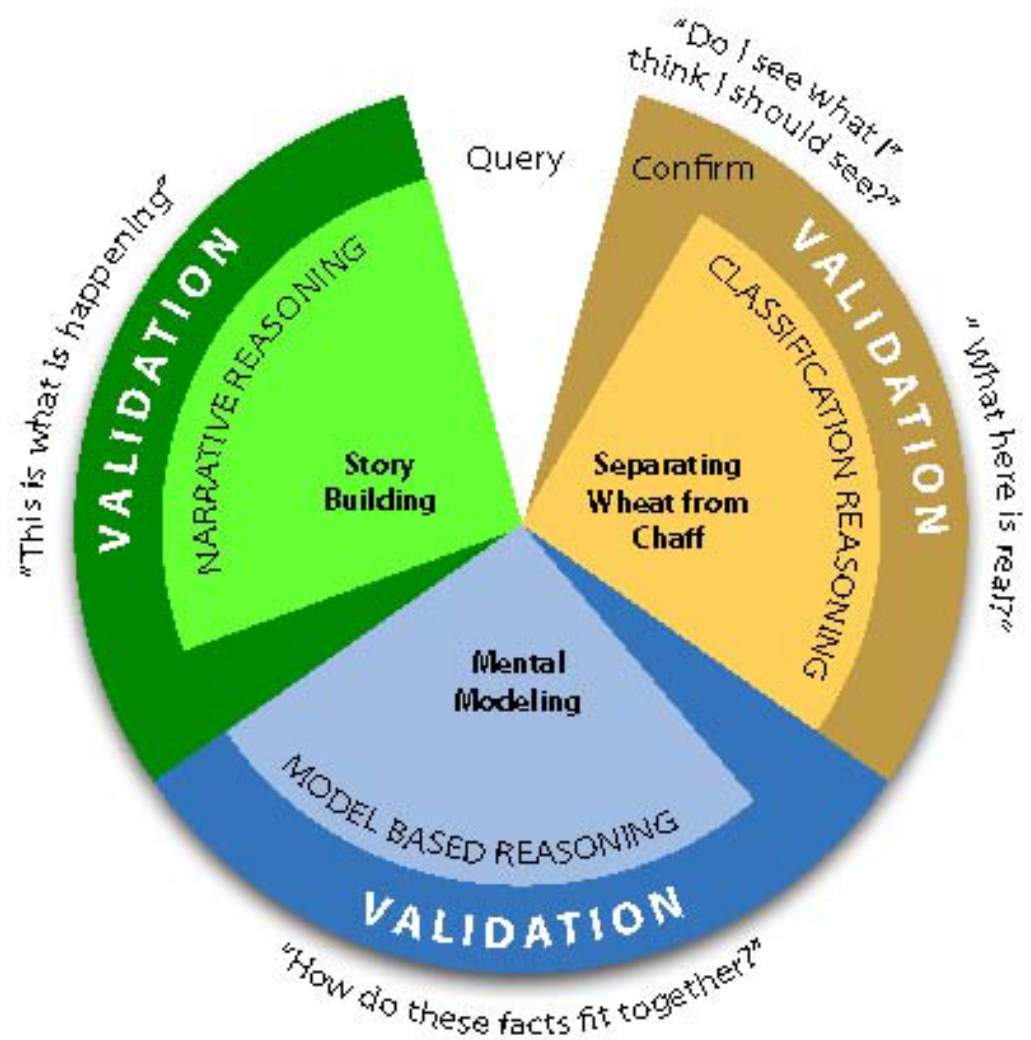
# Workflow Renal Disease

WORKFLOW PIPELINE

HUMAN INTELLIGENCE & COLLABORATION

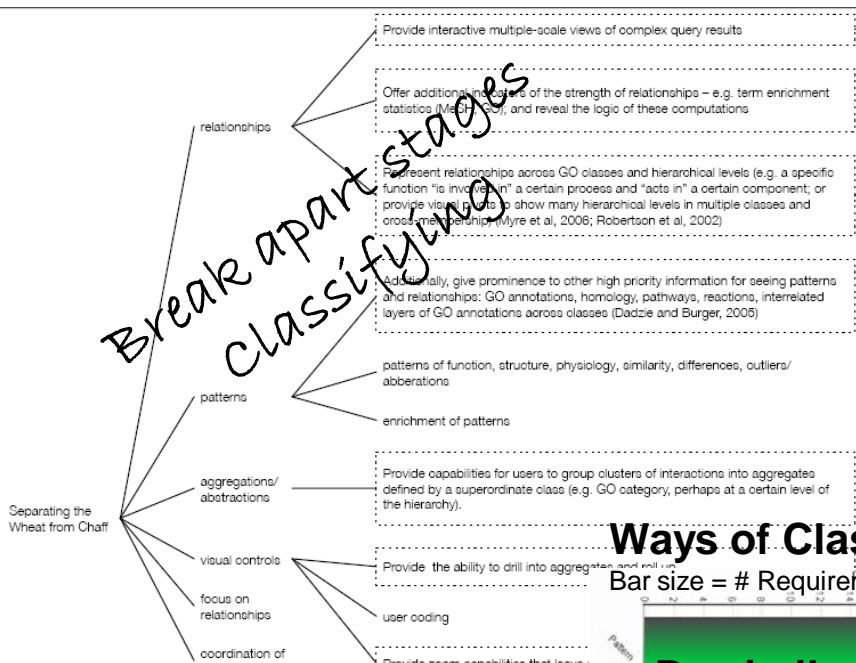


## 1. Useful: Discovery-based analysis



Mirel. **Supporting cognition in systems biology analysis.** *J Biomedical Discovery & Collab*, 2009  
 Mirel, Eichinger, Nair, Kretzler. **Integrating automatic workflows, human intelligence and collaborative** *Proceedings of the AMIA Summit on Translational Bioinformatics*, 2009

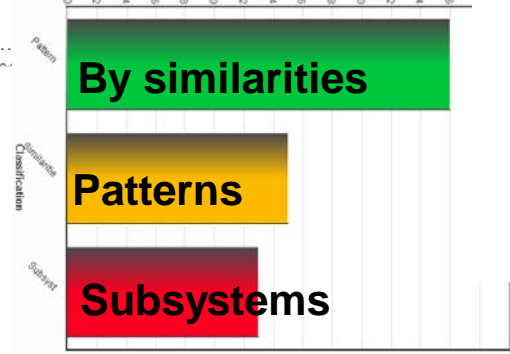
# Useful applied to tools: requirements



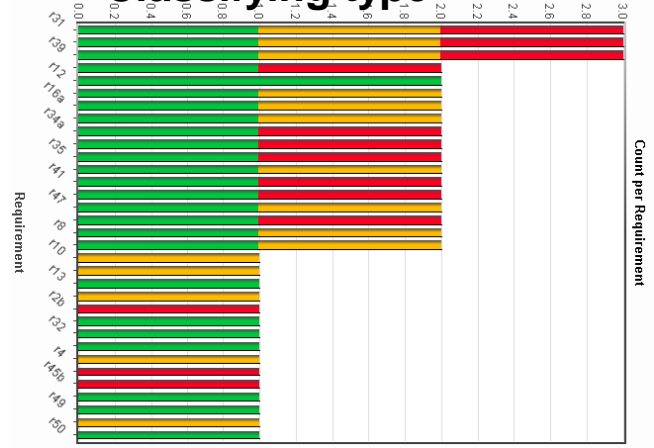
Break apart stages  
classifying

## Ways of Classifying

Bar size = # Requirements



## Requirements by Classifying type



### Required by All 3 ways of classifying:

- Import own data
- Clear indication of the nature of an interaction & type of molecule,
- Visually encode by attribute in networks or pathways

Mirel, Keller, Peleg Altman. **Design of integrated Bioinformatics Systems**. AMIA 2009

## 2. Usable user interfaces

Heuristic evaluations applied to tool fixes



	Gestalt principles		Comments
29	Does the default view use <b>proximity</b> in its arrangement and layout to suggest relationships between like things? (e.g. clusters are spaced to suggest patterns)	1 2 3 4 5 N/A	
30	Do the <b>organization and layout</b> of the default view draw users' eyes to specific spots e.g. through putting certain data/relations in the center or highlighting?	1 2 3 4 5 N/A	
31	Does the default view automatically use <b>other visual cues to emphasize single items</b> ?	1 2 3 4 5 N/A	
32	Does the default view automatically use <b>other visual cues to emphasize groups or relationships</b> (e.g. outlines or hierarchical structures)?	1 2 3 4 5 N/A	
33	Does the default include <b>more than one graphic</b> to show additional information, such as distribution of values in an important field?	1 2 3 4	
34	If <b>x-y axes or matrices</b> are used, do default arrangements automatically draw users' eyes to patterns (e.g. increases/decreases, clusters)?	1 2 3 4	
35	If default visuals do not provide ready entry points, can users perform operations (e.g. user-defined selections, subsetting, layout, filtering) that quickly allow them to find and entry point or other patterns such as similarities, outliers, trends (2-4 steps)?	1 2 3 4	
36	Are users able to manipulate or re-structure visual arrangements to see other patterns/groups?	1 2 3 4	
37	Can users <b>manipulate visual arrangements</b> efficiently (1-3 steps)?	1 2 3 4	

### Modification Report system: Severity rankings

**None** - No immediate issue for performance/satisfaction

**Minor** – Minor slow down in task performance; irritating

**Serious** - Errors or miscomprehension due to UI features:

**Major**- Unacceptably time-consuming, unrecoverable errors, dead-end in task performance

**Critical**- Showstopper; No workarounds possible, cannot complete a given task, possibility of losing data

**Failure** - Catastrophic error, loss of data, system freezes



# 3. Easy to use Effective for tasks

## Usability testing

10 scientists (4 at NCI)

4 integrated tools

Scripted task scenario

Think alouds

N=10, 1-7 scale, 7 strongly agree

**Computer System Usability Questionnaire**

Please rate the usability of the system.

1. Overall, I am satisfied with how easy it is to use this set of tools.	strongly disagree	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	strongly agree
2. It was simple to interact with this set of tools.	strongly disagree	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	strongly agree
3. I could find things of interest relevant to the scenario using the tools	strongly disagree	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	strongly agree
4. I could complete the tasks efficiently									
5. The amount of time spent was worth the effort									
6. I feel comfortable using this set of tools									
7. It was easy to learn to use MiMI, MiMI, Gene2Me									
8. It was easy to use									



Data analysis is in progress  
Will translate into improvements

Q Description	Average	Median
<u>PleasantUIsMiMI</u>	6.4	6
<u>LikeUsingUiMiMI</u>	6.4	6
<u>Easy Learn MiMI</u>	6.3	7
<u>TimeWorthGain</u>	6.2	6
<u>Overall EaseUse</u>	6.1	6
<u>ClearlyOrganized</u>	6.1	6
<u>TrustRetrievedINfo</u>	6.1	6
<u>Easy Understand MiMI</u>	6	6
<u>Overall Satis</u>	6	6





ConceptGen ([tool](#))

ConceptGen ([tutorial](#))

Related gene lists to enriched concepts and other genes enriched for the given concept.



MetScape Plug in for Cytoscape ([tool](#))

MetScapei Plug in for Cytoscape ([tutorial](#))

Displays interactive networks of compounds, enzymes, reactions.



MiMI Plug in for Cytoscape ([via Cytoscape](#))

Mimi Plug in for Cytoscape ([tutorial](#))

Displays molecular networks in Cytoscape.



MiMI Web ([tool](#))

MiMI Web ([tutorial](#))



## 4. Aids for learning

Manuals

Tutorials

Flash demos

YouTube

Classes/HSL  
(Including UG)

Metab2MeSH\*\* ([tool](#))

Metab2MeSH ([tutorial](#))

Relates 1 metabolite to its enriched MeSH terms or 1 MeSH term to its metabolites, and retrieves associated articles



MiSearch ([tool](#))

MiSearch ([tutorial](#))

Ranks orders retrieved articles from PubMed based on a self- customized personal profile.



PubAnatomy([tool](#))

PubAnatomy ([tutorial](#))

Provides new ways to explore relation among anatomical structures, pathop processes, gene expression levels and protein interactions in the context of literature and experimental data.



PubOnto ([tool](#))

PubOnto ([tutorial](#))

MiMI-Cytoscape in Chinese part 1



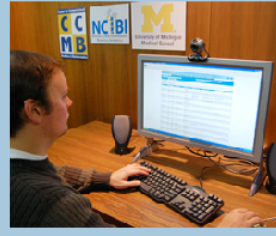
★★★★★ 1 ratings

# Exploratory exercise – articles supporting genes & schizophrenia

1-7 scale, 7 high	<b>PubAnatomy</b> N=15	<b>PubMed</b> N=14
Overall satisfaction (5, 6, 7)	10/15	10/14
Helped me think creatively (5, 6, 7)	10/15	8/14
Useful capabilities for exploration (5, 6, 7)	11/15	10/14
Found relevant items (6, 7)	8/15	6/14

# 5. Ease of access

Navigation	About NCIBI Tools
Home	<p>NCIBI provides the software architecture and tools to generate new knowledge about complex biomedical problems at a molecular and systems level. Diverse sources of experimental data, databases, published literature and text mining are integrated through various methods. Tools give scientists access to these data and help them gain novel conceptual relationships. In addition to the NCIBI tools, various database resources are also available upon investigator request.</p> <p>All NCIBI tools and resources are all free to the research community for internal use. Please read the <a href="#">General Terms of Use</a> for details. Individual tools may have additional use terms that are available on their website.</p> <h3>Getting Started</h3> <p><b>If you are unfamiliar with our tools:</b> We recommend starting with the "Try Our Tools" site.</p> <p>Here you will find NCIBI tools and resources organized into categories and information about how and when to use them. This site is intended to help you plan your work. The links on this site are intended to provide documentation. We encourage you to explore the tools with our help.</p> <p><b>Try Our Tools:</b> You can</p>
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Name	Resource Name:
PeptideAtlas	Peptide Atlas
X_Tandem	Description: Multi-organism, publicly accessible compendium of peptides identified in a large set of tandem mass spectrometry proteomics experiments, some published, many still unpublished. All results of sequence searching are processed through PeptideProphet to derive a probability of correct identification for all results in a uniform manner ensuring a high quality database. All peptides are mapped to Ensembl and can be viewed as custom tracks on the Ensembl genome browser.
ProteinIDatabase	Resource Type: <input type="checkbox"/> BRO (1 Item) BRO:Proteomics
	URL: <a href="http://www.peptideatlas.org">http://www.peptideatlas.org</a>
	Keywords: Proteomics, mass spectrometry, peptides, Ensembl, PeptideProphet, uniform re-analysis of raw data
	Organization: Institute for Systems Biology
	Center: NCIBI
	Contact Person: Eric Deutsch
	Contact Person Email: <a href="mailto:edeutsch@systemsbiology.org">edeutsch@systemsbiology.org</a>
	Contact Person Phone:
	Language:
	License Model: free, but registration required
	Platforms:

**Metab2MeSH\*\*** ([tool](#))  
**Metab2MeSH** ([tutorial](#))

Relates 1 metabolite to its enriched MeSH terms or 1 MeSH term to its metabolites, and retrieves associated articles



**MiSearch** ([tool](#))  
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Ranks orders retrieved articles from PubMed based on a self- customized personal profile.



**PubAnatomy**([tool](#))  
**PubAnatomy** ([tutorial](#))

Provides new ways to explore relationships among anatomical structures, pathophysiological processes, gene expression levels and protein-protein interactions in the context of Medline literature and experimental data.



**PubOnto** ([tool](#))  
**PubOnto** ([tutorial](#))

# Cross-discipline collaborations for integration

## Heuristic evaluations

Developers

HCI specialists

Database specialist

Health science librarian

UI developers

## Undergrad project

MCDB specialist

Neuroinformatics specialist

Usability/instruction specialist

Health science librarian

## Manuals & tutorials

Biomedicine experts

Documentation specialist

Program developers

Project manager

Graphic designers

NCI collaborator

UI developer

Health science librarian

Bioinformatics specialists

# Education, Outreach and Dissemination

**Jim Cavalcoli**