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SCIENCE CENTER



**Medical Imaging Informatics  
Bench to Bedside (mi2b2)**

*Christopher Herrick*

# Why are images important for clinical research?

## ■ Quantify disease burden

- Tumor growth
- Inflammation (lesions in multiple sclerosis, bony erosions of rheumatoid arthritis)
- Hemorrhage
- Infarction

## ■ Quantify the outcome of interventions

- Bone and tumor growth
- Brain loss

## ■ Guide the way to novel diagnostic approaches to disease

- Diffusion Tensor Imaging May Improve Diagnosis and Tracking of Mild Traumatic Brain Injuries

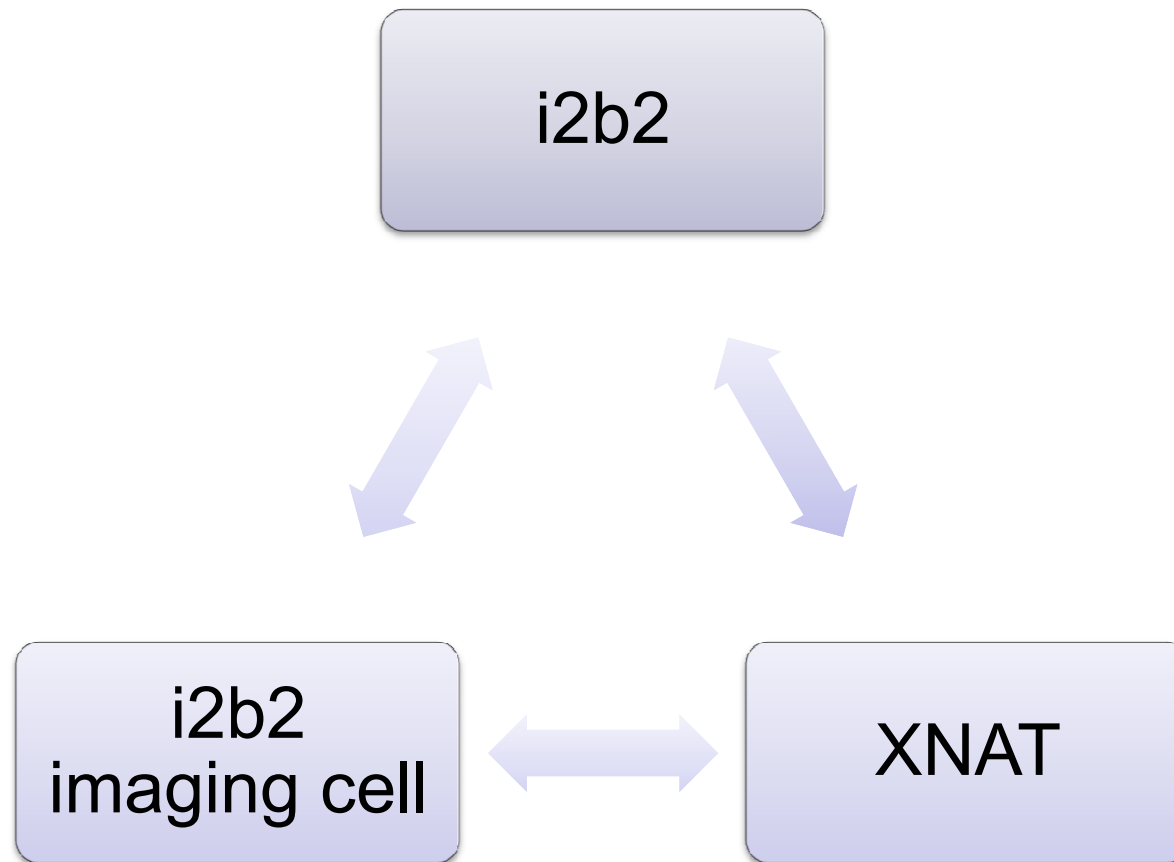


- Mayer, AR *et al.* "A Prospective Diffusion Tensor Imaging Study in Mild Traumatic Brain Injury." *Neurology*, February 23, 2010, Vol. 74, pp. 643-650.
- Bigler, ED and Bazarian, JJ. "Diffusion Tensor Imaging: A Biomarker for Mild Traumatic Brain Injury?" *Neurology*, February 23, 2010, Vol. 74, pp. 626-627.

# Medical Imaging Informatics Bench to Bedside (mi2b2)

- The purpose of this Administrative Supplement project is to develop and disseminate **additions to the Informatics for Integrating Biology and the Bedside (i2b2)-based projects to hospitals that will allow clinical imaging data from sophisticated medical imaging modalities such as MRI, PET, ultrasound and high-speed CT to be used for secondary research purposes.**

# How is mi2b2 structured?

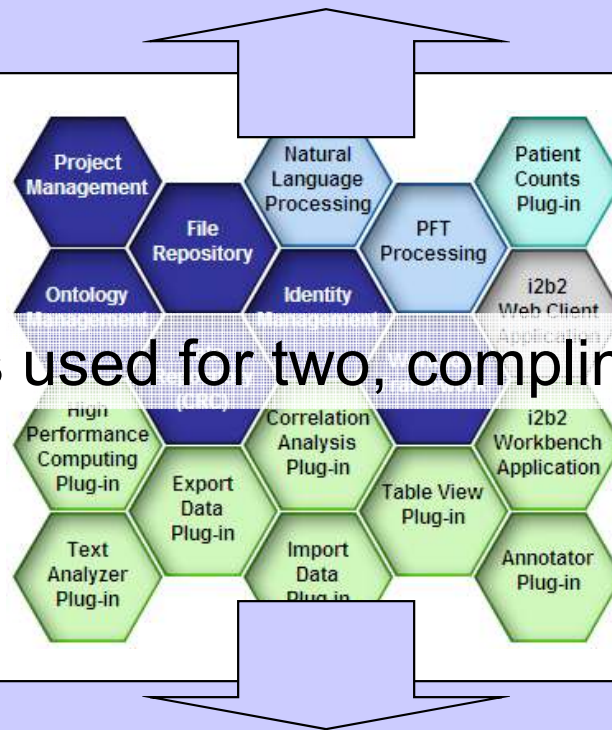


# What is i2b2?

- The National Center for Biomedical Computing entitled Informatics for Integrating Biology and the Bedside (i2b2)
- Software for explicitly organizing and transforming person-oriented clinical data to a way that is optimized for clinical genomics research
  - Allows integration of clinical data, trials data, and genotypic data
- A portable and extensible application framework
  - Software is built in a modular pattern that allows additions without disturbing core parts
  - Available as open source at <https://www.i2b2.org>

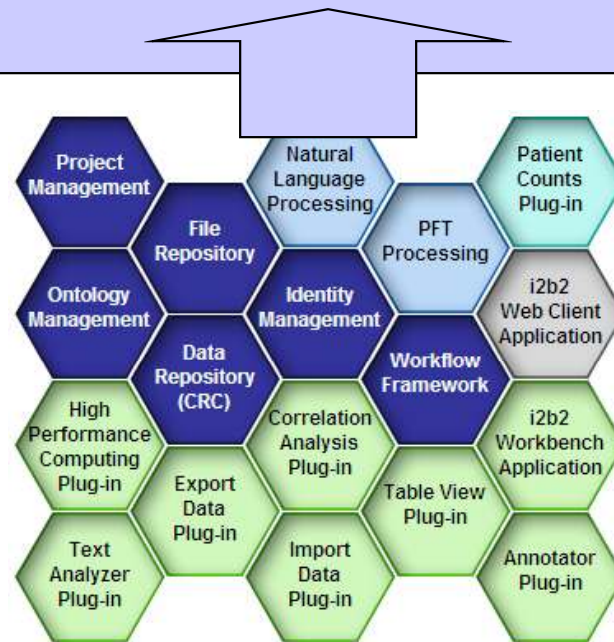
Enterprise-wide repurposing and distribution  
of medical record data for research

An i2b2 Hive is used for two, complimentary purposes



Use of medical record data in clinical studies  
focused upon genomics and pharmacology

## Enterprise-wide repurposing and distribution of medical record data for research



- Enable high performance collection of medical record data for querying and distribution
  - Enterprise web client

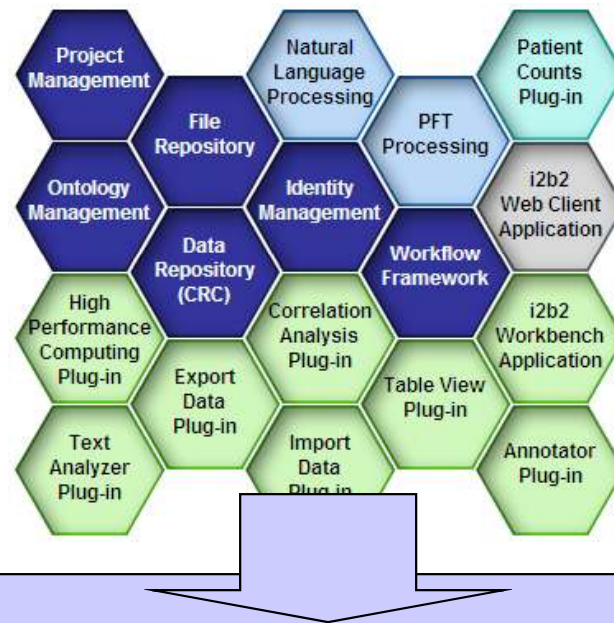
# Enterprise web client

The screenshot displays the i2b2 Query & Analysis Tool interface within a Windows Internet Explorer browser window. The interface is organized into several panels:

- Navigation Panel (Left):** A tree view under "Ontology" with categories like Demographics, Diagnoses, Laboratory Tests, Chemistry, Coagulation, Hematology, Immunology, Pulmonary Function Reports, Urinalysis, Medications, and Procedures. A yellow box prompts "drag an item from here".
- Query Tool (Center):** A "Query Name" field contains "45-54-Circu-Male@18:59:32". Below it are three groups for building a query:
  - Group 1:** Contains "45-54 years old" and "55-64 years old".
  - Group 2:** Contains "Circulatory system".
  - Group 3:** Contains "Male".Logical connectors are placed between groups: "one or more of these" (green) between Group 1 and Group 2, "AND" (blue) between Group 2 and Group 3, and "none of these" (red) for Group 3. Buttons at the bottom include "Run Query", "New Query", "3 Groups", and "New Group".
- Previous Queries (Bottom Left):** A list of recent queries with details like "45-54-Circu-Male@18:59:32 [2008-04-05] [d]".
- Query Status (Bottom Right):** Shows "Executing query...", "Elapsed time (seconds): 0.9", "Query Finished...", and "Matching patients: 5".

The browser's address bar shows "Internet" and the zoom level is set to 100%.

- Repurpose medical record information for research studies
  - I2b2 Workbench
  - Natural language processing



Use of medical record data in clinical studies focused upon genomics and pharmacology

# I2b2 Workbench carries hive activity into a detailed patient view for Investigator

The screenshot displays the 'Patient Recruitment Workbench' software interface. The main window is titled 'Patient Recruitment Workbench' and shows a detailed view for a patient named John Smith. The interface is divided into several panels:

- Concept Tree:** A hierarchical list of medical concepts on the left side, including Demographics, Diagnoses, and various organ systems like the Respiratory system.
- Group Selection:** Three panels at the top showing selected concepts for different groups. Group 1 includes 'Bronchodilator', Group 2 includes 'Prednisolone' and 'Prednisone', and Group 3 is empty.
- Query Results:** A central panel displaying a list of patients with columns for Patient ID, Age, Sex, Race, and various medical conditions. The patient John Smith is highlighted.
- Related Topics:** A panel on the right showing 'About Outline', 'Dynamic Help', and 'Patient Schedule' sections.
- Report Diagnosis (Detail Image):** A panel showing a detailed view of a patient's diagnosis, including a brain scan image.
- Flowchart:** A panel at the bottom showing a flowchart of the patient's medical history and treatment, including 'Deep Patient Object', 'Object of Interest', and 'Measured Disease or Condition'.

The interface also shows the user's name 'Shawn Murphy' and a 'Status' indicator. The bottom right corner features the 'ARVARD ATALYST' logo and the text 'THE HARVARD CLINICAL AND TRANSLATIONAL SCIENCE CENTER'.

# Data integration – Genotype / Phenotype

The image displays a screenshot of the i2b2 Workbench interface on the left and the Entrez Gene website on the right. The i2b2 Workbench shows a list of concepts under 'Ontology' and 'Expression Profiles Data', with a table of gene IDs and their corresponding metric values. The Entrez Gene page shows the details for TMEM208, including its official symbol, full name, primary source, and genomic regions. A diagram at the bottom of the Entrez Gene page shows the gene structure with exons and introns, and a legend for 'colicis region' and 'untranscribed region'.

**i2b2 Workbench for Demo Data**

Ontology

- Demographics
- Diagnoses
- Expression Profiles Data
  - Affymetrix\_HG-U133
    - 221591\_at (54478)
    - 221592\_at (11138)
    - 221593\_at (6160)
    - 221594\_at (9400)
    - 221595\_at (8400)
    - 221596\_s\_at (84060)
    - 221597\_s\_at (29100)
    - 221598\_s\_at (8442)
    - 221599\_at (28971)
    - 221600\_s\_at (28971)
    - 221601\_at (9214)
    - 221602\_s\_at (9214)
    - 221603\_at (9409)
    - 221604\_s\_at (9409)
    - 221605\_s\_at (51268)
    - 221606\_s\_at (79266)
    - 221607\_s\_at (71)
    - 221608\_at (---)
    - 221609\_s\_at (7475)
    - 221610\_at (55620)
    - 221611\_s\_at (51533)
    - 221612\_at (57408)
    - 221613\_s\_at (54469)
    - 221614\_at (9501)
    - 221615\_at (956)
    - 221616\_s\_at (5230)
    - 221617\_at (5230)
    - 221618\_at (51616)
    - 221619\_s\_at (23787)
    - 221620\_at (79125)
    - 221664\_s\_at (50848)
    - 221665\_s\_at (54869)
    - 221666\_s\_at (29108)
    - 221667\_at (26353)
    - 221668\_s\_at (64446)
    - 221669\_at (27034)
    - 221670\_s\_at (8022)
    - 221671\_at (28299)
    - 221672\_s\_at (83696)
    - 221673\_at (52944)
    - 221674\_s\_at (8646)
    - 221675\_s\_at (56994)
    - 221676\_s\_at (23603)
    - 221677\_at (29980)
    - 221678\_at (57406)

Concepts Selection

Search And Compare

Metric

TYPE 1 or TYPE 2

Threshold

Top

Calculation meth

Show

Y-axis Graph Option

- Show metric
- Negative red

Entrez Gene: TMEM208 transmembrane protein 208 [ Homo sapiens ] - Mozilla Firefox

http://www.ncbi.nlm.nih.gov/sites/entrez?db=gene&cmd=Retrieve&opt=full\_report&...&Google

Getting Started Latest Headlines

NCBI Entrez Gene

All Databases PubMed Nucleotide Protein Genome Structure PMC Taxonomy Books OMIM

Search: Gene for [ ] Go Clear

Limits Preview/Index History Clipboard Details

Display: Full Report Show: 20 Sort by: Relevance Send to

All: 1 Current Only: 1 Genes/Genomes: 1 SNP/GenView: 1

1: TMEM208 transmembrane protein 208 [ Homo sapiens ] updated 17-Mar-2008

GeneID: 29100

Summary

Official Symbol: TMEM208 provided by HGNC

Official Full Name: transmembrane protein 208 provided by HGNC

Primary source: HGNC:35015

See related: HPRD:13710

Gene type: protein coding

RefSeq status: Validated

Organism: Homo sapiens

Lineage: Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhina; Catarrhini; Hominoidea; Homo

Also known as: HSPC171

Genomic regions, transcripts, and products

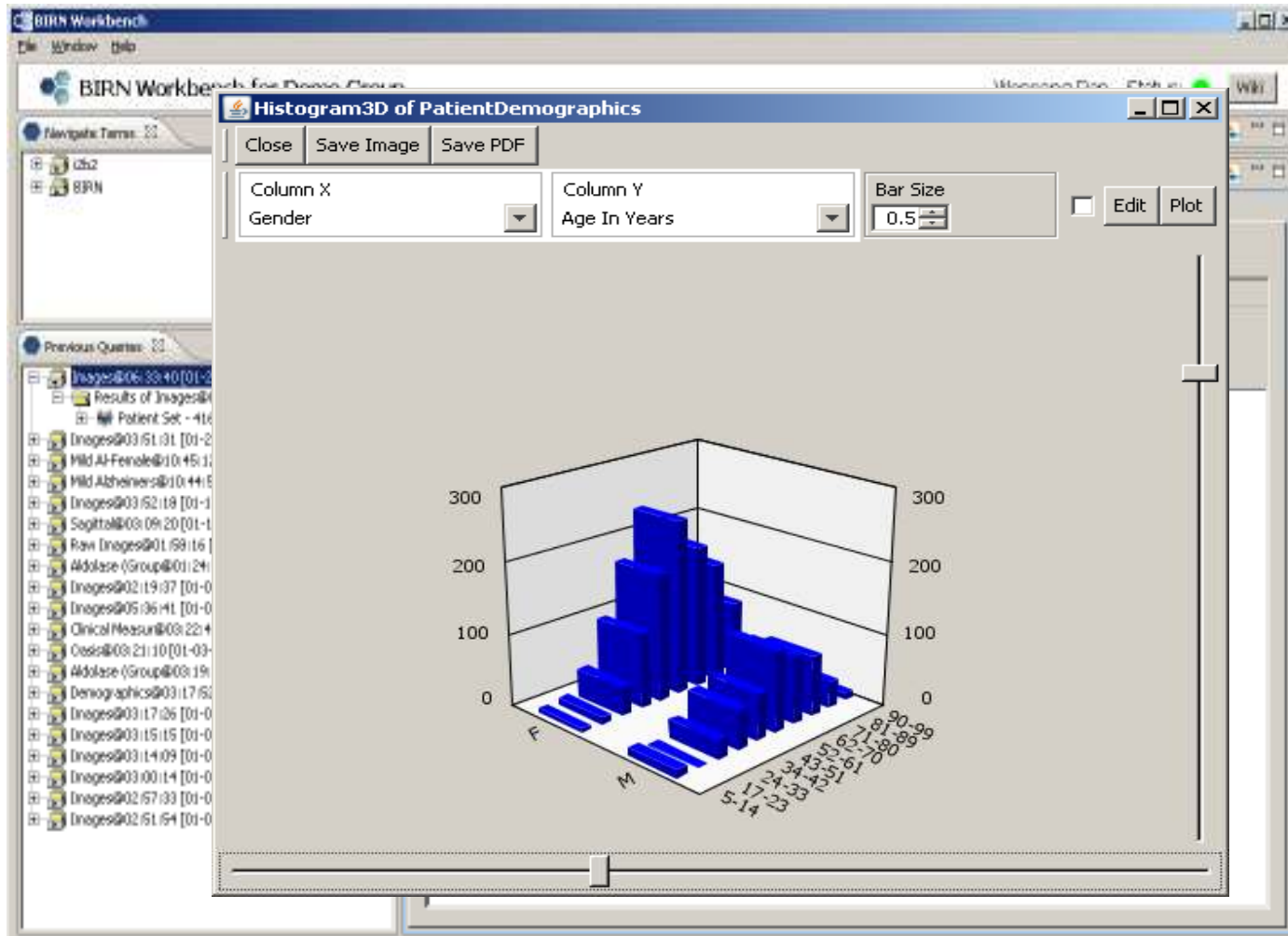
Go to reference sequence details View new Sequence Viewer

MC\_008016\_B

[5581952] 37 [6528400] 37

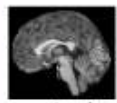
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# Integration of several data export and analysis tools in i2b2 Workbench



# What is XNAT?

- An open source *imaging informatics* platform.
- Core features:
  - DICOM workflow
  - Web interface
  - Extensible data model
  - RESTful web services API
  - Pipeline processing
- Built on various open source Java (Jakarta Turbine, Maven, Restlets, dcm4che) and Javascript (YUI) technologies.



- Projects
  - + Recent
  - + Favorite
  - My projects
  - Other projects
- + Stored Searches
- + Data

PROJECT: DIAN WU 011 > SUBJECT:0013211 > 0013211\_v00\_mr

## MR Session: 0013211\_v00\_mr

Details		Projects	
<b>Accession #</b>	CNDA_E02153	<b>Subject:</b>	0013211
<b>Date Added</b>	2009-09-11 14:08:04.0 (admin)	<b>Gender:</b>	Male
<b>Date:</b>	2009-09-09	<b>Handedness:</b>	Right
<b>Time:</b>	15:06:49	<b>Age:</b>	51.00
<b>Operator:</b>	SML		
<b>Scanner:</b>	CCIRWP-MR30A SIEMENS TrioTim		
<b>Acquisition Site:</b>	DIAN_011		

**Actions**

- Edit**
- View** ▶
- Upload** ▶
- Download** ▶
- Email**
- Build**
- Add Manual QC**
- Manage Files**
- Delete**

Notes:

### Scans

Scan	Type	Usability	Files	Note
+ 1	LOCALIZER	usable	Show Counts	
+ 2	MPRAGE	usable	Show Counts	
+ 3	MPRAGE NORM	usable	Show Counts	
+ 4	MPRAGE	usable	Show Counts	
+ 5	MPRAGE NORM	usable	Show Counts	
+ 6	FLAIR	usable	Show Counts	
+ 7	BOLD	usable	Show Counts	
+ 8	BOLD MOCO	usable	Show Counts	
+ 9	SWI magnitude	usable	Show Counts	
+ 10	SWI phase	usable	Show Counts	
+ 11	SWI minIP	usable	Show Counts	
+ 12	SWI	usable	Show Counts	

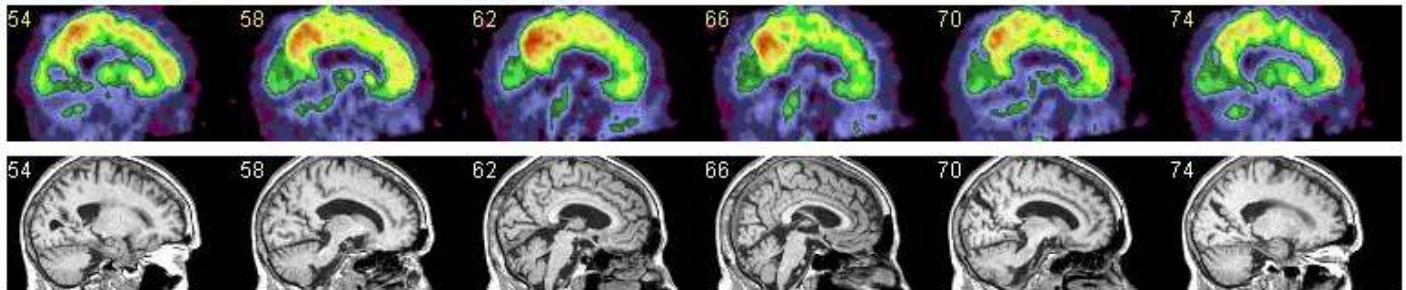
### + History

Add Rad Read

Region	Slope	Binding Pot.	Correl.
Anterior Cingulate	1.801	0.801	0.997368
Caudate	1.535	0.535	0.999370
Gyrus Rectus	1.623	0.623	0.998052
Occipital	1.662	0.662	0.998049
Parietal	2.101	1.101	0.998535
Precuneus	2.448	1.448	0.997597
Prefrontal	2.009	1.009	0.999468
Temporal	1.831	0.831	0.999144
White Matter	1.366	0.366	0.999290

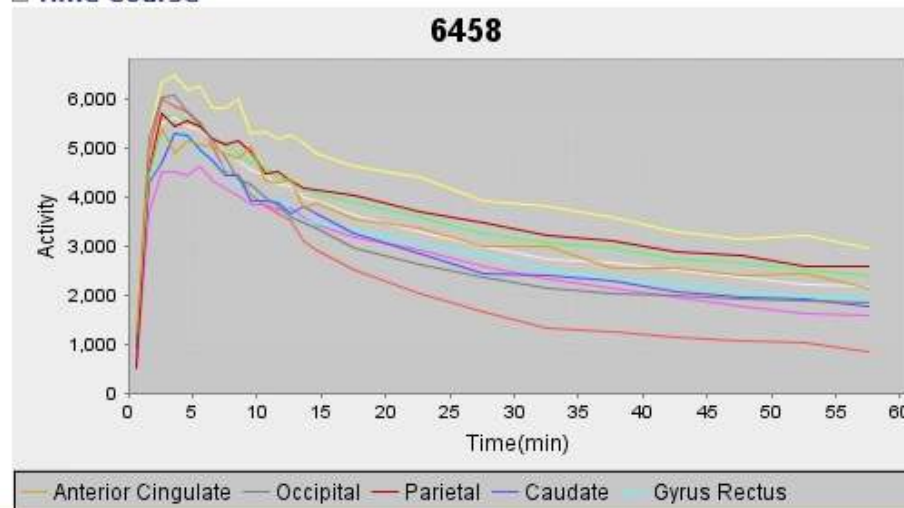
Quality Control Images

Show Overlay PET/MPRAGE Saggital + -

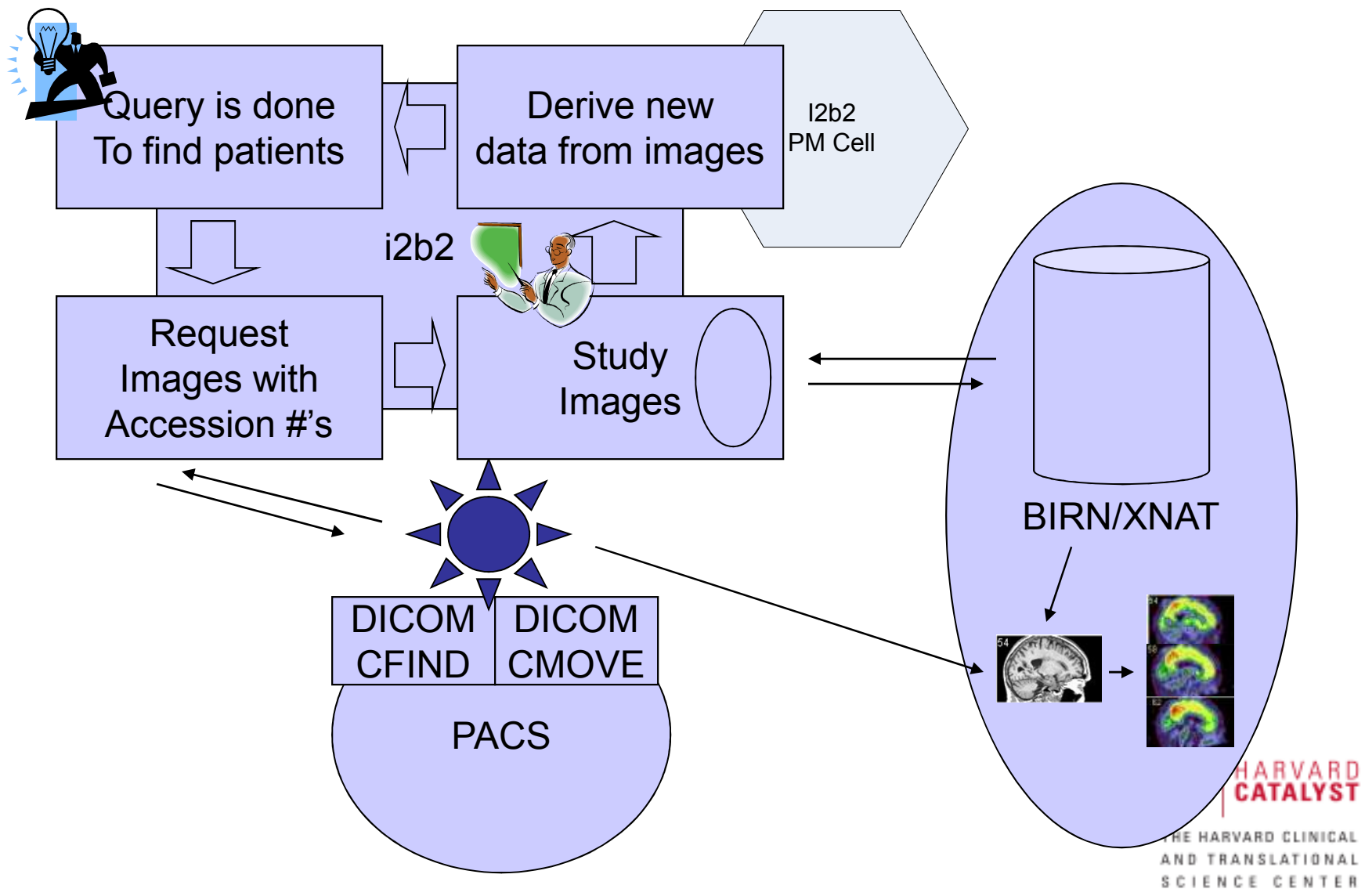


Quality Control

Time Course



# mi2b2 Server Side Architecture



# mi2b2 Client Interface – Enter Patients

The screenshot displays the mi2b2 Workbench interface. The top bar shows the project name 'User Name' and a 'Status' indicator. The left sidebar contains a 'Navigate Terms' tree with categories like Clinical Trials, Demographics (Age, Gender, Language, Marital Status, Race, Religion), and Previous Queries. The main window is split into two panes. The top pane, 'Search Patients', includes dropdowns for 'Select Site' and 'Select PACS', an 'Import Patient Set' button, and a text field for 'Enter Patient Medical Record Numbers'. The bottom pane, 'Formalize Patient Set', features a 'Show/Hide Patients' dropdown and a table of patient information.

Select	Row #	Patient Name	MSS	Found?	Age	Gender	Race	Date of Birth
<input checked="" type="checkbox"/>	1	XXXXX, XXXXX	XXXXXXXXXXXX	Y	74	F	black	
<input checked="" type="checkbox"/>	2	XXXXX, XXXXX	XXXXXXXXXXXX	Y	74	M	white	
<input checked="" type="checkbox"/>	3	XXXXX, XXXXX	XXXXXXXXXXXX	Y	52	F	asian	
<input type="checkbox"/>	4	XXXXX, XXXXX	XXXXXXXXXXXX	N	30	F	black	
<input checked="" type="checkbox"/>	5	XXXXX, XXXXX	XXXXXXXXXXXX	Y	61	F	hispanic	
<input checked="" type="checkbox"/>	6	XXXXX, XXXXX	XXXXXXXXXXXX	Y	52	M	black	
<input checked="" type="checkbox"/>	7	XXXXX, XXXXX	XXXXXXXXXXXX	Y	30	M	asian	
<input checked="" type="checkbox"/>	8	XXXXX, XXXXX	XXXXXXXXXXXX	Y	61	F	hispanic	
<input type="checkbox"/>	9	XXXXX, XXXXX	XXXXXXXXXXXX	N	10	F	hispanic	

# mi2b2 Client Interface – Select Studies

mi2b2 Workbench

Project Name: User Name

Status: ● Wiki

Navigation: Select Patients | Select Studies | Request Management | View Images

Query for Studies by Accession Number

Formalize Patient Set

Show/Hide Patients (Showing 100 out of 190)

Select Studies of Interest:

Select	Row #	Accession #	Site	Department	FOLMIF	# Series	Modalities	Study Date
<input checked="" type="checkbox"/>	1	1000000001	BRH	Oncology	Y	1	URI	05/16/1999
<input checked="" type="checkbox"/>	2	1000000002	MOH	Cardiology	Y	1	URI	09/05/2006
<input checked="" type="checkbox"/>	3	1000000003	BOHC	Oncology	Y	1	URI	12/06/2005
<input type="checkbox"/>	4	1000000004	NRH	Cardiology	N	1	PET	03/06/2010
<input checked="" type="checkbox"/>	5	1000000005	MOH	Oncology	Y	1	URI	06/01/2002
<input checked="" type="checkbox"/>	6	1000000006	MOH	Cardiology	Y	2	URI	11/11/2001
<input checked="" type="checkbox"/>	7	1000000007	BRH	Oncology	Y	1	URI	07/02/1996
<input checked="" type="checkbox"/>	8	1000000008	MOH	Cardiology	Y	1	URI	03/09/1995
<input checked="" type="checkbox"/>	9	1000000009	BRH	Oncology	Y	1	CT	09/10/2007
<input checked="" type="checkbox"/>	10	1000000010	BOHC	Cardiology	Y	8	CT	01/15/2001
<input type="checkbox"/>	11	1000000011	BOH	Oncology	N	2	CT	08/23/1998
<input type="checkbox"/>	12	1000000012	MOH	Cardiology	N	1	URI	07/01/1997
<input type="checkbox"/>	13	1000000013	MOH	Oncology	N	1	URI	08/27/1991
<input checked="" type="checkbox"/>	14	1000000014	BRH	Cardiology	Y	1	CT	01/20/2003
<input checked="" type="checkbox"/>	15	1000000005	BOHC	Oncology	Y	1	CT	11/11/2001
<input checked="" type="checkbox"/>	16	1000000006	BRH	Cardiology	Y	1	CT	07/02/1996
<input checked="" type="checkbox"/>	17	1000000005	MOH	Oncology	Y	1	CT	05/09/1995
<input checked="" type="checkbox"/>	18	1000000005	BOHC	Cardiology	Y	2	CT	09/12/2007

Data Forwarding

Data Destination:  INAT  Local drive

Request Selected Studies

# mi2b2 Client Interface – Check Requests

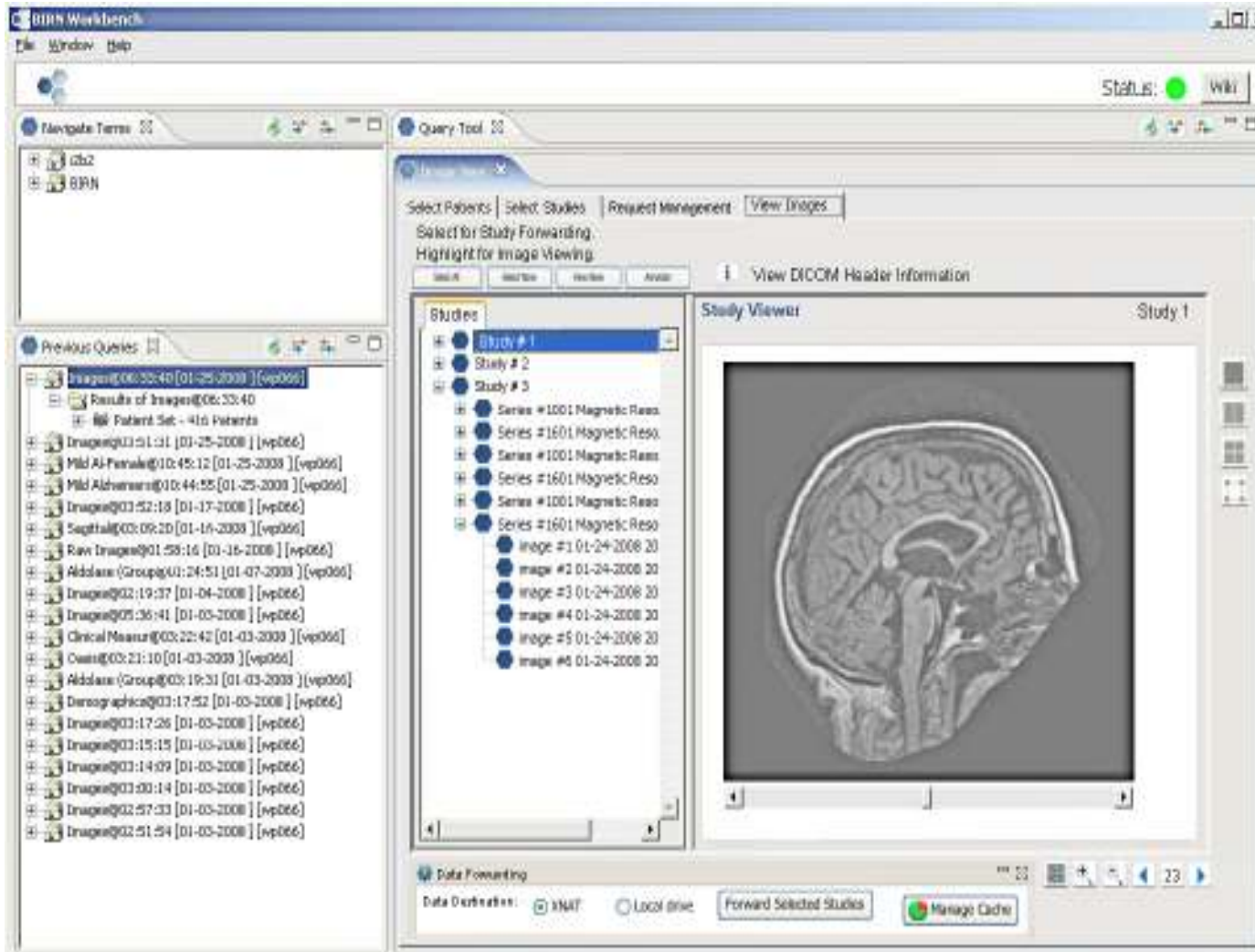
The screenshot displays the mi2b2 Workbench interface. On the left, there are panels for 'Navigate Terms' (showing a tree view of 'Clinical Trials' and 'Demographics') and 'Previous Queries' (listing various image and study sets). The main area is titled 'Image View' and contains a 'Request Management' tab. It shows a table of requests with columns for 'Select', 'Status', 'Priority', 'ID', 'Source', 'Destination', 'Request Date', and 'Full Date'. Request 11 is highlighted in blue. Below the table, there is a section for 'Information for Highlighted Requests' and a 'Data Forwarding' section with radio buttons for 'INAT' and 'Local drive', and a 'Forward Selected Studies' button.

Select	Status	Priority	ID	Source	Destination	Request Date	Full Date
<input checked="" type="checkbox"/>			011000	BWH Oncology	INAT	01/01/2010	01/05/2010
<input checked="" type="checkbox"/>			011003	BWH Cardiology	Cache	01/05/2010	01/16/2010
<input checked="" type="checkbox"/>			MM021	MGH Oncology	Local Drive	02/24/2010	03/05/2010
		1	MM040	MGH Cardiology	INAT	02/23/2010	Downloading
		2	44230	BWH Oncology	Cache	03/05/2010	Waiting
		3	01D100	BWH Cardiology	Local Drive	03/05/2010	Waiting
		4	01D101	BWH Oncology	INAT	03/03/2010	Waiting
		5	01D102	BWH Cardiology	Cache	05/01/2010	Waiting
		6	01D103	MGH Oncology	Local Drive	05/05/2010	Waiting
		7	01D104	MGH Cardiology	INAT	05/03/2010	Waiting
		8	01D105	BWH Oncology	Cache	05/15/2010	Waiting
		9	01D106	BWH Cardiology	Local Drive	05/28/2010	Waiting
		10	01D107	BWH Oncology	INAT	06/23/2010	Waiting
		11	01D108	BWH Cardiology	INAT	07/01/2010	Waiting
		12	01D109	MGH Oncology	Local Drive	07/05/2010	Waiting
		13	01D110	MGH Cardiology	Local Drive	08/05/2010	Waiting

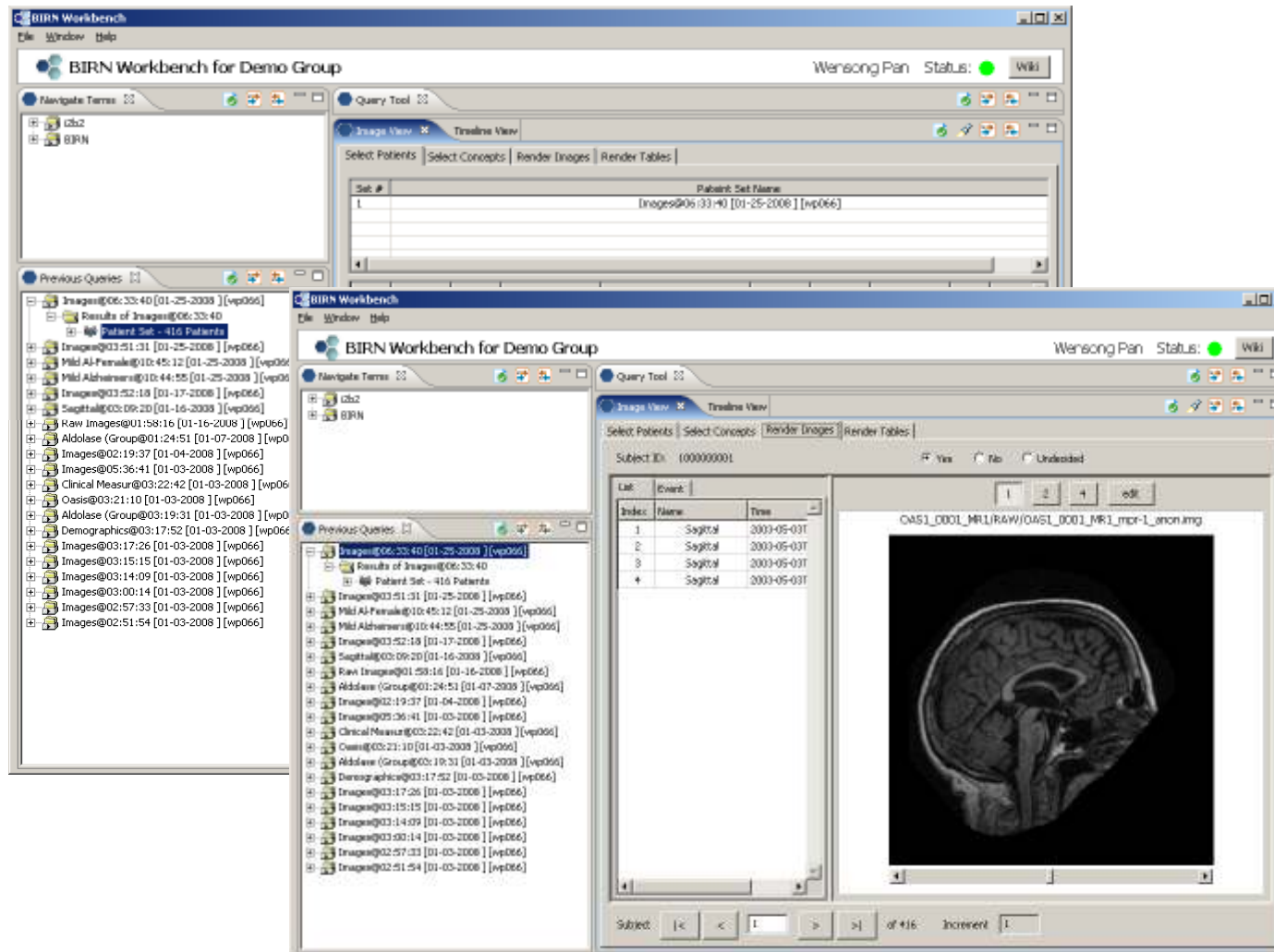
**Information for Highlighted Requests**  
Study 01D108 request is waiting to be processed.  
Will be stored in STAR ID cache.  
No additional data forwarding destinations specified.  
Data use audited by BWH cardiology for user username.

**Data Forwarding**  
Data Destination:  INAT  Local drive

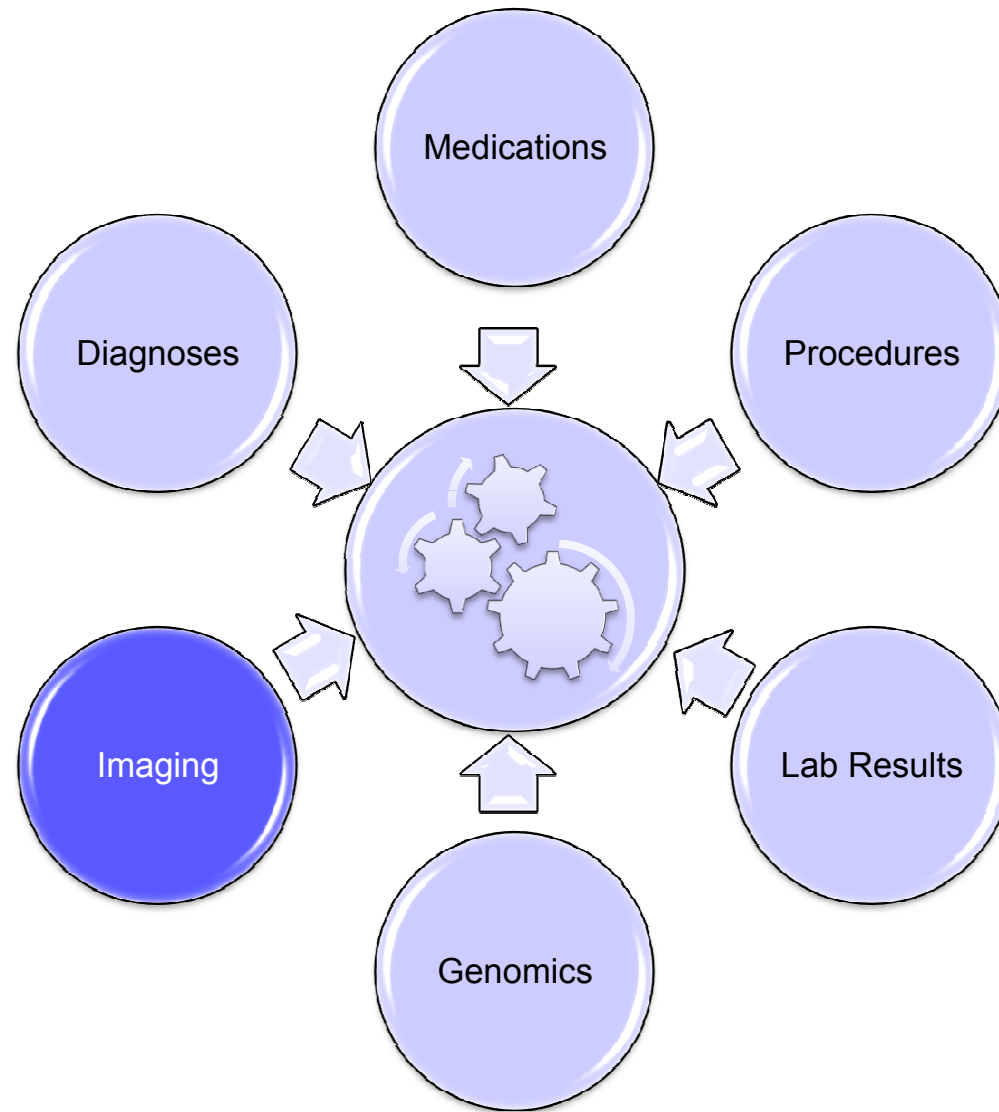
# mi2b2 Client Interface – Review Studies



# mi2b2 Client Interface – Annotating Images



# Enabling research and discovery



## mi2b2: Implementation

i2b2 & Catalyst leadership: Shawn Murphy & Randy Gollub

Project lead architect: Chris Herrick

Project lead scientist: Steve Pieper

Hospital Departments of Radiology IT leaders:

Ramin Khorasani / Kathy Andriole (BWH)

Keith Dreyer / Darren Sack (MGH)

Robert Lenkinski / Jesse Wei (BIDMC)

Daniel Nigrin / Richard Robertson / Bill Tellier /

Paul Lamonica (CHB)

Programmers: Yanbing Wang, Wensong Pan, Yong Gao

Dissemination: Valerie Humblet

XNAT team: Dan Marcus, Tim Olson

BIRN team: Carl Kesselman, Mike D'Arcy

Wiki page: Posting of all Meeting minutes, agendas, etc

[http://www.na-mic.org/Wiki/index.php/CTSC:ARRA\\_supplement](http://www.na-mic.org/Wiki/index.php/CTSC:ARRA_supplement)



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