i2b2 Software

Shawn Murphy MD, Ph.D.
Michael Mendis
Nich Wattanasin MS
Lori Phillips MS
Vivian Gainer MS
Rajesh Kuttan
Wensong Pan MS
Janice Donahue
Griffin Weber MD, Ph.D.
Susanne Churchill Ph.D.
Isaac Kohane MD, Ph.D.
The National Center for Biomedical Computing entitled Informatics for Integrating Biology and the Bedside (i2b2), what is it?

- 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](https://www.i2b2.org)
i2b2 Cell: The Canonical Software Module

- Business Logic
- Data Access
- Data Objects

HTTP XML
(minimum: RESTful)
An i2b2 Environment (the Hive) is built from i2b2 Cells

“Hive” of software services provided by i2b2 cells
I2b2 Software components are distributed as open source
Time align plug-in
Community

United States
- Arizona State University
- Beth Israel Deaconness Hospital, Boston, MA
- Boston University School of Medicine, Boston, MA
- Brigham and Women's Hospital, Boston, MA
- Case Western Reserve Hospital
- Children's Hospital, Boston, MA
- (Denver) Children's Hospital, Denver, CO
- Children's Hospital of Philadelphia, PA
- Children's National Medical Center (GWU)
- Cincinnati Children's Hospital, Cincinnati, OH
- Cleveland Clinic, Cleveland, OH
- (Weill Medical College of) Cornell, NYC, NY
- Duke Medical College
- Group Health Cooperative
- Harvard Pilgrim Healthcare
- Harvard Medical School, Boston, MA
- Health Sciences South Carolina
- Kaiser Permanente Health
- Kimmel Cancer Center (Thomas Jefferson University)
- Massachusetts General Hospital, Boston, MA
- Maine Medical Center, Portland, ME
- Marshfield Clinic, Wisconsin
- Morehouse School of Medicine, Atlanta, GA
- Ohio State University Medical Center, Columbus, OH
- Oregon Health & Science University, Portland, OR
- Renaissance Computing Institute, Chapel Hill, NC
- South Carolina Clinical and Translational Research Institute
- Tufts Medical Center, Boston, MA
- University of Alabama
- University of Arkansas Medical School
- University of California Davis, Davis, CA
- University of California San Francisco, SF, CA
- University of Chicago
- University of Massachusetts Medical School, Worcester, MA
- University of Michigan Medical Center, Ann Arbor, MI
- University of Pennsylvania School of Medicine, Philadelphia, PA
- University of Rochester Medical Center, Rochester, NY
- University of Texas Health Sciences Center at Houston, Houston, TX
- University of Texas Health Sciences Center at San Antonio, SA, TX
- University of Texas Health Sciences Center Southwestern, Dallas, TX
- Utah Health Science Center, Salt Lake City, UT
- University of Washington, Seattle, WA
- University of Wisconsin Madison
- Veterans Administration Boston and Utah

International
- Georges Pompidous Hospital, Paris, France
- Institute for Data Technology and Informatics (IDI), NTNU, Norway
- Karolinska Institute, Sweden
- University of Erlangen-Nuremberg, Germany
- University of Goettingen, Goettingen, Germany
- University of Pavia, Pavia, Italy
- University of Seoul, Seoul, Korea
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
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
Investigator Review
Data mart request form
Support of Driving Biology Projects (DBP’s)

EDR

Selected patients

Data directly from EDR
Data from other sources
Data collected specifically for project

Daily Automated Queries search for Patients and add Data

Project Specific Phenotypic Data
Data Model: Data Requirements

- **Integration** of data from distributed and differently structured databases in order to perform comprehensive analyses.

- **Separation** of data used for research from daily operational or transactional data.

- **Standardization** of a model across systems.

- **Ease** of use by end-users.
Dimensional Modeling

1. **FACTS** - the quantitative or factual data being queried.

2. **DIMENSIONS** – groups of hierarchies and descriptors that define the facts.
Star Schema

One fact table surrounded radially by numerous dimension tables.
i2b2 Star Schema

**patient_dimension**

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In i2b2, a fact is an observation on a patient.

Examples of FACTS:

- Diagnoses
- Procedures
- Health History
- Genetic Data
- Lab Data
- Provider Data
- Demographics Data

An observation is not necessarily the same thing as an event.
i2b2 Dimension Tables

- Dimension tables contain descriptive information about facts.

- In i2b2 there are five dimension tables

  concept_dimension
  provider_dimension
  visit_dimension
  patient_dimension
  modifier_dimension
## Expression of Modifiers in i2b2 data model

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</tbody>
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Modifiers in UI
Modifiers in UI
Modifiers in UI
Modifiers in UI
Modifiers in UI
Modifiers in UI
Modifiers in UI
Modifiers in UI

The image shows a software interface for a query and analysis tool. The interface includes a search bar for terms and a section for finding terms. It also displays groups of terms with criteria such as 'Doses Occurs > 0x', 'Items Instance will be the same', and 'Medication Route = (By Mouth)'. The interface also shows the query status with a finished query and the number of patients resulting from the query.
Modifiers in UI
Modifiers in UI
Constrain observations into the same encounter
FUTURE - UI for temporal query model
I2b2 Version 1.6

- Terms can be Modified and Linked in i2b2 data model
- Ontology editor
- All dimensions can be used in queries as well as Patient Sets and Previous Queries
- Queries find patients that have concepts that occur in the Same Visit and the Same Instance
- Performance enhancements and monitoring
Version 1.7 IM Cell – Needed to get identified data

Main functions

- Converts MRNs to eMRNs which are mapped in CRC cell
- Holds demographics in tables which do not contain clinical data
- Links to enterprise services and converts custom enterprise output to i2b2 PDO
- Lists of patients with real identifiers are managed and linked to a project
Future of i2b2 is through Related and Sponsored Projects …
Crimson

Enabling Sample Management Within i2b2
Pt: Dr. Lynn Bry (LBRY@partners.org)

Synopsis

The i2b2 - Crimson project is designed to provide enhanced sample handling capabilities within the i2b2 framework. Its primary focus is to support both prospective and retrospective sample collection. These modes of collection are dictated by the external systems that are employed to satisfy an i2b2 users query; for prospective sample accrual, requests are typically routed to an external laboratory information management system, for retrospective enquiries, these are usually directed towards an existing sample repository or registry.

The sample collection process has three distinct phases:

- **Sample Request**: A patient set is broadcast to either a LIMS or existing sample repository. Typically the medical record number (encrypted) will be broadcast to the external system. However, alternative patient identifiers can also be supported.
Health Ontology Mapper (HOM)

(The Health Ontology Mapper is an open source general purpose instance mapper for academic research, public hospitals and non-profits.)

Principal Investigators: Rob Wynden (UCSF), Russ Cucina (UCSF) and Nick Anderson (UW)
Ontology Mapper Original Design: Rob Wynden (UCSF), Davena Gabriel (UCD), Marco Casale (Rochester) and Maggie Massary (UPenn)

Lead Terminologist: Ketty Mobed (UCSF)

HOM Interpreter Programming Lead: Prakash Lakshminarayanan (UCSF)
UETL Programming Lead: Vijay Rayankar (UCSF)

License: Open Source BSD License HOM BSD (For an optional commercial license contact: Ellen Kats at UCSF Tech Transfer). If you would like to purchase a Support License for Ontology Mapper please contact Peter Emerson at Recombinant Data Corp at pemerson@recomdata.com.

Genomic Controlled Vocabularies

i2B2 Ontologies

The following controlled vocabularies are provided as i2b2 ontologies.

<table>
<thead>
<tr>
<th>Ontology</th>
<th>Description</th>
<th>Sources</th>
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<td>Genes categorized by locus</td>
<td>Hugo</td>
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<td>Pharmacogenomics</td>
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<td>Hugo, PharmGKB, Mesh, ATC</td>
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HOMERUN

The Hospital Medicine Reengineering Network. HOMERUN is a network of institutions with hospitalists and patients with the primary aim of developing research and implementation studies to reengineer and optimize care delivery. The network includes organizational governance, data sharing infrastructure, and a variety of tools that support clinical research, including therapeutic trials and comparative effectiveness research. HOMERUN currently includes 14 university and community based institutions - where the majority of hospital care is delivered in America. It draws on the experience of the Vermont-Oxford Neonatal Network and National Surgical Quality Improvement Projects (among others). Its infrastructure is built with open-source technologies created by the National Institutes of Health and others that enable secure cross-institutional data sharing that protects the privacy of patient data, tracks patient consent, and enables patient control of their health information.

Each of the current sites uses i2b2 and SHRINE to develop Comparative Effectiveness Research data discovery resources. The project evolved out of the i2b2 Cross-Institutional Clinical Translational Research project (CICTR) - a SHRINE-based federation of UC Davis, UC San Francisco and the University of Washington. The HOMERUN technical collaboration focuses on the policy, data acquisition and mapping processes, and is moving towards harmonizing necessary version-level implementation for local sites. HOMERUN uses the HOM mapper for concept translation.

Current partners (* indicate live data sites)

- UCSF * (Rob Wynden)
- UC Davis *
- UW * (Nick Anderson)
- U Michigan *
- UC Irvine

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I2b2-based Registries

This is the home of the Related Project - i2b2-based Registries space.

The Cincinnati Children’s Hospital Medical Center (CCHMC) i2b2 team has extended i2b2 to create an enhanced patient registry and an associated web-based toolkit. It provides the necessary functionality in a modular fashion, allowing users to choose the capabilities that are appropriate for their project. The enhanced registry architecture includes linkage to the EHR and an application layer that allows the development of functionality to support quality improvement and comparative effectiveness research. There are capabilities for data collection to capture information that is not collected in an EHR, as well as mechanisms for reporting and visualization.

More information can be found on the CCHMC I2b2 project site: http://i2b2.cchmc.org

To help you on your way, we’ve inserted some of our favourite macros on this home page. As you start creating pages, blogging and commenting you’ll see the macros below fill up with all the activity in your space.

Recently Updated

- Home updated by Kern (view change) Jan 03
- Related Project - I2b2-based Registries updated by Kern (view change) Nov 24
- Home updated by Kern (view change) Oct 22
Shared Health Research Information Network (SHRINE)

The Shared Health Research Information Network (SHRINE) helps researchers overcome one of the greatest problems in population-based research. Compiling large groups of well-characterized patients. Qualified investigators may use the SHRINE web-based query tool to determine the aggregate total number of patients at participating hospitals who meet a given set of inclusion and exclusion criteria (currently demographics, diagnoses, medications, and selected laboratory values). Because counts are aggregate, patient privacy is protected.

These data will be most useful for investigators interested in:

- Generating new research hypotheses
- Planning research requiring large sample sizes not easily available at any single institution
- Preparing grant applications that would benefit from pre-identification and/or characterization of a potential research cohort
- Identifying potential cohorts for clinical trials
- Conducting research in the areas of population health and health services

Participating Institutions

- Beth Israel Deaconess Medical Center
- Brigham and Women’s Hospital
- Children’s Hospital Boston
- Dana-Farber Cancer Institute
- Massachusetts General Hospital
Medical Imaging Informatics Bench to Bedside (mi2b2)

Many current and future clinical research studies rely on medical images for quantitative metrics for diagnosis, prognosis and treatment response. Images are used to quantify disease burden such as tumor volume, inflammation, hemorrhage, and infarction. Serial imaging is used to quantify the outcome of interventions, such as changes in tumor size or loss of brain tissue. Importantly, medical images are providing an ever increasing number of sensitive diagnostic approaches to disease, such as the use of susceptibility weighted and diffusion tensor MR imaging in the evaluation of brain trauma.

Here we describe a call within the i2b2 team that allows clinical images to be retrieved from a hospital's clinical Picture Archiving and Communication System.
Research Investigator Workflow enabled by mi2b2

- Query is done to find patients
- Derive new data from images
- Request images with accession #s
- Study images

mi2b2

DICOM CFIND
DICOM CMOVE

PACS

BIRN/XNAT
**i2b2 - SMArt Project**

As part of the Strategic Health IT Advanced Research Projects (SHARP) program and the Substitutable Medical Apps Reusable Technologies (SMArt) initiative, a SMArt-enabled i2b2 cell is being developed to expose a common API for SMArt-applications to interact with health data within the i2b2 analytics platform.

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**SMArt Platform Instance**
“SMART Enabling” i2b2

CRC
ONT
PM
mapper
SMART

SMART APP
SMART APP
SMART APP
SMART Container in i2b2
SNP Terminology development with VISTA

Designing a genomic variant ontology for common use within the open i2b2 community poses a unique challenge. Variants may be defined across several domains: dbSNP rs number, HGVS name, or gene/flanking sequence pairs. It is often difficult to know if variants from different domains are in fact equivalent. This project investigates ways to form a common basis for describing variants.

The project also examines necessary features required for display and comparison of genomic variants within external tools. An application has been developed to show interactive capability within the VISTA suite of visual analysis and functional annotation tools.

Paper and Presentations

Use of Genomic Variants in i2b2 - Lori C. Phillips MS1, Simon Minovitsky2, Igor Ratnere2, Inna Dubchak

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Copyright Info
RS number

- Uniquely identifies a variant over time … but …

- Novel variants may not have rs number
  - User may not want to submit to dbSNP
HGVS Name

- Uniquely identifies variant within a referenced and versioned accession and details the nucleotide substitution.

NM_005228.3:c.2155G>T

- RefSeq accession
- Position
- Nucleotide substitution
- Coding DNA
Common Representation

- All ultimately describe variant location on a chromosome.
- Nucleotide substitution defines the physical manifestation of the variant.

WE PROPOSE:

- HGVS name (n/t subst, positional info)
- Flanking sequences (a way to verify positional info)

AS A WAY TO UNEQUIVOCALLY EQUATE TWO VARIANTS
- ACROSS DOMAINS
- ACROSS VERSIONS
Combining equivalent terms
SMART Container in i2b2
i2b2 Sponsored Project - NCBO Ontology Tools

The i2b2 Hie software is composed of core modules called 'cells' that create a system to allow the use of patient data for research. These cells communicate through web services and use i2b2 standard XML messages to transfer ontology-related metadata. To date, a subset of ICD-9 has been provided with the i2b2 demo software package. There has been a need in the community for access to a complete ICD-9 ontology as well as other clinical-based ontologies.

NCBO hosts a repository of biomedical ontologies. These ontologies are stored in formats that are not understood by i2b2. A tool has been developed to not only extract these ontologies via bioportal REST services, but to transform them into a format that is understood by the i2b2 ONT cell.

Tutorials

i2b2 Ontology Tutorial.pdf - Follow along for a step by step example of how metadata trees are created.
1) make i2b2 formatted ontologies with NCBO Services

- Pull data from NCBO via REST services.
- Reorganize information into format used by i2b2 Ontology cell

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<td>DATE</td>
<td>DATETIME</td>
</tr>
<tr>
<td>SOURCESYSTEM_CD</td>
<td>VARCHAR2(50)</td>
<td>VARCHAR(50)</td>
</tr>
<tr>
<td>VALUETYPE_CD</td>
<td>VARCHAR2(50)</td>
<td>VARCHAR(50)</td>
</tr>
</tbody>
</table>
2) Providing mappings using NCBO services

Mapping cell
- Need for mapping different site-specific ontologies in cross-institutional settings. (SNOMED_CT ↔ ICD-9, RxNORM ↔ NDC)
- First look for locally mapped data
- Then seek mappings through NCBO services.

http://bioportal.bioontology.org/mappings/service/1101/

Request to map local code
ICD9 → SNOMED_CT

Mapper Cell

Locally Mapped data

NCBO REST XML
3) Integrating two i2b2 ontologies with NCBO services

- Integrate ICD-9 into SNOMED
  - For each SNOMED term, find a mapped ICD9 term:

  Request to integrate
  ICD9 into SNOMED_CT
  Integration Workflow
  Add new terms with SNOMED hierarchy, ICD9 name, basecode
  SNOMED with ICD9 Data
  Mapper Cell
  NCBO REST XML
Sponsored Project Development Process
Tools for Community

Shared Wiki Documentation
http://community.i2b2.org/wiki

JIRA Bug Tracking
http://community.i2b2.org/jira

Source Code Subversion Repository
http://svn.i2b2.org/svn/i2b2/trunk

Web site for i2b2 distribution and documentation
https://www.i2b2.org/software
Wiki

Community News
Sponsored Projects
Related Projects
Upcoming Releases
Development Status
Main Branch

Programmer Working

Programmer Gets copy of Code

New Code is Merged

Programmer Checks out Code

Programmer Checks in Code

QA

All other programmers are blocked

Programmer Gets copy of Code
Working on a sponsored project

1. Review the current spreadsheet
2. Select an item you want to work on.
3. Log into JIRA which is http://community.i2b2.org/jira
4. Enter an issue for the bug you are going to fix.
5. Assign the issue to yourself.
6. Keep JIRA updated throughout the development process.
7. Once you are finished the final step is to update the issue in JIRA.
The i2b2 Web Client is a collection of client-side components designed as an YUI AJAX-based plug-ins that communicate with i2b2 Cells and allow the investigator to query and display the data of the hive.
Access sponsored code via SVN
Jira Bug Tracker
Webclient Sponsored Project

New features:

- Performance Report
- Online Help
- Patient Breakdown
- Printing
- Cancel Query
- Query Status
- Patient Count
Patient Breakdown
Online Help

I2B2 WEB CLIENT HELP

I2B2 FIND TERMS VIEW
The Find Terms view is designed to allow users to search for concepts. Users can search by the name or by a particular code. Once the appropriate concept is found it can be used in many of the I2B2 views and plug-ins, such as the Query Tool view and Timeline plug-in.

Introduction
This section describes the layout and contents of this view.

Layout of the Find Terms View
The Find Terms view allows users to search for a concept or group of concepts. There are basically two methods of searching available: (1) by name and (2) by code.
Other Changes
https://www.i2b2.org/software

Shawn Murphy MD, Ph.D.
Michael Mendis
Nich Wattanasin MS
Lori Phillips MS
Vivian Gainer MS
Rajesh Kuttan
Wensong Pan MS
Janice Donahue
Griffin Weber MD, Ph.D.
Susanne Churchill Ph.D.
Isaac Kohane MD, Ph.D.