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Edited by Indra Neil Sarkar

Provides foundational background of key methodological principles in biomedical informatics and their specific applications in biology, medicine and public health.

October 2013
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Welcome

2014 Joint Summits on Translational Science

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Intermountain Healthcare
On behalf of the American Medical Informatics Association (AMIA), we are pleased to welcome you to the 2014 Joint Summits on Translational Science!

The Joint Summits on Translational Science consist of the Summit on Translational Bioinformatics (TBI) on April 7-9 followed by the Summit on Clinical Research Informatics (CRI) on April 9-11. As in years past, the “bridge day” on April 9 focuses on topics of interest to both communities.

The TBI and CRI Summits are the premier forums for interacting with leaders in informatics at the interface of biology and health care. Translational bioinformatics and clinical research informatics are the informatics domains that support translational research in the context of human health and disease, and touch nearly all areas of biological, biomedical, and clinical research. Translational bioinformatics includes innovative methods and discoveries applied to biologic data, with special focus on human application, including personalized medicine. Clinical research informatics focuses on innovations related to the management of information related to clinical trials and includes informatics related to secondary research use of clinical data.

The Joint Summits on Translational Science serve as the primary forum for exchange of ideas, issues, and science in translational bioinformatics and clinical research informatics. The TBI and CRI Scientific Program Committees designed a comprehensive scientific program that will emphasize the aspects of each Summit that distinguish this meeting from others in the informatics community.

The Joint Summits on Translational Science showcase the significant growth and rapidly changing landscape of translational bioinformatics and clinical research informatics.

Our program offers a wide variety of exciting and informative panels, as well as provides a venue for scientists and professionals to accomplish various goals, including professional networking, establishing new collaborations, and seeing the latest developments in research informatics from academia, industry and government. We also planned some novel additions to the program, both to facilitate the dissemination of ideas among established researchers, and to train the next generation of informatics scholars.

We recognize the pressure researchers face to reserve one’s best work for submission to journal publications. We also recognize the value, both to the investigator and to the scientific community, in sharing one’s most exciting work as early as possible. We therefore accepted submissions of proposals that reflect the strongest and most promising innovations from the clinical research informatics and the translational bioinformatics communities in the form of abstract presentations or short papers which can subsequently be extended for follow-up publication in a peer-reviewed journal. New for this year, there is one abstract format. The best abstracts were awarded podium presentations, while others are featured in the poster presentations. We showcase panel presentations, pre-meeting tutorials, and a student paper competition, also new for this year.
AMIA KNOWLEDGE CENTER

The AMIA Knowledge Center is an informatics-specific collection of enduring content designed specifically for members.

**PROCEEDINGS**
The AMIA Knowledge Center is an archive of conference proceedings published by AMIA for activities including:

- Annual Symposium
- Summit on Translational Bioinformatics
- Summit on Clinical Research Informatics
- iHealth
- NI2012
- Annual Policy Conferences

Proceedings volumes include papers, posters, panels and other types of peer-reviewed, state-of-the-art scientific and technical work published by AMIA as a volume at the time of the conference. The Proceedings also includes a PDF of the conference on-site program when available.

**PRESENTATIONS**
The Knowledge Center is a gateway to conference multimedia including presentation slides, posters, and (when available) video and audio.

**WEBINARS**
The Knowledge Center also includes a collection of webinars produced by AMIA and its Working Groups.

**ONC HEALTH IT WORKFORCE CURRICULUM**
Open to members and non-members
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General Information

Attendance Policy at Scientific Sessions
All attendees must be registered and wear their name badges at all times.

Summit on Translational Bioinformatics and Summit on Clinical Research Informatics Proceedings
AMIA provides a dynamic online archive of Proceedings. The Proceedings are fully searchable by title, author, and full text terms. AMIA members and 2014 TBI/CRI registrants have free access to the archives. To access the AMIA Proceedings archive, simply point your browser to http://knowledge.amia.org. Use your AMIA login and password to access the 2014 volume. You can also access the site on web-enabled mobile devices.

Presenter Slides on knowledge.amia.org
Knowledge.amia.org is the new archival home for proceedings, presentations and webinars associated with AMIA meetings and educational programs. TBI and CRI proceedings and slides submitted by participating authors are available to all AMIA members and attendees of the Symposium. Images of posters submitted by participating authors will also be posted. Search by author last name or presentation title.

Please note, that posting slide presentation and poster images is voluntary for authors. If a slide presentation is not listed, the author has chosen not to post his or her proprietary information publicly at this time. Content from participating authors should be available after the meeting.

No Smoking Policy
Smoking is not permitted inside the hotel.

Responsible Drinking Policy
Alcohol will be available at some receptions. Please exercise a responsible drinking policy. Your cooperation will help keep events pleasant and enjoyable for everyone.

Safety First
We want you to have a safe and enjoyable time visiting San Francisco. Please observe the caution appropriate for any major urban area. Don’t forget to remove your name badge before leaving the hotel. The badge clearly identifies you as a tourist in unfamiliar surroundings.

ADA Statement
Special Needs: In accordance with the Americans with Disabilities Act, AMIA seeks to make this live activity accessible to all. If you have a disability which requires special accommodation, please email Dasha Cohen, Director of Meetings, at dasha@amia.org.

Mobile App
The MyItinerary app is available as both a native iOS (iPhone/iPad) app through the iTunes App Store, or as an HTML5 Web app for all major mobile devices (iPhone/iPad, Android, Blackberry 7 and above). Once either version is downloaded to your device, it can be run without the need for an active Internet connection. In addition, you can sync an itinerary that you created online with the app by entering your unique itinerary name.

MyItinerary Mobile App
For optimal use, we recommend: iPhone 3GS, iPod touch (3rd generation+), iPad iOS 4.0 or later. You can download the MyItinerary app by searching for “ScholarOne” in the App Store directly from your mobile device. Alternatively, you can access the link below or scan the QR code to access the iTunes page for the app.

Once the MyItinerary app is downloaded, select the meeting ‘Joint Summits on Translational Science.’

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For optimal use, we recommend: iPhone 3GS, iPod touch (3rd generation+), iPad iOS 4.0 or later. Most mobile devices using Android 2.2 or later with the default browser, Blackberry Torch or later device using Blackberry OS 7.0 with the default browser.

Download the MyItinerary app by accessing the link below or scanning the QR code:

Once downloaded, you can bookmark the site to access it later or add a link to your home screen.

WIFI Connection
Turn on your device’s wireless connections to view available Wi-Fi networks. Choose and connect to “Parc55meeting” network.

Please do not be a bandwidth bully. Users will be cycled off the network to allow others to connect!
# Summits-at-a-Glance

## Monday, April 7

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* T01: Leveraging Public Consortia for Translational Research: An Introduction to ENCODE, Roadmap Epigenomics, and 1000 Genomes Data  
* T02: CDISC Standards in Clinical Research Informatics  
* T03: Enhancing Participant Recruitment to Clinical Trials: Informatics Strategies and Future Directions  | Mission I  
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Stockton |
| 10:00 a.m. – 10:30 a.m. | Coffee Break                                                                                                                      | Cyril Magnin Foyer |
| 1:30 p.m. – 3:00 p.m.  | TBI Opening Plenary Session and Keynote Address: Robert Plenge, MD, PhD                                                         | Cyril Magnin I/II |
| 3:00 p.m. – 3:30 p.m.  | Coffee Break                                                                                                                      | Cyril Magnin Foyer |
| 3:30 p.m. – 5:00 p.m.  | Scientific Sessions  
* TBI01: Panel - Dissemination of Pharmacogenomic Knowledge: Establishing a Pathway to Support Clinical Implementation  
* TBI02: Papers/Podium Presentations - Using Omics for Discovery  
* TBI03: Podium Presentations - Tools to Enhance Understanding and Analysis of Omic Data  
* TBI04: Late Breaking Abstracts - Drugs, RNA, and High-dimensional Data  | Cyril Magnin I  
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Mission |
| 5:00 p.m. – 6:00 p.m.  | Networking Reception                                                                                                              | Cyril Magnin Foyer |
| 6:00 p.m. – 7:00 p.m.  | Genomics Working Group Meeting                                                                                                      | Davidson |
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<td><strong>CRI11</strong>: Papers/Podium Presentations - Researcher Needs</td>
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<td><strong>CRI12</strong>: Late Breaking Abstracts - NLP and Novel Methods for Analyzing Clinical Data</td>
<td>Mission</td>
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<tr>
<td>12:15 p.m. – 1:15 p.m.</td>
<td>Lunch and Learn - <em>with ConvergeHEALTH by Deloitte</em></td>
<td>Cyril Magnin III</td>
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<tr>
<td>1:30 p.m. – 3:00 p.m.</td>
<td>Scientific Sessions</td>
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<td><strong>CRI13</strong>: Podium Presentations - Use of Electronic Health Records for Research</td>
<td>Cyril Magnin II</td>
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<td><strong>CRI14</strong>: Podium Presentations - Engaging Patients in Research</td>
<td>Cyril Magnin III</td>
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<tr>
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<td><strong>CRI15</strong>: Papers/Podium Presentations - Novel Approaches to Data Standards</td>
<td>Mission</td>
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<td><strong>CRI16</strong>: Panel - Architectures for Data Standardization and Interoperability in Patient Centered Outcomes Research</td>
<td>Cyril Magnin I</td>
</tr>
<tr>
<td>3:00 p.m. – 3:30 p.m.</td>
<td>Coffee Break</td>
<td>Cyril Magnin Foyer</td>
</tr>
</tbody>
</table>
### Friday, April 11

<table>
<thead>
<tr>
<th>Time</th>
<th>Event</th>
<th>Room</th>
</tr>
</thead>
<tbody>
<tr>
<td>7:30 a.m. – 8:30 a.m.</td>
<td>Continental Breakfast</td>
<td>Cyril Magnin Foyer</td>
</tr>
<tr>
<td>7:30 a.m. – 11:30 a.m.</td>
<td>Registration Open</td>
<td>Cyril Magnin Foyer</td>
</tr>
<tr>
<td>8:00 a.m. – 2:00 p.m.</td>
<td>AMIA Board of Directors Meeting</td>
<td>Stockton</td>
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<tr>
<td>8:30 a.m. – 10:00 a.m.</td>
<td>Scientific Sessions</td>
<td>Cyril Magnin II</td>
</tr>
<tr>
<td>10:00 a.m. – 10:30 a.m.</td>
<td>Coffee Break</td>
<td>Cyril Magnin Foyer</td>
</tr>
<tr>
<td>10:30 a.m. – 12:00 p.m.</td>
<td><strong>CRI Closing Session and Clinical Research Informatics Year-in-Review:</strong> Peter Embi, MD, MS</td>
<td>Cyril Magnin I</td>
</tr>
</tbody>
</table>
How Can AMIA Best Support Clinical and Translational Informatics?
CTSA/CTSI, IKFC and AMIA: Collaboration, Leadership and the Future

As AMIA continues to serve our translational bioinformatics and clinical research informatics communities, what is our strategic vision for servicing and growing core research and science interests now that the work of the communities has matured?

Join AMIA leaders for an open Town Hall event with Q&A. The AMIA leadership is listening and welcomes full attendance at this session. Topics will include maintaining a professional home for TBI and CRI professionals, member services, and developing informatics competencies for translational research.

The Clinical and Translational Science Awards (CTSA) program in the NCATS Division of Clinical Innovation aims to strengthen and support the entire spectrum of translational research from scientific discovery to improved patient care. Under NCATS leadership, the program supports a national consortium of more than 60 medical research institutions that work together to transform this process. Through this consortium, research teams collaborate to tackle common problems that no one organization can accomplish alone. Its goals are to accelerate the process of translating laboratory discoveries into treatments for patients, train a new generation of clinical and translational researchers, and engage communities in clinical research efforts.

In 2014 the CTSA standing committees will be dissolved, but there is still a great need for ongoing collaboration and community building. AMIA leaders have a deep interest and commitment to the goals of CTSA and an evolving role for AMIA and members in the field.

**Wednesday, April 9**
7:00 a.m. – 8:15 a.m.
(not eligible for CME)

**Blackford Middleton, MD, MPH, MSc  @bfm**
Chair, AMIA Board of Directors
Assistant Vice Chancellor for Health Affairs
Chief Informatics Officer
Professor of Biomedical Informatics and of Medicine
Vanderbilt University Medical Center

**Umberto Tachinardi, MD, MSc  @u_tachinardi**
Chair, AMIA Clinical Research Informatics Working Group (CRI-WG)
Associate Dean for Biomedical Informatics
School of Medicine and Public Health
University of Wisconsin-Madison

**Justin Starren, MD, PhD  @JustinStarren**
AMIA board member, Former Chair of the CTSA Informatics Key Function Committee
Chief, Division of Health and Biomedical Informatics, Department of Preventive Medicine
Deputy Director, Northwestern University Clinical and Translational Science Institute (NUCATS)
Director, Northwestern University Biomedical Informatics Center (NUBIC)
Northwestern University Feinberg School of Medicine

**AMIA Town Hall**

**Informatics Professionals. Leading the Way**
AMIA Board of Directors

Chair
Blackford Middleton, MD, MPH, MSc, FACMI
Vanderbilt University Medical Center

Past Chair
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New York Presbyterian Hospital

Secretary
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Wendy W. Chapman, PhD, FACMI
University of Utah

Theresa Cullen, MD, MS
Veterans Health Administration

Patricia Dykes, DNSc, MA, RN, FACMI
Brigham and Women’s Hospital

R. Scott Evans, MS, PhD, FACMI
Intermountain Healthcare/University of Utah

Cynthia S. Gadd, PhD, FACMI
Vanderbilt University

John H. Holmes, PhD, FACE, FACMI
University of Pennsylvania

Thomas H. Payne, MD, FACMI
University of Washington

Neil Sarkar, PhD
University of Vermont, College of Medicine

Dean F. Sittig, PhD, FACMI, FHIMSS
University of Texas Health Science Center at Houston

Justin B. Starren, MD, PhD, FACMI
Northwestern University Biomedical Informatics Center

Michael S. Weiner, DO, MSM, MSIST
IBM

Ex-Officio Board Members

Alexa T. McCray, PhD, FACMI
American College of Medical Informatics President
Harvard Medical School

Tiffany Kelley, PhD, MBA, RN
Student WG Rep
Continuing Education Credit

STATEMENT OF PURPOSE
Translational bioinformatics and clinical research informatics and are the informatics domains that support translational research in the context of human health and disease, and touch nearly all areas of biological, biomedical, and clinical research. Translational bioinformatics includes innovative methods and discoveries applied to biologic data, with special focus on human application, including personalized medicine. Clinical research informatics focuses on innovations related to the management of information related to clinical trials and includes informatics related to secondary research use of clinical data. Each year the landscapes of translational bioinformatics and clinical research informatics experience significant growth and rapid change. The Joint Summits provide a venue for scientists and professionals to learn about the latest developments in research informatics from academia, industry and government and to consider new collaborations that may contribute to future advances in the fields.

ACCREDITATION STATEMENT
The American Medical Informatics Association is accredited by the Accreditation Council for Continuing Medical Education to provide continuing medical education for physicians.

CREDIT DESIGNATION STATEMENT
The American Medical Informatics Association designates this live activity for a maximum of 27 AMA PRA Category 1 Credits™. Physicians should claim only the credit commensurate with the extent of their participation in the activity.

CRITERIA FOR SUCCESSFUL COMPLETION
Completion of this live activity is demonstrated by attendance at accredited sessions, completion of the evaluation survey sent in a separate email, and verification of attendance through the participant’s electronic report of sessions attended through the individual login at amia.org. The physician participant will be able to generate a CME certificate through the AMIA automated system.

LEARNING OBJECTIVES
After participating in this live activity, learners should be better able to:
- Describe state-of-the-art informatics approaches, theories, and methods relevant to clinical and translational science
- Apply the latest findings from research and development of informatics applications to support clinical and translational biomedical research
- Consider possible frameworks for assessing and deploying clinical research informatics initiatives
- Interact with professionals engaged in clinical and translational science, including clinical and translational investigators, computational biologists, genomics researchers, statistical geneticists, clinical informaticians, public health informaticians, and those involved with clinical and research IT policy and regulatory issues
- Explore research-related issues emerging from national and international clinical and translational research informatics initiatives

TARGET AUDIENCE
The target audience for this live activity includes:
- Clinical and translational investigators with an interest in biomedical informatics as it applies to clinical and translational research
- Sponsors and managers of research institutions and programs
- Bioinformaticians, statistical geneticists, and molecular biologists with interests in informatics applied to clinical research (i.e., research on human subjects or material/data of human origin)
- Biomedical and health informatics researchers, faculty, and students
- Community health advocates and those working to advance community-based research
- Computer scientists and system developers
- Computational biologists with interests in human disease
- Government officials and policy makers concerned with health, healthcare, and biomedical and translational research
- Health information and knowledge management professionals
- Health IT industry professionals and consultants
- Industry representatives related to clinical research and translational research
- Staff members and researchers implementing the informatics components of Clinical and Translational Science Awards (CTSA)
- Standards developers
- Designers and developers of EHRs
- Developers and sponsors of patient registries
COMMERCIAL SUPPORT
No commercial support was received for this activity.

FACULTY
Faculty and their affiliations are noted for each presentation.

DISCLOSURE POLICY
As a provider accredited by the ACCME, AMIA requires that everyone who is in a position to control the content of an educational activity disclose all relevant financial relationships with any commercial interest for 12 months prior to the educational activity.

The ACCME considers relationships of the person involved in the CME activity to include financial relationships of a spouse or partner.

Faculty and planners who refuse to disclose relevant financial relationships will be disqualified from participating in the CME activity. For an individual with no relevant financial relationship(s), the participants must be informed that no conflicts of interest or financial relationship(s) exist.

AMIA uses a number of methods to resolve potential conflicts of interest, including: limiting content of the presentation to that which has been reviewed by one or more peer reviewers; ensuring that all scientific research referred to conforms to generally accepted standards of experimental design, data collection, and analysis; undertaking review of the educational activity by a content reviewer to evaluate for potential bias, balance in presentation, evidence-based content or other indicators of integrity, and absence of bias; monitoring the educational activity to evaluate for commercial bias in the presentation; and/or reviewing participant feedback to evaluate for commercial bias in the activity.

DISCLOSURES FOR THIS ACTIVITY
All speakers and members of the planning committee have been asked to disclose any significant relationships they may have with commercial interests. The presence or absence of relationships will be disclosed at the time of the meeting.

INSTRUCTIONS FOR EARNING CME/CE CREDIT
CME site (MyAMIA) works best with IE 8 or above version, Chrome, and Firefox.

- Login to your AMIA account on the amia.org website
- Go to “My Profile”
- Click “Invoices & Transactions” tab
- Scroll down to Events section and click ‘Credits’ next to 2014 Joint Summits to apply for CME.
- Physicians: Click on the AMIA Activities tab; click “download” under the “My CME” section; you may print out your certificate
- Other attendees: if you require a certificate of participation, please contact Pesha Rubinstein, Director of Education, at pesha@amia.org.
Keynote Speakers

TBI Opening Plenary Session and Keynote Presentation

Robert Plenge, MD, PhD
Vice President, Merck Research Laboratories (MRL) and Worldwide Head, Genetics and Pharmacogenomics (GpGx)

Dr. Plenge’s department, which is part of Early Development and Discovery Sciences (EDDS) under the direction of Dr. Rupert Vessey, is responsible for genetics and pharmacogenomics strategy throughout Merck’s entire pipeline – from early discovery to late-stage clinical development. Prior to joining Merck in July 2013, Dr. Plenge served as Director of Genetics & Genomics in the Division of Rheumatology, Immunology and Allergy at Brigham and Women’s Hospital; Assistant Professor of Medicine at Harvard Medical School; and Associate Member of the Broad Institute of MIT and Harvard. His academic research focused on genetic and genomic underpinnings of complex human disease, with attention to immunemediated diseases such rheumatoid arthritis (RA).

Monday, April 7
1:30 p.m. – 3:00 p.m.
Room: Cyril Magnin I/II

TBI Keynote Presentation

Isaac S. Kohane, MD, PhD
Henderson Professor of Pediatrics and Health Sciences and Technology; Co-Director Center for Biomedical Informatics Harvard Medical School; Director of the Francis A. Countway Library of Medicine

Dr. Kohane is a founder of the Center for Outcome and Policy Research at the Dana-Farber Cancer Institute and founder and Associate Director for the Center for Genetic Epidemiology at Harvard Medical School (HMS). He leads multiple collaborations at HMS and is hospital affiliates in the use of genomics and computer science to study cancer and the development of the brain (with emphasis on autism). He has developed several computer systems to allow multiple hospital systems to be used as “living laboratories” to study the genetic basis of disease while preserving patient privacy. Dr. Kohane’s research builds on his doctoral work in computer science on decision-support and subsequent research in machine-learning applied to biomedicine. Dr. Kohane leads several NIH-funded efforts to translate genomic research into clinical practice and continues his own practice in pediatric endocrinology at Boston Children’s Hospital.

Tuesday, April 8
3:30 p.m. – 5:00 p.m.
Room: Cyril Magnin I/II
CRI Opening Session and Keynote Presentation

Richard Platt, MD, MSc  
Professor and Chair of the Department of Population Medicine; Executive Director of the Harvard Pilgrim Health Care Institute  
Wednesday, April 9  
8:30 a.m. – 10:00 a.m.  
Room: Cyril Magnin I/II

Dr. Platt is a Principal Investigator of the FDA Mini-Sentinel program, which performs post-marketing safety surveillance using the electronic health data from over 125 million people. Dr. Platt is also principal investigator of PCORI’s PCORnet coordinating center, a newly established consortium of 29 networks that will use electronic health data to conduct comparative effectiveness research. He co-leads the coordinating center of the NIH Health Care System Research Collaboratory and leads a CDC Prevention Epicenter, and an AHRQ DEcIDE program. Dr. Platt has been Principal investigator of a CDC Center of Excellence in Public Health Informatics, and an AHRQ CERT.

TBI Closing Session: Translational Bioinformatics Year-in-Review

Russ B. Altman, MD, PhD, FACMI  
Kenneth Fong Professor of Bioengineering, Genetics, Medicine and (by courtesy) Computer Science; Director, Biomedical Informatics Training Program, Stanford University  
Wednesday, April 9  
3:30 p.m. – 5:00 p.m.  
Room: Cyril Magnin I/II

Dr. Altman focuses on the creation and application of computational tools to solve problems in biology and medicine. He focuses particularly on the molecular mechanisms of drug action and drug response, integrating data at the molecular, cellular, organism and population levels. He is interested in methodological innovation in informatics, including knowledge representation, machine learning, natural language processing, data mining, and physical simulation.

CRI Closing Session: Clinical Research Informatics Year-in-Review

Peter J. Embi, MD, MS, FACMI  
Associate Professor and Vice Chair, Department of Biomedical Informatics; The Ohio State University; Chief Research Information Officer, The Ohio State University Medical Center; Physician, Department of Internal Medicine, Division of Rheumatology & Immunology  
Friday, April 11  
10:30 a.m. – 12:00 p.m.  
Room: Cyril Magnin I

Dr. Embi is an internationally recognized researcher and educator in the field of clinical research informatics, with numerous publications and presentations describing his innovations in the field. Dr. Embi joined the Medical Center in 2010 from the University of Cincinnati Academic Health Center where he was Associate Professor of Clinical Medicine and Director of Biomedical Informatics in the Center for Clinical and Translational Science and Training. He has served as an adjunct assistant professor in Ohio State’s Department of Biomedical Informatics since 2008. He is also the founding director of the Center for Health Informatics at the University of Cincinnati Academic Health Center.
BOF01: SciCast Project

Room: Cyril Magnin I

Jessie Tenenbaum, Duke University; Anthony Solomonides, NorthShore University Health System; Judy Logan, Oregon Health & Sciences University

AMIA has been invited to participate in the SciCast project (scicast.org), a prediction market that crowdsources the forecasting of various future innovations in Science and Technology. The Genomics and Clinical Research Informatics Working Groups are sponsoring the first topic leaders through whom questions will be posed and moderated. This BOF session will present the project and encourage attendees to pose new questions.

BOF02: Practical Implementation of Pharmacogenomics

Room: Cyril Magnin II

Joshua Denny, Vanderbilt University

Recently, a few academic medical centers have started implementing genetic data to guide drug prescribing. Prospective and reactive genetic models exist. The NIH Implementing Genomics in Practice (IGNITE) and the Electronic Medical Records and Genomics (eMERGE) Networks seek to propel adoption. Special considerations are needed into how to represent genetic data, where to store it, how to design decision support and surveillance technologies, and how to education patients and providers. Early clinical trials highlight the challenges of implementing pharmacogenomics. This session is designed to gather individuals on the front lines of implementing such systems for an informal discussion.

BOF03: Researching in Big Data

Room: Cyril Magnin III

Nicholas Tatonetti, Columbia University

The explosion of available massive omic and clinical data sets have made possible new classes of research reusing or repurposing existing data. The importance of these data and efforts have been recognized by national and international funding bodies through efforts such as the NIH’s Big Data to Knowledge (BD2K) initiative and data resources such as the Database of Genotypes and Phenotypes (dbGaP) and the Gene Expression Omnibus (GEO).
BOF04: Collecting Clinical Trial Data Using EHR Structured Forms

Room: Cyril Magnin I

Vojtech Huser, National Institutes of Health

Integration of clinical trial data collection into routine care is an ongoing clinical research informatics challenge. For clinical registry studies and certain types of observational trials, it is sometimes possible to directly use form capabilities of the existing EHR system to capture research data. This is possible for studies that do not have study blinding concerns (patient or investigator), existence of incidental findings or research vs. clinical billing issues. This session will be a discussion and exchange of experiences with direct use of EHR system by point of care clinicians/researchers rather than using electronic case report forms in a designated research-only electronic data capture system.

BOF05: Representing Study Eligibility Criteria (SIGEC)

Room: Cyril Magnin II

Chunhua Weng, Columbia University; Ida Sim, University of California San Francisco

With the burgeoning adoption of electronic health records (EHRs), vast amounts of clinical data are increasingly available for computational reuse. It is imperative that the scientific community leverage phenomic data to accelerate clinical research at low cost and large scale. A critical step toward this goal is matching clinical eligibility criteria to clinical data. However, this task is complicated by the semantic gap between free-text eligibility criteria and raw clinical data: each criterion has many ways to describe it and a myriad of clinical data points that represent it. To accelerate advances in this important research area, we would like to create a collaborative community to chart the problem space, to define mission-critical tasks, and to develop a “divide-and-conquer” strategy. We welcome all colleagues and those with interest in formal representations for clinical eligibility criteria and computable phenotype knowledge or with expertise in text-based knowledge engineering to join us in this effort.

BOF06: Future Directions for the Clinical and Translational Research Informatics Community: Life After the Informatics Key Function Committee

Room: Cyril Magnin III

Philip Payne, The Ohio State University; Justin Starren, Northwestern University

With recent changes in the structure and focus on the national CTSA consortium, the TBI and CRI community that had coalesced around the Informatics Key Function Committee (IKFC) has been left without a professional home. This BOF session will explore next steps related to the sustainability and growth of that community, addressing critical questions such as: 1) should AMIA serve as the new professional home for the activities previously housed in the IKFC? 2) are there other stakeholders who should be engaged in an expanded/renewed community derived from the IKFC? and 3) in what existing IKFC or new community-derived activities should an emergent professional home engage?
AMIA's 10x10 Virtual Courses use curricular content from existing informatics training programs and other AMIA educational initiatives with a special emphasis toward those programs with a proven track record in distance learning. The content provides a framework but also covers plenty of detail, especially in areas such as electronic and personal health records, health information exchange, standards and terminology, and health care quality and error prevention.

INFORMATICS EDUCATION ONLINE
10X10 VIRTUAL COURSES SUMMER/FALL 2014
Register now for 2014 CME/CEs

Interprofessional Health Informatics
April 7 – July 7, 2014
University of Minnesota School of Nursing (UMN)
Course Director – Bonnie L. Westra, PhD, RN, FAAN
The UMN 10x10 is directed to both a generic overview of nursing and health informatics and the specific application of information and communication technologies in the clinical area. It focuses on the analysis, modeling, standardization, development and deployment of the electronic health record and safe exchange of patient data. It examines the implications of informatics for practice, including nursing, public health, and healthcare in general.
56.18 ANCC credits available

Introduction to Biomedical and Health Informatics
April 9 – July 23, 2014
Oregon Health & Science University (OHSU)
Course Director – William Hersh, MD
OHSU provides a detailed overview of biomedical and health informatics to those who work at the interface of healthcare and information technology (IT). It provides a broad understanding of the field from the vantage point of those who implement, lead, and develop IT solutions for improving health, healthcare, public health, and biomedical research.
Up to 46.5 CME credits available

Introduction to Biomedical and Health Informatics for Dietitians
May 7 – October 8, 2014
Oregon Health and Science University (OHSU)
Course Director – William Hersh, MD
The Academy of Nutrition and Dietetics, AMIA, and Oregon Health & Science University (OHSU) are pleased to offer this special version of the 10x10 course aimed at RDs and DTRs. The content is geared to nutrition and the in-person session takes place at the 2014 Academy of Nutrition and Dietetics Food & Nutrition Conference & Exposition in Atlanta, GA October 18-21. The course provides a broad understanding of the field from the vantage point of those who implement, lead, and develop IT solutions for improving health, healthcare, public health, and biomedical research.
54.5 CPEU credits available

Coming this Summer:

OHSU in conjunction with the American College of Emergency Physicians
Introduction to Biomedical and Health Informatics for Emergency Medicine
Course begins July 2, 2014

University of Texas Health Science Center at Houston
Healthcare Interface Design Course
Course begins July 7, 2014

To register for any of the above courses and to view full descriptions, please visit: http://www.amia.org/education/10x10-courses
## Lunch and Learn Events

*(not eligible for CME)*

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<th>Date</th>
<th>Time</th>
<th>Title</th>
<th>Speaker</th>
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<tbody>
<tr>
<td><strong>Tuesday, April 8</strong></td>
<td>12:15 p.m. – 1:15 p.m.</td>
<td><strong>Precision Medicine Ascendant: Supporting the Clinical Use of Omics Data</strong></td>
<td>Cyril Magnin III &lt;br&gt;Regis Charlot, MS, President and Chief Technology Officer, Intelligent Medical Objects, Inc.</td>
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<td><em>We have witnessed a sea change in industry attitude towards clinical use of omics data over the last two years, with several pioneers investing significantly in clinical omics strategies focused at the point of care. In this session, the audience will learn:</em>&lt;br&gt;• How the first adopter cohort has leveraged enterprise foundational efforts in translational research towards powering strategies in clinical genomics &amp; precision medicine.&lt;br&gt;• How a second wave of adopters have mobilized in launching their clinical omics strategies.&lt;br&gt;• How the ‘playbooks’ being established by these early adopters can be leveraged by organizations seeking to launch their own clinical omics efforts.</td>
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<tr>
<td><strong>Wednesday, April 9</strong></td>
<td>12:15 p.m. – 1:15 p.m.</td>
<td><strong>ICD10 and Meaningful Use - Opportunity for Innovation</strong></td>
<td>Cyril Magnin III &lt;br&gt;Frederick Lee, MD, MPH, Director, Clinical &amp; Translational Informatics, Oracle Health Sciences; Andrew Boudreau, Product Strategist, Precision Medicine, Oracle Health Sciences</td>
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<td><em>Interface terminology modeling has been positive force in supporting our healthcare transformations and regulatory compliance for ICD10 and Meaningful use. Use of natural language processing and preforming retrospective patient-centric discovery through sophisticated concept tagging is now possible. Connecting our user community to a semantic highway constructed on comprehensive, clinical concept-based interface terminology will be critical for the future of all healthcare organizations and the distribution of HIT innovations. In this presentation, Mr. Charlot will discuss “The Semantic Highway” and outline a new way for healthcare providers currently using IMO as their terminology foundation to create a launching point for innovations that will allow them to thrive in the new healthcare reimbursement environment. Topics include:</em>&lt;br&gt;• Exploring the necessary roles of the Semantic highway for semantically-based commerce&lt;br&gt;• Empowering clinicians and researchers to connect in real time via interface terminology&lt;br&gt;• Exploring academic and corporate symbiotic relationships</td>
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<td><strong>Thursday, April 10</strong></td>
<td>12:15 p.m. – 1:15 p.m.</td>
<td><strong>UC-ReX, Two Years In – Lessons Learned, Future Plans</strong></td>
<td>Cyril Magnin III &lt;br&gt;Regis Charlot, MS, President and Chief Technology Officer, Intelligent Medical Objects, Inc.</td>
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<td><em>The UC-ReX network provides federated access to 12.5 million de-identified patient records across the University of California’s five health sciences campuses. What has been learned in building this network, and what are the future plans for enhancing its utility to the clinical research community?</em></td>
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<td><strong>Precision Medicine, Precision Miner – A Discovery Workbench</strong></td>
<td>Cyril Magnin III &lt;br&gt;Frederick Lee, MD, MPH, Director, Clinical &amp; Translational Informatics, Oracle Health Sciences; Andrew Boudreau, Product Strategist, Precision Medicine, Oracle Health Sciences</td>
</tr>
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<td><em>The goal of precision medicine requires us to develop algorithms that accurately align a patient’s clinical phenotype with their molecular profile in order to arrive at highly specific treatment decisions. How do we develop such algorithms for use in clinical decision support systems? We discuss the Precision Miner tool suite from ConvergeHEALTH by Deloitte and its role as a development environment for the creation of the essential models for personalized, precision medicine.</em></td>
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Jillian’s Billiards Club
Tickets: Free for the Joint Summits registrants. Includes one complimentary drink ticket and heavy hors d’oeuvres.

Guest tickets may be purchased for $50 at the Joint Summits registration desk.

Socialize and enjoy an evening out with colleagues. Fun, food, and FREE entrance for Joint Summits registrants!

Jillian’s Billiards Club is warm and welcoming. The Billiards room offers a relaxed lounge atmosphere, the vibe is easy going, laid back, and most of all fun!

Tuesday, April 8
6:30 p.m. – 8:30 p.m
Located near the Parc 55 Hotel at 175 4th Street, San Francisco. Transportation on your own.

Women in Informatics Networking Event (WINE)
Back by popular demand – WINE II! Network with your colleagues over cocktails. Enjoy a casual get-together at the Parc 55 Hotel Lobby Bar with other women attending the Joint Summits. Cash bar.

Organizer: Jessie Tenenbaum

Wednesday, April 9
6:00 p.m. – 8:00 p.m.
Parc 55 Hotel Lobby Bar
## Working Group Meetings

Everyone is welcome to attend Working Group Meetings. Meals not provided. *(not eligible for CME)*

<table>
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<th>Meeting Name</th>
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<tbody>
<tr>
<td><strong>Monday, April 7</strong></td>
<td>6:00 p.m. – 7:00 p.m.</td>
<td>Genomics Working Group Meeting</td>
<td>Davidson</td>
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<tr>
<td><strong>Wednesday, April 9</strong></td>
<td>12:15 p.m. – 1:15 p.m.</td>
<td>Natural Language Processing Working Group Meeting</td>
<td>Davidson</td>
</tr>
<tr>
<td><strong>Thursday, April 10</strong></td>
<td>6:00 p.m. – 7:00 p.m.</td>
<td>Clinical Research Informatics Working Group Meeting</td>
<td>Cyril Magnin I</td>
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AMIA ANNUAL SYMPOSIUM
NOVEMBER 15 - 19, 2014
WASHINGTON HILTON • WASHINGTON D.C.

Save the Date

amia.org/amia2014
@AMIAinformatics
#AMIA2014

Bonnie L. Westra, PhD, RN, FAAN, FACMI
AMIA 2014 Scientific Program Committee Chair

Neil Sarkar, PhD, MLIS
Foundations Track Chair

Anne M. Turner, MD, MPH, MLIS
Applications Track Chair
Daily Schedule

Monday, April 7

7:30 a.m. – 8:30 a.m.  Continental Breakfast  Cyril Magnin Foyer
7:30 a.m. – 6:00 p.m.  Registration Open  Cyril Magnin Foyer
8:30 a.m. – 12:00 p.m.  Tutorials  Cyril Magnin Foyer

**T01: Leveraging Public Consortia for Translational Research:**
*An Introduction to ENCODE, Roadmap Epigenomics, and 1000 Genomes Data*
*R. Auerbach, Stanford University School of Medicine*

Large-scale consortia such as the Encyclopedia of Coding Elements (ENCODE), 1000 Genomes, the Roadmap Epigenomics, and Gencode have collectively spent hundreds of millions of dollars and generated a wealth of data relating to functional genomics, sequence variation, gene expression and human genome annotation. To date the various consortia have applied these data to explore the intricacies of transcription and how genomics, transcriptomics, and epigenetics work in concert, even using these data to improve the human genome annotation and to identify non-coding elements that may also play a role in regulation; however, the community has only scratched the surface of how these data can be used in a translational context and bridging the gap between basic research and translational medicine will lead to better understanding of diseases and possible cures. Because the depth and breadth of these consortia data sets are so vast and span multiple cell lines, cellular treatments, and assays, external researchers tend to quickly become overwhelmed by what data are available and how to interpret it for use in their own analyses. This tutorial will attempt to simplify the consortium data sets by presenting consortia data sets in the following contexts: DNA binding site analysis, chromatin analysis, DNA methylation, DNA-DNA interactions, transcriptomics, and sequence variation. Attendees should expect to learn about the many different assays used across these consortia and what they measure. The data processing choice made by each consortium and how these choices affect downstream analyses will also be discussed. Finally, the tutorial will end with a discussion of tools and methods to access/view the data, case studies showing how these data have been used in integrative studies to date, and a brainstorming session about how these resources can best be applied in a translational context.

**T02: CDISC Standards in Clinical Research Informatics**
*V. Huser, NIH CC; P. Schaefer, Business Analysis Software & Services, LLC*

This tutorial will provide an introduction to standards defined by the Clinical Data Interchange Standards Consortium (CDISC) to everyone who needs to understand the impact of CDISC standards on clinical research business processes and tools. Part 1 will provide introduction to CDISC as a standard developing organization (SDO), its history and the role of CDISC standards in regulatory approval submission. It will also highlight how CDISC is relevant to clinical research informaticians working at academic medical centers or collaborating with pharmaceutical industry. Part 2 will review individual CDISC standards, such as Operational Data Model (ODM), Study Data Tabulation Model (SDTM), Case Report Tabulation Data Definition Specification (define.xml) and others. Part 2 will also cover cross-standard issues and CDISC controlled terminology. Part 3 will provide practical exposure to XML and examples of clinical trial data represented in CDISC standards (ODM, Study Design Model (SDM-XML), SDTM and define.xml) and overview of free and commercial software products for manipulating data represented in XML-based CDISC standards. Finally, part 4 will focus on future trends in representation of clinical research data, the future of existing CDISC standards and describe emerging new CDISC initiatives and planned future standards. The tutorial targets study data managers, clinical research informaticians, and clinical researchers that need to get an overview of CDISC standards and understand the impact on their work.
T03: Enhancing Participant Recruitment to Clinical Trials: Informatics Strategies and Future Directions
A. Atreja, Mount Sinai School of Medicine; P. Embi, The Ohio State University; P. Harris, Vanderbilt University; C. Weng, Columbia University

Clinical trials are critical to the advancement of medicine and form a crucial link in the translation of basic biological research into routine clinical practice. Finding eligible participants for trials is one of the major bottlenecks in the conduct of clinical research. Despite the great promise of existing health information systems, recruitment rates remain low and are frequently the cause for delays in the completion of trials. The need is great for fundamental, accessible, navigable, and comprehensible solutions to the challenge of participant recruitment. Overcoming these challenges is a fundamentally information-intensive endeavor, and informatics solutions to the problem of inadequate recruitment are beginning to take hold. Through a series of speaker presentations, panel discussion, and breakout sessions, this tutorial will bring together thought leaders to address the challenge of clinical trial participant recruitment through various informatics strategies: (1) Registries, (2) Electronic Health Records, (3) Patient-centric platforms and (4) Social-media based solutions. The panel will discuss the evidence for current strategies and lay out a framework for the future through discussion and break-out groups. Participants will learn various provider-centric and patient-centric approaches to enhance clinical trial recruitment within their research information ecosystems and how to objectively evaluate the effectiveness of these approaches. Through hands-on exercises and use-case scenarios, participants will understand how to combine different strategies to formalize a solution that bests fit within their institutional needs and environment.

10:00 a.m. – 10:30 a.m.
Coffee Break

TBI01: Panel - Dissemination of Pharmacogenomic Knowledge: Establishing a Pathway to Support Clinical Implementation
J. Hoffman, St. Jude Children's Research Hospital; M. Whirl-Carrillo, Stanford University; R. Freimuth, Mayo Clinic; J. Peterson, Vanderbilt University

Pharmacogenomics is often an initial focus for the implementation of genomic medicine. To facilitate the translation of pharmacogenomic knowledge to clinical practice, authoritative resources are needed to form a knowledge base that combines genomic and medication information, which can be used to support gene-based prescribing through the electronic health record (EHR). As these resources are established, the knowledge must be represented in ways that will enable broad dissemination. This session will illustrate how three national initiatives are working together to establish a pathway to support the dissemination and clinical implementation of pharmacogenomics knowledge. Specifically, this panel will highlight the development of clinical guidelines by the Clinical Pharmacogenetics Implementation Consortium (CPIC), including its increased focus on informatics, and the dissemination of that knowledge through PharmGKB. The panel will also summarize lessons learned by the Pharmacogenetics Research Network (PGRN) Translational Pharmacogenetics Program (TPP), which identifies barriers for the implementation of pharmacogenomics, including integration with the EHR, and compares implementation approaches across diverse sites. Finally, because pharmacogenomic expertise may be concentrated in specific organizations and the technical architecture of clinical information systems varies widely, standards must be developed to share pharmacogenomic knowledge, especially genotype interpretations and prescribing recommendations.
**TBI02: Papers/Podium Presentations - Using Omics for Discovery**

Session Chair: Lewis Frey

Towards Personalized Medicine: Leveraging Patient Similarity and Drug Similarity Analytics
P. Zhang, F. Wang, J. Hu, R. Sorrentino, IBM T.J. Watson Research Center

Physiological Predictors based on Temporal Clustering of Patients
R. Moskovitch, N. Tatonetti, Columbia University

Improving Translatability of Biological Networks for Applications in Human Disease and Pharmacology
A. Jacunski, S. Dixon, B. Stockwell, N. Tatonetti, Columbia University

Validation and Portability of Unbiased, Label-free Proteomics
J. Lucas, Quintiles; J. Lucas, J. Thompson, L. Dubois, K. Patel, A. Moseley, Duke University

**TBI03: Podium Presentations - Tools to Enhance Understanding and Analysis of Omic Data**

Session Chair: Will Bush

Biofilter 2.0 for Advanced Predictive Model Development, Testing, and Hypothesis Generation using Expert Domain Knowledge Resources
M. Ritchie, A. Frase, J. Wallace, S. Pendergrass, The Pennsylvania State University

Visualizing Multiple Types of Genomic Information across Chromosomes with PhenoGram
S. Pendergrass, D. Wolfe, S. Dudek, M. Ritchie, The Pennsylvania State University

The ENCODE ChIP-Seq Significance Tool: Enabling the Study of Disease Mechanisms through the Use of Public Data
R. Auerbach, B. Chen, A. Butte, Stanford University School of Medicine

COSMOS: NGS Analysis in the Cloud
J. Hawkins, Harvard Medical School; Y. Soulimi, Faculty of Sciences of Rabat; R. Powles, Virginia Tech; J. Jung, A. Lancaster, D. Wall, Harvard Medical School/Stanford University; P. Tonellato, Harvard Medical School

**TBI04: Late Breaking Abstracts - Drugs, RNA, and High-dimensional Data**

Session Chair: Josh Peterson

Annotating FDA Drug Labels for Drug Indications
R. Khare, U. S. National Library of Medicine; National Center for Biotechnology Information; J. Li, Chinese Academy of Medical Sciences, Institute of Medical Information; Z. Lu, U. S. National Library of Medicine, National Center for Biotechnology Information

Harvest: An Open Platform for Developing Web-based Biomedical Data Discovery and Reporting Applications

Uncovering Differential Multi-microRNA Signatures of Acute Myeloid and Lymphoblastic Leukemias with a Machine-learning-based Network Approach
J. Candia, University of Maryland School of Medicine; S. Cherukuri, University of Maryland, School of Medicine/Noble Life Sciences; J. Banavar, University of Maryland; C. Cuv, University of Maryland School of Medicine; W. Losert, University of Maryland

“N-of-1-pathways” Unveils Personal Deregulated Mechanisms from a Single Pair of RNA-Seq Samples: Towards Precision Medicine
V. Gardeux, University of Illinois at Chicago/EISTI School of Engineering; I. Achour, University of Illinois at Chicago/University of Arizona; M. Maienschein-Cline, G. Parinandi, University of Illinois at Chicago; L. Pesce, University of Illinois at Chicago/Argonne National Laboratory; J. Li, University of Illinois at Chicago/University of Arizona; N. Bahroos, University of Illinois at Chicago; H. Li, University of Illinois at Chicago/University of Arizona; R. Winn, University of Illinois at Chicago/University of Illinois Cancer Center; I. Foster, Argonne National Laboratory/University of Chicago; J. Garcia, University of Arizona; Y. Lussier, University of Illinois at Chicago
Open Faculty Position at UNC - Chapel Hill’s Gillings School of Global Public Health

THE UNIVERSITY of NORTH CAROLINA at CHAPEL HILL

POSITION:
The Departments of Health Policy and Management (http://sph.unc.edu/hpm/) and Epidemiology (http://www.sph.unc.edu/epid/) at the University of North Carolina at Chapel Hill Gillings School of Global Public Health are seeking applicants for a tenured/tenure-track Assistant/Associate Professor position in the field of public health informatics (PHI). This position may involve a joint faculty appointment in both departments. She/he will contribute to the Carolina Health Informatics Program (CHIP), a cross-campus health informatics research and education initiative.

REQUIRED/PREFERRED QUALIFICATIONS:
The core requirements are demonstrated expertise in one or more of the following areas: global/national/state/local health information technology (HIT); public health systems research; or HIT policy and implementation. Candidates must demonstrate formal training in an informatics or a related area (e.g., computer science, health services research, operations research, epidemiology, etc. with an emphasis on informatics and data management). All candidates must demonstrate a research portfolio focused on informatics related to public and population health, strong research skills and record of scholarship, as well as the ability to teach and advise students.

DUTIES/RESPONSIBILITIES:
This individual will contribute to the successful development of the University of North Carolina PHI program through research, education, and related activities with a focus on improving public health systems performance and population health. The individual will be expected to engage in research that spans both departments and may include, but is not limited to outcomes research, comparative effectiveness research, health services research, pharmacoepidemiology, HIT policy evaluation, systems analysis, relational data theory, surveillance systems, data warehousing, and decision support. This individual also will be expected to teach in the new certificate and Master’s/PhD programs in Health Informatics with tracks dedicated to PHI intended to integrate information sciences and technology in public health practice and research. Successful candidates will be able to demonstrate how they will help improve public health systems performance and population health by utilizing public health information systems such as surveillance systems, health information exchange networks for monitoring public health, web-based health education and promotion, national electronic health record adoption/implementation, and/or “big-data” research.

ADDITIONAL INFORMATION:
Applications, including a cover letter describing their qualifications, a complete curriculum vitae, and contact information for three professional references, should be submitted electronically to the attention of Dr. Andy Olshan at the following website: http://unc.peopleadmin.com/postings/37248.
Tuesday, April 8

7:00 a.m. – 6:00 p.m.  Registration Open  Cyril Magnin Foyer

7:00 a.m. – 8:15 a.m.  Birds-of-a-Feather Sessions - open to all  Cyril Magnin I

**BOF01: SciCast Project**
*(not eligible for CME)*  
J. Tenenbaum, Duke University; A. Solomonides, NorthShore University Health System; J. Logan, Oregon Health & Sciences University

AMIA has been invited to participate in the SciCast project (scicast.org), a prediction market that crowdsources the forecasting of various future innovations in Science and Technology. The Genomics and Clinical Research Informatics Working Groups are sponsoring the first topic leaders through whom questions will be posed and moderated. This BOF session will present the project and encourage attendees to pose new questions.

**BOF02: Practical Implementation of Pharmacogenomics**
*(not eligible for CME)*  
J. Denny, Vanderbilt University

Recently, a few academic medical centers have started implementing genetic data to guide drug prescribing. Prospective and reactive genetic models exist. The NIH Implementing Genomics in Practice (IGNITE) and the Electronic Medical Records and Genomics (eMERGE) Networks seek to propel adoption. Special considerations are needed into how to represent genetic data, where to store it, how to design decision support and surveillance technologies, and how to educate patients and providers. Early clinical trials highlight the challenges of implementing pharmacogenomics. This session is designed to gather individuals on the front lines of implementing such systems for an informal discussion.

**BOF03: Researching in Big Data**
*(not eligible for CME)*  
N. Tatonetti, Columbia University

The explosion of available massive omic and clinical data sets have made possible new classes of research reusing or repurposing existing data. The importance of these data and efforts have been recognized by national and international funding bodies through efforts such as the NIH’s Big Data to Knowledge (BD2K) initiative and data resources such as the Database of Genotypes and Phenotypes (dbGaP) and the Gene Expression Omnibus (GEO).

7:00 a.m. – 8:30 a.m.  Continental Breakfast  Cyril Magnin Foyer
TUESDAY, APRIL 8
Scientific Sessions
8:30 a.m. – 10:00 a.m

8:30 a.m. – 10:00 a.m  Scientific Sessions

**TBI05: Papers/Podium Presentations - Phenotyping Toolkits and Resources**
Session Chair: Robert Freimuth

- Informatics for the International Mouse Phenotyping Consortium
  T. Meehan, European Molecular Biology Laboratory/European Bioinformatics Institute

- The PhenX Toolkit: Promoting Data Sharing and Translational Research

  R. Walker, University of California San Diego

- Creating Scalable Research Infrastructure to Enable Translational Science: The Synthetic Derivative
  J. Cowan, M. Basford, X. Wang, S. Osgood, P. Harris, J. Denny, Vanderbilt University School of Medicine

**TBI06: Podium Presentations - Machine Learning Omics for Cancer**
Session Chair: Joshua Stuart

- Proteogenomic Characterization of Human Colorectal Cancer

- Cancer Patient Integrative Stratification via a Two-step Consensus Clustering of Molecular Expression and Clinical Attributes
  C. Wang, R. Machiraju, K. Huang, The Ohio State University

- New Genetic Variants Improve Personalized Breast Cancer Diagnosis
  J. Liu, D. Page, University of Wisconsin; P. Peissig, Marshfield Clinic Research Foundation; C. McCarty, Essentia Institute of Rural Health; A. Oriti, Marshfield Clinic Research Foundation/Marshfield Clinic Weston Center/University of Queensland; A. Trentham-Dietz, E. Burnside, University of Wisconsin

- Identification of Transcriptionally-defined Cancer Subpopulations through Integration of Public Microarray Data with Single Cell Gene Expression Profiling
  M. Januszzyk, M. Sorkin, R. Rennert, G. Gurtner, P. Khatri, A. Butte, Stanford University

**TBI07: Papers/Podium Presentations - Using Omic Data for Prediction and Prioritization**
Session Chair: Zhongming Zhao

- Automatic Gene Prioritization in Support of the Inflammatory Contribution to Alzheimer’s Disease
  S. Furniss, R. Yao, G. Gonzalez, Arizona State University

- Generalized Linear Models for Identifying Predictors of the Evolutionary Diffusion of Viruses
  R. Beard, D. Magee, Arizona State University; M. Suchard, University of California; P. Lemey, KU Leuven; M. Scotch, Arizona State University

- Intra-host Evolution and Subclonal Diversity in Acute Infections using Unphased Genomic Data
  H. Khabanian, Z. Carpenter, Columbia University; J. Kugelman, The U.S. Army Medical Research Institute of Infectious Diseases; J. Chan, V. Trifonov, Columbia University; E. Nagle, T. Warren, The U.S. Army Medical Research Institute of Infectious Diseases; P. Iversen, Sarepta Therapeutics; S. Bavari, G. Palacios, The U.S. Army Medical Research Institute of Infectious Diseases; R. Rabadian, Columbia University

- Searching for Master Regulators of Disease-related Gene Expression Profiles by Network Analysis of the LINCS Library of Transcriptional Signatures of Cellular Perturbations
  J. Chen, M. Phatak, University of Cincinnati Medical Center; S. Sivaganesan, University of Cincinnati; J. Reichard, Toxicology Excellence for Risk Assessment (TERA); W. Niu, V. Joshi, M. Medvedovic, University of Cincinnati Medical Center
TBI08: Late Breaking Abstracts - Biology to Phenotype Prediction and Biobanks
Session Chair: Nicholas Tatonetti

Findings from the Third Critical Assessment of Genome Interpretation, AGI 2013, a Community Experiment to Evaluate Phenotype Prediction
S. Brenner, University of California, Berkeley; J. Moult, University of Maryland

Phenome-wide Association Studies on a Quantitative Trait: Application to TPMT Enzyme Activity and Thiopurine Therapy in Pharmacogenomics
A. Neuraz, University Hospital HEGP, AP-HP/Universite Paris Descartes Faculte-de-Medecine, INSERM UMR_S 872; L. Chouchana, Universite Paris Descartes, INSERM UMR_S 775; G. Malamut, C. LeBeller, D. Roche, University Hospital HEGP, AP-HP; P. Beaune, Universite Paris Descartes, INSERM UMR_S 775/University Hospital HEGP; AP-HP; P. Degoulet, University Hospital HEGP, AP-HP/Universite Paris Descartes Faculte-de-Medecine, INSERM UMR_S 872; A. Bergun, University Hospital HEGP, AP-HP/Universite Paris Descartes Faculte-de-Medecine, INSERM UMR_S 872; M. Lorlot, Universite Paris Descartes, INSERM UMR_S 775/University Hospital HEGP, AP-HP; P. Avillach, University Hospital HEGP, AP-HP/Universite Paris Descartes Faculte-de-Medecine, INSERM UMR_S 872

Lessons Learned: Building the IT Infrastructure for the Million Veterans Program
L. D'Avolio, Ariadne Labs/Harvard University School of Public Health

A Method for Predicting MicroRNA Regulation-altering Genomic Variants from Matched Genotype, miRNA Expression and Gene Expression
E. Maxwell, National Human Genome Research Institute, National Institutes of Health/Boston University; J. Campbell, Boston University School of Medicine; A. Labadorf, Boston University/Boston University School of Medicine; V. Kartha, Boston University School of Medicine; A. Spira, R. Myers, Boston University/Boston University School of Medicine; A. Baxevanis, National Human Genome Research Institute, National Institutes of Health

10:00 a.m. – 10:30 a.m.  Coffee Break  Cyril Magnin Foyer
10:30 a.m. – 12:00 p.m.  Scientific Breaks  Cyril Magnin II

TBI09: Podium Presentations - Tools to Support Pharmacogenomics
Session Chair: Christoph Brockel

Use of RxNorm and NDF-RT to Normalize and Characterize Participant-reported Medications in an i2b2-based Research Repository
C. Blach, Duke University; G. Del Fiol, University of Utah; C. Dundee, J. Frund, R. Richesson, M. Smerek, A. Walden, J. Tenenbaum, Duke University

The Pharmacogenomic Guideline Repository: A Resource of Structured Guidelines to Facilitate Clinical Implementation
R. Freimuth, Q. Zhu, C. Chute, Mayo Clinic

PGxpress: A Pharmacogenomic Mobile Website
M. Whirl-Carrillo, R. Whaley, T. Klein, R. Altman, Stanford University

Towards an Integrated Framework of Pharmacovigilance Signal Detectors through Semantic Mediation
V. Koutkias, M. Jaulent, INSERM
TUESDAY, APRIL 8
Scientific Sessions
10:30 a.m. – 12:00 p.m. | CONTINUED

**TBI10: Papers/Podium Presentations - Method Development**
Session Chair: Gil Alterovitz

**Categorizing the Relationships between Structurally Congruent Concepts from Pairs of Terminologies for Semantic Harmonization**
Z. He, J. Geller, New Jersey Institute of Technology; G. Elhanan, Halfpenny Technologies

**Efficient Algebraic Interval Queries on Biomedical Sequence Annotations**
Y. Luo, P. Szolovits, MIT

**Evaluating CTSA Publication Output Using the Triangle of Biomedicine**
G. Weber, Harvard Medical School

**Selective Model Averaging with Bayesian Rule Learning for Predictive Biomedicine**
J. Balasubramanian, S. Visweswaran, G. Cooper, V. Gopalakrishnan, University of Pittsburgh

**TBI11: Papers/Podium Presentations - EHR Phenotypes and Methods**
Session Chair: Abel Kho

**Standardized Representation for Electronic Health Record-driven Phenotypes**
R. Richesson, Duke University School of Nursing; S. Rusincovitch, Duke University Health System; M. Smerek, Duke Clinical Research Institute; J. Pathak, Mayo Clinic

**Identifying Patients with Hypertension in the Electronic Medical Record**
P. Teixeira, W. Wei, R. Cronin, J. Denny, Vanderbilt University

**Creation and Validation of an EMR-based Algorithm for Identifying Major Adverse Cardiac Events while on Statins**
W. Wei, Vanderbilt University; Q. Feng, P. Weeke, W. Bush, M. Waitara, O. Iwuchukwu, D. Roden, Vanderbilt University School of Medicine; R. Wilke, Sanford Healthcare; C. Stein, Vanderbilt University School of Medicine; J. Denny, Vanderbilt University

**SPIRIT - Integrated Platform for Protocol Decision Trees, Eligibility Screening and Cohort Identification**
A. Shah, J. Meng, S. Achuthan, S. Bolisetty, A. Nagender, J. Niland, City of Hope

**TBI12: Late Breaking Panel - Corporate-academic Collaboration: Lessons Learned Navigating the Pitfalls and Promises of Industry Partnerships**
L. D’Avolio, Ariadne Labs; A. Butte, Stanford University School of Medicine; M. Williams, Geisinger Health System

By nearly all indications the opportunity for industry-academic partnerships has never been more promising. Low cost, high throughput sequencing is creating new markets in everything from cloud computing to diagnostics and more targeted interventions. Shifting reimbursement policies are suddenly prioritizing quality and creating unprecedented opportunity for those capable of turning clinical data into knowledge. Faced with an explosion of new biological data and pressures to better understand the use of their compounds, pharmaceutical companies are seeking new relationships with clinical and academic partners. At the same time the research budgets of traditional research funding agencies are shrinking. Finally, discovery enables the opportunities to commercial results through startup companies or technology licensing. In this session a panel of experts in straddling the fine line between academia and industry speak to the challenges and opportunities presented when navigating these two very different paradigms.

12:15 p.m. – 1:15 p.m.
**Lunch and Learn with Oracle Health Sciences**
(not eligible for CME)

**Precision Medicine Ascendant: Supporting the Clinical Use of Omics Data**
Frederick Lee, MD, MPH, Director, Clinical & Translational Informatics, Oracle Health Sciences; Andrew Boudreau, Product Strategist, Precision Medicine, Oracle Health Sciences

1:00 p.m. – 5:00 p.m.
**10x10 with OHSU In-person Session**
(not eligible for the Joint Summits CME)
1:30 p.m. – 3:00 p.m.  Scientific Sessions

**TBI13: Papers/Podium Presentations - Data Sharing and Data Repositories**  
Session Chair: James Hoffman

**Automated Batch Randomization for Better Study Design**  
M. Maienschein-Cline, Z. Lei, V. Gardeux, N. Bahrroos, Y. Lussier, University of Illinois at Chicago

**Developing Governance for Federated Community-based EHR Data Sharing**  
C. Lin, K. Stephens, L. Baldwin, G. Keppel, R. Whitener, A. Echo-Hawk, D. Korngiebel, University of Washington

**tranSMART: An Open Source Knowledge Management and High Content Data Analytics Platform**  
E. Scheufele, Recombinant by Deloitte/Harvard University; D. McDuffie, M. Kapoor, C. Urich, J. Avitable, J. Liu, D. Housman, Recombinant by Deloitte; M. Palchuk, Recombinant by Deloitte/Harvard University

**AACT-results: The Results Dataset Extensions for the AACT Database**  

**TBI14: Panel - Building a Richly Connected and Highly Analyzed Genotype/Phenotype Ecosystem in a World of Data Silos**  
D. Heinze, Zato Healthcare; S. Kahn, Illumina; P. McOwen, Zato Healthcare; J. Vengco, Baystate Health; E. Worthey, Medical College of Wisconsin

The ability to index, aggregate, search, navigate, analyze and share genomic and clinical data across departmental, institutional, geographic and political boundaries while maintaining security, privacy and data rights is critical to the success of translational medicine. We discuss advances in the technology of cooperative computing, information fusion and surface form ontologies with application to the translation of genomic research to clinical practice and, conversely, the application of phenotypic data to genomic research. Specifically, we describe a seminal collaboration of genomic R&D with clinical medicine as facilitated over a secure, clinically appropriate, ontology enabled, multi-centric platform for discovery across diverse genomic and clinical data sets that are stored and administered on diverse and disparate data centers and data types. This environment motivates the investigation of a variety of genotype/phenotype issues. We discuss the migration in the clinical context from sparse phenotype information to fully extracted phenotype data from the full clinical record to ontologically structured phenotype data. In the genetic research context, we discuss the migration toward a structure of deeply analyzed and organized clusters of genotype/phenotype data.

**TBI15: Papers/Podium Presentations - Machine Learning and Phenotype Discovery**  
Session Chair: Leonard D’Avolio

**Focused Proteomic Profiling for Late Onset Neonatal Sepsis**  
S. Mani, D. Cannon, C. Hartenberger, University of New Mexico; K. Ballard, Myriad RBM; H. Peceny, R. Ohls, University of New Mexico

**Heterogeneity within and across Pediatric Pulmonary Infections: From Bipartite Networks to At-risk Subphenotypes**  
S. Bhavnani, B. Dang, M. Cara, UTMB; G. Bellala, Hewlett Packard Laboratories; S. Visweswaran, University of Pittsburgh; A. Mejias, The Ohio State University; R. Divekar, Mayo Clinic

**Prioritizing Experimental Validations of Computational Predictions based on Estimated Biomedical Impact**  
M. Ganapathiraju, University of Pittsburgh, M. Ganapathiraju, Carnegie Mellon University; L. Viswanathan, University of Pittsburgh/Carnegie Mellon University

**Preliminary Classification of Cancer Sites Using Machine Learning and Somatic Mutations from the COSMIC Database**  
Y. Chen, M. Kochen, Z. Zhao, Vanderbilt University, H. Xu, The University of Texas Health Science Center at Houston
TUESDAY, APRIL 8
Scientific Sessions
1:30 p.m. – 3:00 p.m. | CONTINUED

**TBI16: Papers/Podium Presentations - Natural Language Processing**
Session Chair: Hua Xu

**Using SemRep and a Medication Indication Resource to Extract Treatment Relations from Clinical Notes**
C. Bejan, W. Wei, J. Denny, Vanderbilt University

**Facilitating Post-surgical Complication Detection through Sublanguage Analysis**
H. Liu, S. Sohn, S. Murphy, J. Naessens, Mayo Clinic; M. Burton, Mayo Clinic/Mayo Clinic College of Medicine; D. Larson, Mayo Clinic College of Medicine

**Phonetic Spelling Filter for Keyword Selection in Drug Mention Mining from Social Media**
P. Pimpalkhute, A. Patki, G. Gonzalez, Arizona State University

**Adapting a Natural Language Processing Tool to Facilitate Clinical Trial Curation for Personalized Cancer Therapy**
J. Zeng, The University of Texas MD Anderson Cancer Center; Y. Wu, The University of Texas Health Science Center at Houston; A. Bailey, A. Johnson, V. Holla, The University of Texas MD Anderson Cancer Center; E. Bernstam, The University of Texas Health Science Center at Houston; H. Xu, F. Meric-Bernstam, The University of Texas MD Anderson Cancer Center

3:00 p.m. – 3:30 p.m. Coffee Break Cyril Magnin Foyer
3:30 p.m. – 5:00 p.m. Plenary Session Cyril Magnin I/II

**TBI Keynote Presentation**

**Isaac S. Kohane, MD, PhD**
Henderson Professor of Pediatrics and Health Sciences and Technology, Co-Director Center for Biomedical Informatics Harvard Medical School; Director of the Francis A. Countway Library of Medicine

For details see page 16

5:00 p.m. – 6:00 p.m. TBI Poster Session
(not eligible for CME)

See page 48 for list of TBI posters, listed alphabetically by first author.

6:30 p.m. – 8:30 p.m. Billiards Meet-up at Jillian’s Billiards
(not eligible for CME)

For details see page 22
## Wednesday, April 9

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<tr>
<th>Time</th>
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<th>Location</th>
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<tr>
<td>7:00 a.m. – 6:00 p.m.</td>
<td>Registration Open</td>
<td>Cyril Magnin Foyer</td>
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<tr>
<td>7:00 a.m. – 8:15 p.m.</td>
<td><strong>AMIA Town Hall</strong>&lt;br&gt;<strong>How Can AMIA Best Support Clinical and Translational Informatics?</strong>&lt;br&gt;CTSA/CTSI, IKFC and AMIA: Collaboration, Leadership and the Future</td>
<td>Cyril Magnin I/II</td>
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<tr>
<td>7:00 a.m. – 8:30 a.m.</td>
<td>Continental Breakfast</td>
<td>Cyril Magnin Foyer</td>
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<tr>
<td>8:30 a.m. – 10:00 a.m.</td>
<td>Plenary Session&lt;br&gt;<strong>CRI Opening Session and Keynote Presentation</strong>&lt;br&gt;<strong>Richard Platt</strong>, MD, MSc&lt;br&gt;Professor and Chair of the Department of Population Medicine; Executive Director of the Harvard Pilgrim Health Care Institute</td>
<td>Cyril Magnin I/II</td>
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<tr>
<td>10:00 a.m. – 10:30 a.m.</td>
<td>Coffee Break</td>
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<tr>
<td>10:30 a.m. – 12:00 p.m.</td>
<td>Scientific Sessions</td>
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### CRI01: Podium Presentations - Novel Analytic Methods

**Session Chair: Joyce Niland**

- **SNAPL-CAT: Catalyzing the Rate-limiting Step of Big Data Psychometrics with Item-response Theory and Advanced Computerized Adaptive Testing**<br>
  M. Kao, Stanford School of Medicine; K. Cook, Northwestern University; T. Pacht, G. Olson, B. Darnall, S. Weber, S. Mackey, Stanford School of Medicine

- **Joint Analysis of Multiple Data Types in Electronic Health Records**<br>
  J. Lucas, Quintiles/Duke University
Discovery of Seasonal Patterns in Incidence of Disease from EHR Data
R. Melamed, H. Khiabanian, R. Rabadan, Columbia University

Utilizing Temporal Information to Improve Adverse Drug Event Prediction Models
A. Cami, B. Reis, Boston Children’s Hospital/Harvard Medical School

**CRIO2: Late Breaking Panel - Direct Use of EHR for Clinical Trial Data Collection Instead of a Dedicated Research EDC System**
V. Huser, NIH Clinical Center; K. Marsolo, Cincinnati Children’s Hospital; J. McKeey, NIH Clinical Center; B. Wells, Cleveland Clinic Research Institute

Seamless collection of clinical trial data in the context of routine care is a significant clinical research informatics (CRI) challenge. In recent years, despite existence of dedicated research electronic data capture (EDC) systems, such as REDCap or MediData Rave, collecting clinical trial data or registry data directly within an Electronic Health Record System (EHR) is emerging as a viable platform for certain type of studies. This panel will explore challenges and applicable standards in this domain and feature 3 case studies where research data capture is done in an EHR system.

**TBI17: Papers/Podium Presentations - Pharmacogenomics and Adverse Events**
Session Chair: Joshua Swamidass

**Efficiently Mining Adverse Event Reporting System for Multiple Drug Interactions**
Y. Xiang, A. Albin, K. Ren, The Ohio State University; P. Zhang, Indiana University School of Medicine; J. Etter, The Ohio State University; S. Lin, Marshfield Clinic Research Foundation; L. Li, Indiana University School of Medicine

**Implementation of Genotype-tailored Antiplatelet Therapy Following Percutaneous Coronary Stent Placement: A Mixed Methods Study**

**An Integrated Framework for the Pharmacogenomic Characterization of Oncological Drug Response to Enable Precision Medicine**
K. Bhuvaneshwar, M. Harris, T. Natarajan, L. Sheahan, Georgetown University; J. Deeken, Inova Translational Medicine Institute; S. Madhavan, Georgetown University

**Pharmacogenomic Analysis of Pathways in Multiple Rat Strains: Implications for Drug Testing in Models**

**TBI18: Student Paper Competition**
Session Chairs: Joshua Denny and Rachel Richesson

**Automated Physician Order Recommendations and Outcome Predictions by Data-mining Electronic Medical Records**
J. Chen, Stanford University Hospital; R. Altman, Stanford University

**Modeling Clinical Context: Rediscovering the Social History and Evaluating Language from the Clinic to the Wards**
C. Walsh, N. Elhadad, Columbia University

**Longitudinal Analysis of New Information Types in Clinical Notes**
R. Zhang, S. Pakhomov, G. Melton, University of Minnesota

**Considerations for Using Research Data to Verify Clinical Data Accuracy**
D. Fort, C. Weng, S. Bakken, Columbia University; A. Wilcox, Intermountain Healthcare

**How Essential are Unstructured Clinical Narratives and Information Fusion to Clinical Trial Recruitment?**
12:15 p.m. – 1:15 p.m. Lunch and Learn with IMO (not eligible for CME)

ICD10 and Meaningful Use - Opportunity for Innovation
Regis Charlot, MS, President and Chief Technology Officer, Intelligent Medical Objects, Inc.

12:15 p.m. – 1:15 p.m. Natural Language Processing Working Group Meeting (not eligible for CME)

Lunch not provided

1:30 p.m. – 3:00 p.m. Scientific Sessions

**CRI03: Papers/Podium Presentations - Ontologies in CRI**
Session Chair: Elmer Bernstam

**ClinMiner: Ontology Based Clinical Data Portal**
M. Shimoyama, T. Adamusiak, Medical College of Wisconsin

**Application of HL7/LOINC Document Ontology to a University-affiliated Integrated Health System Research Clinical Data Repository**
Y. Wang, S. Pakhomov, J. Dale, University of Minnesota; E. Chen, University of Vermont; G. Melton, University of Minnesota

**Standards-based Representation of Open Clinical Trials Data for Public Dissemination and Reanalysis.**
R. Shankar, A. Butte, Stanford University

**Semantator: Semantic Annotator for Converting Biomedical Text to Linked Data**
C. Tao, University of Texas Health Sciences Center at Houston; D. Song, D. Sharma, C. Chute, Mayo Clinic

**CRI04: Papers - Text Mining**
Session Chair: Stephane Meystre

**Discovering Associations among Diagnosis Groups Using Topic Modeling**
D. Li, T. Therneau, C. Chute, H. Liu, Mayo Clinic

**Semi-supervised Learning to Identify UMLS Semantic Relations**
Y. Luo, MIT; O. Uzuner, MIT/University at Albany

**Towards Transforming Expert-based Content to Evidence-based Content**
S. Moosavinasab, M. Rastegar-Mojarad, Mayo Clinic/University of Wisconsin-Milwaukee; H. Liu, Mayo Clinic; S. Jonnalagadda, Northwestern University/Mayo Clinic

**Detecting Associations between Major Depressive Disorder Treatment and Essential Hypertension using Electronic Health Records**
J. Pathak, Mayo Clinic; G. Simon, University of Minnesota; D. Li, J. Biernacka, G. Jenkins, C. Chute, D. Hall-Flavin, R. Weinshilboum, Mayo Clinic
**Scientific Sessions**

**WEDNESDAY, APRIL 9**

1:30 p.m. – 3:00 p.m. | CONTINUED

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**TBI19: Papers/Podium Presentations – Phenomic Analysis and Interpretation**

Session Chair: Paul Avillach

**Using a Biobank Linked to Electronic Medical Records to Identify Non-specific Clinically Associated Genetic Variants**


**Improving the Translation of Model Organism Research into Disease Diagnostics**

N. Washington, Lawrence Berkeley National Laboratory; M. Haendel, Oregon Health & Science University; S. Kohler; Charité - Universitätsmedizin Berlin; S. Lewis, Lawrence Berkeley National Laboratory; P. Robinson, Charité - Universitätsmedizin Berlin; D. Smedley, Wellcome Trust Sanger Institute; C. Mungall, Lawrence Berkeley National Laboratory

**Phenome Wide Association Studies Demonstrating Pleiotropy of a Genetic Variant within FTO with and without Adjustment for Body Mass Index**

R. Cronin, L. Bastarache, J. Field, D. Crawford, J. Denny, Vanderbilt University

**EHR-based Phenome Wide Association Study in Pancreatic Cancer**

T. Adamusiak, M. Shimoyama, Medical College of Wisconsin

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**TBI20: Panel – Strategies for Sustainable Open Source Projects for Clinical and Translational Research: Lessons from the Trenches**

E. Nelson, LabKey Software; L. Rozenblit, Prometheus Research; M. Mendis, Harvard Partners; B. Bauman, OpenClinica; M. Igra, LabKey Software

Theoretically, taking an open source approach can broaden the public benefits of grant-funded software projects; increase the leverage of informatics investments; draw upon a wider pool of contributors and expertise; and improve transparency, reproducibility, and extensibility. However, as Dr. Isaac Kohane has warned, open source software is “...free like a pony. You still have to feed it and clean up after it” (TEDMed, 2013). Furthermore, simply making software open source does not ensure that it will become immediately useful to others. This panel will cover practical strategies for generalizing, sustaining, and evolving open source software developed for clinical and translational research. Panel members will address sustainable business models, feasibility of grant support, implications of different open source licenses, modes of dissemination (including community norms for attracting open-source evangelists), community-building approaches, practical trade-offs, and unexpected challenges. Panelists represent open source platforms for clinical and translational research that have proven useful across multiple organizations and shown sustainability over time. Platforms include LabKey Server (http://labkey.org), RexDB (http://rexdb.org/), i2b2 (https://i2b2.org/), and OpenClinica (https://openclinica.com/).

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3:00 p.m. – 3:30 p.m. | Cyril Magnin Foyer

Coffee Break

3:30 p.m. – 5:00 p.m. | Cyril Magnin I/I

Plenary Session

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**TBI Closing Session:**

Translational Bioinformatics Year-in-Review

**Russ B. Altman**, MD, PhD, FACMI

*Kenneth Fong Professor of Bioengineering, Genetics, Medicine and (by courtesy) Computer Science; Director, Biomedical Informatics Training Program, Stanford University*

For details see page 17

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5:00 p.m. – 6:00 p.m. | Cyril Magnin Foyer

Networking Reception

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6:00 p.m. – 8:00 p.m. | Lobby Bar

Women in Informatics Networking Event

*(not eligible for CME)*

For details see page 22
### Thursday, April 10

<table>
<thead>
<tr>
<th>Time</th>
<th>Event</th>
<th>Location</th>
<th>Speaker(s)</th>
<th>Notes</th>
</tr>
</thead>
<tbody>
<tr>
<td>7:00 a.m. – 6:00 p.m.</td>
<td>Registration Open</td>
<td>Cyril Magnin Foyer</td>
<td>V. Huser, National Institutes of Health</td>
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<tr>
<td>7:00 a.m. – 8:15 a.m.</td>
<td>Birds-of-a-Feather Sessions - <em>open to all</em></td>
<td>Cyril Magnin Foyer</td>
<td>V. Huser, National Institutes of Health</td>
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<tr>
<td><strong>BOF04</strong>: Collecting Clinical Trial Data using EHR Structured Forms</td>
<td><em>not eligible for CME</em></td>
<td>Cyril Magnin I</td>
<td>V. Huser, National Institutes of Health</td>
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<td>Integration of clinical trial data collection into routine care is an ongoing clinical research informatics challenge. For clinical registry studies and certain types of observational trials, it is sometimes possible to directly use form capabilities of the existing EHR system to capture research data. This is possible for studies that do not have study blinding concerns (patient or investigator), existence of incidental findings or research vs. clinical billing issues. This session will be a discussion and exchange of experiences with direct use of EHR system by point of care clinicians/researchers rather than using electronic case report forms in a designated research-only electronic data capture system.</td>
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<td><strong>BOF05</strong>: Representing Study Eligibility Criteria (SIGEC)</td>
<td><em>not eligible for CME</em></td>
<td>Cyril Magnin II</td>
<td>C. Weng, Columbia University; I. Sim, University of California San Francisco</td>
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<td>With the burgeoning adoption of electronic health records (EHRs), vast amounts of clinical data are increasingly available for computational reuse. It is imperative that the scientific community leverage phenomic data to accelerate clinical research at low cost and large scale. A critical step toward this goal is matching clinical eligibility criteria to clinical data. However, this task is complicated by the semantic gap between free-text eligibility criteria and raw clinical data: each criterion has many ways to describe it and a myriad of clinical data points that represent it. To accelerate advances in this important research area, we would like to create a collaborative community to chart the problem space, to define mission-critical tasks, and to develop a “divide-and-conquer” strategy. We welcome colleagues with interest in formal representations for clinical eligibility criteria and computable phenotype knowledge or with expertise in text-based knowledge engineering to join us in this effort. We also welcome anyone who is just interested in this topic to join us and share your insights and feedback.</td>
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<td><strong>BOF06</strong>: Future Directions for the Clinical and Translational Research Informatics Community</td>
<td><em>not eligible for CME</em></td>
<td>Cyril Magnin III</td>
<td>P. Payne, The Ohio State University; J. Starren, Northwestern University</td>
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<td>With recent changes in the structure and focus on the national CTSA consortium, the TBI and CRI community that had coalesced around the Informatics Key Function Committee (IKFC) has been left without a professional home. This BOF session will explore next steps related to the sustainability and growth of that community, addressing critical questions such as: 1) should AMIA serve as the new professional home for the activities previously housed in the IKFC? 2) are there other stakeholders who should be engaged in an expanded/renewed community derived from the IKFC? and 3) what existing IKFC or new community-derived activities should an emergent professional home engage in.</td>
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<tr>
<td>7:00 a.m. – 8:30 a.m.</td>
<td>Continental Breakfast</td>
<td>Cyril Magnin Foyer</td>
<td>Stockton</td>
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<tr>
<td>8:00 a.m. – 5:00 p.m.</td>
<td>AMIA Board of Directors Meeting</td>
<td>Stockton</td>
<td>Stockton</td>
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</tbody>
</table>
8:30 a.m. – 10:00 a.m.  Scientific Sessions

**CRI05: Panel - Big Data Analytics**

L. Frey, University of Utah School of Medicine; L. Lenert, Medical University of South Carolina; S. DuVall, University of Utah School of Medicine/VA Salt Lake City Health Care System; L. Dahm, University of California Irvine Medical Center

The panel will discuss improvements and issues with the use of big data methodologies for predictive analytics in clinical research. The panel is made up of four clinical informatics researchers that are involved with the development of big data systems in healthcare. Dr. Lisa Dahm is the Director of Clinical Informatics at Irvine and oversees the development and operations of Saritor Hadoop Distributed File System, a big data solution for Irvine’s electronic medical records. Dr. Scott DuVall is the Associate Director for the VA’s corporate data warehouse VINCI, which includes all VA patient records. Drs. Leslie Lenert and Lewis Frey are Co-PIs on a NIH funded Clinical Personalized Pragmatic Prediction of Outcomes (Clinical3PO) big data system deployed at the VA. The Clinical3PO initiative is focused on predictive analytics within the VA using similarity matching technology. Dr. Lenert will present an overview of the Clinical3PO system and its implications for clinical care. Dr. Frey will discuss the technology development and preliminary results from the near-term prediction algorithm within the Clinical3PO system. Hadoop and other big data systems provide an ecosystem that is affordable, scalable and highly available, while allowing clinical research and clinical practice to coexist in the same system.

**CRI06: Papers/Podium Presentations - Enterprise Approaches for Support Clinical Research**

Session Chair: Phillip Payne

- **Implementing a Clinical Research Management System: One Institution’s Successful Approach Following Previous Failures**
  T. Campion, V. Blau, S. Brown, D. Izcovich, C. Cole, Weill Cornell Medical College

- **A Scalable Approach to Dynamically Populating REDCap-enabled Research Registries from an Enterprise Data Warehouse**
  F. Lamantia, R. Rice, D. Ervin, W. Stephens, Ohio State University Wexner Medical Center; G. Young, The Ohio State University; T. Borlawsky, Ohio State University Wexner Medical Center

- **Design and Implementation of an Automated Geocoding Infrastructure for the Duke Medicine Enterprise Data Warehouse**

- **When Should We Share? Securely Measuring the Overlap between Private Datasets**
  S. Swamidass, Washington University; L. Rozenblit, Prometheus Research LLC

**CRI07: Papers/Podium Presentations - Natural Language Processing**

Session Chair: Jyotishman Pathak

- **Natural Language Processing of Free-text Problem List Sections in Structured Clinical Documents: a Case Study at NIH Clinical Center**
  V. Huser, J. Cimino, NIH CC

- **Who’s Counting? Probability Statements and Risk in Medical Literature**
  L. Deiens, IBM Research; L. Tounsi, Dublin City University; B. Sacaleanu, IBM Research

- **Open Source Clinical NLP - More than Any Single System**
  J. Masanz, Mayo Clinic; S. Pakhomov, University of Minnesota; H. Xu, University of Texas at Houston; S. Wu, C. Chute, H. Liu, Mayo Clinic

- **Extracting and Standardizing Medication Information in Clinical Text - the MedEx-UIMA System**
  M. Jiang, Y. Wu, University of Texas at Houston; A. Shah, Vanderbilt University; P. Priyanka, University of Texas at Houston; J. Denny, Vanderbilt University; H. Xu, University of Texas at Houston
**CRI08: Papers/Podium Presentations - Data-driven Models**  
*Session Chair: Chunhua Weng*

**On the Bayesian Derivation of a Treatment-based Cancer Ontology**  
Z. Gao, Harvard Medical School; J. Warner, Vanderbilt University; P. Yang, Massachusetts General Hospital; G. Alterovitz, Harvard Medical School/Massachusetts Institute of Technology

**Ontology-based Tools to Expedite Predictive Model Construction**  
P. Haug, J. Holmen, Intermountain Healthcare/University of Utah; X. Wu, K. Mynam, M. Ebert, Intermountain Healthcare; J. Ferraro, Intermountain Healthcare/University of Utah

**Methodological Approach for Incorporating Socioecological Context into Translational Research**  
M. Breitenstein, University of Minnesota/Mayo Clinic; J. Pathak, Mayo Clinic

**Chicago Health Insights: A Novel Approach for Regional Integration of Electronic Health Record Data**  
A. Kho, K. Jackson, J. Behrens, S. Goel, Northwestern University

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10:00 a.m. – 10:30 a.m.  
**Coffee Break**  
*Cyril Magnin Foyer*

10:30 a.m. – 12:00 p.m.  
**Scientific Sessions**

**CRI09: Panel - TRANSFoRm Digital Infrastructure:**  
*The Architecture for the Learning Healthcare System in Europe*  
*Session Chair: Jihad Obeid*  
V. Curcin, Imperial College London; T. Arvanitis, University of Warwick; P. Brodka, Wroclaw University of Technology; D. Corrigan, Royal College of Surgeons of Ireland; B. Delaney, King’s College London

The Learning Healthcare System (LHCS) refers to the close coupling of clinical research and the translation of research into practice in a cycle of continuous improvement. This vision permeates multiple domains, clinical as well as technical, and its realization is dependent on establishing standardized, secure, and traceable flows of data between these domains to maximize the research and clinical benefits. This panel presents the model-driven software architecture designed in the TRANSFoRm project (www.transformproject.eu), a large EU FP7 Integrated Project to develop a digital infrastructure for the LHCS in European Primary Care. The discussion will cover various components of the system, comparing them with similar tools in USA and Europe, and analyze how our modular approach supports collaboration with related efforts.

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**CRI10: Papers/Podium Presentations - Clinical Data Repositories (Design and Management Aspects)**  
*Session Chair: Jihad Obeid*

**Sample and Clinical Information Link (SCI-Link) - Standardized Data Registry Management System**  
M. Ahuja, J. Schappet, R. Lorentzen, Y. Wang, P. Hylock, University of Iowa; L. Kimberly, University of Iowa Hospital and Clinics; H. Davis, B. Knosp, University of Iowa; M. Santillan, D. Santillan, University of Iowa Hospital and Clinics

**LabKey Server: An Open Source Platform for Large-scale, Translational Research**  
M. Igra, E. Nelson, B. Piehler, J. Eckels, M. Bellew, P. Hussey, A. Rauch, LabKey Software

**Creating a Next-generation Research Informatics Infrastructure: WICER Lessons for Data Integration**  
A. Wilcox, Intermountain Healthcare; D. Fort, S. Bakken, Columbia University

**Toward a Cognitive Task Analysis for Biomedical Query Mediation**  
G. Hruby, J. Cimino, V. Patel, C. Weng, Columbia University
CRI11: Papers/Podium Presentations - Researcher Needs
Session Chair: Nicholas Anderson

Using Software to Elicit User Needs for Clinical Research Visit Scheduling

Transforming Research Program Management: From a Ticketing System to a Computerized Research Record (CoRR)
P. Embi, M. Lopetegui, T. Borlawsky, F. Lamantia, R. Rice, The Ohio State University

Are EHR Data Suitable for Secondary Use? Researcher Views
N. Weiskopf, S. Bakken, C. Weng, Columbia University

Workflows for a Web-based Consent Management System with Electronic Consent
K. Marsolo, J. Nix, Cincinnati Children’s Hospital Medical Center

CRI12: Late Breaking Abstracts - NLP and Novel Methods for Analyzing Clinical Data
Session Chair: Paul Harris

Clinical Research Data Warehouse Enrichment via NLP Over Discharge Summaries
M. Burton, E. Sadhu, X. Dong, Z. Lei, N. Bahroos, University of Illinois at Chicago

Population Epidemiology from Clinical Text: Replicating the ACE Study in Gulf War Veterans
K. Hammond, A. Ben-Ari, R. Laundry, VA Puget Sound Health Care System/University of Washington

Patient-level Temporal Aggregation for Text-based Asthma Status Ascertainment
S. Wu, Y. Juhn, S. Sohn, H. Liu, Mayo Clinic

12:15 p.m. – 1:15 p.m. Lunch and Learn with ConvergeHEALTH by Deloitte
(not eligible for CME)

UC-ReX, Two Years In – Lessons Learned, Future Plans
Lisa Dahm, Director of Clinical Informatics for UC-ReX, Director Center for Biomedical Informatics, UC Irvine

Precision Medicine, Precision Miner – A Discovery Workbench
Michael Kamerick, Specialist Leader, Informatics, ConvergeHEALTH; Matvey Palchuk, CMIO, ConvergeHEALTH

1:30 p.m. – 3:00 p.m. Scientific Sessions

CR13: Podium Presentations - Use of Electronic Health Records for Research
Session Chair: Michael Kahn

National Institutes of Health’s Biomedical Translational Research Information System (BTRIS) Data Query Tool
J. Cimino, E. Ayres, National Institutes of Health

Use of the Epic Electronic Health Record for Comprehensive Clinical Research Management at Duke

Analyzing Problem List Data for Real-time Re-Use
C. Hebert, The Ohio State University Wexner Medical Center; C. Shivade, The Ohio State University; P. Payne, P. Embi, The Ohio State University Wexner Medical Center

Comparison of Medication Extraction Methods in the Cleveland Clinic Electronic Health Record
B. Wells, A. Milinovich, S. Griffith, Cleveland Clinic
**CRI14: Podium Presentations - Engaging Patients in Research**  
*Session Chair: Adam Wilcox*

*Cross-system Evaluation of Clinical Trial Search Engines*  
S. Jiang, C. Weng, Columbia University

*Impact of Electronic Health Record Alerts on Recruitment for Clinical Trials: A Study of Patients’ Perceptions*  
E. Patterson, C. Roth, Ohio State University; N. Elder, S. Cotton, University of Cincinnati; P. Embi, Ohio State University

*Weaving a Strong Trust Fabric through Community-engaged Research: Lessons from the WICER Project about Digital Infrastructure for the Learning Health System*  
S. Bakken, N. Suero-Tejeda, T. Bigger, Columbia University; A. Wilcox, Intermountain Health Care; B. Boden-Albala, Mount Sinai Medical Center

*Spreading Research and Engaging Disease Communities - One Automated Tweet at a Time*  
K. Reuter, University of Southern California; A. Chatterjee, San Francisco; J. Daigre, University of California, San Francisco; B. Voytek, University of California, San Diego

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**CRI15: Papers/Podium Presentations - Novel Approaches to Data Standards**  
*Session Chair: Rachel Richesson*

*City of Hope Research Informatics Common Data Elements Information Architecture Framework*  
A. Shakir, K. Olsen, A. Londrc, S. Pannoni, S. Berger, J. Niland, City of Hope

*Temporal Knowledge Acquisition from Clinical Research Documents for Community-based Clinical Research Data Standards Development*  
C. Weng, Columbia University

*Simplifying Complex Clinical Element Models to Encourage Adoption*  
R. Freimuth, Q. Zhu, J. Pathak, C. Chute, Mayo Clinic

*Enhancing Electronic Health Records to Support Clinical Research*  
D. Vawdrey, C. Weng, Columbia University; D. Herion, NIH; J. Cimino, Columbia University/NIH

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**CRI16: Panel - Architectures for Data Standardization and Interoperability in Patient Centered Outcomes Research**  
*Session Chair: Cyril Magnin III*

J. Campbell, University of Nebraska; R. Waitman, University of Kansas; A. Kho, Northwestern University Feinberg School of Medicine; T. Campion, Weill Cornell Medical College; S. Rosenbloom, Vanderbilt University

The Patient Centered Outcomes Research Institute's (PCORI) Clinical Data Research Network (CDRN) initiative promises to test the reusability of electronic health records (EHR) and other data sources to support comparative effectiveness research. This effort is concurrent with a national investment in EHRs compliant with Nationwide Health Information Network (NwHIN) standards designed to develop interoperable shared data. The interoperation and utility of this data is untested by clinical research at a national scale. This panel will bring together four recently funded CDRNs who will describe the approaches to interoperability, data models, and standardization they are incorporating in their network.
THURSDAY, APRIL 10
Scientific Sessions
3:00 p.m. – 3:30 p.m. Coffee Break Cyril Magnin Foyer
3:30 p.m. – 5:00 p.m. Scientific Sessions

CRI17: Papers/Podium Presentations - Using Electronic Health Records for Research in Multiple Settings
Session Chair: Leslie Lenert

Detailed Clinical Modeling Approach to Data Extraction from Heterogeneous Data Sources for Clinical Research
S. Lim Choi Keung, L. Zhao, J. Rossiter, University of Warwick; M. McGilchrist, F. Culross, University of Dundee; J. Ethier, A. Burgun, INSERM; R. Verheij, N. Khan, Netherlands Institute for Health Services Research; A. Taweel, King’s College London; V. Curcin, Imperial College London; B. Delaney, King’s College London; T. Arvanitis, University of Warwick

A Data Set Authoring Tool and Code Generator for Secondary Analysis in Distributed Research Networks
D. Meeker, C. Skeels, RAND Corporation; L. Pearlman, K. Czajkowski, University of Southern California Information Sciences Institute; L. Ohno-Machado, University of California, San Diego

C. Daniel, AP-HPC/INSERM

Variation in Cohorts Derived from EHR Data in Four Care Delivery Settings
S. Rea, Intermountain Healthcare; K. Bailey, J. Pathak, Mayo Clinic; P. Haug, Intermountain Healthcare

CRI18: Podium Presentations - Tools and Support for Clinical Studies
Session Chair: Denise Hynes

RexInstrument: Exploring an Open-source Standard for Configuring Clinical Research Instruments
C. Tirrell, L. Rozenblit, F. Farach, Prometheus Research, LLC

Government-developed Software for Clinical Research - Open-season on Open-source: The NICHD Clinical Trials Database (CTDB) and Toolkit (CTK) Development and Adoption Strategy
C. Sastry, M. Breymaier, A. Idriss, S. Ivusic, R. Annechiarico, NIH/NICHD; T. Caruso, NIH/NICHDT/University of North Carolina at Chapel Hill

Protocol Decision Trees to Facilitate Protocol Planning and Patient Enrollment

A Decision Framework for Selecting a Federated Data Sharing Platform
M. Ames, University of Colorado; J. Bondy, Colorado Clinical and Translational Sciences Institute; A. Davidson, Denver Public Health; T. Wade, National Jewish Health; M. Kahn, Colorado Clinical and Translational Sciences Institute
CRI19: Papers/Podium Presentations - Social Networking for Scientists
Session Chair: David Eichmann

Open Proposals: A Pre-competitive Interactive Space for the Research Community
O. Gologorskaya, M. Kahlon, L. Yuan, L. Schoonerman, C. Piontkowski, R. Sac, C. McFall, University of California, San Francisco

Research Networking Across an Entire University
G. Weber, Harvard Medical School

Temporal Analysis of the Usage Log of a Research Networking System
S. Yoon, S. Trenbowski, R. Steinman, S. Bakken, C. Weng, Columbia University

Visualizing and Evaluating the Growth of Multi-institutional Collaboration Based on Research Network Analysis
J. Luo, University of Wisconsin Milwaukee; C. Pelfrey, G. Zhang

CRI20: Late Breaking Abstracts - Highlights of CRI Work in Press
Session Chair: Judy Logan

Data Governance Requirements for Distributed Clinical Research Networks: Triangulating Perspectives of Diverse Stakeholders
K. Kim, San Francisco State University/Betty Irene Moore School of Nursing, UC Davis; D. Browe, H. Logan, San Francisco State University; R. Holm, L. Hack, Object Health; L. Ohno-Machado, UC San Diego

Profiling Risk Factors for Chronic Uveitis in Juvenile Idiopathic Arthritis: A New Model for EHR-based Research
T. Cole, Stanford University; J. Frankovich, Stanford University School of Medicine; S. Iyer, P. LePendu, A. Bauer-Mehren, N. Shah, Stanford University

Inappropriate Access Detection for Electronic Health Records Using Collaborative Filtering
A. Menon, X. Jiang, J. Kim, J. Vaidya, Rutgers University; L. Ohno-Machado, UC San Diego

CRI Challenges in Studies Using EHRs of Deceased Patients: Piloting Analyses Via the “No IRB” Route
V. Huser, NIH Clinical Center; M. Kayaalp, Z. Dodd, National Library of Medicine; J. Cimino, NIH Clinical Center

5:00 p.m. – 6:00 p.m.  
CRI Poster Session and Reception
(not eligible for CME)

See page 51 for list of CRI posters, listed alphabetically by first author.

6:00 p.m. – 7:00 p.m.  
Clinical Research Informatics Working Group Meeting
(not eligible for CME)
**Friday, April 11**

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<thead>
<tr>
<th>Time</th>
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<tr>
<td>7:30 a.m. – 11:30 a.m.</td>
<td>Registration Open</td>
<td>Cyril Magnin Foyer</td>
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<td>8:30 a.m. – 10:00 a.m.</td>
<td>Scientific Sessions</td>
<td>Cyril Magnin II</td>
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**CRI21: Podium Presentations - Clinical Data Repositories - Data/results-oriented**
Session Chair: Yuan Luo

- **Being PRO ACTive- What can a Clinical Trials Database Reveal about ALS?**
  - N. Zach, Prize4Life; R. Kueffner, Ludwig-Maximilians-University; A. Shui, A. Sherman, J. Walker, E. Sinani, I. Katsovskiy, D. Schoenfeld, Massachusetts General Hospital; G. Stolowtzyk, R. Norel, IBM; N. Atassi, J. Berry, M. Cudkowicz, Massachusetts General Hospital; M. Leitner, Prize4Life

- **Understanding Diagnosis Assignment from Billing Systems Relative to Electronic Health Records for Clinical Research Cohort Identification**
  - R. Waitman, K. Gerard, D. Connolly, G. Ator, University of Kansas Medical Center

- **Discrepancy-reducing Feedback Loops Based on Intra- and Inter-validation of Synoptic Pathology Data**

- **Design and Implementation of a Real-time Location Sensing System for Determining Interpersonal Social Contacts in the Emergency Department**
  - S. Hilton, Georgia Regents University; D. Lowery-North, V. Hertzberg, L. Elon, G. Cotsonis, Emory University

M. Paterno, Partners Healthcare/Brigham and Women’s Hospital; P. Dayan, Columbia University; E. Tham, University of Colorado/Children’s Hospital Colorado; H. Goldberg, Partners Healthcare/Brigham and Women’s Hospital; R. Grundmeier, The Children’s Hospital of Philadelphia; N. Kuppermann, University of California Davis

The overall goal of this multi-center study is to decrease inappropriate use of cranial CT for children with minor blunt head trauma (BHT) by creating a generalizable model to translate evidence into clinical practice. Participating sites used either a web-based, platform-independent Clinical Decision Support (CDS) Service provided by the Enterprise Clinical Rules Service (ECRS) team at Partners Healthcare System (PHS) or locally produced CDS (i.e., using the EHR’s CDS rules engine) developed at a central site and exported to sites selecting the local CDS option. This panel will describe the process of creating specific, computable knowledge from evidence for use across multiple institutions. A key contribution to the field of generalizable computer decision support that we provide is our experience using the same decision support content in disparate CDS systems. Our learning goals for this panel are three-fold: [a] to understand the processes needed to provide CDS for multiple sites both within a local EHR internal rules engine and from an external, remote, cloud-based CDS service; [b] to consider the pros and cons of each approach; and [c] to understand how best to provide shareable, reusable, scalable, and maintainable CDS. We will provide initial findings from implementation from two sites in our assessment. All panelists are key participants in this research, and each brings specific expertise in his/her presentation area.
**CRI23: Podium Presentations - Special Focus on i2b2**  
Session Chair: Vojtech Huser

**Importing Continuity of Care Documents into i2b2 and SMART**  
J. Klann, Harvard Medical School/Massachusetts General Hospital/Partners Healthcare System; A. Porter, N. Wattanasin, Partners Healthcare System; S. Murphy, Harvard Medical School/Massachusetts General Hospital/Partners Healthcare System

**Leveraging Big Data Technology within i2b2 Platform**  
X. Dong, N. Bahroos, M. Chukhman, E. Sadhu, R. Johnson, H. Sharma, D. Hynes, University of Illinois at Chicago

**Components and Workflow for Patient Identification using i2b2 for Clinical Trials (i2b2-CT)**  
N. Wattanasin, M. Mendis, A. Porter, S. Ubaha, Partners HealthCare; J. Bickel, K. Mandl, I. Kohane, Boston Children’s Hospital; S. Murphy, Partners HealthCare/Massachusetts General Hospital

**Implementing i2b2 as a Research Portal to the Carolina Data Warehouse through OpenFurther**  
R. Bradford, A. Farrag, J. Mostafa, University of North Carolina at Chapel Hill

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**CRI24: Late Breaking Abstracts - Collaborative Research Models and Methods**  
Supporting Privacy and Research Efficiencies  
Session Chair: Russ Waitman

**Unzipping Zip Codes: A Methodology to Assign De-identified Health Data to Smaller Geographic Localities**  
A. Pah, J. Behrens, S. Goel, A. Kho, Northwestern University

**Protecting Privacy and Promoting Large-scale Research Using an Informatics Framework for Multisite Longitudinal Pediatric Biorepository Studies**  
A. Felmeister, T. Rivera, A. Masino, J. Pennington, The Children’s Hospital of Philadelphia; P. White, The Children’s Hospital of Philadelphia/Perelman School of Medicine at the University of Pennsylvania

**Accelerating Multi-center Research through a Statewide Electronic Collaborative IRB Review System in South Carolina: Initial Experiences**  
R. Alexander, J. Obeid, L. Lenert, Health Sciences South Carolina/Medical University of South Carolina

**NIH/NICHD’s Clinical Research Informatics Team Collaboration with a Wounded Warrior Rehabilitation Research Consortium**  
C. Sastry, NIH/NICHD; S. Milbourne, R. Sacher, M. Mattera, BADER Consortium-University of Delaware; F. Velez, R. Annechiarico, NIH/NICHD

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10:00 a.m. – 10:30 a.m.  
**Coffee Break**  
Cyril Magnin Foyer

10:30 a.m. – 12:00 p.m.  
**Plenary Session**

**CRI Closing Plenary Session and Year-in-Review**  
Peter J. Embi, MD, MS, FACMI  
Associate Professor and Vice Chair, Department of Biomedical Informatics, The Ohio State University; Chief Research Information Officer, The Ohio State University Medical Center; Physician, Department of Internal Medicine, Division of Rheumatology & Immunology

*For details see page 17*
# TBI Poster Session

(not eligible for CME)

**Tuesday, April 8**

5:00 p.m. – 6:00 p.m.

Room: Cyril Magnin Foyer

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<td>Z. Abrams, A. Pattanayak, W. Kenworthy, L. Dalton, P. Payne, The Ohio State University</td>
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<td>A. Alexander, Mayo Clinic</td>
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<td>S. Ayvaz, Kent State University; Q. Zhu, Mayo Clinic; H. Hochheiser; University of Pittsburgh; M. Brochhausen, University of Arkansas; J. Horn, University of Washington; M. Dumontier, Stanford University; M. Samwald, Medical University of Vienna; R. Boyce, University of Pittsburgh</td>
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<td>D. Barash, M. Drany, Ben-Gurion University</td>
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<td>How Bipartite Network Visualizations Complement Ingenuity Pathway Analysis: A Case Study in Methylation Related to Preterm Births</td>
<td>S. Bhavnani, B. Dang, M. Caro, R. Menon, UTMB</td>
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<td>Visualizing Clinically Similar Phenotypes</td>
<td>C. Borromeo, University of Pittsburgh, C. Mungall, Lawrence Berkeley National Lab; J. Espina, University of Pittsburgh; M. Haendel, Oregon Health and Science University; D. Smedley, J. Jacobsen, Wellcome Trust Sanger Institute; H. Hochheiser, University of Pittsburgh</td>
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<td>Population-specific Manifestation of Insulin Signaling/Action Pathways: A Case Study of Chronic Metabolic Diseases in Colombians</td>
<td>M. Caro, B. Dang, UTMB; G. Bedoya, University of Antioquia; S. Bhavnani, UTMB</td>
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<td>Predicting Gene-level Pathogenicity Using Variation in Asymptomatic Individuals</td>
<td>C. Cassa, Harvard Medical School</td>
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<td>Y. Chang, C. Chen, P. Chen, H. Yang, Taipei Medical University; G. Lin, Institute for Information Industry</td>
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<td>D. Chhabra, S. Sharma, Brigham and Women’s Hospital; A. Kho, Brigham and Women’s Hospital/Boston Children’s Hospital; V. Carey, S. Weiss, K. Tantisira, Brigham and Women’s Hospital</td>
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<td>B. Conkright, K. Bhuvaneshwar, M. Harris, L. Song, Y. Gusev, S. Madhavan, Georgetown University Medical Center</td>
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<td>Revealing Heterogeneity in Gene Regulation through Network Edge Coloring: A Case Study in Pediatric Pulmonary Infections</td>
<td>B. Dang, UTMB; S. Visweswaran, University of Pittsburgh; A. Mejias, The Ohio State University; R. Divekar, Mayo Clinic; S. Bhavnani, UTMB</td>
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<td>A. Demartini, University of Pavia; D. Capozzi, Biomeris s.r.l./University of Pavia; A. Malovini, Biomeris s.r.l./University of Pavia/IRCCS Fondazione Salvatore Maugeri; A. Puca, IRCCS Multimedica/Università degli Studi di Salerno; R. Bellazzi, Biomeris s.r.l./University of Pavia/IRCCS Fondazione Salvatore Maugeri</td>
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<td>L. Frey, University of Utah; L. Lenert, Medical University of South Carolina</td>
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<td>Integrating Genetic Variants within the i2b2 Framework: The NoSQL Way</td>
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<td>H. Han, Seoul National University College of Medicine/CHA University General Hospital/Seoul National University Systems; J. Ohn, Seoul National University College of Medicine/Seoul National University Systems; J. Moon, CHA University General Hospital; J. Kim, Seoul National University College of Medicine/Seoul National University Systems</td>
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<td>D. Li, J. Okamoto, S. Leischow, H. Liu, Mayo Clinic</td>
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<td>P. Li, Shanghai Jiaotong University; X. Jiang, S. Wang, University of California-San Diego; J. Kim, Shanghai Jiaotong University; H. Xiong, L. Ohno-Machado, University of California-San Diego</td>
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<td>A. Loisacana, N. Rejock, C. Barnes, M. Conlon, E. Schmidt, University of Florida</td>
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<td>S. Nafisi, Harvard Medical School; M. Maitituoheti, Harvard Medical School/Beth Israel Deaconess Medical Center; E. Przybytkowski, McGill University; D. Wall, Harvard Medical School/Beth Israel Deaconess Medical Center; M. Baski, McGill University; P. Tonellato, Harvard Medical School/Beth Israel Deaconess Medical Center</td>
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<td>M. Panahiazar, Knoesis Center</td>
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<td>Phenocarta: A Comprehensive Gene-disease Database for the Interpretation of Genomics Studies</td>
<td>E. Portales-Casamar; N. St-Georges; P. Pavlidis, University of British Columbia/NeuroDevNet</td>
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<td>Derived Gene Network</td>
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<td>A Reverse Translational Bioinformatics Approach to Validate an Association between HIV Warts and Breast Cancer</td>
<td>S. Syed-Abdul, Y. Li, Taipei Medical University College of Medical Science and Technology</td>
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<td>F. Vitali, F. Mulas, University of Pavia; A. Zambelli, Fondazione Salvatore Maugeri; R. Bellazzi, University of Pavia</td>
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### CRI Poster Session

*(not eligible for CME)*

**Thursday, April 10**

5:00 p.m. – 6:00 p.m.

Room: Cyril Magnin Foyer

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<td>The Colibri Project: A Shared Database of Pediatric Patients’ Examinations</td>
<td>C. Altomare, G. Lanzola, R. Bellazzi, University of Pavia; G. Reni, IRCCS E. Medea - La Nostra Famiglia</td>
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<td>Automating Data Re-use Policies for NIH Intramural Clinical Research Data</td>
<td>E. Ayres, J. Cimino, NIH</td>
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<td>A Pilot Evaluation of Patient Data Sharing Preferences</td>
<td>E. Bell, M. Grando, L. Ohno-Machado, UCS D</td>
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<td>Dynamical Approaches to Clinical Artificial Intelligence, Decision-making, and Cognitive Computing</td>
<td>C. Bennett, Indiana University/Centerstone Research Institute; K. Hauser, Indiana University; T. Doub, Centerstone Research Institute</td>
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<td>Methods for Identification of Sexual Health Variables in a Research Data Warehouse</td>
<td>W. Brown, W. Bockting, New York State Psychiatric Institute/Columbia University; N. Reame, S. Bakken, Columbia University</td>
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<td>Supporting the Discoverability of Research Objects by Connecting Research and Researchers with ORCID</td>
<td>R. Bryant, ORCID; K. Holmes, Washington University</td>
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<td>Role of Citation Tracking in Updating of Systematic Reviews</td>
<td>M. Choong, G. Tsafnat, University of New South Wales</td>
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<td>Connecting the Fred Hutchinson Cancer Research Center to the eagle-i Network: An Open Source Solution</td>
<td>A. Clark, Fred Hutchinson Cancer Research Center; B. Bahl, D. Bourges-Waldeck, Harvard Medical School; J. Locke, FreeLock; J. McMurry, D. Macfadden, Harvard Medical School</td>
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<td>B. de Veer, C. Fong, S. Lee, C. Nefcy, S. Prager, T. Black, University of Washington</td>
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<td>D. Gabriel, University of California, Davis; D. Ludwig, University of California, San Francisco; D. Bell, University of California, Los Angeles; P. Paul, W. Zhu, University of California, San Diego; A. Patel, University of California, Los Angeles; T. Nagler, University of California, Davis; D. Berman, University of California, San Francisco; L. Dahm, University of California, Irvine</td>
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<td>D. Harris, R. Kavuluru, Z. Yu, R. Theakston, J. Jaramczyk, T. Johnson, University of Kentucky</td>
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<td>A Person-centered Health Information Delivery Tool for Dementia Caregivers on an Ontological Semantic Basis</td>
<td>C. Hempelmann, Texas A&amp;M University-Commerce; V. Gurupur, Louisiana Tech University</td>
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<td>Comparative Analysis of Online Health Information Search by Device Type</td>
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<td>W. Jiang, P. Li, Shanghai Jiaotong University/UC San Diego; S. Wang, UC San Diego; Y. Wu, Duke University; M. Xue, Shanghai Jiaotong University/UC San Diego, L. Ohno-Machado, X. Jiang, UC San Diego</td>
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<td>H. Joo, H. Lee, P. Bow, J. Blum, University of Michigan</td>
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<td>Stanford-NIH Pain Registry: Open Source Platform for Large-scale Longitudinal Assessment of Clinical Data and Patient-reported Outcomes</td>
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<td>M. Kao, Stanford University; K. Cook, Northwestern University; G. Olson, T. Pacht, B. Damall, S. Weber, S. Mackey, Stanford University</td>
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