accelerating precision medicine and patient-centered outcomes research through discovery, development, and delivery
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Follow Twitter @AMIAinformatics for real time updates
Use hashtag #TBICRI15 to share with others
Check twubs.com/TBICRI15 to track the conversation
Connect via WiFi access Wireless Network: Parc55meeting
Username: N/A Password: tbicri (available on Level 4 only)
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Summit on Translational Bioinformatics
March 23-25, 2015

Scientific Program Committee

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Jihad S. Obeid, MD
Medical University of South Carolina

Nicholas P. Tatonetti, PhD
Columbia University

Shyam Visweswaran, MD, PhD
University of Pittsburgh

Hua Xu, PhD
University of Texas Health Science Center
Dear Colleagues and Friends,

On behalf of AMIA, the track chairs and scientific program committee, I am excited to welcome you to a phenomenal 2015 AMIA Summit on Translational Bioinformatics! We have received a range of high quality submissions covering the gamut of translational bioinformatics topics including pan-omics, phenotyping, machine learning, big data analysis, data integration and discovery.

This year we have a terrific program with tutorials, lectures, panels, and posters that showcase the latest advances in applying informatics to translational biomedical research and clinical care. I want to thank the community for their contributions to the Summit that makes it stand out as a leading pioneer in Translational Bioinformatics.

This year we will have a special focus on big data, kicked off with a keynote from Dr. Philip Bourne, NIH Associate Director for Data Science, and brought home with an invited panel consisting of thought leaders from five Big Data Centers of Excellence. We are pleased to offer two tutorials that promise to strengthen your understanding of electronic phenotyping algorithms with Dr. Jyotishman Pathak and Dr. Joshua Denny, as well as experimental approaches to validating mined data, Dr. Hua Fan Minogue.

Moreover, we have put you in a difficult position of choosing one of three highly relevant Birds-of-a-Feather (BOF) sessions covering: 1) Precision Medicine, Dr. Jessie Tenenbaum, 2) Deep phenotyping, Dr. Jyotishman Pathak, and 3) Big Data to Knowledge, Dr. Nicholas Tatonetti.

TBI will have four tracks covering the following:

- **Track 1** focuses primarily on pan-omics and includes one late breaking session on analysis methods.
- **Track 2** includes a series of methods and analysis sessions along with two late breaking sessions on big data and ontologies.
- **Track 3** covers extant phenotyping topics with an emphasis on the EHR. These include computational approaches, using the OMOP common data model and semantic phenotyping along with other methods.
- **Track 4** incorporates knowledge discovery topics related to drug repurposing, drug discovery, crowd sourcing and heterogeneous data sources. This track includes the student paper competition that highlights our up and coming talent.

We have also added a new design challenge that focuses on novel analysis of lung cancer using The Cancer Genome Atlas (TCGA). Dr. Warren Kibbe, Director of the NCI Center for Biomedical Informatics and Information Technology (CBIIT), will provide an introduction to TCGA.

We will close the conference with Dr. Russ Altman’s Year-in-Review covering the key contributions in translational bioinformatics.

One last comment, this conference is chock-full of highly relevant and timely topics. I suggest you divide and conquer with your colleagues—after all it is big data. I hope you all thoroughly enjoy the summit and leave with many new collaborators and insights!

Sincerely,

Lewis J. Frey, PhD
Chair, Scientific Program Committee for TBI
Associate Professor, Public Health Sciences,
College of Medicine
Medical University of South Carolina
Summit on Clinical Research Informatics
March 25-27, 2015

Scientific Program Committee

Chair
Chunhua Weng, PhD, MS
Columbia University

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University of Alabama at Birmingham

Judith R. Logan, MD, MS
Oregon Health & Science University

Philip R. O. Payne, PhD, FACMI
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Kavishwar Wagholikar
Mayo Clinic

Russ Waitman, PhD
University of Kansas

Colin Walsh, MD
Columbia University

Nicole Weiskopf, PhD
Oregon Health & Science University
Dear Colleagues and Friends,

On behalf of the 2015 Joint Summits Scientific Program Committee, I extend a warm welcome to AMIA members, students, practitioners, informatics researchers, industry partners, and others interested in the rapidly emerging field of informatics to attend the AMIA 2015 Clinical Research Informatics (CRI) Summit.

The CRI Summit is the premier forum for interacting with leaders and practitioners in clinical research informatics. It publicizes the latest accomplishments in clinical research informatics, highlights innovations and best practices for managing Big Clinical Data for observational studies and clinical trials, and discusses informatics science related to secondary research use of Big Clinical Data.

The theme of the 2015 Clinical Research Informatics Summit is **accelerating precision medicine and patient-centered outcomes research through discovery, development and delivery**. Dr. Paul Wicks from PatientsLikeMe will open the meeting with his keynote speech. This meeting will bring together translational scientists and informatics researchers and practitioners from academia, industry, government and non-profit sectors to share knowledge and best practices, and to forge interdisciplinary collaborations across boundaries. Dr. Peter Embi from The Ohio State University will conclude the meeting with his “CRI Year in Review”.

Equally emphasizing discovery and impact, this Summit highlights translational research from bench to bedside, practice, and communities. The past year of 2014 witnessed multiple exciting events for the CRI community, including the launch of the nationwide Patient-Centered Outcomes Research Network (PCORnet), the continued increase in the use of electronic health records in physician offices in the United States, the rise in sharing results of clinical trial studies, and the establishment of the NIH Big Data to Knowledge (BD2K) center. The CRI community has been presented with more and larger electronic data sources for clinical research than ever, which come with old and new challenges for data quality, interoperability, privacy, security, and Big Data Analytics.

This CRI Summit offers great learning opportunities with informative expert panels, scientific sessions, and posters covering all of the above topic areas. It also newly created **Peer-based Learning Workshops** to facilitate group learning among practitioners and to enable sharing of best practices for these topic areas. To further nurture junior trainees in this field, there are dedicated **Student Paper Competition** sessions. A special session for **Design Challenge** will showcase working solutions to structuring clinical research eligibility criteria, a fundamental challenge in the CRI community.

The Scientific Program Committee has prepared a fantastic program in the beautiful city of San Francisco. I look forward to seeing you at this exciting meeting!

Sincerely,

Chunhua Weng, PhD, MS
Chair, Scientific Program Committee for CRI
Associate Professor of Biomedical Informatics
Columbia University
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 2015 TBI/CRI registrants have free access to the archives. To access the AMIA Proceedings archive, simply point your browser to [http://knowledge.amia.org](http://knowledge.amia.org). Use your AMIA login and password to access the 2015 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 publically 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.

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**MyItinerary 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 “2015 Joint Summits on Translational Science”.

**MyItinerary Web App**
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.

**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, March 23

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<td>Continental Breakfast</td>
<td>Cyril Magnin Foyer</td>
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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>8:30 a.m. – 12:00 p.m.</td>
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<td></td>
<td><strong>T01</strong>: Authoring, Sharing, and Executing Electronic Phenotyping Algorithms: Past, Present and the Future</td>
<td>Cyril Magnin III</td>
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<td><strong>T02</strong>: Taking Control of Your Findings: A Guide to Experimental Approaches for Validating Mined Data</td>
<td>Mission</td>
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<td>10:00 a.m. – 10:30 a.m.</td>
<td>Coffee Break</td>
<td>Cyril Magnin Foyer</td>
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<td>12:00 p.m. – 1:30 p.m.</td>
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<tr>
<td>1:30 p.m. – 3:00 p.m.</td>
<td><strong>TBI Opening Session and Keynote Presentation:</strong> Philip E. Bourne, PhD</td>
<td>Cyril Magnin I/II</td>
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<td>3:00 p.m. – 3:30 p.m.</td>
<td>Coffee Break</td>
<td>Cyril Magnin Foyer</td>
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<td>3:30 p.m. – 5:00 pm</td>
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<td><strong>TBI01</strong>: Podium Presentations - Variants, Clusters and Palindromes in the Genome-Environment</td>
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<td><strong>TBI04</strong>: Podium Presentations - Drug Repurposing and Interactions</td>
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<td>5:00 – 6:00 p.m.</td>
<td>Networking Reception</td>
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<td>6:00 p.m. – 7:00 p.m.</td>
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<td>TBI Birds-of-a-Feather Sessions</td>
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<td><strong>TBI-BOF01</strong>: Precision Medicine</td>
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<td><strong>TBI-BOF02</strong>: Deep Phenotyping</td>
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<td>7:00 a.m. – 6:00 p.m.</td>
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<td><strong>TBI05</strong>: Papers/Podium Presentations – Systems Biology and Protein Biomarkers</td>
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<td><strong>TBI06</strong>: Podium Presentations - Drugs and Phenotype</td>
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<td><strong>TBI11</strong>: Peer-based Learning Workshop - Semantic Phenotyping for Translational Medicine</td>
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<td><strong>TBI12</strong>: Podium Presentations - Crowd Sourcing and Heterogeneous Data Sources</td>
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<td><strong>TBI13</strong>: Papers/Podium Presentations - Cancer Networks</td>
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<td><strong>TBI14</strong>: NLP, Ontologies, and Data Standards</td>
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<td><strong>TBI15</strong>: Papers/Podium Presentations - Phenotyping Methods</td>
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<td><strong>TBI19</strong>: Papers/Podium Presentations - Phenotyping with EHRs</td>
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<td><strong>TBI20</strong>: Design Challenge - Improving Understanding through TCGA Data Integration</td>
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<td>6:30 p.m. – 9:00 p.m.</td>
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<td>Jillian’s Billiards Club</td>
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<td>7:00 a.m. – 8:15 a.m.</td>
<td>AMIA Town Hall</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>
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<td>7:00 a.m. – 6:00 p.m.</td>
<td>Registration Open</td>
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<tr>
<td>8:30 a.m. – 10:00 a.m.</td>
<td>CRI Opening Session and Keynote Presentation: Paul Wicks, PhD</td>
<td>Cyril Magnin I/II</td>
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<td>10:00 a.m. – 10:30 a.m.</td>
<td>Coffee Break</td>
<td>Cyril Magnin Foyer</td>
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<td>10:30 a.m. – 12:00 p.m.</td>
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<td><strong>TBI21</strong>: Didactic Panel - Challenges of Implementing Genomic Decision Support in the Real World—Experience from the eMERGE and CSER Networks</td>
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<td><strong>TBI22</strong>: Papers/Podium Presentations - Data Querying and Quantification</td>
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<td><strong>CRI01</strong>: Student Paper Competition, Part 1 – Text Mining for Clinical Research</td>
<td>Cyril Magnin II</td>
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<td><strong>CRI02</strong>: Papers/Podium Presentations – Phenotyping</td>
<td>Embarcadero, Level 3</td>
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<td><strong>CRI03</strong>: Didactic Panel - OHDSI - An Open Collaborative Approach for Rapid Evidence Generation</td>
<td>Cyril Magnin I</td>
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<td>12:00 p.m. – 1:30 p.m.</td>
<td>Lunch on own</td>
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<td>12:00 p.m. – 1:30 p.m.</td>
<td>IMO Corporate Roundtable (by invitation)</td>
<td>Hearst</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>TBI23</strong>: Papers/Podium Presentations - NGS and Gene Analysis Methods</td>
<td>Cyril Magnin I</td>
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<td><strong>TBI24</strong>: Papers/Podium Presentations - Natural Language Processing Methods</td>
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<td><strong>CRI04</strong>: Student Paper Competition, Part 2 - Health Data Analytics for Clinical Research</td>
<td>Cyril Magnin II</td>
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<td><strong>CRI05</strong>: Papers/Podium Presentations - Personalized Predictive Modeling</td>
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<td><strong>CRI06</strong>: Design Challenge - Structuring Clinical Research Eligibility Criteria</td>
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<td>3:00 p.m. – 3:30 p.m.</td>
<td>Coffee Break</td>
<td>Cyril Magnin Foyer</td>
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<tr>
<td>3:30 p.m. – 5:00 p.m.</td>
<td>TBI Closing Session and Translational Bioinformatics Year in Review: Russ B. Altman, MD, PhD</td>
<td>Cyril Magnin I/II</td>
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<tr>
<td>5:00 p.m. – 6:00 p.m.</td>
<td>CRI Poster Session 1 and Reception</td>
<td>Cyril Magnin Foyer</td>
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<tr>
<td>6:00 p.m. – 7:00 p.m.</td>
<td>OSU Great Lakes Region Meeting (by invitation) – Affiliate Event</td>
<td>Cyril Magnin III</td>
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<td>6:00 p.m. – 7:30 p.m.</td>
<td>Signet Accel Corporate Roundtable (by invitation)</td>
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<td>6:00 p.m. – 8:00 p.m.</td>
<td>Women in Informatics Networking Event (WINE)</td>
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<tr>
<td>7:00 p.m. – 9:00 p.m.</td>
<td>OSU Reception (by invitation) – Affiliate Event</td>
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<td>7:00 a.m. – 8:15 a.m.</td>
<td>Birds-of-a-Feather Sessions</td>
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<tr>
<td>CRI-BOF01:</td>
<td>Sustaining the Effective Use of Health Care Data</td>
<td>Cyril Magnin I</td>
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<td>CRI-BOF02:</td>
<td>Common Data Models for Patient-centered Comparative Effectiveness Research</td>
<td>Cyril Magnin II</td>
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<tr>
<td>CRI-BOF03:</td>
<td>Creating a Home for the Clinical and Translational Research Informatics Community within AMIA and Beyond</td>
<td>Cyril Magnin III</td>
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<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>7:00 a.m. – 8:30 a.m.</td>
<td>TriNetX Corporate Roundtable (by invitation)</td>
<td>Hearst</td>
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<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. – 10:00 a.m.</td>
<td>CRI10: Peer-based Learning Workshop - Visualizing Business Analytics and HIT for PCORI</td>
<td>Mission</td>
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<tr>
<td>8:30 a.m. – 10:00 a.m.</td>
<td>Scientific Sessions</td>
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<tr>
<td>CRI07:</td>
<td>Didactic Panel - Clinical Trials Results Data Sharing: The Time is Now</td>
<td>Cyril Magnin III</td>
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<tr>
<td>CRI08:</td>
<td>Papers - Modeling Clinical Data to Support Clinical Research</td>
<td>Cyril Magnin I</td>
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<tr>
<td>CRI09:</td>
<td>Podium Presentations - Data Sharing and Research Collaboration</td>
<td>Cyril Magnin II</td>
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<tr>
<td>CRI11:</td>
<td>Papers/Podium Presentations - Secure Processing of PHI</td>
<td>Embarcadero, Level 3</td>
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<tr>
<td>10:00 a.m. – 10:30 a.m.</td>
<td>Coffee Break</td>
<td>Cyril Magnin Foyer</td>
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<tr>
<td>10:30 a.m. – 12:00 p.m.</td>
<td>Scientific Sessions</td>
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<tr>
<td>CRI12:</td>
<td>Didactic Panel - PCORnet CDRN Data Quality Challenges and Solution</td>
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<tr>
<td>CRI13:</td>
<td>Podium Presentations - Data Integration and Information Fusion</td>
<td>Cyril Magnin I</td>
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<tr>
<td>CRI14:</td>
<td>Podium Presentations – Standards</td>
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<tr>
<td>CRI15:</td>
<td>Papers - Text Mining</td>
<td>Mission</td>
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<tr>
<td>CRI16:</td>
<td>Papers/Podium Presentations - Data Abstraction and Text Mining</td>
<td>Embarcadero, Level 3</td>
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<tr>
<td>12:15 p.m. – 1:15 p.m.</td>
<td>Lunch &amp; Learn with ConvergeHEALTH by Deloitte</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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<tr>
<td>CRI17:</td>
<td>Interactive Panel - Where is the Science in Big Data Visual Analytics? From Pretty Pictures to Transformative Biomedical Discoveries</td>
<td>Cyril Magnin III</td>
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<tr>
<td>CRI18:</td>
<td>Papers/Podium Presentations - Data Integration, Exploration and Mining</td>
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<td>CRI19:</td>
<td>Papers/Podium Presentations - Semantic Interoperability</td>
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<tr>
<td>CRI20:</td>
<td>Papers/Podium Presentations - User Needs and Consenting Methods and Considerations</td>
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<tr>
<td>CRI21:</td>
<td>Papers/Podium Presentations - Workflow Architecture</td>
<td>Mission</td>
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<td>3:00 p.m. – 3:30 p.m.</td>
<td>Coffee Break</td>
<td>Cyril Magnin Foyer</td>
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<td>3:30 p.m. – 5:00 p.m.</td>
<td>Scientific Sessions</td>
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<td><strong>CRI22</strong>: Papers/Podium Presentations - Temporal Data Analytics</td>
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<td><strong>CRI23</strong>: Papers/Podium Presentations - Adverse Outcomes</td>
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<td><strong>CRI24</strong>: Podium Presentations - Collective Knowledge Mining</td>
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<td><strong>CRI25</strong>: Papers/Podium Presentations - Real-time Decision Support</td>
<td>Mission</td>
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<td><strong>CRI26</strong>: Peer-based Learning Workshop - IRBShare and Honest Broker</td>
<td>Embarcadero, Level 3</td>
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<td>5:00 p.m. – 6:00 p.m.</td>
<td>CRI Poster Session 2 and Reception</td>
<td>Cyril Magnin Foyer</td>
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**Friday, March 27**

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<thead>
<tr>
<th>Time</th>
<th>Event</th>
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<tr>
<td>7:00 a.m. – 8:30 a.m.</td>
<td>Prometheus Research Corporate Roundtable (by invitation)</td>
<td>Powell, Level 3</td>
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<td>7:30 a.m. – 8:30 a.m.</td>
<td>Continental Breakfast</td>
<td>Cyril Magnin Foyer</td>
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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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<tr>
<td>8:30 a.m. – 10:00 a.m.</td>
<td>Scientific Sessions</td>
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<td><strong>CRI28</strong>: Papers/Podium Presentations - Disease Detection, Diagnosis, and Monitoring: State of the Art</td>
<td>Cyril Magnin I</td>
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<td><strong>CRI29</strong>: Papers/Podium Presentations – Buttons</td>
<td>Cyril Magnin II</td>
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<td><strong>CRI30</strong>: Papers/Podium Presentations - Ontology-based Semantic Methods</td>
<td>Mission</td>
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<td><strong>CRI31</strong>: Peer-based Learning Workshop - Everything about Scientific Profiles: Resource Sharing and Networking</td>
<td>Embarcadero, Level 3</td>
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<td>10:00 a.m. – 10:30 a.m.</td>
<td>Coffee Break</td>
<td>Cyril Magnin Foyer</td>
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<tr>
<td>10:30 a.m. – 12:00 p.m.</td>
<td><strong>CRI Closing Session and Year in Review: Peter Embi, MD, M5, FACMI</strong></td>
<td>Cyril Magnin I</td>
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AMIA Town Hall

The Precision Medicine Initiative Update

Join AMIA leaders for an open Town Hall event with updates on AMIA activities, President Obama’s Precision Medicine Initiative, and Q&A with the audience. We want to keep AMIA members informed of these activities, and to brainstorm about how we can continue to leverage the expertise of the informatics community. We welcome your engagement and full participation in this exciting initiative.

In January, AMIA leaders and members were invited to the White House and heard President Obama announce his $2.15 million investment in the Precision Medicine Initiative. This is a White House and National Institute of Health priority, and has the potential to affect hundreds of millions of Americans. Finding ways for us to engage the public and leveraging the expertise of AMIA members will be critical to the success of this work. While this initiative is research-based, precision medicine goes beyond the traditional -omics. Precision medicine is about asking the question “what kind of information do I need to more precisely target interventions to improve a person’s health?” We can’t ask or answer these questions without informatics.

In addition to the President’s announcement, NIH has convened a Precision Medicine Workshop and a series of working groups that will engage experts from government, academe, industry, non-profit, health system providers, and advocacy groups. The topics to examine include:

- Genomics/PGx/Other omics
- Epidemiology, population & clinical
- Policy, Ethics, Law
- Computer science (mobile platforms, UI)
- EHRs
- Measures of the personal environment
- Health services, implementation, & outcomes research

These groups are expected to address critical issues affecting the Precision Medicine Initiative and EHR-derived health data with the goal to establish a national cohort of 1 million plus individuals.

Doug Fridsma, MD, PhD
@fridsma
President and CEO, AMIA

Atul Butte, MD, PhD, FACMI
@atulbutte
Professor of Pediatrics (Systems Medicine) and of Genetics and, by courtesy, of Computer Science, of Medicine (Immunology and Rheumatology) and of Pathology
Stanford School of Medicine

Blackford Middleton, MD, MPH, MSc
@bfrm
Chair, AMIA Board of Directors
Professor of Biomedical Informatics, and of Medicine
Vanderbilt University Medical Center

Joshua C. Denny, MD, MS, FACMI
@jdnashville
Associate Professor of Biomedical Informatics
Associate Professor of Medicine
Vanderbilt University School of Medicine

Jessie Tenenbaum, PhD
@jessiet1023
Associate Director, Bioinformatics
Duke Translational Medicine Institute

Wednesday, March 25
7:00 a.m. – 8:15 a.m.
(not eligible for CME)

Cyril Magnin I & II
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Vanderbilt University Medical Center

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Brigham and Women’s Hospital

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Neil Sarkar, PhD, FACMI
University of Vermont

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

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

Jessica Tenenbaum, PhD
Duke Translational Medicine Institute

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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.

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

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 28.5 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 certified sessions
- Completion of individual session evaluations using QR codes in back of this program book (required for nurses)
- Completion of the evaluation survey sent via email post-meeting
- Verification of attendance through the participant’s electronic report of sessions attended through the individual login at www.amia.org. The physician participant will be able to generate a CME certificate through the AMIA automated system.
- Requesting credit by April 27, 2015

For Nurse CE and the most up-to-date disclosure information, see http://www.amia.org/jointsummits2015 and the hard copy handout with this program book.
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 2015 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@amia.org

TARGET AUDIENCE
The target audience for this live activity includes:

- 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
Keynote Speakers

TBI Opening Plenary Session and Keynote Presentation

**Philip E. Bourne, PhD**  
*Associate Director for Data Science, National Institutes of Health (NIH)*

Bourne’s professional interests focus on service and research. He serves the national biomedical community through contributing ways to maximize the value (and hence accessibility) of scientific data. His research focuses on relevant biological and educational outcomes derived from computation and scholarly communication. This implies algorithms, text mining, machine learning, metalanguages, biological databases, and visualization applied to problems in systems pharmacology, evolution, cell signaling, apoptosis, immunology and scientific dissemination. He is committed to maximizing the societal benefit derived from university research and to furthering the free dissemination of science through new models of publishing and better integration and subsequent dissemination of data and results.

Monday, March 23  
1:30 p.m. – 3:00 p.m.  
Cyril Magnin I/II

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*

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.

Wednesday, March 25  
3:30 p.m. – 5:00 p.m.  
Cyril Magnin I/II
CRI Opening Session and Keynote Presentation

Paul Wicks, PhD
Vice President of Innovation, PatientsLikeMe

Specializing in the conduct of clinical research using the Internet, Paul is responsible for shaping the scientific validity of the PatientsLikeMe platform and generating insights from the personal health data shared by members. This sharing of online medical data has led to over 50 novel studies including a patient-led observational trial of lithium in ALS, digital tools to develop patient-reported outcome measures, a “dose–response” curve for the benefits of friendship between patients, and new methods for gaining patient input into clinical trial design. Prior to joining PatientsLikeMe, Paul worked at the Institute of Psychiatry (King’s College London) studying cognition and neuroimaging in rare forms of ALS, and the psychological consequences of Parkinson’s disease. In 2011 he was awarded MIT Technology Review’s TR35 “Humanitarian of the Year” award and was recognized as a TED Fellow in 2012.

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

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.
Birds-of-a-Feather Sessions
(not eligible for CME)

Tuesday, March 24    7:00 a.m. – 8:15 a.m.

**TBI-BOF01: Precision Medicine**

*J. Tenenbaum, Duke University*  
*Cyril Magnin I*

President Obama’s announcement of the Precision Medicine initiative puts the Translational Bioinformatics Summit on center stage for articulating how to integrate health data and ‘omics’ data to achieve precision medicine. Dr. Jessie Tenenbaum will lead a discussion informed by input from leaders in the field. If you want to be part of this timely discussion on the future of translational research make sure you attend this BOF.

**TBI-BOF02: Deep Phenotyping**

*J. Pathak, Mayo Clinic*  
*Cyril Magnin II*

Deep phenotyping has been described as a critical methodology on the path to precision medicine. Dr. Jyotishman Pathak will describe his efforts at Mayo Clinic and how they can be used, expanded and generalized to create well-specified phenotypes for genomic studies. Be part of the discussion on how we can work to achieve deep phenotype identification and utilization across healthcare.

**TBI-BOF03: Big Data to Knowledge**

*N. Tantonetti, Columbia University*  
*Cyril Magnin III*

The Big Data to Knowledge initiative is the perfect storm of patient centered information, metadata, genomics, phenotyping and causal knowledge discovery. Dr. Nicholas Tatonetti will lead the BOF in a discussion of the current state of research and how it impacts our progress toward precision medicine. Be sure to attend this BOF to discuss the successes, questions and challenges that the field will need to tackle in order to transform data into knowledge in this big data era.
Thursday, March 26  7:00 a.m. – 8:15 a.m.

**CRI-BOF01: Sustaining the Effective Use of Health Care Data**

*A. Wilcox, Intermountain Healthcare; E. Holve, AcademyHealth*

This birds-of-a-feather (BOF) session will discuss lessons learned in sustaining health research data infrastructures. Specifically, it will address (a) what sustainability models exist for health research data infrastructures, (b) what are the common and important attributes of those models that lead to sustainability, (c) what are other lessons learned from both successful and unsuccessful models, and (d) what are current important trends in sustainability. A recent informatics journal issue focused on sustaining large projects working with clinical data, and initial information will be drawn from the examples in that issue. These examples created an initial set of sustainability examples from which patterns may be identified; however, more examples are needed to best identify important characteristics of successful sustainability plans. With this BOF session, we can identify both more examples and more themes from existing examples to inform others developing such plans. Sustainability is a critical topic, with better understanding and application needed to maximize the benefit of investments in clinical research data infrastructures.

**CRI-BOF02: Common Data Models for Patient-centered Comparative Effectiveness Research**

*A. Solomonides, NorthShore University HealthSystem; J. Logan, Oregon Health & Science University*

This birds-of-a-feather session (BOF) will address two issues: (a) From the point of view of scientists and clinical/biomedical researchers, what are the merits of the many alternative data models that have been used or proposed for comparative effectiveness research? (b) From the point of view of practical informaticians who must extract-transform-load (ETL) data from EHRs into data marts built to the specification of an abstract model, what are the common virtues and challenges of these models?

The Patient-centered Outcomes Research Institute has funded 11 Clinical Data Research Networks and 18 Patient-powered Research Networks with the goal of setting up a national network to support patient-centered comparative effectiveness research. A lively debate has taken place since then to determine the most appropriate and effective data models and standards to be adopted by such networks so as to ensure accuracy, longevity, sustainability, usability, and comparability of data. The issues and problems of using electronic health record data for research, and observational comparative effectiveness research in particular, have been extensively discussed in the literature. Aspects that have attracted less attention include the diversity of models and standards adopted and the difficulties of extraction of meaningful data for research. The BOF will discuss particular choices and their rationale, issues in relation to data domains, standards and terminologies for different domains, problems with extraction of reliable data from electronic health records and examples of uses of the data models in comparative effectiveness research.

**CRI-BOF03: Creating a Home for the Clinical and Translational Research Informatics Community within AMIA and Beyond**

*N. Anderson, University of California, Davis; P. Payne, The Ohio State University; J. Starren, Northwestern University; J. Tenenbaum, Duke University*

Over the last several years, substantial discussion has taken place within AMIA and in the broader biomedical research community concerning how to create, sustain, and engage a robust community of practice focusing upon clinical and translational research informatics. As part of these conversations, AMIA has emerged as a leading professional home for such individuals. In addition, emergent efforts by the CI4CC, CTSA IDTF, and Clinical Research Forum are providing convening venues for clinical and translational research informatics investigators, practitioners, and trainees. This birds-of-a-feather session will provide a forum for both discussing such developments and defining new and emergent priorities for AMIA in this constantly evolving and critical domain.
Lunch and Learn Events

Capture of Structured Clinical Data at the Point of Care to Support Translational Medicine: The IMO 2.x Platform

Eric Rose, MD, FAAFP, Director of Clinical Terminology, and Regis Charlot, MS, Chief Technology Officer and President, IMO

Complex analysis of clinical data for purposes of process or outcomes measurement, population health management, and knowledge discovery (e.g. genome-wide association studies) requires that clinical information be faithfully captured at the point of care. Standardized clinical terminologies are an absolute necessity for performing such activities on a large scale, particularly when aggregating data across multiple systems. However, there are numerous challenges to their successful use for clinical data capture. While such terminologies can often represent clinical information at a fine level of granularity, they often also provide very coarse-grained representation of such information, and in everyday usage, clinicians may not avail themselves of the available granularity, limiting secondary use of such data. Furthermore, standardized terminologies often have limited conceptual coverage in various areas. Lastly, for many semantic domains, there are multiple standardized terminologies in use. The introduction of ICD-10-CM has complicated the situation by forcing granularity in often non-intuitive ways and this will have a potentially distorting impact on structured data.

This presentation will describe a clinical interface terminology solution that addresses these issues. By providing clinician-friendly terms mapped to standardized terminologies, the semantic limitations of those terminologies can be overcome, and codes from multiple standardized terminologies can be retrieved for a single term. By providing frequent updates, IMO terminology and technology can keep up with rapid developments in clinical science, emerging diseases, and changes in clinical nomenclature. In addition, the solution links different terms in a semantic hierarchy, allowing end-users to be prompted, when they select a coarsely-granular term, with potential additional specificity, increasing the likelihood of capturing data at a fine level of specificity. This will initially be used to provide point-of-care decision support to assist with ICD-10-CM coding while maintaining clinical relevance.

The second portion of this presentation will describe the technical platform that supports this terminology solution, which allows organizations to deploy and update rapidly and seamlessly across multiple systems and environments, to monitor its use, and to understand the implications of any update of content.

The Convergence of Delivery and Discovery to Enhance Quality, Performance, and Cost in a Value-based Era

Fred Lee MD, MPH, VP Healthcare Analytics, ConvergeHEALTH by Deloitte

Providers who can effectively leverage their organization’s discovery capabilities towards improving care delivery will likely realize significant competitive advantages in a value-based environment. Predictive models, simulations, and AI methods can be used to enhance care for at-risk populations, help improve operational performance, and forecast financial impacts of assuming risk. Yet enabling learning healthcare loops at the enterprise level requires an integration of (1) statistically founded analytic technologies, (2) professional services, (3) data science, and (4) a collaborative network of peers and partners that can share content, insights, and experience.

In this session, attendees will be presented with how industry approaches centered on these four factors are accelerating the convergence of the discovery and delivery missions within AMCs, children’s hospitals, and other providers to enable evidence-based practice and practice-based evidence to operate in a self-reinforcing cycle.
Corporate Roundtables

*not eligible for CME* (by invitation)

AMIA Corporate Roundtables are fully catered private events coordinated by AMIA and hosted by organizations looking to engage directly with leaders in the field. These events allow AMIA Corporate Members to engage conference attendees and receive feedback on corporate strategies and product development while informing participants on current biomedical and health informatics issues. Corporate Roundtables are by invitation only and are not eligible for CME/CE.

For more information on Corporate Membership or sponsoring a Corporate Roundtable at an upcoming AMIA Event, please contact Ross Martin, MD, MHA, Vice President, Policy and Development, ross@amia.org, 301-657-1291 ext. 133.

**Wednesday, March 25**

12:00 p.m. – 1:30 p.m.

**Wednesday, March 25**

6:00 p.m. – 7:30 p.m.

**Thursday, March 26**

7:00 a.m. – 8:30 a.m.

**Friday, March 27**

7:00 a.m. – 8:30 a.m.
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.

Introduction to Biomedical and Health Informatics
April 1 – July 15, 2015
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 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 CMEs available.

Interprofessional Health Informatics
April 8, 2015 – July 8, 2015
University of Minnesota School of Nursing (UMN)
Course Director – Bonnie L. Westra, PhD, RN, FAAN
This course provides 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.

Biomedical and Health Informatics for Dietitians and Nutritionists
April 15 – October 3, 2015
OHSU in conjunction with the Academy of Nutrition and Dietetics
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 2015 Academy of Nutrition and Dietetics Food & Nutrition Conference & Exposition in Nashville, TN on October 3, 2015.
Up to 54.5 CPEU's are available.

Healthcare Interface Design Course
July 6 – September 11, 2015
University of Texas Health Science Center at Houston
Course Director – Jiajie Zhang, PhD
The University of Texas Health Science Center at Houston’s contribution to the AMIA 10x10 is an online course that focuses on EMR, human-computer interaction, human factors and Health IT usability. This virtual course will allow the student to master the fundamental principles and methods in health interface design, learn how to evaluate the usability of existing systems, and also learn how to design new systems with built-in good usability by applying related theories, principles, methodologies and techniques. CME not available with this course.

To register for any of the above courses and to view full descriptions, please visit: http://www.amia.org/education/10x10-courses
Social Events
(not eligible for CME)

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, March 24
6:30 p.m. – 9:00 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, March 25
6:00 p.m. – 8:00 p.m.
Parc 55 Hotel Lobby Bar
Save the Date

AMIA 2015 Annual Symposium

NOVEMBER 14 - 18
SAN FRANCISCO

Chair, 2015 Scientific Program Committee

Christoph U. Lehmann, MD, FAAP, FACMI
Vanderbilt University
@culehmann

The 2015 Annual Symposium will be held in San Francisco at the Hilton San Francisco Union Square
Daily Schedule

Monday, March 23

7:00 a.m. – 6:00 p.m. Registration Open

7:00 a.m. – 8:30 a.m. Continental Breakfast

8:30 a.m. – 12:00 p.m. Tutorials

**T01: Authoring, Sharing, and Executing Electronic Phenotyping Algorithms: Past, Present and the Future**

J. Pathak, Mayo Clinic; J. Denny, Vanderbilt University School of Medicine; W. Thompson, NorthShore University HealthSystem; L. Rasmussen, Northwestern University

This tutorial will cover basic themes about use of Electronic Health Records (EHRs) for generating cohorts of patients to serve as cases and controls for given clinical phenotypes. EHRs can be used for many different types of research including disease-based, response to treatment, clinical biomarkers, redefining “normal”, and analysis of changes over time of clinical variables and parameters. Deriving such phenotypes from EHR data can be challenging. Methods typically involve use of structured data such as billing codes, medication records, and laboratory data, as well as unstructured data such as narrative reports, for which natural language processing (NLP) systems are often used. After derivation of these phenotypes, populations can be used for clinical research. Linkage to DNA biobanks also enables the possibility of genomic and pharmacogenomic associations.

Research within the electronic MEDical Records and GEnomics (eMERGE; http://gwas.org) network has demonstrated success with EHR-based phenotypes for use in genome-wide association studies (GWAS). In addition, use of EHR-linked genetic data uniquely enables phenome-wide associations studies (PheWAS), which allows an unbiased scan of what diseases may be associated with a given genotype.

This tutorial will review the design of EHR-linked biobanks; methods for creating phenotype algorithms with integrated use of NLP, billing codes, laboratory and test results, and medication records (with review of a number of case studies); use of standard vocabularies in representing phenotype data, use of standards-based approaches for constructing and representing phenotype algorithms; and application of PheWAS to further characterize clinical variants. The tutorial will also include a hands-on session using a novel platform for authoring, sharing, and execution of electronic phenotyping algorithms (http://informatics.mayo.edu/PhEMA).

*Cyril Magnin III

#T01

* CTS-AMIA

All Attendees: Session Evaluation

Use QR codes to evaluate each session (required for nursing CE). If you are unable to access the surveys via QR code visit amia.org/jointsummits2015/TBI-evaluation
**T02: Taking Control of Your Findings: A Guide to Experimental Approaches for Validating Mined Data Mission**

*H. Fan Minogue, Stanford University School of Medicine*

In the last decade, advances in the technology have drastically speeded up the harvest of biological data and generated unprecedented amount of information. Modern biology has become a data-driven science, which also posed considerable challenges to experimental scientists in data processing and extraction of biological meanings. Bioinformatics has taken an increasingly vital role to meet the need for the effective management, analysis and integration of the data. New insights about diseases and their molecular basis have been identified through mining of massive-scale datasets and some have even led to new therapies. However, the role of bioinformatics researchers is often defined as a service provider, who facilitates the discovery of new biological insights by providing new clues, yet the validation of their predictions often needs to be performed by experimental scientists. Thus bioinformatics researchers often have to hand over their data and wish positive feedback or end up as the middle author of the work.

This tutorial will attempt to demonstrate the capability of data scientists to take control of their in silico findings by revealing the principle and application of approaches to experimental validation, the resources for validation assays, and the strategies to apply them for the specific questions of interest. Attendees should expect to learn about the essential experimental approaches used for validation and what they measure. The application of each assay and the resources for performing them will be discussed. The strategies to carry out a successful validation will also be discussed. Finally, the tutorial will end with three use cases showing what kind of assays can be utilized for each specific question, a discussion of hurdles and the cycle of experimentation and evaluation, and a brainstorming session about how these approaches can in turn empower and motivate the data mining.
### 3:30 p.m. – 5:00 p.m.  Scientific Sessions

<table>
<thead>
<tr>
<th>TBI01: Podium Presentations - Variants, Clusters and Palindromes in the Genome-environment</th>
<th>Cyril Magnin I  #TBI01</th>
</tr>
</thead>
</table>
| **Session Chair:** Zhongming Zhao  
**Identification of Zoonotic Disease Clusters by Integrating Phylogeography**  
*R. Beard, M. Scotch, Arizona State University* |  |
| **A Systems Biology Approach to Genome-environment Interactions Using Zebrafish (Danio rerio)**  
*G. Hardiman, Medical University of South Carolina* |  |
| **DNA Palindromes in Human Genome**  
*H. Li, University of Pittsburgh; A. Gupta, Carnegie Mellon University; M. Ganapathiraju, University of Pittsburgh/Carnegie Mellon University* |  |
| **Pathways Analysis of Rare, High-impact Variants in Mothers of Children with Autism**  
*C. O’Connell, S. Sharma, J. Jung, Stanford University, D. Wall, Stanford University/Hartwell Autism Informatics Initiative (iHART)* |  |

<table>
<thead>
<tr>
<th>TBI02: Podium Presentations - Machine Learning</th>
<th>Cyril Magnin II  #TBI02</th>
</tr>
</thead>
</table>
| **Session Chair:** Riccardo Bellazzi  
**Predicting Papillary Thyroid Carcinoma Patient Outcomes through Gene Expression Data**  
*K. Yu, W. Wang, C. Wang, M. Snyder, Stanford University* |  |
| **Meta-analysis of Gene Expression Using the Elastic Net**  
*J. Hughey, A. Butte, Stanford University* |  |
| **Weighting of Sensitivity and Specificity Estimates to Obtain Unbiased Performance Estimates for Classifiers Using Stratified Test Sets**  
*D. Morrison, T. Hernandez-Boussard, Stanford University School of Medicine* |  |
| **Clinical Diagnoses Prediction with Temporal Data Analytics**  
*R. Moskovitch, Columbia University* |  |
MONDAY, MARCH 23
Scientific Sessions
3:30 p.m. – 5:00 p.m. | CONTINUED

TBI03: Didactic Panel - Computational Phenotyping from Electronic Health Records across National Networks
J. Denny, Vanderbilt University; J. Sun, Georgia Institute of Technology; A. Kho, Northeastern University; J. Pathak, Mayo Clinic; R. Richesson, Duke University

Wide-spread adoption of electronic health records (EHRs) containing rich amounts of longitudinal clinical data has led to expanded opportunities to repurpose these data for clinical and genomic research. We will present experiences and lessons learned across five national networks, including the Electronic Medical Records & Genomics (eMERGE) Network, Strategic Health IT Advanced Research Project (SHARPn), Pharmacogenomics Research Network (PGRN), Pharmacogenomics in Very Large Populations (PGPop), and PCORnet. We will also discuss the future of phenotyping research and its impact to both clinical research and operation. Topics covered will include strengths and weaknesses of EHR data for secondary research; computational approaches to phenotype representation and applications; novel methods of creating computational phenotypes; refining and sharing phenotypes; phenotype validation; and the standardization, interoperability, access, management, and governance of phenotype definitions across clinical sites and research networks. We will also discuss informatics successes and clinical and genomic discoveries, as well as current challenges using case studies from aforementioned networks.

TBI04: Podium Presentations - Drug Repurposing and Interactions
Session Chair: Subha Madhavan

Assessing the Plausibility of Drug Interactions Signals Learned from the EHR
J. Banda, Stanford University; H. Strasberg, Wolters Kluwer Health; N. Shah, Stanford University

Prediction of Drug-drug Interactions Based on Clinical Side Effects
P. Zhang, F. Wang, J. Hu, IBM T.J. Watson Research Center

Identifying Candidate Ataxin-2 Inhibitors in High-throughput Screening Data Using Molecular Descriptors
D. Jones, J. Wen, D. Scales, University of Utah; T. Dexheimer, H. Sun, D. Maloney, A. Simeonov, A. Jadhav, National Institutes of Health; S. Pulst, J. Facelli, University of Utah

The Use of Cytogenetic Data to Enable Drug Repurposing Studies
Z. Abrams, P. Payne, The Ohio State University

5:00 p.m. – 6:00 p.m. Networking Reception (not eligible for CME)

6:00 p.m. – 7:00 p.m. Genomics Working Group Meeting (not eligible for CME)
## Tuesday, March 24

<table>
<thead>
<tr>
<th>Time</th>
<th>Event Description</th>
<th>Location</th>
<th>Facilitators</th>
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<tbody>
<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>
<tr>
<td>7:00 a.m. – 8:15 a.m.</td>
<td>TBI Birds-of-a-Feather Sessions</td>
<td>Cyril Magnin Foyer</td>
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</tr>
<tr>
<td><strong>TBI-BOF01: Precision Medicine</strong></td>
<td><em>J. Tenenbaum, Duke University</em></td>
<td>Cyril Magnin I</td>
<td>#PMI</td>
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<td></td>
<td>President Obama’s announcement of the Precision Medicine initiative puts the Translational Bioinformatics Summit on center stage for articulating how to integrate health data and ‘omics’ data to achieve precision medicine. Dr. Jessie Tenenbaum will lead a discussion informed by input from leaders in the field. If you want to be part of this timely discussion on the future of translational research make sure you attend this BOF.</td>
<td>* CTS-AMIA</td>
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<tr>
<td><strong>TBI-BOF02: Deep Phenotyping</strong></td>
<td><em>J. Pathak, Mayo Clinic</em></td>
<td>Cyril Magnin II</td>
<td>#PHENO</td>
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<td></td>
<td>Deep phenotyping has been described as a critical methodology on the path to precision medicine. Dr. Jyotishman Pathak will describe his efforts at Mayo Clinic and how they can be used, expanded and generalized to create well-specified phenotypes for genomic studies. Be part of the discussion on how we can work to achieve deep phenotype identification and utilization across healthcare.</td>
<td>* CTS-AMIA</td>
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<tr>
<td><strong>TBI-BOF03: Big Data to Knowledge</strong></td>
<td><em>N. Tatonetti, Columbia University</em></td>
<td>Cyril Magnin III</td>
<td>#BIGDATA</td>
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<td></td>
<td>The Big Data to Knowledge initiative is the perfect storm of patient centered information, metadata, genomics, phenotyping and causal knowledge discovery. Dr. Nicholas Tatonetti will lead the BOF in a discussion of the current state of research and how it impacts our progress toward precision medicine. Be sure to attend this BOF to discuss the successes, questions and challenges that the field will need to tackle in order to transform data into knowledge in this big data era.</td>
<td>* CTS-AMIA</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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### TBI05: Papers/Podium Presentations – Systems Biology and Protein Biomarkers

**Session Chair: Hua Xu**

<table>
<thead>
<tr>
<th>Title</th>
<th>Authors</th>
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</thead>
<tbody>
<tr>
<td>Druggability Profiling of Protein Biomarkers</td>
<td>S. Mani, D. Cannon, R. Ohls, D. Perkins, T. Oprea, S. Mathias, University of New Mexico; K. Ballard, Rules Based Medicine Inc.; O. Ursu, C. Bologa, University of New Mexico</td>
</tr>
<tr>
<td>Analysis of Viral Genetics for Estimating Diffusion of Influenza A H6N1</td>
<td>M. Scotch, Arizona State University; M. Suchard, University of California, Los Angeles; P. Rabinowitz, University of Washington</td>
</tr>
</tbody>
</table>

### TBI06: Podium Presentations - Drugs and Phenotype

**Session Chair: Jessica Tenenbaum**

<table>
<thead>
<tr>
<th>Title</th>
<th>Authors</th>
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<tbody>
<tr>
<td>Resources from the Clinical Pharmacogenetic Implementation Consortium (CPIC) to Enable Pharmacogenomic Clinical Decision Support</td>
<td>J. Hoffman, St. Jude Children’s Research Hospital; M. Whirl-Carrillo, Stanford University; R. Freimuth, Mayo Clinic; C. Haidar, K. Caudle, St. Jude Children’s Research Hospital; T. Klein, Stanford University; M. Relling, St. Jude Children’s Research Hospital</td>
</tr>
<tr>
<td>Extension of RxNorm for Medication Clinical Decision Support</td>
<td>R. Freimuth, K. Wix, M. Siska, C. Chute, Mayo Clinic</td>
</tr>
<tr>
<td>Identification of Similar Variables in the Database of Genotypes and Phenotypes (dbGaP)</td>
<td>K. Lin, S. Doan, A. Hsieh, H. Kim, University of California San Diego</td>
</tr>
<tr>
<td>Informing the Hunt for Rare Disease Causal Variants: The International Mouse Phenotyping Consortium</td>
<td>T. Meehan, European Bioinformatics Institute</td>
</tr>
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</table>

### TBI07: Peer-based Learning Workshop - Use of the OMOP Common Data Model within the PCORI CDRN Initiative

**Session Chair: Cyril Magnin**

<table>
<thead>
<tr>
<th>Title</th>
<th>Authors</th>
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<tbody>
<tr>
<td>M. Matheny, TVHS Veterans Administration/Vanderbilt University; D. Meeker, University of Southern California; M. Kahn, University of Colorado; R. Beienkaya, Albert Einstein College of Medicine; L. Frey, Medical University of South Carolina; P. Ryan, Janssen Research &amp; Development</td>
<td>Cyril Magnin III</td>
</tr>
</tbody>
</table>

* CTS-AMIA
**TBI08: Papers/Podium Presentations - Cancer Patient Status and Drug Discovery**  
*Session Chair: Joshua Denny*

**Mining Biomedical Literature to Explore Interactions between Cancer Drugs and Dietary Supplement**

R. Zhang, T. Adam, G. Simon, University of Minnesota; M. Cairelli, T. Rindflesch, National Library of Medicine; S. Pakhomov, G. Melton, University of Minnesota

**Adverse Drug Events-based Tumor Stratification for Ovarian Cancer Patients Receiving Platinum Therapy**

C. Wang, M. Zimmermann, C. Chute, G. Jiang, Mayo Clinic

**Discovering Synergistic Multi-drug Combinations for Breast Cancer**


**Cancer Registry Control Panel (CRCP): A System for the Discovery of Patient Cancer Status Using the EMR**

J. Osborne, M. Wyatt, A. Westfall, J. Willig, G. Gordon, University of Alabama at Birmingham

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

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

**TBI09: Papers/Podium Presentations - Epigenetic and Genomic Approaches**  
*Session Chair: Gary Hardiman*

**DNA Methylation Data Analysis with SPIRIT-ML**

S. Achuthan, K. Donyo, Z. Chen, R. Natarajan, J. Niland, A. Shah, City of Hope

**Personalized Medicine on Cancer Treatment: Using Big Data Techniques to Integrate Clinical and Genomic Data**

F. Utro, P. Zhang, F. Wang, J. Hu, IBM T.J. Watson Research Center

**Novel Application of Junction Trees to the Interpretation of Epigenetic Differences among Lung Cancer Subtypes**

A. Lopez Pineda, V. Gopalakrishnan, University of Pittsburgh School of Medicine

**Identification of Epigenetic Modifications that Contribute to Pathogenesis in Therapy-related AML: Effective Integration of Genome-wide Histone Modification with Transcriptional Profiles**

X. Yang, the University of Chicago

All Attendees: Session Evaluation

Use QR codes to evaluate each session *(required for nursing CE)*. If you are unable to access the surveys via QR code visit amia.org/jointsummits2015/TBI-evaluation
### TBI10: Big Data to Knowledge (BD2K) Centers of Excellence

L. Frey, Medical University of South Carolina; I. Kohane, Harvard Medical School; M. Musen, Stanford University; D. Page, University of Wisconsin-Madison; D. Haussler, University of California Santa Cruz; G. Cooper, University of Pittsburgh

Leaders of the Big Data to Knowledge (BD2K) Centers of Excellence will discuss their perspectives regarding using big data to improve our understanding of disease and improving patient outcomes. Dr. Isaac Kohane will present the use of a Patient-centered Information Commons (PIC) to conduct large-scale analysis to improve understanding of causation in Precision Medicine. Dr. Mark Musen will describe methods for improving metadata collection in healthcare through his Center for Expanded Data Annotation and Retrieval (CEDAR). Dr. David Haussler will discuss the coordination of multi-institutional partners through the Center for Big Data in Translational Genomics (CBDTG) to improve precision diagnosis and treatments based on genomic information. Dr. David Page from the Center for Predictive Computational Phenotyping (CPCP) will describe the extraction of relevant phenotypes from complex data. Dr. Gregory Cooper from the Center for Causal Modeling and Discovery of Biomedical Knowledge from Big Data (CMD) will discuss how we can tie big data research together through causal modeling. Together these thought leaders will provide a comprehensive view of the state of the art of translating big data to knowledge via approaches that are patient focused, metadata informed, integrated with genomic data, well phenotyped and oriented toward causal discovery to improve our understanding of health and disease.

### TBI11: Peer-based Learning Workshop - Semantic Phenotyping for Translational Medicine

M. Haendel, Oregon Health & Sciences University; N. Washington, C. Mungall, Lawrence Berkeley National Laboratory

### TBI12: Podium Presentations - Crowd Sourcing and Heterogeneous Data Sources

**Search Tag Analyze Resource (STAR): An Online Platform to Crowdsource Genomic Disease Signatures from Open Digital Samples**

D. Hadley, J. Pan, M. Sirota, B. Chen, B. Oskotsky, R. Auerbach, A. Morgan, B. Pinsky, A. Butte, Stanford University

**medTurk: An In-house Crowdsourcing Approach to Extracting Information from Clinical Notes**

R. Johnson, S. Rao, P. Kasturirangan, K. Tercyak, A. Shad, S. Madhavan, Georgetown University

An Inter-patient Heterogeneity Model for Biomarker Discovery Studies

M. Winerip, G. Wallstrom, Arizona State University

Partial Integration Strategy of Heterogeneous Datasets to Prognosticate Survival in Glioblastoma

H. Itakura, O. Gevaert, Stanford University
### 12:15 p.m. – 1:15 p.m. IMO Lunch and Learn

*IMO Lunch and Learn (Not eligible for CME/CE)*

** IMO Lunch and Learn **

**Capture of Structured Clinical Data at the Point of Care to Support Translational Medicine: The IMO 2.x Platform**

Eric Rose, MD, FAAFP  
*Director of Clinical Terminology, and Regis Charlot, MS, Chief Technology Officer and President, IMO*

*For details see page 23*

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

#### TBI13: Papers/Podium Presentations - Cancer Networks  
**Session Chair: Warren Kibbe**

- **Detecting Cancer Pathway Crosstalk with Distance Correlation**  
  M. Sharpnack, K. Huang, The Ohio State University

- **Definition and Exploration of LUAD-LUSC Hybrid Subtype via Integrative Omics Module Networks**  
  K. Planey, O. Gevaert, Stanford University

- **Disease Comorbidity Network Guides the Detection of Molecular Evidence for the Link Between Colorectal Cancer and Obesity**  
  Y. Chen, L. Li, R. Xu, Case Western Reserve University

- **Integrating Gene Regulatory Networks to Identify Cancer-specific Genes**  
  V. Bo, A. Tucker, Brunel University

#### TBI14: Podium Presentations - NLP, Ontologies, and Data Standards  
**Session Chair: Jihad Obeid**

- **Evaluating the Use of Star Allele Nomenclature with High-throughput Sequence Data: Implications for Research and Clinical Practice**  
  A. Gordon, D. Nickerson, C. Chute, Johns Hopkins University; R. Freimuth, Mayo Clinic

- **NLP-TAB: A System for Integration and Visualization of Diverse Biomedical NLP Applications**  
  B. Knoll, G. Melton, University of Minnesota; H. Liu, Mayo Clinic; H. Xu, University of Texas; S. Pakhomov, University of Minnesota

  *Automating i2b2 Ontology Mappings with MetaMap*  
  L. Phillips, Partners Healthcare Systems; S. Murphy, Partners Healthcare Systems/Massachusetts General Hospital

  *Development of Standardized Common Data Elements for Biobanking of Human Biospecimens*  
  H. Ellis, Duke University
TBI15: Papers/Podium Presentations - Phenotyping Methods
Session Chair: Joshua Denny

Definition and Application of Phenotype Design Patterns
L. Rasmussen, Northwestern University; W. Thompson, NorthShore University HealthSystem; J. Pacheco, A. Kho, Northwestern University; D. Carrell, Group Health Research Institute; J. Pathak, Mayo Clinic; P. Peissig, Marshfield Clinic Research Foundation; G. Tromp, Geisinger Health System; J. Denny, Vanderbilt University; J. Starren, Northwestern University

A Knowledge-based, Automated Method for Phenotyping in the EHR Using Only Clinical Pathology Reports
A. Yahi, N. Tatonetti, Columbia University

A Toolkit Enabling Efficient, Repeatable Phenotype Algorithm Development and Sharing
J. Kirby, Vanderbilt University Medical Center; L. Rasmussen, Northwestern University; P. Speltz, Vanderbilt University Medical Center; J. Pathak, Mayo Clinic; J. Pacheco, Northwestern University; W. Thompson, NorthShore University Health System; J. Cowan, S. Osgood, L. Bastarache, Vanderbilt University Medical Center; P. Peissig, Marshfield Clinic Research Foundation; S. Stallings, P. Harris, M. Basford, J. Denny, Vanderbilt University Medical Center

Translation of Pathway-based trans-eQTL to Human Phenotypes

TBI16: Student Paper Competition
Session Chair: Lewis Frey

Concept Modeling-based Drug Repositioning
J. Patchala, University of Cincinnati; A. Jegga, Cincinnati Children’s Hospital and Medical Center/University of Cincinnati

Conceptualizing a Novel Quasi-continuous Bayesian Phylogeographic Framework for Spatiotemporal Hypothesis Testing
D. Magee, M. Scotch, Arizona State University

Are All Vaccines Created Equal? Using Electronic Health Records to Discover Vaccines Associated With Clinician-coded Adverse Events
M. Boland, N. Tatonetti, Columbia University

Secure Genomic Computation through Site-wise Encryption
Y. Zhao, X. Wang, H. Tang, Indiana University Bloomington

3:00 p.m. – 3:30 p.m. Coffee Break

Mission #TBI15

*[CTS-AMIA]*

Cyril Magnin Foyer
### Scientific Sessions

**TBI17: Podium Presentation: Analysis Methods**  
*Session Chair: Robert Freimuth*

- **A Risk Model for 30-Day Heart Failure Re-admission using Electronic Medical Records**  
  U. Kartoun, S. Shaw, Massachusetts General Hospital/Harvard Medical School

- **A Data Safe Haven to Securely Bring Analysis to Distributed Cancer Genome Data**  

- **Big Data for Little Babies: Early Prediction of Adverse Events in the Neonatal Intensive Care Unit**  
  K. Unnikrishnan, NorthShore University HealthSystem

- *** Inter-network Cluster Validation: A Case Study in Co-Occurring Comorbidities**  
  S. Bhavnani, B. Dang, UTMB; S. Visweswaran, University of Pittsburgh; R. Divekar, Mayo Clinic

**TBI18: Papers/Podium Presentations - Drugs, Events, and Outcomes**  
*Session Chair: Nigam Shah*

- **Biocuration of Chemopredictive Markers and Direct Drug Targets from Public Data to Determine Associated Targeted Therapy Benefit and Clinical Outcomes**  
  S. Rao, S. Riazi, S. Boca, V. Singh, M. Harris, P. McGarvey, M. Pishvaian, Georgetown University; J. Brody, Thomas Jefferson University; S. Madhavan, Georgetown University

- **Adverse Drug Event Ontology: Gap Analysis for Clinical Surveillance Application**  
  T. Adam, J. Wang, University of Minnesota

- **Data-integration and Information Propagation for Drug Discovery in Triple Negative Breast Cancer: A Network-based Approach**  
  F. Vitali, L. Cohen, F. Mulas, University of Pavia; A. Zambelli, IRCCS-Fondazione S. Maugeri; R. Bellazzi, University of Pavia

- **The AEExplorer, its Developments and Applications in Clinical Trials, Especially for Investigating the Effects of Concomitant Proton Pump Inhibitors (PPIs) in Osteoporosis Clinical Trials**  
  Z. Luo, FDA; J. Yang, University of North Carolina at Charlotte; Z. Zuo, N. Xu, M. Whitaker, R. Tiwari, L. Huang, FDA; Z. Luo, South University of Science and Technology of China; C. Cooper, Becton, Dickinson and Company; W. Tong, L. Rosario, E. Navarro Almario, S. Buckman-Garner, FDA
TBI19: Papers/Podium Presentations - Phenotyping with EHRs
Session Chairs: Jihad Obeid

Mining Electronic Health Records Using Linked Data
D. Odgers, M. Dumontier, Stanford University

Leveraging an Electronic Health Record-linked Biorepository to Generate a Metformin Pharmacogenomics Hypothesis
M. Breitenstein, Mayo Clinic/University of Minnesota; L. Wang, Mayo Clinic; G. Simon, University of Minnesota; E. Ryu, S. Armasu, B. Ray, R. Weinshilboum, J. Pathak, Mayo Clinic

Automated Biospecimens Annotation Model for Scalable Mesothelioma Biobanking
W. Amin, A. Parwani, University of Pittsburgh School of Medicine; J. Melamed, New York University School of Medicine; G. Mandava, R. Uppal, University of Pittsburgh School of Medicine; C. Morrison, C. Gaudioso, Roswell Park Cancer Institute; M. Feldman, University of Pennsylvania School of Medicine; H. Pass, New York University School of Medicine; M. Becich, University of Pittsburgh School of Medicine

Improving Phenotypic Granularity with NLP-PheWAS in Multiple Sclerosis
P. Teixeira, Vanderbilt University; M. Davis, Brigham Young University; L. Wiley, L. Bastarache, J. Smith, R. Carroll, D. Fabbri, D. Roden, J. Denny, Vanderbilt University

TBI20: Design Challenge - Improving Understanding through TCGA Data Integration
Session Chair: Lewis Frey

GenePool: A Cloud-based Platform for Interactive Visualization and Integrative Analysis of Genomics and Clinical Data
H. Fan Minogue, M. Sirota, Stanford University School of Medicine; S. Sanga, Station X; D. Hadley, A. Butte, Stanford University School of Medicine; T. Klingler, Station X

A Prototype Software Pipeline to Identify Mutated Genes that Have a Similar Effect on Tumor Transcription
S. Piccolo, Brigham Young University

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

See page 59 for list of TBI posters, listed alphabetically by the first author.

6:30 p.m. – 9:00 p.m.
Billiard Meet-up at Jillian's Billiards
(Not eligible for CME/CE)

For details see page 25
Wednesday, March 25

7:00 a.m. – 6:00 p.m.  Registration Open

7:00 a.m. – 8:15 a.m  AMIA Town Hall

Join AMIA leaders for an open Town Hall event with updates on AMIA activities, President Obama’s Precision Medicine Initiative, and Q&A with the audience. We want to keep AMIA members informed of these activities, and to brainstorm about how we can continue to leverage the expertise of the informatics community. We welcome your engagement and full participation in this exciting initiative.

Doug Fridsma, MD, PhD  @fridsma
President and CEO, AMIA

Blackford Middleton, MD, MPH, MSc  @bfm
AMIA Board of Directors

For details see page 14

7:00 a.m. – 8:30 a.m.  Continental Breakfast

8:30 a.m. – 10:00 a.m.  Plenary Session

CRI Summit Opening Plenary Session and Keynote Presentation

Paul Wicks, MD, PhD
Vice President of Innovation, PatientsLikeMe

For details see page 19

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

CRI01: Student Paper Competition, Part 1 – Text Mining for Clinical Research
Session Chair: James Cimino

Structuring Free-text Microbiology Culture Reports for Secondary Use
W. Yim, H. Evans, M. Yetisgen, University of Washington

Incorporating Statistical Topic Models in the Retrieval of Healthcare Documents
K. Caballero Barajas, R. Akella, University of California Santa Cruz/University of California Berkeley

Automating Identification of Multiple Chronic Conditions in Clinical Practice Guidelines
T. Leung, H. Jalal, D. Zulman, VA Palo Alto Health Care System/Stanford University; M. Dumontier, Stanford University; D. Owens, VA Palo Alto Health Care System/Stanford University; M. Musen, Stanford University; M. Goldstein, VA Palo Alto Health Care System/Stanford University

Phenotyping Adverse Drug Reactions: Statin-related Myotoxicity
L. Wiley, J. Moretz, J. Denny, J. Peterson, Vanderbilt University; W. Bush, Case Western Reserve University

CRI02: Papers/Podium Presentations – Phenotyping
Session Chair: Peggy Peissig

A Modular Architecture for Electronic Health Record-driven Phenotyping
L. Rasmussen, Northwestern University; R. Kiefer, Mayo Clinic; H. Mo, P. Speltz, Vanderbilt University; W. Thompson, NorthShore University HealthSystem; G. Jiang, Mayo Clinic; J. Pacheco, J. Xu, Northwestern University; Q. Zhu, University of Maryland Baltimore County; J. Denny, Vanderbilt University; E. Montague, Northwestern University; J. Pathak, Mayo Clinic

Electronic Phenotyping for Measuring Quality of Care
S. Tamang, T. Podchiyska, T. Hernandez-Boussard, N. Shah, Stanford University

Mining Phenotypic Keywords from a Large Collection of Clinical Narratives
C. Bejan, R. Nash, D. Conway, E. Bowton, K. Johnson, J. Denny, Vanderbilt University

Learning Semantic Tags from Big Data for Clinical Text Representation
Y. Li, H. Liu, Mayo Clinic

CRI03: Didactic Panel - Observational Health Data Sciences and Informatics (OHDSI): An Open Collaborative Approach for Rapid Evidence Generation
D. Vawdrey, Columbia University; J. Duke, Regenstrief Institute; G. Hripcsak, Columbia University; P. Ryan, Janssen Research and Development; N. Shah, Stanford University

Observational Health Data Sciences and Informatics (OHDSI) is an international collaborative creating open-source solutions for performing large-scale analytics using observational health data. OHDSI facilitates collaborative research by establishing a worldwide network of observational health databases and providing a community where advanced analytic methods and interoperable software tools can be easily shared. This panel will discuss the opportunities and challenges associated with OHDSI’s approach to big data analytics in healthcare, including efforts to map clinical data to standardized formats, and the availability of new tools to perform clinical characterization, population-level estimation, and patient-level predictive modeling research. Panelists will discuss relationships between OHDSI and data sharing initiatives such as the Patient-centered Outcomes Research Institute (PCORI) Clinical Data and Patient-powered Research Networks, the Informatics for Integrating Biology & the Bedside (i2b2) Center, and the NIH Accrual to Clinical Trials (ACT) effort. Moving beyond technical infrastructure and data standardization, panelists will emphasize OHDSI’s approach for generating evidence about disease progression, health service utilization, and the effects of medical interventions. Ample time will be allotted for interactive discussion based on questions from the audience.
TBI21: Didactic Panel - Challenges of Implementing Genomic Decision Support in the Real World—Experience from the eMERGE and CSER Networks
J. Starren, Northwestern University; P. Tarczy-Hornoch, B. Shirts, University of Washington; M. Williams, Geisinger Health System; T. Herr, Northwestern University

While the need for genomic decision support has been universally recognized and discussed in numerous papers, the number of actual implementations has been few. Many commercial EHR vendors have stated publicly that they do not have near-term plans to store genomic data within the EHR itself, although they anticipate exposing genomic computerized decision support (GCDS) within their workflows. Several papers have explicitly commented on the need for Ancillary Genomic Systems (AGS) to mediate between the large volumes of genomic data that is anticipated and the limited data capacity of most EHR systems. The Electronic Medical Records and Genomics (eMERGE) network and the Clinical Sequencing Exploratory Research (CSER) network are to multi-institution networks exploring the challenges of implementing GCDS in real-world situations. This panel brings together representatives of both networks to discuss the collective experience of 16 different health systems that have incorporated genomic results into the process of care.

TBI22: Papers/Podium Presentations - Data Querying and Quantification
Session Chair: Nicholas Tatonetti

Mining Relation Reversals in the Evolution of SNOMED CT Using MapReduce
S. Tao, L. Cui, W. Zhu, M. Sun, Case Western Reserve University; O. Bodenreider, National Library of Medicine; G. Zhang, Case Western Reserve University

RED-i Data Integrator for REDCap Projects
E. Schmidt, K. Hanson, C. Barnes, J. Hanna, W. Hogan, University of Florida

Brain Injury Cognitive Screening (BICS): A Simple, Quick and Effective Application for Screening Mild Traumatic Brain Injury
J. Kumar, MDS University/Neurology and TBI Rehabilitation Center; S. Kumar, P. Shah, A. Jawahar, Neurology and TBI Rehabilitation Center

Quantifying Geo-imputation Error: Using Gaussian Geostatistical Simulation (GGS) to Dis-aggregate Zip Code Data & Estimate Positional Error
J. Behrens, A. Pah, A. Kho, Northwestern University Feinberg School of Medicine

12:00 p.m. – 1:30 p.m.
IMO Corporate Roundtable (by invitation)
(Not eligible for CME/CE)

All Attendees: Session Evaluation
Use QR codes to evaluate each session (required for nursing CE). If you are unable to access the surveys via QR code visit amia.org/jointsummits2015/CRI-evaluation
<table>
<thead>
<tr>
<th>Session</th>
<th>Title</th>
<th>Chair(s)</th>
<th>Location</th>
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<tbody>
<tr>
<td>CRI04</td>
<td>Predicting New Target Conditions for Drug Retesting Using Temporal Patterns in Clinical Trials: A Proof of Concept</td>
<td>Z. He, C. Weng, Columbia University</td>
<td>Embarcadero, Level 3</td>
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<td></td>
<td>An Ontology Driven Clinical Evidence Service Providing Diagnostic Decision Support in Family Practice</td>
<td>D. Corrigan, HRB Center for Primary Care Research/Royal College of Surgeons in Ireland</td>
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<td>Data-mining Electronic Medical Records for Clinical Order Recommendations: Wisdom of the Crowd or Tyranny of the Mob?</td>
<td>J. Chen, Veteran Affairs/Stanford University; R. Altman, Stanford University</td>
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<td>Measuring Mortality Information in Observational Clinical Databases</td>
<td>B. Jones, Brigham Young University; D. Vawdrey, Columbia University</td>
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<td>CRI05</td>
<td>Personalized Predictive Modeling and Risk Factor Identification Using Patient Similarity</td>
<td>K. Ng, IBM Research; J. Sun, Georgia Institute of Technology; J. Hu, IBM Research; F. Wang, IBM Research/University of Connecticut</td>
<td>Embarcadero, Level 3</td>
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<td>Predictive Modeling for Pressure Ulcers from Intensive Care Unit Electronic Health Records</td>
<td>P. Kaewprag, The Ohio State University; C. Newton, The Ohio State University Wexner Medical Center; B. Vermillion, S. Hyun, K. Huang, R. Machiraju, The Ohio State University</td>
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<td>Cloud-based Predictive Modeling Platform for Healthcare Research</td>
<td>H. Su, J. Sun, Georgia Institute of Technology</td>
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<td>Prediction of Hospital Readmission for Psychiatric Diagnoses Using Clinical Narrative and Medication Data on the Day of Admission</td>
<td>C. Walsh, H. Salmasian, C. Friedman, G. Hripcsak, Columbia University</td>
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<td>CRI06</td>
<td>A Standardized Approach to Cohort Definition Applied across a Network of OMOP-compliant Observational Databases for Clinical Trial Feasibility Assessment</td>
<td>C. Knoll, F. DeFalco, P. Ryan, Janssen Research and Development</td>
<td>Embarcadero, Level 3</td>
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<td>Structuring Clinical Trial Eligibility Criteria with the Common Data Model</td>
<td>G. Levy-Fix, A. Yaman, C. Weng, Columbia University</td>
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TBI23: Papers/Podium Presentations - NGS and Gene Analysis Methods
Session Chair: Gary Hardiman

Identifying Cancer Driver Mutations and Genes from Next-generation Sequencing Data
Z. Zhao, P. Jia, J. Xia, Vanderbilt University

Development of Bioinformatics Pipeline for Analyzing Clinical Pediatric NGS Data
E. Crowgey, University of Delaware

A Comprehensive Time-course-based Meta-analysis of Sepsis and Sterile Inflammation Reveals a Robust Diagnostic Gene Set
T. Sweeney, A. Shidham, Stanford University; H. Wong, Cincinnati Children’s Hospital; P. Khatri, Stanford University

An Approach for Partial Automation of Next Generation Sequencing Trio Analysis
A. Murphy, University of Minnesota

3:00 p.m. – 3:30 p.m. Coffee Break
Cyril Magnin Foyer

3:30 p.m. – 5:00 p.m. Plenary Session

TBI Summit Closing Session and Translational Bioinformatics Year-in-Review

Russ B. Altman, MD, PhD, FACMI  @rbaltman
Stanford University
Kenneth Fang Professor of Bioengineering, Genetics, Medicine and (by courtesy) Computer Science; Director, Biomedical Informatics Training Program, Stanford University

For details see page 18
WEDNESDAY, MARCH 25

5:00 p.m. – 6:00 p.m.  CRI Poster Session 1 and Reception  
(Not eligible for CME/CE)  
Cyril Magnin Foyer

See page 63 for list of CRI Poster Session 1 posters,  
listed alphabetically by first author.

6:00 p.m. – 7:00 p.m.  OSU Great Lakes Region Meeting (by invitation – Affiliate Event)  
Cyril Magnin III

6:00 p.m. – 7:30 p.m.  Signet Accel Corporate Roundtable (by invitation)  
(Not eligible for CME/CE)  
Hearst

6:00 p.m. – 8:00 p.m.  Women in Informatics Networking Event (WINE)  
(Not eligible for CME/CE)  
For details see page 25  
Lobby Bar

7:00 p.m. – 9:00 p.m.  OSU Reception (by invitation) – Affiliate Event  
Cyril Magnin II

Thank you for attending the Summit on Translational Bioinformatics. Don’t forget to evaluate the entire TBI Summit.

If you are unable to access the survey via QR code visit amia.org/jointsummits2015/TBI-evaluation
Thursday, March 26

7:00 a.m. – 6:00 p.m.  Registration Open

7:00 a.m. – 8:15 a.m.  Birds-of-a-Feather Sessions

**CRI-BOF01: Sustaining the Effective Use of Health Care Data**
A. Wilcox, Intermountain Healthcare; E. Holve, AcademyHealth

This meeting will discuss lessons learned in sustaining health research data infrastructures. Specifically, it will address (a) what sustainability models exist for health research data infrastructures, (b) what are the common and important attributes of those models that lead to sustainability, (c) what are other lessons learned from both successful and unsuccessful models, and (d) what are current important trends in sustainability. A recent informatics journal issue focused on sustaining large projects working with clinical data, and initial information will be drawn from the examples in that issue. These examples created an initial set of sustainability examples from which patterns may be identified; however, more examples are needed to best identify important characteristics of successful sustainability plans. With this BoF session, we can identify both more examples and more themes from existing examples to inform others developing such plans. Sustainability is a critical topic, with better understanding and application needed to maximize the benefit of investments in clinical research data infrastructures.

**CRI-BOF02: Common Data Models for Patient-centered Comparative Effectiveness Research**
A. Solomonides, NorthShore University HealthSystem; J. Logan, Oregon Health & Science University

This birds-of-a-feather session (BOF) will address two issues: (a) From the point of view of scientists and clinical/biomedical researchers, what are the merits of the many alternative data models that have been used or proposed for comparative effectiveness research? (b) From the point of view of practical informaticians who must extract-transform-load (ETL) data from EHRs into data marts built to the specification of an abstract model, what are the common virtues and challenges of these models?

The Patient-centered Outcomes Research Institute has funded 11 Clinical Data Research Networks and 18 Patient-Powered Research Networks with the goal of setting up a national network to support patient-centered comparative effectiveness research. A lively debate has taken place since then to determine the most appropriate and effective data models and standards to be adopted by such networks so as to ensure accuracy, longevity, sustainability, usability, and comparability of data. The issues and problems of using electronic health record data for research, and observational comparative effectiveness research in particular, have been extensively discussed in the literature. Aspects that have attracted less attention include the diversity of models and standards adopted and the difficulties of extraction of meaningful data for research. The BOF will discuss particular choices and their rationale, issues in relation to data domains, standards and terminologies for different domains, problems with extraction of reliable data from electronic health records and examples of uses of the data models in comparative effectiveness research.

**CRI-BOF03: Creating a Home for the Clinical and Translational Research Informatics Community within AMIA and Beyond**
N. Anderson, University of California, Davis; P. Payne, The Ohio State University; J. Starren, Northwestern University; J. Tenenbaum, Duke University

Over the last several years, substantial discussion has taken place within AMIA and in the broader biomedical research community concerning how to create, sustain, and engage a robust community of practice focusing upon clinical and translational research informatics. As part of these conversations, AMIA has emerged as a leading professional home for such individuals. In addition, emergent efforts by the CI4CC, CTSA IDTF, and Clinical Research Forum are providing convening venues for clinical and translational research informatics investigators, practitioners, and trainees. This birds-of-a-feather session will provide a forum for both discussing such developments and defining new and emergent priorities for AMIA in this constantly evolving and critical domain.
**THURSDAY, MARCH 26**

### Scientific Sessions
7:00 a.m. – 10:00 a.m.

<table>
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<tr>
<th>Time</th>
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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>7:00 a.m. – 8:30 a.m.</td>
<td>TriNetX Corporate Roundtable (by invitation) (Not eligible for CME/CE)</td>
<td>Hearst</td>
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<td>7:00 a.m. – 10:00 a.m.</td>
<td>Scientific Session</td>
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Note: This session begins early. The remainder of the Scientific Sessions begin at 8:30 a.m.

### CRI10: Peer-based Learning Workshop - Visualizing Business Analytics and HIT for PCORI

**Session Chair:** Judith Logan

**Note:** This session begins at 7:00 a.m.

**Use of Innovative HIT Solutions in Clinical Data Research Networks for Optimization of Patient-centered Clinical Outcomes Research**

A. Kho, Northwestern University; P. Harris, Vanderbilt University Medical Center; K. Mandl, Harvard Medical School/Boston Children’s Hospital; T. Carton, Louisiana Public Health Institute; L. Ohno-Machado, University of California, San Diego; R. Waitman, University of Kansas Medical Center; M. Zirkle, PCORI

**Visualizing Operational Informatics Data Using R**

L. McIntosh, C. Zabarovskaya, Washington University School of Medicine

### CRI07: Didactic Panel - Clinical Trials Results Data Sharing: The Time is Now

**Chair:** I. Sim, UCSF; P. Fu, Harbor-UCLA Medical Center; D. Louzao, Duke Clinical Research Institute; P. Embi, Ohio State University Wexner Medical Center

There is great potential value to sharing clinical trial results to accelerate reproducibility, meta-analysis, and hypothesis generation. While there have been numerous company, institution, and project-specific data sharing initiatives, large scale sharing has been limited by complex questions about the who, what, when, and how of data sharing.

To advance data sharing, the Institute of Medicine (IOM) conducted a consensus study in 2014 on Strategies for Responsible Sharing of Clinical Trial Data. The committee’s report identifies critical questions around data sharing aims, principles, policy, technical infrastructure, incentives, and intellectual property and legal issues. The report includes direct recommendations for action aimed at academic health centers, research funders, and professional organizations, among others. It also lays out specific considerations regarding technical and informatics infrastructure. This panel will discuss the opportunities and challenges facing academia in this anticipated “new normal” of data sharing. Presentations will include an overview of the IOM report; cost, data governance, IT infrastructure, and information security concerns of a non-academic health care provider; an example of an independent scientific review program to adjudicate access requests for secondary use of commercial clinical trials data; and an overview of the governance, organizational, and ethical concerns of an academic health center.
CRIO8: Papers - Modeling Clinical Data to Support Clinical Research

Session Chair: Nick Anderson

Modeling Flowsheet Data for Clinical Research
S. Johnson, University of Minnesota; M. Byrne, St. Catherine University; B. Christie, Fairview Health Services; C. Delaney, University of Minnesota; A. LaFlamme, Fairview Health Services; J. Park, L. Pruinelli, University of Minnesota; S. Sherman, Fairview Health Services; S. Speedie, B. Westra, University of Minnesota

Towards the Standardized Documentation of E-cigarette Use in the Electronic Health Record for Population Health Surveillance and Research
T. Winden, Allina Health/University of Minnesota; E. Chen, University of Vermont; Y. Wang, University of Minnesota; I. Sarkar, E. Carter, University of Vermont; G. Melton, University of Minnesota

Drug Normalization for Cancer Therapeutic and Druggable Genome Target Discovery
G. Jiang, S. Sohn, M. Zimmermann, C. Wang, H. Liu, C. Chute, Mayo Clinic

A Probabilistic Reasoning Method for Predicting the Progression of Clinical Findings from Electronic Medical Records
T. Goodwin, S. Harabagiu, University of Texas at Dallas

CRIO9: Podium Presentations - Data Sharing and Research Collaboration

Session Chair: Elmer Bernstam

Promoting Data Quality in a Clinical Data Research Network Using GitHub
A. Browne, J. Pennington, C. Bailey, Children’s Hospital of Philadelphia/Perelman School of Medicine/University of Pennsylvania

UC TrialQuest: Supporting Multisite Clinical Trials across the University of California
N. Buscher, UC BRAID; A. Chatterjee, E. Mah, UCSF; R. Sak, UC BRAID

Data Impact Factor – Recognizing Data Sharing within the NIH Intramural Clinical Research Community
E. Ayres, J. Cimino, NIH Clinical Center

CRIO10: Peer-based Learning Workshop - Visualizing Business Analytics and HIT for PCORI

Session Chair: Judith Logan

Note: This session begins at 7:00 a.m.

See full description of session CRIO10 listed at 7:00 a.m. – 10:00 a.m.
THURSDAY, MARCH 26
Scientific Sessions
8:30 a.m. – 10:00 a.m. | CONTINUED

**CRI11: Papers/Podium Presentation - Secure Processing of PHI**

*Session Chair: Michael Kahn*

**EU FP7 TRANSFoRm Project: Query Workbench for Participant Identification and Data Extraction**
L. Zhao, S. Lim Choi Keung, C. Golby, University of Warwick; J. Ethier, Université Paris Descartes - Sorbonne Paris Cité; V. Curcin, King’s College London; H. Bastiaens, University of Antwerp; A. Burgun, Université Paris Descartes - Sorbonne Paris Cité; B. Delaney, King’s College London; T. Arvanitis, University of Warwick

**Enabling Use of High Performance Computing for Secure Processing of Protected Health Information**
R. Bill, G. Melton, B. Gottschalk, A. Ring, J. Dale, J. Vinals, A. Lamblin, S. Pakhomov, University of Minnesota

**Early Detection of Heart Failure Using Structured and Unstructured Information in Electronic Health Records**
Y. Wang, K. Ng, R. Byrd, S. Ebadollahi, IBM T.J. Watson Research Center; W. Stewart, Sutter Health

**A Bibliometric Analysis on Cancer Population Science with Topic Modeling**
D. Li, M. Rastegar-Mojarad, J. Okamoto, H. Liu, S. Leischow, Mayo Clinic

10:00 a.m. – 10:30 a.m. **Coffee Break**

Cyril Magnin Foyer

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

**CRI12: Didactic Panel - PCORnet CDRN Data Quality Challenges and Solution**

*Session Chair: Michael Kahn*

**The Patient-Centered Outcomes Research Institute (PCORI) Clinical Data Research Networks (CDRNs) will scale the capacity to conduct comparative effectiveness research (CER) using data from clinical practice in large populations. It is therefore critical to ensure that information collected and provided by CDRNs are based on credible, high-quality data. This panel gives a thorough overview of the CDRNs Data Quality (DQ) perspectives, challenges, and proposed strategies at the level of participating institutions and networks, and entirety of the distributed and integrated collaborative research infrastructure that it intends to build. Panelists will present state of the art DQ methods and solutions to address these challenges. The panel stresses systematic, model-driven, and standard-based approaches to solving some of the outstanding DQ challenges.**

*CTS-AMIA*
CR13: Podium Presentations - Data Integration and Information Fusion
Session Chair: Paul Harris

Derivation of Non-invasive PaO2/FiO2 Ratio Scoring for Critical Care by Synchronizing Asynchronously Charted Electronic Health Record Data
J. Adams, A. Riedl, H. Black, C. Phan, N. Anderson, University of California, Davis

Effect of Care Fragmentation on Performance of Asthma Phenotype Algorithm Using Electronic Health Records
K. Jackson, J. Pacheco, A. Pah, A. Kho, Northwestern University

Linking Structured and Unstructured Clinical Phenotypes through the OMOP Common Data Model
J. Duke, C. Hilton, C. J. Cummins, Regenstrief Institute

Integrating Patient Reported Outcomes and Clinical Data for Patient Centered Outcomes Research: An i2b2 Approach
J. Klann, Harvard Medical School/Massachusetts General Hospital/Partners Healthcare; M. Natter, Boston Children’s Hospital/Harvard Medical School; W. Adams, Boston University School of Medicine; S. Murphy, Partners Healthcare/Massachusetts General Hospital/Harvard Medical School

CR14: Podium Presentations – Standards
Session Chair: Rachel Richesson

Common Data Schemas for Mobile Health: The Open mHealth Approach
I. Sim, S. Canin, UCSF/Open mHealth; A. de Paula Hanika, K. McCurdy, Open mHealth; M. McConnell, Stanford University; E. Farrugia, D. Bonilla, Open mHealth

* Developing a Suite of Electronic Data Capture Applications Based on an Open-source Instrument Definition Standard
C. Tirrell, J. Simeone, F. Farach, L. Rozenblit, Prometheus Research

Evaluating Common Data Models for Use on a Longitudinal Community Registry
M. Younes, Duke University; G. Del Fiol, University of Utah; J. Tenenbaum, A. Walden, M. Zozus, Duke University

* Developing HL7 Standards to Improve Clinical Research in Emergency Medicine: The Common Model of Emergency Care Information
J. McClay, University of Nebraska Medical Center; L. Langford, Intermountain Healthcare

CR15: Papers: Text Mining
Session Chair: Cosmin Bejan

Integrating Multiple On-line Knowledge Bases for Disease-lab Test Relation Extraction
Y. Zhang, E. Soysal, S. Moon, J. Wang; C. Tao, H. Xu, The University of Texas Health Science Center at Houston

Prescription Extraction from Clinical Notes: Towards Automating EMR Medication Reconciliation
Y. Wang, IBM TJ. Watson Research Center; S. Steinhubl, Scripps Translational Science Institute; C. Defilippi, University of Maryland Medical Center; K. Ng, S. Ebadiollahi, IBM TJ. Watson Research Center; W. Stewart, Sutter Health; R. Byrd, IBM TJ. Watson Research Center

Granular Quality Reporting for Cervical Cytology Testing
K. Wagholikar, K. MacLaughlin, C. Chute, Mayo Clinic; R. Greenes, Arizona State University; H. Liu, R. Chaudhry, Mayo Clinic

Toward a Natural Language Interface for EHR Questions
K. Roberts, D. Demner-Fushman, National Library of Medicine
**THURSDAY, MARCH 26**

**Scientific Sessions**

10:30 a.m. – 12:00 p.m. | CONTINUED

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**CRI16: Papers/Podium Presentations - Data Abstraction and Text Mining**
Session Chair: Genevieve Melton-Meaux

- **Leveraging Expert Knowledge to Improve Machine-learned Decision Support Systems**
  F. Kuusisto, University of Wisconsin - Madison; J. Dutra, University of Porto; M. Elezaby, E. Mendonça, J. Shavlik, E. Burnside, University of Wisconsin - Madison

- **A Hybrid Approach to Extracting Disorder Mentions from Clinical Notes**
  C. Wang, R. Akella, University of California Santa Cruz

- **Characterizing Secondary Use of Clinical Data**
  E. Lee, T. Black, R. Harrington, P. Tarczy-Hornoch, University of Washington

- **Automated Data Abstraction with Natural Language Processing in a Surgical Quality Improvement Platform**
  M. Yetisgen, P. Klassen, P. Tarczy-Hornoch, University of Washington

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12:15 p.m. – 1:15 p.m.

**ConvergeHEALTH by Deloitte Lunch and Learn**
(Not eligible for CME/CE)

**The Convergence of Delivery and Discovery to Enhance Quality, Performance, and Cost in a Value-based Era**

- **Fred Lee, MD, MPH**
  VP Healthcare Analytics, ConvergeHEALTH by Deloitte

*For details see page XX*

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1:30 p.m. – 3:00 p.m.

**CRI17: Interactive Panel - Where is the Science in Big Data Visual Analytics? From Pretty Pictures to Transformative Biomedical Discoveries**

- **S. Bhavnani, UTMB; S. Visweswaran, University of Pittsburgh; R. Divekar, Mayo Clinic; G. Bellala, Hewlett Packard Laboratories**

Numerous visual analytical representations (e.g., networks visualizations) have been developed to analyze big biomedical data obtained from sources such as electronic medical records and whole genome assays. The goal of using these methods is to make unplanned discoveries leading to transformative changes in healthcare. However, such discovery-based approaches are often referred to as “fishing expeditions” that capture mere correlations, and therefore inferior to gold standard methods such as hypothesis testing and machine learning. Given the vast opportunities offered by big data visual analytics, there is an urgent need for the informatics community to address this analytical debate and define a path forward. Towards that goal, this panel will assemble analysts from informatics, clinical practice, and industry to debate the role of visual analytics in biomedical informatics research. Two proponents of visual analytics will stress why visual analytics is indispensable in the age of big biomedical data, and two critics will argue that visual analytics does not adequately address the limitations of correlation, multiple testing, and human bias. This debate format is designed to engage the audience in a spirited discussion about the future role of big data visual analytics in biomedical informatics.
CRI18: Papers/Podium Presentations - Data Integration, Exploration and Mining
Session Chair: Russ Waitman

The NIH/NICHD Clinical Trials Database (CTDB): A Bio-specimen Management System Solution
R. Anneckarico, A. Idriss, NICHD

Visualizing Anomalies in Electronic Health Record Data: The Variability Explorer Tool
H. Estiri, Y. Chan, L. Baldwin, H. Jung, A. Cole, K. Stephens, University of Washington

Research Data Explorer: Lessons Learned in Design and Development of Context-based Cohort Definition and Selection
A. Wilcox, Intermountain Healthcare; D. Vawdrey, C. Weng, M. Velez, S. Bakken, Columbia University

Catalyzing Tissue-based Brain Tumor Research Using Integrated Tumor Versus Somatic Variant Data
A. Felmeister, The Children's Hospital of Philadelphia/Drexel University; T. Rivera, The Children's Hospital of Philadelphia; Y. Zhu, A. Resnick, J. Lilly, The Children's Hospital of Philadelphia/Perelman School of Medicine at the University of Pennsylvania; D. Stokes, J. Pennington, The Children's Hospital of Philadelphia; T. Curran, The Children's Hospital of Philadelphia/Perelman School of Medicine at the University of Pennsylvania

CRI19: Papers/Podium Presentations - Semantic Interoperability
Session Chair: Philip Payne

A Prototype for Executable and Portable Electronic Clinical Quality Measures Using the KNIME Analytics Platform
H. Mo, Vanderbilt University; J. Pacheco, L. Rasmussen, Northwestern University; P. Speltz, Vanderbilt University; J. Pathak, Mayo Clinic; J. Denny, Vanderbilt University; W. Thompson, NorthShore University HealthSystem

Case Study for Integration of an Oncology Clinical Site in a Semantic Interoperability Solution Based on HL7 v3 and SNOMED-CT: Data Transformation Needs
A. Ibrahim, A. Bucur, Philips Research Europe; D. Perez-Rey, E. Alonso, Universidad Politecnica de Madrid; A. Dekker, M. de Hoog, M. Marshall, Maastro Radiation Oncology Clinic

NEO: Systematic Non-lattice Embedding of Ontologies for Comparing the Subsumption Relationship in SNOMED CT and in FMA Using MapReduce
W. Zhu, G. Zhang, S. Tao, M. Sun, L. Cui, Case Western Reserve University

Semantic Enrichment of CDISC Operational Data Model
S. Lim Choi Keung, L. Zhao, University of Warwick; J. Ether, Université Paris Descartes - Sorbonne Paris Cité; V. Curcin, King's College London; A. Burgun, Université Paris Descartes - Sorbonne Paris Cité; B. Delaney, King's College London; T. Arvanitis, University of Warwick

All Attendees: Session Evaluation

Use QR codes to evaluate each session (required for nursing CE). If you are unable to access the surveys via QR code visit amia.org/jointsummits2015/CRI-evaluation
THURSDAY, MARCH 26
Scientific Sessions
1:30 p.m. – 3:00 p.m. | CONTINUED

**CRI20: Papers/Podium Presentations - User Needs and Consent Methods and Considerations**
Session Chair: Nicole Weiskopf

- Examining Researcher Needs and Barriers for Using Electronic Health Data for Translational Research

- Operationalizing Semantic Medline for Meeting the Information Needs at Point of Care
  M. Rastegar-Mojarrad, D. Li, H. Liu, Mayo Clinic

- Sociodemographic Factors and Health Literacy are Related to Consent for Collection, Use, and Storage of Biospecimens in a Latino Community Sample
  S. Bakken, S. Yoon, N. Suero-Tejeda, C. Weng, N. Reame, Columbia University

- A Telemedicine Platform for Remote Electronic Informed Consent
  J. Obeid, B. Welch, L. Lenert, Medical University of South Carolina

**CRI21: Papers/Podium Presentations - Workflow Architecture**
Session Chair: Bernard LaSalle

- Embracing the Sparse, Noisy, and Interrelated Aspects of Patient Demographics for Use in Clinical Medical Record Linkage
  S. Ash, K. Lin, University of Memphis

  B. Granger, Duke University School of Nursing/Duke University Health System; M. Staton, Coordinated Care of North Carolina; L. Peterson, Duke University School of Nursing; S. Rusincovitch, Duke Translational Medicine Institute

- Studying the Confounding Effects of Socio-ecological Conditions in Retrospective Clinical Research: A Use Case of Social Stress
  M. Breitenstein, University of Minnesota/Mayo Clinic; J. Pathak, Mayo Clinic; G. Simon, University of Minnesota

- Using Software as Hypothesis to Develop a System for Tracking Research Activity
  A. Das, B. Levin, S. Andrews, Geisel School of Medicine at Dartmouth

3:00 p.m. – 3:30 p.m. Coffee Break

Embarcadero, Level 3
* CTS-AMIA

Mission
#CRI21

#CRI20
3:30 p.m. – 5:00 p.m.  Scientific Sessions

**CRI22: Papers/Podium Presentations - Temporal Data Analytics**

*Session Chair: Jianying Hu*

- Clinical Procedures Prediction with Temporal Data Analytics  
  R. Moskovitch, Columbia University

- Cumulative Time Series Representation for in Hospital Code Blue Prediction  
  R. Salas-Boni, University of California San Francisco; Y. Bai, University of California Los Angeles; X. Hu, University of California San Francisco

- ClinicalTime: Identification of Patients with Acute Kidney Injury Using Temporal Abstractions and Temporal Pattern Matching  
  D. Capurro, Pontificia Universidad Catolica de Chile/University of Washington; M. Barbe, C. Daza, J. Santa Maria, J. Trincado, I. Gomez, Pontificia Universidad Catolica de Chile

- Designing Ontology-based Patterns for the Representation of the Time-relevant Eligibility Criteria of Clinical Protocols  
  C. Tao, UTHealth; C. Crowe, University of Virginia

**CRI23: Papers/Podium Presentations - Adverse Outcomes**

*Session Chair: Justin Starren*

- A System for Identifying and Investigating Unexpected Response to Treatment  
  M. Ozery-Flato, L. Ein-Dor, H. Neuvirth, N. Parush, IBM Research - Haifa; M. Kohn, Sentrian; J. Hu, IBM Research - T.J. Watson; R. Aharonov, IBM Research - Haifa

- Automated Determination of Publications Related to Adverse Drug Reactions in PubMed  
  H. Adams, Stony Brook University; C. Friedman, Columbia University; J. Finkelstein, Johns Hopkins University

- Rediscovering Drug Side Effects: The Impact of Analytical Assumptions on the Detection ofAssociations in EHR Data  
  J. Diaz-Garelli, E. Bernstam, M. Rahbar, T. Johnson, University of Texas Health Science Center at Houston

- Using Electronic Health Record Data to Study Disease-specific Effects of Metformin and Insulin in Breast Cancer  
  M. Breitenstein, University of Minnesota/ Mayo Clinic; L. Wang, R. Weinshilboum, Mayo Clinic; G. Simon, University of Minnesota; J. Pathak, Mayo Clinic
**THURSDAY, MARCH 26**

**Scientific Sessions**

3:30 p.m. – 5:00 p.m. | CONTINUED

### CRI24: Podium Presentations - Collective Knowledge Mining

**Session Chair:** Kavishwar Wagholikar

- **A Method for Assessing the Collective Population Representativeness of Multiple Related Clinical Trials Using Public Data Resources**
  
  Z. He, Columbia University; P. Ryan, Janssen Research and Development; S. Wang, C. Weng, Columbia University

- **Piloting a Comprehensive Knowledge Base for Pharmacovigilance Using Standardized Vocabularies**
  
  V. Huser, NIH CC; J. Jao, University of Pittsburg; J. Duke, Regenstrief Institute; P. Ryan, OHDSI; S. Nelson, University of Utah; R. Boyce, University of Pittsburgh

- **XPRESS – Extraction of Phenotypes from Clinical Records Using Silver Standard Corpora**
  
  T. Podchiyska, V. Agarwal, N. Shah, Stanford University

- **Use of i2b2 for the MURDOCK Study’s Integrated Data Repository**
  
  C. Blach, Duke University; G. Del Fiol, University of Utah; J. Frund, K. Morehouse, A. Walden, J. Tenenbaum, Duke University

### CRI25: Papers/Podium Presentations - Real-time Decision Support

**Session Chair:** Adam Wilcox

- **It’s Just (Academic) Business: A Use Case in Improving Informatics Operations with Business Intelligence**
  
  L. McIntosh, C. Zabarovskaya, M. Uhlmansiek, Washington University School of Medicine

- **How Comorbidities Co-occur in Readmitted Hip Fracture Patients: From Bipartite Networks to Insights for Post-discharge Planning**
  
  S. Bhavnani, B. Dang, UTMB; S. Visweswaran, University of Pittsburgh; R. Divekar, Mayo Clinic; A. Karmarkar, K. Ottenbacher, UTMB

- **Are Patients with Similar Names at Greater Risk for Wrong-patient Orders?**
  
  H. Salmasian, R. Green, C. Friedman, G. Hripcsak, D. Vawdrey, Columbia University

- **Real-time Scoring of Patient-reported Outcomes in FORCE-TJR: National Total Joint Replacement Research Registry**
  
  H. Zheng, W. Li, L. Harrold, D. Ayers, P. Franklin, University of Massachusetts Medical School

### CRI26: Peer-based Learning Workshop - IRBShare and Honest Broker

**Session Chair:** David Vawdrey

- **IRBshare: Enabling Flexibility while Streamlining IRB Oversight and Administrative Management of Multicenter Trials**
  
  P. Harris, E. Sheffer, Vanderbilt University

- **Implementation of an Electronic Honest Broker-based Toolkit for Integrated Data and Biorepository Research**
  
  A. Felmeister, The Children’s Hospital of Philadelphia/Drexel University; T. Rivera, The Children’s Hospital of Philadelphia

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5:00 p.m. – 6:00 p.m.

**CRI Poster Session 2 and Reception**

(Not eligible for CME/CE)

See page 67 for list of CRI Poster Session 2 posters, listed alphabetically by first author.
## Friday, March 27

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<td>Prometheus Research Corporate Roundtable (by invitation) (Not eligible for CME/CE)</td>
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<td>7:30 a.m. – 8:30 a.m.</td>
<td>Continental Breakfast</td>
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<td>7:30 a.m. – 11:30 a.m.</td>
<td>Registration Open</td>
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<tr>
<td>8:30 a.m. – 10:00 a.m.</td>
<td>Scientific Sessions</td>
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**CRI27: Interactive Panel – Tug of Ontology Wars: How Many Information Models Does It Take to Weave a Nationwide Clinical Data Research Network?**

P. Mirhaji, Albert Einstein College of Medicine; S. Murphy, Partners Healthcare; C. Reich, AstraZeneca LP; K. Marsolo, Cincinnati Children’s Hospital Medical Center

This panel will introduce and comparatively review the information models, ontologies, and terminologies used by Informatics for Integrating Biology and the Bedside (i2b2), Observational Medical Outcomes Partnership (OMOP), and the PCORnet Common Data Model. This panel will also discuss the corresponding vocabulary systems of these models and their value proposition for investigators and research organizations. Panelists will share perspectives that have informed the original design and conceptualization of these frameworks, and will address the topics of adoption, utility and impact within the current ecosystem of collaborative, distributed research initiatives. They will also discuss their vision for the evolution and future extensions of these frameworks.

The panel will engage the audience to discuss the need for multiple data models, why we lack a “single bullet” solution, and how returns on research resources invested in one framework can be maximized through innovative interoperability and interchange solutions between them. Panelists will interact with audience and among each other to discuss opportunities that exist in current high profile national and international initiatives (such as the PCORI CDRN and PPRN initiatives, the CTSA accrual to clinical trials (ACT), and OHDSI OMOP platform) for large-scale multi-disciplinary research collaborations, informatics, and analytics.

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**All Attendees: Session Evaluation**

Use QR codes to evaluate each session *(required for nursing CE)*. If you are unable to access the surveys via QR code visit amia.org/jointsummits2015/CRI-evaluation
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<tr>
<td>K. McManus, E. Mallory, R. Goldfeder, W. Haynes, J. Tatum, Stanford University</td>
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<tr>
<td>Automated Home Monitoring of High-risk Inter-stage Surgical Infants with Complex Congenital Heart Disease</td>
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<td>R. Stroup, Children's Mercy Hospitals and Clinics</td>
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<tr>
<td>Leveraging Interaction between Genetic Variants and Mammographic Findings for Personalized Breast Cancer Diagnosis</td>
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<tr>
<td>J. Liu, Y. Wu, I. Ong, D. Page, UW-Madison; P. Peissig, Marshfield Clinic Research Foundation; C. McCarty, Essentia Institute of Rural Health; A. Onitilo, Marshfield Clinic Research Foundation; E. Burnside, UW-Madison</td>
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<td>What Chronic Conditions Predict an Index Depression Diagnosis in Adults?</td>
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<td>E. Ryu, A. Chamberlain, R. Pendegraft, W. Bobo, J. Pathak, Mayo Clinic</td>
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<td>N. Shah, B. Gallego, Y. Low, C. Longhurst, Stanford University</td>
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<td>Infobutton Usage in Patient Portal MyHealth</td>
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<td>J. Long, Intermountain Healthcare; N. Hulse, Intermountain Healthcare/University of Utah; C. Tao, UTHealth</td>
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<td>Methods for Linking EHR Notes to Education Materials</td>
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<td>J. Zheng, University of Massachusetts, Amherst; H. Yu, University of Massachusetts Medical School</td>
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<td>ISIDRO: Interactive Secure Institutional Data Release Overseer</td>
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<td>B. Levin, A. Das, Dartmouth College</td>
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<td>ResearchIQ: Design of a Semantically Anchored Integrative Query Tool</td>
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<td>O. Lele, S. Raje, P. Yen, P. Payne, The Ohio State University</td>
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<td>A Semantic Web-based System for Mining Genetic Mutations in Cancer Clinical Trials</td>
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<td>S. Priya, Lehigh University/Mayo Clinic; G. Jiang, D. Dasari, M. Zimmermann, C. Wang, Mayo Clinic; J. Heflin, Lehigh University; C. Chute, Mayo Clinic</td>
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<td>Provenance Metadata as a Method of Validating the Learning Healthcare System</td>
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<td>V. Curcin, King’s College London; R. Danger, Imperial College London; T. Arvanitis, University of Warwick; B. Delaney, King’s College London</td>
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<tr>
<td>A Semantic Framework for Quality Data Model to Support EHR-driven Phenotype Authoring and Execution</td>
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<td>G. Jiang, H. Solbrig, R. Kiefer, Mayo Clinic; L. Rasmussen, Northwestern University; H. Mo, P. Speltz, Vanderbilt University; W. Thompson, Northwestern University; J. Denny, Vanderbilt University; C. Chute, J. Pathak, Mayo Clinic</td>
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* CTS-AMIA
**CRI31: Peer-based Learning Workshop - Everything about Scientific Profiles: Resource Sharing and Networking**  
*Session Chair: David Eichmann*

**eagle-i: a VIVO-ISF Ontology Enabled Tool to Promote Resource Sharing, Discovery and Integration with Harvard Catalyst Profiles**  
B. Bahl, D. Bourges-Waldegg, G. Weber, Harvard Medical School; M. Haendel, Oregon Health & Science University; K. Holmes, Northwestern University

**Profiles Research Networking Software**  
G. Weber, Harvard Medical School; E. Meeks, University of California San Francisco

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<tr>
<th>Time</th>
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<td>10:00 a.m. – 10:30 a.m.</td>
<td>Coffee Break</td>
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<td>10:30 a.m. – 12:00 p.m.</td>
<td><strong>CRI Summit Closing Session and Year-in-Review</strong></td>
<td>Cyril Magnin I</td>
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**Peter 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 19

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Thank you for attending the Summit on Clinical Research Informatics. Don’t forget to evaluate the entire CRI Summit.

If you are unable to access the survey via QR code visit amia.org/jointsummits2015/CRI-evaluation
AMIA seeks to recognize individuals who maintain their membership commitment and continue to represent the values of AMIA. We strive to recognize the amazing people who choose to belong to AMIA’s membership community.

All members, new and experienced, are valuable to the AMIA community. The diversity of AMIA’s multidisciplinary members makes the AMIA community special. In a world where knowledge is expanding exponentially through the use of informatics, AMIA welcomes and values members who continue to:

- Sustain interest in the organizations mission
- Value networking with informatics professionals
- Pursue a professional life of learning and sharing information
- Apply knowledge to pose questions and solve problems
- Seek opportunities to lead and serve

For more information about AMIA’s Member Loyalty Program
Contact Nicole Washington, Member Services Coordinator by phone at 301-657-1291 or email nicole@amia.org.
TBI Poster Session
(Not eligible for CME/CE)

Tuesday, March 24
5:00 p.m. – 6:00 p.m.

Room: Cyril Magnin Foyer

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T. Altman, Stanford University; D. Relman, Stanford University/VA Palo Alto Health Care System; D. Dill, Stanford University

| Widespread Parainflammation in Human Cancer | 3 |
D. Aran, Stanford University/The Hebrew University of Jerusalem; A. Lasry, A. Zinger, M. Biton, E. Pikarsky, Y. Ben-Neriah, A. Hellman, The Hebrew University of Jerusalem

| G-DOC Plus: The Next-generation Systems Medicine Platform for Precision Medicine | 4 |
K. Bhuvaneshwar, A. Belouali, V. Singh, R. Johnson, L. Song, S. Rao, A. Alaaou, M. Harris, Y. Gusev, S. Madhavan, Georgetown University

| Using Electronic Health Records to Uncover Disease-birth Month Dependencies | 5 |
M. Boland, Z. Shahn, D. Mogdian, G. Hripcsak, N. Tatonetti, Columbia University

| Identifying the Impact of Genomic Variation on Glycemic Response to Metformin Using EHR-linked Biorepository Data | 6 |
M. Breitenstein, University of Minnesota/ Mayo Clinic; E. Ryu, L. Wang, S. Armasu, R. Weinshilboum, Mayo Clinic; G. Smirn, University of Minnesota; J. Pathak, Mayo Clinic

| Connecting Chemical Structure to Cellular Response: An Integrative Analysis of Gene Expression, Bioactivity, and Structural Data Across 11000 Compounds | 7 |

| FHIR-based Web Services for Computational Phenotyping from Electronic Health Records | 8 |
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| SysBioCube Tools for Integration of Omics and Phenotype Datasets | 9 |
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| Functional Characterization of Disease-associated Genes in Autism Spectrum Disorders Using Intelligent Literature Extraction | 10 |
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| Planning Clinically Relevant Biomarker Validation Studies Using the “Number Needed to Treat” Concept | 11 |
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| Spike in Interdisciplinary Research Helps Decode Autism’s Complexity | 12 |
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| Identification of Causal Cascades and Unobserved Intermediate Structure in Input/Output Systems | 14 |
C. Glymour, Carnegie Mellon University

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| Connecting the Signatures: Associations between Small Molecules and microRNA in Malignant Melanoma | 16 |
A. Jha, K. Kegan, P. Payne, Ohio State University
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2016 Joint Summits on Translational Science

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Subha Madhavan, PhD
Director, Innovation Center for Biomedical Informatics Georgetown University Medical Center
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CRI Summit
Nick Anderson, PhD
Director of Informatics Research and Assistant Professor Robert D. Cardiff Professor of Informatics, University of California, Davis
@nick_r_anderson
## CRI Poster Session 1

*(Not eligible for CME/CE)*

**Wednesday, March 25**

**5:00 p.m. – 6:00 p.m.**

Room: Cyril Magnin Foyer

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<td>Development of a National Distributed Research Network Data Infrastructure: Design of the PCORnet Common Data Model</td>
<td>J. Brown, Harvard Medical School/Harvard Pilgrim Health Care Institute; S. Rusincovitch, Duke Translational Medicine Institute; A. Kha, Northwestern University; K. Marsolo, Cincinnati Children's Hospital Medical Center; L. Curtis, Duke University School of Medicine</td>
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<td>Predicting Risk of ICU Transfer, Intubation, or Death for Pediatric Asthma, RSV, and Pneumonia Patients by Mining Data in Electronic Medical Records Using Machine-learning Techniques</td>
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<td>Automated Extraction of Vascular Findings from Computed Tomographic Angiogram (CTA) Reports</td>
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<td>A Semi-automatic Method for Generating Ontology of the Common Terminology Criteria for Adverse Events</td>
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CRI Poster Session 2
(Not eligible for CME/CE)

Thursday, March 26
5:00 p.m. – 6:00 p.m.
Room: Cyril Magnin Foyer

**Design and Implementation of NYC-CDRN Informatics Infrastructure: A Preliminary Report**
R. Belenkaya, Albert Einstein College of Medicine; T. Campion, Weill Cornell Medical College; T. Bloom, New York Genome Center; C. Weng, Columbia University College of Physicians and Surgeons; R. Chandras, New York University Langone Medical Center; T. Check, Healthx; G. Hripcsak, Columbia University College of Physicians and Surgeons; R. Kaushal, Weill Cornell Medical College; P. Mirhaji, Albert Einstein College of Medicine

**CliNER: A Lightweight Tool for Clinical Named Entity Recognition**
W. Boag, K. Waxcome, UMass Lowell; T. Naumann, Massachusetts Institute of Technology; A. Rumshisky, UMass Lowell/Massachusetts Institute of Technology

**Implementing a Distributed Network to Share Electronic Health Record Data for Surveillance and Research: Colorado Health Observation Regional Data Service (CHORDS)**
J. Bondy, Colorado Clinical and Translational Sciences Institute; E. McCormick, Denver Public Health; J. Wade, National Jewish Health; B. Doyle, University of Colorado Cancer Center; D. Tabano, J. Stein, Kaiser Permanente Colorado; M. Kahn, Colorado Clinical and Translational Sciences Institute; A. Davidson, Denver Public Health

**A Comparative Evaluation of Open Source Data Quality Tools**
T. Callahan, M. Kahn, University of Colorado Denver

**An Image Phenotyping Infrastructure for Clinical Research**
B. Chapman, W. Liu, University of Utah

**Expressing Research Data from Multiple Interconnected REDCap Projects in i2b2**
J. Craig, K. Reilly, J. Oates, D. Kamen, J. Obeid, Medical University of South Carolina

**Automated Diabetes Surveillance Using Natural Language Processing and Artificial Neural Networks**
M. Crosskey, E. Pfaff, J. Klein, UNC Chapel Hill; V. Zhong, E. Mayer-Davis, UNC Chapel Hill/Gillings School of Public Health

**RexMart: Empowering Analysts to Configure Research Data Marts to Improve End-user Data Exploration**
P. Farach, O. McGettrick, A. Mesa, L. Rozenblit, Prometheus Research

**Leveraging Technology to Assist in Management of Diabetic Conditions**
K. Feldman, S. Li, University of Notre Dame; W. Mikes-Carrasco, Interdisciplinary Center for Network Science & Applications (CeNSA); M. Krchekf, Saint Joseph Regional Medical Center; N. Chawla, Interdisciplinary Center for Network Science & Applications (CeNSA)

**Data Validation Systems - An Unmet Need for National Patient Safety Indicator Reporting**
M. Fennessy, The Ohio State University; M. Bethel, A. Lorenz, T. Latimer, L. Yahe-Dunbar, The Ohio State University Wexner Medical Center; S. Moffatt-Bruce, The Ohio State University Wexner Medical Center/The Ohio State University

**Making Work Visible in Systems for Enterprise-wide Research Activities**
C. Ganoe, S. Thompson, S. Punjasthitkul, A. Das, Geisel School of Medicine at Dartmouth

**Patient Care Snapshot: An Automated Integrated Patient Care Tool**

**A Population Level Adherence Model for Diabetes**
T. Gupta, E. Manigandan, G. Soto-Campos, S. Narayanan, ConvergeHEALTH by Deloitte; E. Scheufele, ConvergeHEALTH by Deloitte/University of California, San Francisco; J. Kohler, ConvergeHEALTH by Deloitte

**Patient Centered Ontology Development for a Personal Health Information System**
C. Hempelmann, Texas A&M University- Commerce; V. Gurupur, University of Central Florida; U. Sakaglu, Texas A&M University- Commerce

**Predicting Length of Hospital Stay Using the Polarity of Nursing Statements**
E. Jeon, H. Park, Y. Kim, Y. Min, Seoul National University
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### Characterizing Common Features of Recipe Management and Recommender Systems in Mobile Applications

D. Walker, M. Murtaugh, G. Luo, University of Utah

### Identification Rate of Patients with Systemic Lupus Erythematosus Using Structured Data in an Electronic Health Record

T. Walunas, K. Jackson, A. Chung, K. Mancera-Cuevas, R. Ramsey-Goldman, A. Kho, Northwestern University

### Temporal Identification of Type 2 Diabetes Using Structured Data from an Electronic Health Record

B. Wells, A. Milinovich, K. Pantalone, C. Yu, J. Bauman, Cleveland Clinic

### Text Annotation of Serious Adverse Event Reports for Identification of Clinical Trial Endpoints

M. Williams, R. Pridgen, M. Wilson, B. McCourt, Duke University

### Modeling Trajectories for Diabetes Complications

P. Yadav, L. Prunelli, A. Hangsleben, S. Dey, K. Hauwiller, B. Westra, C. Delaney, V. Kumar, M. Steinbach, G. Simon, University of Minnesota

### Correspondence of Topic Models and MeSH Terms for PubMed Abstracts

Z. Yu, E. Bernstam, T. Cohen, T. Johnson, University of Texas Health Science Center at Houston

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Cyril Magnin
55’ x 103’
5,670
12’
6’
255
400
120
100
1000
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900
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Cyril Magnin I
55’ x 34’
1,890
12’
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Cyril Magnin II
55’ x 35’
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Cyril Magnin III
55’ x 34’
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Cyril Magnin Foyer*
57’ x 120’
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12’
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1200
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Balboa
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Davidson
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Mission II
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Mission III
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10’
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