driving discovery and dissemination of precision medicine to improve patient and population health outcomes

2016 JOINT SUMMITS ON TRANSLATIONAL SCIENCE

SAN FRANCISCO

Summit on Translational Bioinformatics
MARCH 21-23

Summit on Clinical Research Informatics
MARCH 22-24

Informatics Implementation Track
MARCH 21-24

#TBICRI16
amia.org/jointsummits2016
@AMIAinformatics
The Joint Summits on Translational Science is supported by

TriNetx

IMO
Intelligent Medical Objects

Duke Clinical Research Institute
From Thought Leadership to Clinical Practice

Thank You
Welcome
2016 Joint Summits on Translational Science

Questions? Concerns? E-mail feedback@amia.org
Click amia.org/jointsummits2016/updates for daily changes to the schedule
Follow Twitter @AMI Ainformatics for real time updates
Use hashtag #TBICRI16 to share with others
Connect via Wi-Fi access Wireless Network: Parc55meeting
Username: N/A
Password: tbicri (available on Level 4 only)
Bookmark jointsummits2016.zerista.com
Visit registration in the Cyril Magnin Foyer for AMIA HQ staff support
Claim CME/CE Credits amia.org/jointsummits2016/cme

NEW! The Joint Summits has a new networking platform and mobile app. Connect and plan with personal profiles, interest tags, social media, direct messaging, note taking, and a customized schedule.

- Check your email for an AMIA Meetings app invitation link
- Download the AMIA Meetings app
- Create your new account, profile and select your interest tags (initial set-up is easier with laptop or tablet)
- If you cannot find your AMIA Meetings app invitation ...
- Go to the Registration Desk in Cyril Magnin Foyer and ask an AMIA staff member to assist.
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
Dear Colleagues and Friends,

On behalf of AMIA and the scientific program committee, we would like to extend a warm welcome to the Joint Summits on Translational Science, which combines the Summit on Translational Bioinformatics and the Summit on Clinical Research Informatics.

The Joint Summits serve as the primary forum to connect with leaders in the field of informatics who are advancing translational science at the nexus of bioinformatics and clinical research. The theme of the 2016 Joint Summits is driving discovery and dissemination of precision medicine to improve patient and population health outcomes.

This meeting brings together translational scientists, data scientists, informatics researchers and practitioners from academia, industry, government and non-profit sectors to share knowledge and best practices, and to forge collaborations across boundaries.

We have a terrific program with tutorials, lectures, expert panels and posters showcasing the latest advances in translational science.

We have a great lineup of keynotes for you this year. Russ B. Altman, MD, PhD, FACMI, will provide the Year-in-Review on Translational Bioinformatics. Deborah Estrin, PhD, founder of the Health Tech Hub at Cornell Tech and co-founder of the startup Open mHealth, will provide her thoughts on Tuesday. David Haussler, PhD, a collaborator on the Human Genome Project will speak on Wednesday. Peter Embi, MD, MS, FACMI, will provide the Clinical Research Informatics Year-in-Review on Thursday.

New for 2016 is the “Informatics Implementation Track,” which features sessions focusing on the bridge between clinical research informatics and translational informatics. Led by Paul Harris, PhD, Vanderbilt University, these sessions will be of particular interest to those researchers and organizations who are committed to advancing the translation of discovery into real-world settings.

Moreover, awards to be presented include:

- Marco Ramoni Distinguished Paper Award for Translational Bioinformatics
- Clinical Research Informatics (CRI) Distinguished Paper Award (sponsored by The Ohio State University)
- Translational Bioinformatics Student Paper Award
- Clinical Research Informatics Student Paper Award

We hope you enjoy the summit and the fantastic program the committee has put together!

Sincerely,

Subha Madhavan, PhD  
Chair, 2016 TBI Scientific Program Committee

Nicholas Anderson, PhD  
Chair, 2016 CRI Scientific Program Committee
Scientific Program Committees

Summit on Translational Bioinformatics

Chair

Subha Madhavan, PhD
Georgetown University

Track Chairs

Nicholas Tatonetti, PhD
Columbia University

Zhongming Zhao, PhD
Vanderbilt University

Members

Xiaohong (Sherry) Cao, PhD
Genzyme Sanofi Corporation

Maricel G. Kann, PhD
University of Maryland-Baltimore

Jason H. Moore, PhD
University of Pennsylvania - The Perelman School of Medicine

Radha Nagarajan, PhD
University of Kentucky

Peggy Peissig, PhD, MBA
Marshfield Clinic

Marylyn D. Ritchie, PhD
Geisinger Health System

Shyam Visweswaran, MD, PhD
University of Pittsburgh

Rong Xu, PhD
Case Western Reserve University

Summit on Clinical Research Informatics

Chair

Nicholas Anderson, PhD
University of California, Davis

Track Chairs

Jihad Obeid, MD
Medical University of South Carolina

Russ Waitman, PhD
University of Kansas Medical Center

Members

Daniel Capurro, MD, PhD
Pontificia Universidad Católica de Chile

David Eichmann, PhD
University of Iowa

Kate Fultz Hollis, MS
Oregon Health & Science University

Davera Gabriel, RN
University of California, Davis

Kelly Grindrod, PharmD, MSc
University of Waterloo

Vojtech Huser, MD, PhD
National Institutes of Health

Dipti Ranganathan
University of Texas Southwestern Medical Center

Kari Stephens, PhD
University of Washington
Informatics Implementation Track

Chair
Paul Harris, PhD
Vanderbilt University

Track Leads
Denise Hynes, PhD, MPH, RN
University of Illinois at Chicago and
Veterans Affairs Information Resource Center (VIReC)

Bernie LaSalle
University of Utah

Sorena Nadaf, MS, MMI
University of California, San Francisco

Robert Schuff, MS
Oregon Health & Science University

Bonnie Westra, PhD, RN, FACMI
University of Minnesota
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 2016 TBI/CRI registrants have free access to the archives. To access the AMIA Proceedings archive, simply point your browser to http://knowledge.amia.org. Use your AMIA login and password to access the 2016 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 Joint Summits. 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.

Mobile App
NEW! The Joint Summits has a new networking platform and mobile app. Connect and plan with personal profiles, interest tags, social media, direct messaging, note taking, and a customized schedule.

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- Download the AMIA Meetings app
- Create your new account, profile and select your interest tags (initial set-up is easier with a laptop or tablet) https://jointsummits2016.zerista.com

Wi-Fi Connection
Turn on your device’s wireless connections to view available Wi-Fi networks. Choose and connect to “Parc55meeting” network. The password is tbicri on Level 4 only.

Please do not be a bandwidth bully. Users will be cycled off the network to allow others to connect!
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<th>Time</th>
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<tr>
<td>7:00 a.m. – 8:15 a.m.</td>
<td>Birds-of-a-Feather Sessions</td>
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<td></td>
<td><strong>TBI-BOF01</strong>: Informatics for Mental Health</td>
<td>Mission</td>
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<td><strong>TBI-BOF02</strong>: Integrating data with Electronic Health Records for Exploration of Common Disease</td>
<td>Market Street, 3rd Floor</td>
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<tr>
<td>7:00 a.m. – 8:30 a.m.</td>
<td>Continental Breakfast</td>
<td>Cyril Magnin Foyer</td>
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<tr>
<td>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. – 10:00 a.m.</td>
<td>Translational Bioinformatics Year-in-Review: Russ B. Altman, MD, PhD, FACMI</td>
<td>Cyril Magnin Ballroom</td>
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<tr>
<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>Scientific Sessions</td>
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<td><strong>II01</strong>: Scaling up Data and Technology (Why and How this Matters)</td>
<td>Cyril Magnin III</td>
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<td><strong>S01</strong>: Panel - Precision Medicine: Leveraging Genomics in Diverse Indications</td>
<td>Cyril Magnin I</td>
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<td><strong>S02</strong>: Panel - The Many Meanings of Precision Medicine</td>
<td>Cyril Magnin II</td>
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<td><strong>S03</strong>: Podium Presentations - Genomics-based Decision Support and Knowledge Platforms</td>
<td>Mission</td>
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<td><strong>S04</strong>: Papers/Podium Presentations - Using Clinical Data to Make Biological Discoveries</td>
<td>Market Street, 3rd Floor</td>
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<td>1:30 p.m. – 3:00 p.m.</td>
<td>Scientific Sessions</td>
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<td><strong>II02</strong>: How do I Become an Operational Leader?</td>
<td>Cyril Magnin III</td>
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<td><strong>S05</strong>: Panel - Funding Opportunities and Government-funded Initiatives in the Areas of Translational Bioinformatics and Clinical Research Data Infrastructure</td>
<td>Cyril Magnin I</td>
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<td><strong>S06</strong>: Panel - Career Opportunities to the Many Paths to Informatics</td>
<td>Cyril Magnin II</td>
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<td><strong>S07</strong>: Papers/Podium Presentations - Data-driven Omics</td>
<td>Stockton</td>
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<td><strong>S08</strong>: Papers/Podium Presentations - Pharmacogenomics and Clinical Decision Support</td>
<td>Market Street, 3rd Floor</td>
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<tr>
<td>1:30 p.m. – 5:00 p.m.</td>
<td><strong>T01</strong>: Tutorial - Fundamentals and Applications of Computational Causal Discovery in Biomedicine</td>
<td>Mission</td>
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<tr>
<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>Scientific Sessions</td>
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<td><strong>II03</strong>: Efficiently and Sustainably Delivering Integrated Research Registries in Academic Health Centers: Experiences from the Trenches</td>
<td>Cyril Magnin III</td>
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<td><strong>S09</strong>: Papers/Podium Presentations - Drug Discovery and Drug Repurposing</td>
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<td><strong>S10</strong>: Podium Presentations - Machine Learning for Biomedicine</td>
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<td><strong>S11</strong>: Podium Presentations - Systems Biology and Gene Discovery</td>
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<tr>
<td>5:00 p.m. – 6:00 p.m.</td>
<td>Networking Reception</td>
<td>Cyril Magnin Foyer</td>
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<tr>
<td>5:30 p.m. – 7:00 p.m.</td>
<td>Genomics and Translational Bioinformatics Working Group Meeting</td>
<td>Stockton</td>
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<tr>
<td>6:30 p.m. – 8:30 p.m.</td>
<td>REDCap Community Discussion and Tutorial</td>
<td>Cyril Magnin I</td>
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## Tuesday, March 22

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<tr>
<td>7:00 a.m. – 8:15 a.m.</td>
<td>Birds-of-a-Feather Sessions</td>
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<td><strong>TBI-BOF03</strong>: Envisioning Informatics for the NIH Precision Medicine Initiative</td>
<td>Cyril Magnin I</td>
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<td><strong>TBI-BOF04</strong>: Tools for Reproducible Research in Translational Bioinformatics</td>
<td>Cyril Magnin II</td>
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<tr>
<td>7:00 a.m. – 8:30 a.m.</td>
<td>Continental Breakfast</td>
<td>Cyril Magnin Foyer</td>
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<tr>
<td>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. – 10:00 a.m.</td>
<td>Scientific Sessions</td>
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<td><strong>II04</strong>: Why &amp; How This Matters</td>
<td>Cyril Magnin III</td>
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<td><strong>S12</strong>: Podium Presentations - Precision Medicine in Action</td>
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<td><strong>S13</strong>: Panel - BD2K (Big Data to Knowledge) Program Driving Clinical Genomic and Disease Discovery</td>
<td>Cyril Magnin II</td>
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<td><strong>S14</strong>: Papers - Data and Text Processing</td>
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<td><strong>S15</strong>: Papers - Infrastructure for Data Driven Translational Science</td>
<td>Market Street, 3rd Floor</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>
<td>Scientific Sessions</td>
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<td><strong>II05</strong>: Implementing Data Standards to Enable the Learning Health System</td>
<td>Cyril Magnin III</td>
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<td><strong>S16</strong>: TBI Student Paper Competition</td>
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<td><strong>S17</strong>: Podium Presentations - Addressing the Data Problem</td>
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<td><strong>S18</strong>: Papers - Data Mining or Knowledge Discovery</td>
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<td><strong>S19</strong>: Panel - Insight Generation from Real-world and Real-time Treatment Pathways</td>
<td>Cyril Magnin II</td>
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<tr>
<td>11:00 a.m. – 3:00 p.m.</td>
<td>10x10 with the Ohio State University In-person Session (10x10 students only)</td>
<td>Balboa</td>
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<td>1:30 p.m. – 3:00 p.m.</td>
<td>Scientific Sessions</td>
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<td><strong>II06</strong>: Secondary Use of Data for Research - EHR, Omics, and Environmental Data</td>
<td>Cyril Magnin III</td>
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<td><strong>S20</strong>: Podium Presentations - Drugs, Text, and EHRs: Analytics Methods for Health Data</td>
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<td><strong>S21</strong>: Panel - ClinGen Informatics Resources for Researchers, Clinicians, and Laboratories</td>
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<td><strong>S22</strong>: Papers - Data Mining or Knowledge Discovery</td>
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<td><strong>S23</strong>: Papers - Clinical and Research Data Visualization</td>
<td>Market Street, 3rd Floor</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><strong>Plenary Session and Keynote Presentation: Deborah Estrin, PhD</strong></td>
<td>Cyril Magnin Ballroom</td>
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<tr>
<td>5:00 p.m. – 6:00 p.m.</td>
<td>Poster Session 1</td>
<td>Cyril Magnin Foyer</td>
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<tr>
<td>6:30 p.m. – 8:30 p.m.</td>
<td>Billiards Networking Meet-up</td>
<td>Jillian’s Billiards</td>
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**Wednesday, March 23**

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<td>7:00 a.m. – 8:15 a.m.</td>
<td>AMIA Town Hall</td>
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<td>7:00 a.m. – 8:30 a.m.</td>
<td>Continental Breakfast</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>8:00 a.m. – 12:00 p.m.</td>
<td>10x10 with Oregon Health &amp; Science University In-person Session (10x10 students only)</td>
<td>Stockton</td>
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<td>8:30 a.m. – 10:00 a.m.</td>
<td>Scientific Sessions</td>
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<td><strong>II07:</strong> Leveraging Participant-generated and Environmental Data (Why and How this Matters)</td>
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<td><strong>S24:</strong> Panel - Practical Implementation of Genomic Sequencing in Healthcare Settings</td>
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<td><strong>S25:</strong> CRI Student Paper Competition</td>
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<td><strong>S26:</strong> Podium Presentations - Data Mining and Knowledge Discovery</td>
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<tr>
<td>8:30 a.m. – 12:00 p.m.</td>
<td><strong>T02:</strong> Tutorial - Immuno-informatics Coming of Age: Emerging Approaches and Applications</td>
<td>Mission</td>
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<td>10:00 a.m. – 10:30 a.m.</td>
<td>Coffee Break</td>
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<tr>
<td>10:30 a.m. – 12:00 p.m.</td>
<td>Scientific Sessions</td>
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<td><strong>II08:</strong> Innovative Informatics Approaches to Assist with Recruitment and Retention (Interactive Learning)</td>
<td>Cyril Magnin III</td>
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<td><strong>S27:</strong> Podium Presentations - Clinical and Research Data Collection, Curation, Preservation, or Sharing</td>
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<td><strong>S28:</strong> Podium Presentations - Data Integration and Standardization</td>
<td>Cyril Magnin I</td>
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<td>10:30 a.m. – 3:00 p.m.</td>
<td><strong>T03:</strong> Tutorial - Cancer Precision Medicine</td>
<td>Cyril Magnin II</td>
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<td>12:30 p.m. – 1:30 p.m.</td>
<td>Lunch Break <em>(lunch on own)</em></td>
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<td>1:30 p.m. – 3:00 p.m.</td>
<td>Scientific Sessions</td>
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<td><strong>II09:</strong> i2b2: Challenges and Solutions to integrate FHIR and PCORI CDM</td>
<td>Cyril Magnin III</td>
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<td><strong>S29:</strong> Papers/Podium Presentations - Data Standards, Terminologies, Ontologies</td>
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<td><strong>S30:</strong> Podium Presentations - Machine Learning for Clinical Applications</td>
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<td><strong>S31:</strong> Podium Presentations - Ethical, Legal, and Social Issues</td>
<td>Market Street, 3rd Floor</td>
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<td>3:00 p.m. – 3:30 p.m.</td>
<td>Coffee Break</td>
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<td>3:30 p.m. – 5:00 p.m.</td>
<td><strong>Plenary Session and Keynote Presentation: David Haussler, PhD</strong></td>
<td>Cyril Magnin Ballroom</td>
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<td>5:00 p.m. – 6:00 p.m.</td>
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<td>i2b2 Community Discussion and Tutorial</td>
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<td>6:30 p.m. – 8:30 p.m.</td>
<td>WINE - Women in Informatics Networking Event</td>
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<td>Birds-of-a-Feather Sessions</td>
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<td><strong>CRI-BOF01</strong>: Clinical Research Informatics Working Group: The Role of the Chief Research Informatics Officer</td>
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<td><strong>CRI-BOF02</strong>: CTSA Informatics Domain Task Force – Looking Forward</td>
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<td>Continental Breakfast</td>
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<td>Scientific Sessions</td>
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<td><strong>II10</strong>: Supporting Research Using Mobile Platforms (Interactive Learning)</td>
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<td><strong>S32</strong>: Podium Presentations - Outcomes Research</td>
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<td><strong>S33</strong>: Panel - Observational Health Data Sciences and Informatics (OHDSI): A Rapidly Growing International Network for Open Science and Data Analytics in Healthcare</td>
<td>Cyril Magnin I</td>
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<td><strong>S34</strong>: Podium Presentations - Clinical and Research Data Collection, Curation, Preservation, or Sharing</td>
<td>Market Street, 3rd Floor</td>
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<tr>
<td>8:30 a.m. – 12:00 p.m.</td>
<td><strong>TO4</strong>: Tutorial - Developing Executable Phenotype Algorithms Using the KNIME Analytics Platform</td>
<td>Cyril Magnin II</td>
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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>Scientific Sessions</td>
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<td><strong>II11</strong>: Creating Collaborative Opportunities in Research Data Management: Implementation and Impact of REDCAP in U.S. Department of Veterans Affairs</td>
<td>Cyril Magnin III</td>
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<td><strong>S35</strong>: Podium Presentations - Pharmacogenomics, Dosing, and Drug Interactions</td>
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<td><strong>S36</strong>: Podium Presentations - Infrastructure for Data-driven Translational Science</td>
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<td><strong>S37</strong>: Papers - Machine Learning for Clinical Applications</td>
<td>Mission</td>
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<td>12:15 p.m. – 1:15 p.m.</td>
<td>Lunch &amp; Learn – TriNetX</td>
<td>Cyril Magnin III</td>
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<tr>
<td>1:30 p.m. – 3:00 p.m.</td>
<td>Scientific Sessions</td>
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<td><strong>II12</strong>: Informatics Landscape: How Your Work Matters and the Implementation of Research</td>
<td>Cyril Magnin III</td>
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<td><strong>S38</strong>: Panel - Advanced Machine Learning for Healthcare</td>
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<td><strong>S39</strong>: Panel - Completing the Learning Health Care System Cycle: Developing and Testing eCQM in pSCANNER, a PCORNet Research Network</td>
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<td><strong>S40</strong>: Podium Presentations - Data Mining and Knowledge Discovery</td>
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<td><strong>S41</strong>: Papers - Clinical and Research Data Collection, Curation, Preservation, or Sharing</td>
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<td>3:00 p.m. – 3:30 p.m.</td>
<td>Coffee Break</td>
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<tr>
<td>3:30 p.m. – 5:00 p.m.</td>
<td><strong>Clinical Research Informatics Year-in-Review: Peter Embi, PhD</strong></td>
<td>Cyril Magnin Ballroom</td>
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**Thursday, March 24**
Tom Payne, AMIA Board Chair and Doug Fridsma, President and CEO of AMIA, will chair this session, an overview of the new 2015-2020 Strategic Plan.

After listening intently to the membership over the past two years, conducting surveys, exploring task force recommendations, and reviewing member feedback, the new Strategic Plan is designed to advance the membership, the organization and the broader impact of AMIA. Information is also available at amia.org/about-amia/strategic-plan. Q&A follows the presentation.

The plan was presented at the AMIA 2015 Annual Symposium and via live webinar in January. For members who did not have an opportunity to attend the prior presentations and those who have questions about the exciting direction where AMIA is headed, please join Tom and Doug for a thoughtful discussion.

**AMIA Strategic Plan 2016-2020**
**Working Together to Transform Health and Healthcare**

**Wednesday, March 23**
7:00 a.m. – 8:15 a.m.

Cyril Magnin I

(Complimentary Continental Breakfast begins in the Cyril Magnin Foyer at 7:00 a.m.)

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

---

**Tom Payne, MD, FACMI**
@tompayne2
Chair, AMIA Board of Directors
University of Washington
AMIA Board of Directors

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

Peter J. Embi, MD, MS, FACMI
The Ohio State University

Cynthia S. Gadd, PhD, FACMI
Vanderbilt University

Gretchen Purcell Jackson, MD, PhD
Vanderbilt University Medical Center

Curtis P. Langlotz, MD, PhD, FACMI, FSiIM
Stanford University

Wanda Pratt, PhD, FACMI
University of Washington

Neil Sarkar, PhD, FACMI
Brown University

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

Jessica Tenenbaum, PhD
Duke Translational Medicine Institute

Adam Wright, PhD
Brigham and Women’s Hospital/Harvard Medical School

Ex-Officio Board Members
Suzanne Bakken, RN, PhD, FACMI
American College of Medical Informatics President
Columbia University

John T. Finnell, MD
Academic Forum Executive Committee Chair
Regenstrief Institute/Indiana University School of Medicine

Douglas B. Fridsma, MD, PhD, FACP, FACMI
President and Chief Executive Officer
AMIA

Michael Weiner, DO
Industry Advisory Council Chair
IBM

Laura K. Wiley
Student Working Group Representative
Vanderbilt University
STATEMENT OF PURPOSE
Translational bioinformatics and clinical research informatics are the informatics domains that support translational research in the context of human health and disease, and touch nearly all areas of biological, biomedical, and clinical research. Translational bioinformatics includes innovative methods and discoveries applied to biologic data, with special focus on human application, including personalized medicine. Clinical research informatics focuses on innovations related to the management of information related to clinical trials and includes informatics related to secondary research use of clinical data.

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. In addition, the 2016 Joint Summits include an implementation track of sessions, focusing on operationalizing informatics tools and support models to support local and global research.

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

And, in addition, for the Informatics Implementation Track:

- Implement more effective operational leadership practices in the clinical research enterprise through practically-focused direct and interactive learning methods
- Develop and adopt best practices for streamlining and improving regulatory processes, clinical trial protocols, study costs, patient recruitment, and data collection and management
- Create and sustain multidisciplinary collaborations in the biomedical research community to expand access to diverse expertise, sophisticated technologies, and unique tools and resources

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 24 AMA PRA Category 1 Credits™. Physicians should claim only the credit commensurate with the extent of their participation in the activity.

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

CONTINUING EDUCATION FOR NURSES
This continuing nursing education activity was approved by the Maryland Nurses Association, an accredited approver by the American Nurses Credentialing Center’s Commission on Accreditation.

Activity Approval Code: A15-49-0321-0210
Approved Contact Hours: 24

Deadline for claiming credit for this activity: April 24, 2016

Nurse Planner for this activity: Bonnie Westra, PhD, RN, FACMI, Associate Professor, School of Nursing and Director, Center for Nursing Informatics, University of Minnesota

Bonnie Westra has disclosed that neither she nor her life partner has relevant financial relationships with ACCME-defined commercial interests.
COMMERCIAL SUPPORT
No commercial support was received for this activity.

FACULTY
Faculty and their affiliations are noted for each presentation.

Disclosures for all planners and presenters will be made in advance of the activity in person and at www.amia.org/jointsummits2016/cme.

INSTRUCTIONS FOR EARNING CME/CE CREDIT
CME site (MyAMIA) works best with IE 9 or above version, Chrome, and Firefox.

- Login to your AMIA account on the AMIA.org website
- Go to “My Events” under Membership/Activities
- Click “Apply for Credits” for this meeting.
- Follow the instruction on the Credit Registration page.
- **Nurses**: Complete your CNE credit claim by April 24, 2016. You will receive your CNE certificate via email from AMIA.
- **Physicians**: To print out your certificate, go to “My CME/CE Credits” under Membership/Activities. under Membership/Activities.
- Other attendees: if you require a certificate of participation, please contact pesha@amia.org.

CONTACT INFORMATION
For questions about continuing education, contact pesha@amia.org.

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.

TARGET AUDIENCE
The target audience for this live activity includes:

- Clinical and translational investigators with an interest in biomedical informatics as it applies to clinical and translational research
- Sponsors and managers of research institutions and programs
- Bioinformaticians, statistical geneticists, and molecular biologists with interests in informatics applied to clinical research (i.e., research on human subjects or material/data of human origin)
- Biomedical and health informatics researchers, faculty, and students
- Community health advocates and those working to advance community-based research
- Computer scientists and system developers
- Computational biologists with interests in human disease
- Government officials and policy makers concerned with health, healthcare, and biomedical and translational research
- Health information and knowledge management professionals
- Health IT industry professionals and consultants
- Industry representatives related to clinical research and translational research
- Staff members and researchers implementing the informatics components of Clinical and Translational Science Awards (CTSA)
- Standards developers
- Designers and developers of EHRs
- Developers and sponsors of patient registries
Translational Bioinformatics Year-in-Review

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

**Deborah Estrin, PhD**  
@deborahestrin  
Professor of Computer Science, Cornell Tech  
Professor of Healthcare Policy and Research, Weill Cornell Medical College

Dr. Estrin is founder of the Health Tech Hub at Cornell Tech in New York City. She is also a and co-founder of the non-profit startup Open mHealth. Her current focus is on mobile health and small data, leveraging the pervasiveness of mobile devices and digital interactions for health and life management (TEDMED, Small data Lab).

Estrin is credited for being a thought leader in the subfield of wireless sensing systems, and in high impact, application-driven computer systems research. She chaired the National Research Council study on Networked Embedded Computing, which produced the report, Embedded Everywhere; and in 2001 shortly after joining the UCLA faculty, she founded the NSF-funded Science and Technology Center for Embedded Networked Sensing (CENS). Estrin spent the early part of her career on faculty at USC (1986-2000) in the Internet research and development community (IETF and Sigcomm) with a focus on protocol design and scalability. Estrin received her PhD (1985) in Computer Science from the Massachusetts Institute of Technology, and her BS (1980) from U.C. Berkeley.

Estrin’s contributions to technology and application innovation have been recognized internationally, including: first ACM Athena Lecturer (2006), the Anita Borg Institute’s Women of Vision Award for Innovation (2007), Doctor Honoris Causa from EPFL Switzerland (2008) and Uppsala University Sweden (2010), and induction into the American Academy of Arts and Sciences (2007) and the National Academy of Engineering (2009).
David Haussler, PhD
Investigator, Howard Hughes Medical Institute
Distinguished Professor, Biomolecular Engineering,
University of California, Santa Cruz
Scientific Director, UC Santa Cruz Genomics Institute,
University of California, Santa Cruz
Director, UCS Cancer Genomics Hub, University of California, Santa Cruz
Scientific Co-Director, California Institute for Quantitative Biosciences (QB3)

David Haussler develops new statistical and algorithmic methods to explore the molecular function, evolution, and disease process in the human genome, integrating comparative and high-throughput genomics data to study gene structure, function, and regulation. As a collaborator on the international Human Genome Project, his team posted the first publicly available computational assembly of the human genome sequence. His team subsequently developed the UCSC Genome Browser, a web-based tool that is used extensively in biomedical research. He built the CGHub database to hold NCI’s cancer genome data, co-founded the Treehouse Childhood Cancer Project to enable international comparison of childhood cancer genomes, and is a co-founder of the Global Alliance for Genomics and Health (GA4GH), a coalition of the top research, health care, and disease advocacy organizations. He is a member of the National Academy of Science and the American Academy of Arts & Science.

Clinical Research Informatics Year-in-Review

Peter J. Embi, MD, MS, FACMI @embimd
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, The Ohio State University

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.
INFORMATICS EDUCATION ONLINE

10x10 VIRTUAL COURSES 2016

Register now for 2016 CME/CEs

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.

Pharmacogenomics
March 21 – May 16, 2016
Stanford University
Course Director – Russ Altman, MD, PhD
The 10x10 with Stanford University provides an introduction to the relevant pharmacology, genomics, experimental methods for high-throughput measurements (sequencing, expression, genotyping), analysis methods for GWAS, chemoinformatics, and natural language processing. Review of key gene classes (cytochromes, transporters, GPCRs), key drugs for which genetics is critical (warfarin, clopidogrel, statins, NSAIDs, neuropsychiatric drugs and cancer drugs). Also reviews resources for pharmacogenomics (PharmGKB, Drugbank, CMAP, and others) as well as issues in doing clinical implementation of pharmacogenomics testing.

Introduction to Biomedical and Health Informatics
April 7 – July 13, 2016
Oregon Health and Science University (OHSU)
Course Director – William Hersh, MD
The goal of the OHSU 10x10 course is to provide a detailed overview of biomedical and health informatics to those who will work at the interface of healthcare and information technology (IT). The course also aims to provide an entry point for those wishing further study (and/or career development) in the field. 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 AMA PRA Category 1 credits

Interprofessional Health Informatics
April 7 – July 7, 2016
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.
56.25 ANCC credits available

Patient Safety and Health Information Technology
June 6 – September 7, 2016
University of Illinois Chicago (UIC)
Course Director – Annette Valenta, DrPH
For 2016, the UIC College of Applied Health Sciences, Department of Biomedical and Health Information Sciences, focuses its 10x10 course on examining how health information technology (HIT) can be used to support...and inhibit...patient safety. The 10x10 course will examine the informatics and information technology issues surrounding the implementation and use of HIT that have contributed to robust discussion over the past decade. Participants will gain an understanding of the sociotechnical aspects of information technology, including why implementation of the best software or hardware sometimes fails to meet expectations.
Up to 56 AMA PRA Category 1 credits

To register for any of the above courses and to view full descriptions, please visit: amia.org/education/10x10-courses
Informatics Implementation Track

The AMIA 2016 Joint Summits Informatics Implementation Track is dedicated to exchange of information and ideas, report-outs from best-of-breed software teams, gap analyses, requirements gathering, professional development opportunities, networking sessions and mentoring opportunities geared specifically to support existing or new CRI implementation experts.

The field of clinical research informatics (CRI) is rapidly evolving to support new frameworks for data sharing, network creation, data access policies, privacy and de/re-identification models, common use data models, phenotype creation and sharing, standards harmonization and other areas of study essential for making new advancements.

CRI implementation and organizational experts are creating innovative tools, support models, sustainable funding cores, local and global training initiatives and software dissemination approaches, all essential requirements for making real-world impact and democratizing access to data resources across all research domains.

Evening Exploratory Sessions

Monday, March 21  6:30 p.m. – 8:30 p.m.  Cyril Magnin I
REDCap Community Discussion and Tutorial
Members of the REDCap team will be present to discuss models for supporting data capture, management and dissemination across small- and large-scale research enterprises. We will begin with a broad overview of the REDCap platform and consortium model, then break into two cross-over tutorial / discussion groups. One group will focus on REDCap’s ‘out of the box’ functionality and discuss strategies for workforce training and engagement with local compliance/regulatory offices to ensure widespread adoption across the local research enterprise. A second group will focus on ‘extending’ REDCap functionality and promoting large-systems interoperability using REDCap’s plug-in architecture and an extensive suite of web services.

Wednesday, March 23  6:30 p.m. – 8:30 p.m.  Cyril Magnin I
i2b2 Community Discussion and Tutorial
In the first half of the session, members of the i2b2 core team will be present and lead a general discussion which will focus on the core roadmap and the new, automated plug-in distribution method. Members of the i2b2 community will learn how they can make their own i2b2 plug-ins available for automated distribution. In the second half of the session, there will be a tutorial on creating web-client and server-side plug-ins for i2b2 and how these can work in tandem to add enormous amounts of functionality to the core i2b2 implementation.
Informatics Implementation Track

Monday, March 21

II01: Scaling up Data and Technology: (Why and How this Matters)
A. Kho, Northwestern University; Z. Landis-Lewis, University of Michigan; T. Box, Department of Veterans Affairs; J.M. Gaziano, VA Boston Healthcare System/Brigham and Women's Hospital/Harvard Medical School

Early development of informatics tools and information systems necessarily may be focused on building and fine tuning functionality, feasibility testing, and usability evaluation in limited settings. Implementation may be restricted to users and sites that are highly invested. As interest and scope expands, implementation requirements may also evolve with expanded volume of users, multiplicity of user expectations, greater heterogeneity of sites, new challenges with interoperability, and increased compliance requirements. Intellectual property and warranty issues may also differ with project expansions. This panel will focus on examples of shifting from a small scale implementation of informatics to a larger scale and scope. Panelists will describe both organizational and technical aspects they encountered in the shift from a smaller scale development phase to a larger scale implementation. Two examples from clinical settings focused on implementation of electronic medical records enhancements and care management and workflow tools, and two examples from research network implementation of tools for disambiguation and expanded data for precision medicine will be highlighted.

II02: How do I Become an Operational Leader?
P. Embi, The Ohio State University; G. Graham, Department of Veterans Affairs; R. Kennedy, Sotera Wireless, Inc.; L. Lenert, Medical University of South Carolina

As our field of medical informatics grows and evolves, with expanded educational opportunities, and new roles, best routes for career advancement may be difficult to discern. From Chief Information Officers, Chief Medical Information Officers, Chief Nursing Information officers, Chief Health Information Officer, Chief Research Information Officers, Informatics Directors, Technology Officers, there are many paths and opportunities for operational leadership. Join us for this panel in a first ever candid discussion with operational leaders about how to become an informatics leader. In a moderated discussion, four accomplished operational leaders from government, private sector and academia will share experiences about specific events and capabilities that can propel a career, skill sets that are most useful for specific positions, and the role of mentors in supporting career development.

II03: Efficiently and Sustainably Delivering Integrated Research Registries in Academic Health Centers: Experiences from the Trenches
L. Rozenblit, Prometheus Research, LLC; I. Brooks, The University of Tennessee Health Science Center; P. Embi, The Ohio State University; M. Ahuja, T. Campion, Weill Cornell Medical College

Integrated research registries are a rapidly growing class of clinical research informatics systems that support investigators by bringing together data collected primarily for research purposes with clinical data and other institutional data. Unfortunately, many existing tools and approaches for delivering research registries are inadequate because they are either very expensive or unacceptably ad hoc. Research activities undertaken inside academic medical centers place considerable demands on informaticists supporting those efforts. On the one hand, there is tremendous demand for registries and data repositories that support research activities. On the other hand, priority, support and budgets for creating such systems are small to nonexistent, limiting their supply. In the background, institutional IT is desperate to control access to PHI and to avoid a proliferation of ill-designed, hard-to-maintain ad hoc solutions.

This panel will discuss various approaches for closing the gap between the demand and the supply for integrated research registries by focusing on highly efficient strategies for delivery. Panelists will describe both organizational and technical strategies for reducing the cost of delivery to a number that a typical research department can afford. Our ultimate goal is to establish a common approach to meeting the growing need for integrated research registries.
Tuesday, March 22

II04: Why & How This Matters  
C. McDonald, National Library of Medicine; B. LaSalle, University of Utah  
8:30 a.m. – 10:00 a.m.

Invited presentation followed by Informatics Implementation Track networking exercise.

Speed Networking Exercise: The final 30 minutes of the session will feature a content-focused speed networking exercise moderated by Program Committee member Bernie LaSalle designed to foster connections between learners from different operational settings. Bernie is a clinical instructor in the Department of Biomedical Informatics with a focus on research data management, terminology and data integration. His areas of expertise include the following: clinical research data management, database design, clinical trials, data ethics, and biospecimen management.

II05: Implementing Data Standards to Enable the Learning Health System  
N. Shah, Stanford University; M. N. Zozus, Duke University  
10:30 a.m. – 12:00 p.m.

Academic health centers, pharmaceutical and device vendors, clinical care providers and others have spent considerable resources during the last several years responding to national initiatives (Meaningful Use, Accrual for Clinical Trials, Precision Medicine) the popular trend of leveraging Big Data. While there is no shortage of data sources and data standards, there continues to be a need for evidence of practical implementation and sharing of successful strategies and the outcomes of those that were not as successful. This session will include an example of using a variety of data standards for the ultimate goal of (machine) learning from electronic medical data and an example of an implementation of an early version of the CDISC STDM data model in the clinical trials and the use of a common data model for a large pragmatic trial. We will review the entire spectrum of medical data and the applicable standards using specific use cases.

II06: Secondary Use of Data for Research - EHR, Omics, and Environmental Data  
S. Visweswaran, University of Pittsburgh; J. Tenenbaum, Duke University; R. Gouripeddi, University of Utah  
1:30 p.m. – 3:00 p.m.

Modern healthcare transformation depends on having access to and understanding a composite ‘data picture’ of the person, cohort or population environment that is being treated. This understanding includes the sharing, aggregation of many data sources and the ability to reuse these data. This session will present three use cases: 1) electronic health records (EHR); 2) metabolomic and 3) environmental (exposome) as examples of secondary data use. The interactive learning session will feature “show-and-tell” style examples of best practices in the use of secondary data for research purposes from three of the leading informatics institutions in the United States. An emphasis will be placed on providing solutions that are generalizable across research settings.
Informatics Implementation Track

Wednesday, March 23

**II07: Leveraging Participant-generated and Environmental Data (Why and How this Matters)**
R. Gerson, Northwestern University; J. Puro, OCHIN; I. Sim, University of California San Francisco

Classic clinical and translational research utilizes data collected in typically highly controlled research settings often embedded in academic medical centers. These settings produce high-quality research datasets of limited scope designed to answer specific research questions. However, these settings and the datasets they produce often only capture a thin cross-section of a research participant. New technologies and approaches are creating opportunities to efficiently collect and integrate non-traditional data into the research dataset enabling a much more precise characterization of a participant in the broader context of their lives. In this moderated panel, we will hear from three experts with deep knowledge in patient reported outcomes data, social determinants of health data, and mobile and sensor health data.

**II08: Innovative Informatics Approaches to Assist with Recruitment and Retention (Interactive Learning)**
P. Embi, The Ohio State University; R. Schuff, Oregon Health & Science University

The lack of successful recruitment into clinical trials is a well known major obstacle to the advancement of clinical research. The widespread implementation of electronic health records, patient portals, and mobile technologies has created new opportunities to go beyond the classic approaches to recruitment. In this moderated panel, we’ll introduce and explore the implementation issues surrounding three complementary approaches to EHR-based recruitment.

**II09: i2b2: Challenges and Solutions to Integrate FHIR and PCORI CDM**
K. Wagholikar, S. Murphy, J. Klann, Massachusetts General Hospital/Harvard University; J. Mandel, Boston Children’s Hospital

This panel will introduce the challenges posed in integrating FHIR and CDM into the platform for Informatics for Integrating Biology and the Bedside (i2b2). Panelists will share the experience on projects involving these models and standards. They will address the topics of impact of adoption of the standards within the current ecosystem of collaborative, distributed research, and on innovations to develop health care applications. They will also discuss ways to resolve the challenges and will share their views on evolution of the i2b2 framework and ongoing projects. The panel will engage the audience to discuss the challenges faced by the audience to adopt their informatics infrastructure to the FHIR and PCORI-CDM and how they can leverage the work done by i2b2 and SMART to address the challenges.
Thursday, March 24

**II10: Supporting Research Using Mobile Platforms (Interactive Learning)**

L. Lander, Apple, Inc.; M. Lunn, UCSF School of Medicine; S. Leachman, Knight Cancer Institute; D. Waggot, Stanford University

**Apple ResearchKit:** An open source software framework that makes it easy for researchers and developers to create apps for application to medical studies.

**PRIDE Research:** The PRIDE Study, this allows healthcare providers to understand how lesbian, gay, bisexual, transgender, queer (LGBTQ), and other sexual and gender minority people’s health, lives, thoughts, and experiences change over time. With this information, we can better understand how sexual orientation and gender identity affects health and how to promote health and combat disease.

**Mole Mapper:** A personalized tool to help you map, measure, and monitor the moles on your skin. Using a familiar Maps-like interface, you can measure the size of a mole using the camera and a common reference object like a coin for possible melanoma.

**MyHeart Counts:** A research app designed to study activity and heart health through your phone. It is also one of the largest cardiovascular research trials ever conducted. Stanford University scientists plan to use data gathered from app users to improve methods of preventing and treating heart disease.

**II11: Creating Collaborative Opportunities in Research Data Management: Implementation and Impact of REDCAP in U.S. Department of Veterans Affairs**

E. Whittier, Department of Veterans Affairs; P. Harris, Vanderbilt University School of Medicine and School of Engineering; C. Francis, Iowa City VA Health Care System; P. Addy, Connecticut Healthcare System/Department of Veterans Affairs; D. Hynes, Department of Veterans Affairs/University of Illinois at Chicago

Collaboration across university and US Department of Veterans Affairs (VA) affiliated medical centers is common in many multisite studies and large program projects, however use of comparable data management systems has long been a challenge. With the recent centralized and national deployment of REDCAP in the VA, new and innovative opportunities to collaborate using REDCAP are now available. This panel focuses on implementation of REDCAP, Research Electronic Data Capture, in the VA as a web-based tool to collect and manage research and quality improvement data. REDCAP provides functionality that enables multisite collaboration across VA sites and with university-based affiliates. With parallel design, data collection using REDCAP at VA and non-VA sites can be accomplished using the same schema and forms. The tool enables systematic clinical and research data collection, integration of external data sources, and export of data to statistical analysis packages.

**II12: Informatics Landscape: How Your Work Matters and the Implementation of Research**

M. Goldstein, Stanford University; D. Hynes, VA Information Resource Center; P. Harris, Vanderbilt University

Where are we and where are we going? Mary K. Goldstein studies innovative methods of implementing evidence-based clinical practice guidelines for quality improvement. She leads the ATHENA Decision Support System project that has developed and implemented an automated clinical decision support system for primary care clinicians, using hypertension as a model, and now extended into several other clinical domains. Goldstein’s research also explores older adults’ health preferences (health utility) for application to cost-effectiveness analysis. Goldstein is a fellow of the American Geriatrics Society, and an emerita of the Society’s board of directors. Goldstein has received a number of honors and awards including an Advanced Career Development award from the Department of Veterans Affairs Health Services Research and Development (HSR&D) program. She received a BA in philosophy and an MD, both from Columbia University, and completed her residency in family medicine at Duke University Medical Center. At the Stanford School of Medicine she completed an AHRQ-funded fellowship and an MS in health services research.

What will you do next? In the final 30 minutes of the inaugural Implementation Informatics Track, Denise Hynes and Paul Harris will lead a session that talks about your work can influence health outcomes for patients, families and communities. Through their research to improve the exchange and use of electronic health data and the collective learning experiences at the conference, attendees will discuss the lessons learned over the four-day conference and ideas to discuss and operationalize in your home institutions.
Birds-of-a-Feather Sessions

(not eligible for CME/CE)

Monday, March 21

**TBI-BOF01: Informatics for Mental Health**
Facilitator: Jessica Tenenbaum, Duke University

In this session we will discuss challenges and opportunities related to informatics for mental health research: relevant datasets and terminologies; limited existing biomarkers; overlap of symptoms between diagnoses and its implications for a systems biology approach; and ethical, legal, and social issues around privacy and secondary use of data.

**TBI-BOF02: Integrating Data with Electronic Health Records for Exploration of Common Disease**
Facilitator: Marylyn Ritchie, Geisinger Health System

In this session, we will discuss strategies and challenges for bringing multiple dimensions of data (genomics, transcriptomics, metabolomics, environmental, social, mobile health, etc.) together with EHR data to enable research.

Tuesday, March 22

**TBI-BOF03: Envisioning Informatics for the NIH Precision Medicine Initiative**
Facilitator: Joshua Denny, Vanderbilt University

We will begin with a brief overview of the NIH Precision Medicine Initiative, which aims to collect more than a million individuals in the US with health and molecular data, and will then have a free-form discussion of informatics tools and advances required to making PMI an effective platform to advance health.

**TBI-BOF04: Tools for Reproducible Research in Translational Bioinformatics**
Facilitator: Nicholas Tatonetti, Columbia University

Reproducibility is essential for replication. We will discuss the software and methods available to make research in translational bioinformatics reproducible.
Thursday, March 24

**CRI-BOF01: The Role of the Chief Research Informatics Officer**

*Sponsored by AMIA Clinical Research Informatics Working Group*

Facilitators: Peter J. Embi, The Ohio State University Wexner Medical Center, and Umberto Tachinardi, University of Wisconsin School of Medicine and Public Health

The role of chief research informatics officer (CRI) is developing at academic institutions and has been the subject of active discussions at the Joint Conference. In 2012 and 2013, very popular panels discussed the CRI role as critical to managing the interface between clinical systems and research needs. In this Birds-of-a-Feather session, we will discuss the growing responsibilities of the CRI and how to better manage all these responsibilities for medical research. All joint conference participants welcome.

**CRI-BOF02: CTSA Informatics Domain Task Force – Looking Forward**

*Facilitator: Paul Harris, Vanderbilt University*

This birds-of-a-feather session will connect individuals in the AMIA CRI Working group, the CTSA Informatics Domain Task Force community and research infrastructure implementation leaders. A desired outcome will be alignment of activities relevant for future collaborations across local institutions and across large program-sponsored networks.

Tweet your sessions!

Follow @AMIAinformatics

Use hashtag #TBICRI16
Lunch and Learn Events

(not eligible for CME/CE)

Thursday, March 24  12:15 p.m. – 1:15 p.m.

Cyril Magnin II

TriNetX: A Public/Private Network For Accelerating Clinical Trials

Michael Kamerick, VP Provider Acquisition, TriNetX

The TriNetX mission is to help bring new therapies to market faster by enhancing clinical trial design and accelerating patient recruitment. TriNetX facilitates collaboration between healthcare providers, pharmaceutical companies and contract research organizations (CROs) through the creation of a global, federated clinical data network that connects researchers in real-time to the patient populations they are seeking to study. This session will include an update on the rapid growth of the network, an overview of the architecture, security policies, and governance principles, and a demonstration of the new capabilities of the TriNetX network.
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 22
6:30 p.m. – 8:30 p.m.

Located near the Parc 55 Hotel at 175 4th Street, San Francisco. Transportation on your own.

Women in Informatics Networking Event (WINE)
Back by popular demand – WINE! 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: Davera Gabriel

Wednesday, March 23
6:30 p.m. – 8:30 p.m.

Parc 55 Hotel Lobby Bar
Daily Schedule

Monday, March 21

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

**TBI-BOF01: Informatics for Mental Health**
*(not eligible for CME/CE)*

Facilitator: Jessica Tenenbaum, Duke University

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**TBI-BOF02: Integrating Data with Electronic Health Records for Exploration of Common Disease**
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In this session, we will discuss strategies and challenges for bringing multiple dimensions of data (genomics, transcriptomics, metabolomics, environmental, social, mobile health, etc.) together with EHR data to enable research.

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

Cyril Magnin Foyer

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

Cyril Magnin Foyer

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

Translational Bioinformatics Year-in-Review

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

@rbaltman

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

For details see page 16

10:00 a.m. – 10:30 a.m.  Coffee Break

Cyril Magnin Foyer
### II01: Scaling up Data and Technology: (Why and How this Matters)

For details see page 20.

### S01: Panel - Precision Medicine: Leveraging Genomics in Diverse Indications

A. Butte, University of California, San Francisco; D. McGovern, Cedars-Sinai Medical Center; O. Morozova, University of California, Santa Cruz; C. Chiu, University of California, San Francisco

Precision medicine holds tremendous potential to improve health outcomes in many different disease areas across broad socioeconomic strata. By continually expanding our understanding of the molecular and other determinants of disease, diagnoses will become more accurate and prevention and treatment strategies more targeted toward the mechanisms driving disease in different individuals. This panel focuses on nucleic acid sequence-based precision medicine advances, covering diverse approaches and diverse disease indications. Panelists will address the use of computational approaches, employing existing large data sets, for drug repositioning, for comparative analyses that enable discovery of clinical leads based on tumor genomics and for rapid and accurate identification of pathogens. They will also highlight how molecular characterization and stratification of patient populations has the potential to improve clinical management of debilitating diseases. In addition, panelists will discuss the challenges associated with integrating large and diverse data sets and how outcomes research is an integral part of advancing precision medicine into clinical practice.

### S02: Panel - The Many Meanings of Precision Medicine

A. Solomonides, NorthShore University HealthSystem; R. Altman, Stanford University; J. Denny, Vanderbilt University; L. Ozeran, Clinical Informatics; J. Tenenbaum, Duke University

Some interpret “Precision Medicine” as synonymous with Molecular Medicine, while others treat it as an improvement over the term Personalized Medicine. The concept of Translational Medicine is also linked in some way. How do these concepts interrelate? How should AMIA and its constituent Working Groups, with the different foci, view Precision Medicine—as an extension of what we have already been doing, or as a radical change of direction? Why should we consider the President’s initiative to be part of our mission? How do we interpret our own efforts in Ethics, in Genomics, in Clinical Research Informatics in the context of Precision Medicine? Speakers at this panel will assert personal positions to provoke fresh thought and a lively debate, both among themselves and with participants from the floor. There are probably as many points of view as there are possible discussants, so this will be a great opportunity to air opinions among our peers.
S03: Podium Presentations - Genomics-based Decision Support and Knowledge Platforms
Session Chair: Mariel Kahn

Usage of Electronic Medical Record Data to Characterize the APOL1 Risk Allele Association with Blood Pressure Traits
G. Galameau, G. Nadkarni, S. Ellis, R. Nadukuru, J. Zhang, S. Scott, Icahn School of Medicine at Mount Sinai; R. Li, National Human Genome Research Institute; L. Rasmussen-Torvik, A. Kho, G. Hayes, J. Pacheco, R. Chisholm, Northwestern University Medical Center; D. Roden, J. Denny, Vanderbilt University Medical Center; E. Kenny, E. Battinger, Icahn School of Medicine at Mount Sinai

Genomic Clinical Decision Support in Pediatric Primary Care
J. Pennington, D. Karovite, The Children’s Hospital of Philadelphia; R. Grundmeier, The Children’s Hospital of Philadelphia/Perelman School of Medicine; B. Bernhardt, N. Spinner, Perelman School of Medicine; E. Krause, J. Michel, J. Miller, The Children’s Hospital of Philadelphia; I. Krantz, Perelman School of Medicine

Enhancing tranSMART by Integrating with Patient Data in i2b2 and Machine Learning
H. Li, S. Achuthan, M. Guirgus, A. Shah, City of Hope

Biomarker Extraction and Discovery from Clinical Narratives Using Ontology-supported Natural Language Processing (NLP) Algorithms
J. Lin, W. Chan, S. Hmwe, A. Shah, W. Zhu, City of Hope

S04: Papers/Podium Presentations - Using Clinical Data to Make Biological Discoveries
Session Chair: Nicholas Tatonetti

Discovering Novel Genetic Aberrations for Leukemia Using Karyotype Data
Z. Abrams, S. Raje, K. Coombes, P. Payne, The Ohio State University

Constraints on Biological Mechanism from Disease Comorbidity Using Electronic Medical Records and Database of Genetic Variants
S. Bagley, Stanford University; M. Sirota, UCSF; R. Chen, Personalis; A. Butte, UCSF; R. Altman, Stanford University

PheWAS and Bayesian Networks to Describe and Understand Complex Genetic, Clinical, and Comorbidity Relationships
R. Carroll, J. Denny, Vanderbilt University School of Medicine

A Use Case to Support Precision Medicine for Frequently Hospitalized Older Adults with Polypharmacy
M. Cabrera, J. Finkelstein, Columbia University

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

II02: How do I Become an Operational Leader?
For details see page 20.

S05: Panel - Funding Opportunities and Government-funded Initiatives in the Areas of Translational Bioinformatics and Clinical Research Data Infrastructure
J. Skaper, HHS; I. Lee, NIH; E. Collier, NCATS; J. Larkin, ADDS; J. Rutter, NIH; M. Rocca, FDA

This panel will bring leaders across the Department of Health and Human Services to discuss key funding opportunities and government-funded initiatives in the areas of translational bioinformatics and clinical research data infrastructure.
MONDAY, MARCH 21
Scientific Sessions
1:30 p.m. – 3:00 p.m. | CONTINUED

**S06: Panel - Career Opportunities to the Many Paths to Informatics**
L. Wiley, Vanderbilt University; C. Overby, University of Maryland; L. Rozenblit, Prometheus Research LLC; M. Sirota, University of California San Francisco

Translational Bioinformatics (TBI) and Clinical Research Informatics (CRI) are young, diverse fields with increasing workforce demands. However due to the youth and breadth of the fields, the diversity of career opportunities are not always clear. Following the successful tradition of AMIA Student Working Group organized “career panels” at the AMIA Annual Symposium, we propose a TBI/CRI focused career panel to offer perspectives and advice for students on career opportunities and professional development. This year, the panelists include an interdisciplinary academician with work in both the TBI and CRI space, an CRI entrepreneur and a TBI academician who has also spent significant time in the pharmaceutical industry. They will share their career and educational experiences and discuss upcoming trends in informatics careers. This panel will help future and current TBI and CRI students and other early-career professionals to better prepare for and develop their careers.

**S07: Papers/Podium Presentations - Data-driven Omics**
Session Chair: Nicholas Tantonetti

- **Application of Deep Learning Algorithms with Feature Selection for DNA Methylation Data Analysis**
  A. Jayasekara, University of Southern California; Z. Chen, R. Natarajan, A. Shah, S. Achuthan, City of Hope

- **Smoking vs Genetic Effects on Disease Expression: A Gene Environment Interaction Study**
  L. Bastarache, T. Osterman, W. Wei, J. Denny, Vanderbilt University

- **Single-sample Expression-based Chemo-sensitivity Score Improves Survival Associations Independently from Genomic Mutations for Ovarian Cancer Patients**
  M. Zimmermann, G. Jiang, C. Wang, Mayo Clinic

- **Towards the Identification of Tissue-based Proxy Biomarkers**
  V. Popovici, Masaryk University

**S08: Papers/Podium Presentations - Pharmacogenomics and Clinical Decision Support**
Session Chair: Rong Xu

- **Integrating Genomic Resources with Electronic Health Records using the HL7 Infobutton Standard**
  B. Heale, University of Utah; C. Overby, University of Maryland School of Medicine; W. Rubinstein, D. Maglott, The National Center for Biotechnology Information/National Institutes of Health; T. Nelson, Geisinger Health System; A. Milosavljevic, Baylor College of Medicine; C. Martin, S. Goehringer, Geisinger Health System; R. Freimuth, Mayo Clinic; G. Del Fiol, University of Utah; M. Williams, Geisinger Health System

- **Modeling the Costs of Clinical Decision Support for Genomic Precision Medicine**
  P. Mathias, P. Tarczy-Hornoch, B. Shirts, University of Washington

- **A Public Repository for Structured Knowledge Artifacts Based on Pharmacogenomic Clinical Guidelines**
  R. Kiefer, R. Freimuth, Mayo Clinic

- **Genomic Clinical Decision Support: From Desiderata to Action**
  M. Williams, Geisinger Health System; D. Masys, University of Washington School of Medicine; R. Freimuth, Mayo Clinic; J. Ostell, National Center for Biotechnology Information; A. Butte, University of California-San Francisco; J. Peterson, Vanderbilt University Medical Center; K. Kawamoto, University of Utah; C. Overby, University of Maryland School of Medicine; B. Welch, Medical University of South Carolina; T. Manolio, National Human Genome Research Institute; B. Middleton, Harvard TH Chan School of Public Health
1:30 p.m. – 5:00 p.m.  Tutorial

**T01: Tutorial - Fundamentals and Applications of Computational Causal Discovery in Biomedicine**
*R. Scheines, D. Danks, Carnegie Mellon University; X. Lu, University of Pittsburgh*

The last 25 years have produced a revolution in statistical and computational tools for causal inference and discovery in biomedicine. In this tutorial, we focus on causal discovery in large data sets drawn from clinical and translational research.

In the first half, we explain the basics of graphical causal models using multiple examples from biomedicine and other fields. We teach the basic graphical causal model framework, including how to represent and model causal systems, how to model and compute the effects of interventions, and the assumptions that make causal search possible. We also cover several search algorithms for learning about causal structure from background knowledge and data. We discuss why regression and related techniques are unreliable for causal discovery and demonstrate superior alternatives. Throughout, we use the freely available Tetrad program to teach these ideas with hands-on exercises using simulated and real data sets.

In the second half, we turn to more complex causal learning situations. We discuss the problem of causal discovery in the presence of unmeasured confounders (latent variables) and algorithms that can reliably extract causal information even when the measured variables fail to include hidden common causes. We examine causal learning from time series data (repeated measurements, dynamic streams, etc.), as well as feedback systems. Time permitting, we conclude by opening discussion to the types of complex clinical and translational data that tutorial attendees are analyzing and the questions they seek to answer with them.

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

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

**II03: Efficiently and Sustainably Delivering Integrated Research Registries in Academic Health Centers: Experiences from the Trenches**
*For details see page 20.*

**S09: Papers/Podium Presentations - Drug Discovery and Drug Repurposing**
*Session Chair: Sherry Cao*

**A Bioinformatics Approach to Identify Novel Drugs against Liver Cancer**
*T. Motiwala, K. Regan, R. Reyes, S. Jacob, P. Payne, The Ohio State University*

**Identifying Plant-human Disease Associations in Biomedical Literature: A Case Study**
*V. Sharma, Brown University; W. Law, M. Balick, New York Botanical Garden; I. Sarkar, Brown University*

**Explore Small Molecule-induced Genome-wide Transcriptional Profiles for Novel Inflammatory Bowel Disease Drug**
*X. Cai, Y. Chen, Z. Gao, R. Xu, Case Western Reserve University*

**Imputing Drug-perturbed Gene Expression Profiles for LINCS L1000 Data**
*R. Hodos, Icahn School of Medicine at Mount Sinai/New York University; P. Zhang, IBM T. J. Watson Research Center; Q. Duan, A. Ma'ayan, N. Clark, Icahn School of Medicine at Mount Sinai; F. Wang, IBM T. J. Watson Research Center; D. Sontag, New York University; J. Hu, IBM T. J. Watson Research Center; J. Dudley, Icahn School of Medicine at Mount Sinai*
### S10: Podium Presentations - Machine Learning for Biomedicine
Session Chair: Rong Xu

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<tr>
<th>Title</th>
<th>Authors</th>
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<tbody>
<tr>
<td>Gene Co-expression Analysis Predicts Genetic Variants Associated with Drug Responsiveness in Lung Cancer</td>
<td>K. Huang, The Ohio State University; S. Shroff, Cornell University; J. Zhang, The Ohio State University</td>
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<tr>
<td>A Prediction Model to Assess Mortality Risk in Cirrhosis</td>
<td>U. Kartoun, K. Corey, Massachusetts General Hospital/Harvard Medical School; H. Zheng, Massachusetts General Hospital; S. Shaw, Massachusetts General Hospital/Harvard Medical School</td>
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<td>SPIRIT ML – 2.0</td>
<td>D. Dodd, University of California Santa Barbara; E. Jiang, Arcadia High School; S. Bolisetty, A. Shah, S. Achuthan, City of Hope</td>
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<td>Hybrid Feature Clustering for Predicting and Explaining Novel Drug-drug Interactions that Prolong the QT interval</td>
<td>T. Lorberbaum, N. Tatonetti, Columbia University</td>
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### S11: Podium Presentations - Systems Biology and Gene Discovery
Session Chair: Marylyn Ritchie

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<th>Title</th>
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<tbody>
<tr>
<td>Filtering Small-scale Genomic Data Sets to Find Genes Consistently Linked to Rett Syndrome: A Novel Approach for Orphan Diseases Gene Expression Analysis</td>
<td>J. Von Stein, Z. Abrams, P. Payne, The Ohio State University</td>
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<td>Systematic Pan-cancer Analysis of Tumor Purity</td>
<td>D. Aran, M. Sirota, A. Butte, University of California, San Francisco</td>
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<td>Cause and Effect Modeling of Disease Linked Protein Biomarkers</td>
<td>S. Mani, D. Cannon, R. Ohls, D. Perkins, University of New Mexico; K. Ballard, Rules Based Medicine; C. Bologa, University of New Mexico</td>
</tr>
<tr>
<td>Obtaining High-quality, Genome-wide Genotypes from Archival FFPE Tissue Samples</td>
<td>M. Maienschein-Cline, P. Kanabar, O. Karpenko, Z. Lei, H. Hu, N. Bahoos, Z. Arbieva, University of Illinois at Chicago</td>
</tr>
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5:00 p.m. – 6:00 p.m. Networking Reception  
Cyril Magnin Foyer

5:30 p.m. – 7:00 p.m. Genomics and Translational Bioinformatics Working Group Meeting  
(Not eligible for CME/CE)  
Stockton

6:30 p.m. – 8:30 p.m. REDCap Community Discussion and Tutorial  
(Not eligible for CME/CE)  
Cyril Magnin I

For details see page 19.
Tuesday, March 22

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

**TBI-BOF03: Envisioning Informatics for the NIH Precision Medicine Initiative**
*(not eligible for CME/CE)*

Facilitator: Joshua Denny, Vanderbilt University

We will begin with a brief overview of the NIH Precision Medicine Initiative, which aims to collect more than a million individuals in the US with health and molecular data, and will then have a free-form discussion of informatics tools and advances required to making PMI an effective platform to advance health.

**TBI-BOF04: Tools for Reproducible Research in Translational Bioinformatics**
*(not eligible for CME/CE)*

Facilitator: Nicholas Tatonetti, Columbia University

Reproducibility is essential for replication. We will discuss the software and methods available to make research in translational bioinformatics reproducible.

7:00 a.m. – 8:30 a.m.  Continental Breakfast  Cyril Magnin Foyer

7:00 a.m. – 6:00 p.m.  Registration Open  Cyril Magnin Foyer
TUESDAY, MARCH 22
Scientific Sessions
8:30 a.m. – 10:00 a.m.

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

II04: Why & How This Matters

For details see page 21.

S12: Podium Presentations - Precision Medicine in Action
Session Chair: William Riley

Trastuzumab Treatment and Cardiotoxicity in Breast Cancer Patients
M. Harris, B. Conkright, R. Johnson, S. Boca, S. Riazi, Georgetown University Medical Center; R. Torguson, MedStar Cardiovascular Research Network; A. Alouai, Georgetown University Medical Center; F. Asch, MedStar Cardiovascular Research Network; P. Pohlmann, Georgetown University Medical Center; A. Barac, MedStar Cardiovascular Research Network; S. Madhavan, Georgetown University Medical Center

CDS-KB: A KnowledgeBase of Lessons Learned for Clinical Decision Support Implementation
J. Kirby, Vanderbilt University; L. Rasmussen, Northwestern University Feinberg School of Medicine; P. Harris, J. Denny, Vanderbilt University; P. Dexter, Indiana University School of Medicine; S. Ellis, Icahn School of Medicine at Mount Sinai; A. Hartzler, Group Health Research Institute; C. Overby, University of Maryland School of Medicine; P. Caraballo, Mayo Clinic; M. Levy, Vanderbilt University Medical Center; P. Peissig, Marshfield Clinic Research Foundation; B. Phelps, Vanderbilt University; J. Starren, Northwestern University Feinberg School of Medicine; M. Williams, Geisinger Health System; J. Peterson, Vanderbilt University

Omics Analysis System for Precision Oncology (OASISPRO): A Web-based Omics Analysis Tool for Clinical Phenotype Prediction

Deciphering Patient-specific Disease Trajectories Using an Ensemble Classification Framework
R. Nagarajan, C. Miller, J. Ebersole, University of Kentucky

S13: Panel - BD2K (Big Data to Knowledge) Program Driving Clinical Genomic and Disease Discovery
S. Madhavan, Georgetown University; J. Tenenbaum, Duke University; M. Haendel, OHSU; J. Cherry, M. Musen, Stanford University

In June 2012, a Working Group of the Advisory Committee to the NIH Director (ACD) on Data and Informatics delivered a report1 that addressed the rapid growth in biomedical data. The report contained a series of recommendations for bringing NIH and its total investigator community into the era of Big Data. The NIH Director Francis Collins accepted the recommendations and initiated the Big Data to Knowledge (BD2K) extramural program under the leadership of Dr. Phil Bourne who was appointed as Associate Director of Data Science in early 2014. On this panel, we present four BD2K funded initiatives including Standards coordination center and CEDAR.
### S14: Papers - Data and Text Processing

**Session Chair:** Jihad Obeid

1. **NLP-PIER: A Scalable Natural Language Processing, Indexing, and Searching Architecture for Clinical Notes**  
   R. McEwan, G. Melton, B. Knoll, Y. Wang, G. Hultman, J. Dale, T. Meyer, S. Pakhomov, University of Minnesota

2. **A Quantitative and Qualitative Evaluation of Sentence Boundary Detection for the Clinical Domain**  
   D. Griffis, The Ohio State University/National Institutes of Health; C. Shivade, E. Fosler-Lussier, A. Lai, The Ohio State University

3. **A Decompositional Approach to Executing Quality Data Model Algorithms on the i2b2 Platform**  
   H. Mo, Vanderbilt University; G. Jiang, Mayo Clinic; J. Pacheco, Northwestern University Feinberg School of Medicine; R. Kiefer, Mayo Clinic; L. Rasmussen, Northwestern University Feinberg School of Medicine; J. Pathak, Weill Cornell Medical College; J. Denny, Vanderbilt University; W. Thompson, NorthShore University HealthSystem

4. **Towards Evidence-based Precision Medicine: Extracting Population Information from Biomedical Text Using Binary Classifiers and Syntactic Patterns**  
   K. Raja, Northwestern University; N. Dasot, P. Goyal, Indian Institute of Technology; S. Jonnalagadda, Northwestern University

### S15: Papers - Infrastructure for Data Driven Translational Science

**Session Chair:** Kate Fultz Hollis

1. **Applying a Participatory Design Approach to Define Objectives and Properties of a “Data Profiling” Tool for Electronic Health Data**  
   H. Estiri, T. Lovins, University of Washington; N. Afzalan, University of Redlands; K. Stephens, University of Washington

2. **Metadata-driven Clinical Data Loading into i2b2 for Clinical and Translational Science Institutes**  
   A. Post, A. Pai, R. Willard, B. May, A. West, S. Agravat, Emory University; S. Granite, R. Winslow, Johns Hopkins University; D. Stephens, Emory University

3. **Cohort Selection and Management Application Leveraging Standards-based Semantic Interoperability and a Groovy DSL**  
   A. Bucur, J. van Leeuwen, N. Chen, Philips Research Europe; D. Perez-Rey, R. Alonso-Calvo, S. Paraiso-Medina, Universidad Politécnica de Madrid; B. Claerhout, K. de Schepper, Custodix NV; K. Mehta, German Breast Group; C. Krykwinski, Institut Jules Bordet

4. **Developing a Prioritization Schema for Matching Patients to Clinical Trials**  
   M. Cantor, Y. Darwish, NYU Langone Medical Center

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**10:00 a.m. – 10:30 a.m.**  
**Coffee Break**  
**Cyril Magnin Foyer**
TUESDAY, MARCH 22
Scientific Sessions
10:30 a.m. – 12:00 p.m.

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

II05: Implementing Data Standards to Enable the Learning Health System
For details see page 21.

S16: TBI Student Paper Competition
Session Chair: Nicholas Tatonetti

Using a Novel Ontology to Inform the Discovery of Therapeutic Peptides from Animal Venoms
J. Romano, N. Tatonetti, Columbia University Medical Center

Finding Related Publications: Extending the Set of Terms Used to Assess Article Similarity
W. Wei, R. Marmor, S. Singh, S. Wang, UCSD; D. Demner-Fushman, National Library of Medicine; T. Kuo, C. Hsu, L. Ohno-Machado, UCSD

In Search of ‘Birth Month Genes’: Using Existing Data Repositories to Locate Genes Underlying Birth Month-disease Relationships
M. Boland, N. Tatonetti, Columbia University

A Novel Framework for Assessing Metadata Quality in Epidemiological and Public Health Research Settings
C. McMahon, S. Denaxas, University College London

PALME: Patients Like My gEnome
L. Wang, Y. Fang, Northwest A&F University; D. Aref, New Jersey Institute of Technology; S. Rathi, Syracuse University; L. Shen, Donghua University; X. Jiang, S. Wang, University of California San Diego

S17: Podium Presentations - Addressing the Data Problem
Session Chair: Radha Nagarajan

Metabolomics Data Management: A View from the Trenches
J. Tenenbaum, Duke University

D2R: The Next Generation of Sequence Read Repository
P. Nagahawatte, V. Nagisetty, R. Jose, University of Tennessee Health Science Center; M. Shankar, Oak Ridge National Laboratory; R. Davis, University of Tennessee Health Science Center

Bringing Genomes Back to Biology: How Integration of Public Genomic Data Sets with a Biorepository Translate Genomic Discoveries into Biological Insight

Breast Cancer Prognostics Using Multi-omics Data
S. Ma, J. Ren, D. Fenyö, New York University Langone Medical Center
**S18: Papers - Data Mining or Knowledge Discovery**

*Session Chair: Vojtech Huser*

**A Data Mining Approach to Determine Sepsis Guideline Impact on Inpatient Mortality and Complications**

L. Pruinelli, P. Yadav, A. Hangsleben, J. Johnson, University of Minnesota; S. Dey, IBM T.J. Watson Research Center; M. McCarty, Hennepin County Medical Center; V. Kumar, C. Delaney, M. Steinbach, B. Westra, University of Minnesota; G. Simon, Mayo Clinic

**Learning Low-dimensional Representations of Medical Concepts**

Y. Choi, C. Chiu, D. Santag, New York University

**Predicting Hospital Visits from Geo-tagged Internet Search Logs**

V. Agarwal, L. Han, I. Madan, S. Saluja, A. Shidham, N. Shah, Stanford University

**Using LASSO Regression to Predict Rheumatoid Arthritis Treatment Efficacy**

D. Odgers, N. Telis, H. Hall, M. Dumontier, Stanford University

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**S19: Panel - Insight Generation from Real-world and Real-time Treatment Pathways**

*Z. Cai, Celgene; D. Gotz, University of North Carolina at Chapel Hill; A. Kamauu, Anolinx LLC; G. Petratos, Hiteks Solutions Inc*

Understanding of patient outcomes in relation to patient treatment pathways is critical for Comparative Effectiveness Research (CER) and healthcare quality improvement. The recent growing prevalence of longitudinal healthcare data from Electronic Health Records (EHR), health insurance claims, and disease/patient registries has made it possible to retrospectively reconstruct patient-level treatment pathways based on real-world data. Real-time decision support at the point of care for treatment pathways is also becoming available as the EHR systems are incorporating alerting and recommendation functionality into their user interface for physicians. The panel will focus on such retrospective and prospective pathway reconstructions and temporal visualization and analysis for better understanding treatment patterns in real-world. From a medical informatics perspective, this panel will address the needs to: 1) reconstruct real-patient treatment pathways by introducing high performance platforms or tools to extract relevant data elements and information out of structured and unstructured healthcare data, 2) identify real-world treatment patterns using visual analytics, and to associate patient outcomes with treatment pathways, and 3) enable answering “what if” questions by predicting outcomes of new interventions in the context of prospective treatment pathways.

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**11:00 a.m. – 3:00 p.m.**

**Special Event**

10x10 with the Ohio State University In-person Session

(10x10 students only)

*(Not eligible for CME/CE)*
1:30 p.m. – 3:00 p.m.  Scientific Sessions

II06: Secondary Use of Data for Research - EHR, Omics, and Environmental Data

For details see page 21.

S20: Podium Presentations - Drugs, Text, and EHRs: Analytics Methods for Health Data

Session Chair: Nicholas Tantonetti

Provenance in Practice: Data Lineage in Clinical and Biomedical Research
B. Ruth, Y. Kushleyeva, J. Pennington, The Children’s Hospital of Philadelphia

The Phenotype Execution and Modeling Architecture (PhEMA) – A Standards-based Composition of Software for Phenotype Algorithm Development
L. Rasmussen, Northwestern University; R. Kiefer, Mayo Clinic; H. Mo, Vanderbilt University; W. Thompson, NorthShore University HealthSystem; G. Jiang, Mayo Clinic; J. Pacheco, Northwestern University; P. Speltz, Vanderbilt University; J. Xu, Northwestern University; J. Denny, Vanderbilt University; E. Montague, Northwestern University; J. Pathak, Mayo Clinic

Systematic and Longitudinal Approach to Height, Weight, and Body Mass Index Data Cleaning for Efficient Reuse of EHR Data for Research
Y. Jiang, M. Basford, J. Kirby, X. Wang, P. Harris, J. Denny, Vanderbilt University Medical Center

Porting a Natural Language Processing Algorithm to Extract Findings from Colonoscopy Pathology Reports
J. Pacheco, Northwestern University Feinberg School of Medicine; A. Gawron, University of Utah; K. Borthwick, Geisinger Health System; P. Peissig, Marshfield Clinic; D. Carrell, Group Health Research Institute; L. Rasmussen, Northwestern University Feinberg School of Medicine; H. Mo, Vanderbilt University; W. Thompson, NorthShore University HealthSystem; Northwestern University Feinberg School of Medicine


J. Cherry, Stanford University; A. Milosavljevic, Baylor College of Medicine; S. Prabhu, Stanford University; M. Williams, Geisinger Health System

ClinGen, the Clinical Genome Resource, is a National Institutes of Health (NIH)-funded project to create a centralized repository and interconnected resources for clinically annotated genes and variants that can be leveraged to improve our understanding of genomic variation and optimize its use in clinical care. In this panel, we propose highlighting the tools, resources, and standards developed by the ClinGen consortium to improve patient care in the information age of genomics.
**S22: Papers - Data Mining or Knowledge Discovery**
*Session Chair: David Eichmann*

**Drug-drug Interaction Profiles of Medication Regimens Extracted from a De-identified Electronic Medical Records System**
M. Butkiewicz, N. Restrepo, J. Haines, D. Crawford, Case Western Reserve University

**Searching in the Dark: Phenotyping Diabetic Retinopathy in a De-identified Electronic Medical Record Sample of African Americans**
N. Restrepo, Case Western Reserve University; E. Farber-Eger, Vanderbilt University Medical Center; D. Crawford, Case Western Reserve University

**Inferring the Interactions of Risk Factors from EHRs**
T. Goodwin, S. Harabagiu, University of Texas at Dallas

**Cross Border Semantic Interoperability for Clinical Research: The EHR4CR Semantic Resources and Services**
C. Daniel, AP-HP/LIMICS - INSERM UMRS1142; D. Ouagne, LIMICS - INSERM UMRS1142; E. Sadou, AP-HP; K. Forsberg, Astra Zeneca; M. McGilchrist, Dundee University; E. Zapletal, N. PARIS, AP-HP; S. Hussain, M. Jaulent, LIMICS - INSERM UMRS1142; D. Kolra, EUROREC

**S23: Papers - Clinical and Research Data Visualization**
*Session Chair: Kate Fultz Hollis*

**How Have Cancer Clinical Trial Eligibility Criteria Evolved Over Time?**
A. Yaman, S. Chakrabarti, A. Sen, C. Weng, Columbia University

**i2b2t2: Unlocking Visualization for Clinical Research**
D. Harris, D. Henderson, University of Kentucky

**Research Reproducibility in Longitudinal Multi-center Studies Using Data from Electronic Health Records**
M. Zozus, R. Richesson, A. Walden, I. Tenenbaum, W. Hammond, Duke University

**Test Case Selection in Pre-deployment Testing of Complex Clinical Decision Support Systems**
G. Tso, Veteran Affairs Palo Alto/Stanford University School of Medicine; K. Yuen, S. Martins, Veteran Affairs Palo Alto; S. Tu, Stanford University School of Medicine; M. Ashcraft, P. Heidenreich, Veteran Affairs Palo Alto; B. Hoffman, Veteran Affairs Boston/Harvard Medical School; M. Goldstein, Veteran Affairs Palo Alto/Stanford University School of Medicine
TUESDAY, MARCH 22
3:30 p.m. – 9:00 p.m. | CONTINUED

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<tr>
<th>Time</th>
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<tr>
<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>Plenary Session and Keynote Presentation</td>
<td>Cyril Magnin Ballroom</td>
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<td><strong>Deborah Estrin, PhD @deborahestrin</strong></td>
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<td>Professor of Computer Science, Cornell Tech</td>
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<td>Professor of Healthcare Policy and Research, Weill Cornell Medical College</td>
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<td>5:00 p.m. – 6:00 p.m.</td>
<td>Poster Session 1</td>
<td>Cyril Magnin Foyer</td>
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<td>Both TBI and CRI posters are displayed. TBI authors present, with CRI authors optional.</td>
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<td>See page 57 for list of posters, listed alphabetically by the first author.</td>
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<td>6:30 p.m. – 8:30 p.m.</td>
<td>Social Event</td>
<td>Jillian’s Billiards</td>
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<td>Billiards Networking Meet-up</td>
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<td><em>(Not eligible for CME/CE)</em></td>
<td>San Francisco</td>
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<td>For details see page 28.</td>
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Wednesday, March 23

7:00 a.m. – 8:15 a.m.
AMIA Town Hall
(Not eligible for CME/CE)
For details see page 12.

7:00 a.m. – 8:30 a.m.
Continental Breakfast
Cyril Magnin Foyer

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

8:00 a.m. – 12:00 p.m.
Special Event
10x10 with the Oregon Health & Science University
In-person Session
(10x10 students only)
(Not eligible for CME/CE)

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

II07: Leveraging Participant-generated and Environmental Data (Why and How this Matters)
For details see page 22.

S24: Panel - Practical Implementation of Genomic Sequencing in Healthcare Settings
C. Overby, University of Maryland; M. Williams, Geisinger Health System; D. Crosslin, University of Washington; Z. Zhao, Vanderbilt University; W. Chung, Columbia University
Implementing whole genome sequencing and exome sequencing in a healthcare setting will require biomedical informatics approaches that facilitate feasible and appropriate management, analysis and return of results over an individual's lifetime. Our panel will describe experiences with and lessons learned from current processes of receiving and using genomic sequencing results for the diagnosis and treatment of genetic disease (Dr. Wendy Chung), establishing infrastructure for reporting genome and exome sequencing results to providers and patients in a large integrated health care delivery system (Dr. Marc S. Williams), current processes for managing genomic sequencing data across electronic medical records and genomics (eMERGE) network institutions (Dr. Casey Overby), and reporting actionable results from the targeted Pharmacogenomics Research Network sequence platform (Dr. David Crosslin).
WEDNESDAY, MARCH 23
Scientific Sessions
8:30 a.m. – 10:00 a.m.

**S25: CRI Student Paper Competition**
Session Chair: Nicholas Anderson

- To Share or Not to Share: Ethical Acquisition and Use of Medical Data
  K. Fultz Hollis, OHSU

- Tumor Information Extraction in Radiology Reports for Hepatocellular Carcinoma Patients
  W. Yim, T. Denman, S. Kwan, M. Yetisgen, University of Washington

- An Infinite Mixture Model for Coreference Resolution in Clinical Notes
  S. Liu, University at Buffalo, SUNY; H. Liu, Mayo Clinic; V. Chaudhary, University at Buffalo, SUNY; D. Li, Mayo Clinic

- Predicting Emergency Department Visits
  S. Poole, Stanford University; S. Grannis, Regenstrief Institute; N. Shah, Stanford University

- Comparative Evaluation for Brain Structural Connectivity Approaches: Towards Integrative Neuroinformatics Tool for Epilepsy Clinical Research
  S. Yang, Case Western Reserve University; C. Tatsuoka, University Hospitals Case Medical Center; K. Ghosh, University of Nevada; N. Lecumberri, S. Lhatoo, University Hospitals Case Medical Center; S. Sahoo, Case Western Reserve University

**S26: Podium Presentations - Data Mining and Knowledge Discovery**
Session Chair: Peter Embi

- Modeling an Efficient Data Mart for High-performance Clinical Data Analytics Using Neo4j Graph Database
  F. Sen, T. Viangteeravat, O. Ajayi, Le Bonheur Children’s Hospital

- Identification of an Acute Kidney Injury Phenotype from Electronic Health Record Data
  M. Semanik, M. Yetisgen, A. Pollack, University of Washington

- Use of Administrative Data to Predict Risk of Liver Disease
  T. Motiwala, Z. Abrams, K. Regan, B. Kite, The Ohio State University; G. Gascon, The Ohio State University Health Plan, Inc; P. Payne, The Ohio State University

- Quality of Race and Ethnicity Data in Electronic Health Records
  F. Polubriaginof, M. Boland, A. Perotte, D. Vawdrey, Columbia University, NewYork-Presbyterian Hospital
8:30 a.m. – 12:00 p.m.  Tutorial

**T02: Tutorial - Immuno-informatics Coming of Age: Emerging Approaches and Applications**  
H. Fan-Minogue, Stanford University

The immune system is a complex system of the human body and composed of numerous cellular components. Traditional immunology approaches have been very successful in analyzing each component and its function in average and across samples, but they often miss the network functioning principles that rely on and arise from interactions among immunological components. Recent advances in genomics technology and bioinformatics approaches have allowed high-resolution acquisition and analysis of high dimensional immunologically relevant data. Immuno-informatics, or computational immunology, thus emerged as a research area that encompasses high-throughput genomic and bioinformatics approaches to immunology. Immuno-informatics also plays an essential role in Systems Immunology that aims to gain integrated comprehension of the immune system structure and function. In this tutorial, I will give an introduction to immuno-informatics by revealing the principle of emerging genomics and single cell technologies that allow deep profiling of immune components, demonstrating new computational and statistical tools that provides comprehensive analysis and visualization of high-dimensional immunological data, and describing applications of immuno-informatics in understanding immune responses during diseases. Attendees should expect to learn about the essential technologies used for capturing immunophenotypes at single-cell level and what they measure. The advantages and trade-offs of these new technologies in contrast to traditional immunology approaches will be discussed. Attendees should also expect to learn about the machine learning approaches used to analyze single-cell data and how they are implemented. Finally, the tutorial will end with a discussion of immunology databases and tools to access/view the data, case studies showing how these data have been used to gain new insights of immune system to date, and a brainstorming session about how these resources can best be applied in a translational context.

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

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

**II08: Innovative Informatics Approaches to Assist with Recruitment and Retention**  
(Interactive Learning)

For details see page 22.

**S27: Podium Presentations - Clinical and Research Data Collection, Curation, Preservation, or Sharing**  
Session Chair: Davera Gabriel

An Informatics Approach for the Curation and Standardization of Data Elements on Multi-center Clinical Trial Networks  
K. Wilson, M. Ham, RTI International

Bridging the Big Data/Small Data Gap  
P. Harris, Vanderbilt University; T. Campion, Weill Cornell Medical Center; R. Taylor, Vanderbilt University; M. Davila, Weill Cornell Medical Center; J. Kirby, Vanderbilt University; D. Phillips, Weill Cornell Medical Center; J. Scherdin, Vanderbilt University

Comparison of Two Distributed Data Network Approaches: Democratic and Self-governed vs. Centrally Managed  
J. Klann, Harvard Medical School/Massachusetts General Hospital; V. Raghavan, D. Macfadden, S. Weiler, Harvard Medical School; K. Mandl, Harvard Medical School/Boston Children’s Hospital; S. Murphy, Harvard Medical School/Massachusetts General Hospital

Issues in the Capture of Patient Reported Outcomes in a Heterogeneous Research Network  
J. McClay, J. Campbell, A. Mudgapalli, University of Nebraska Medical Center; R. Waitman, University of Kansas Medical Center
WEDNESDAY, MARCH 23
Scientific Sessions
10:30 a.m. – 12:00 p.m.  | CONTINUED

### S28: Podium Presentations - Data Integration and Standardization
*Session Chair: Kari Stephens*

**The Human Genomic Data Solution within the NIH Biomedical Translational Research Information System (BTRIS)**
L. Remennik, E. Ayres, S. Rath, NIH Clinical Center

**Assessment of Factors and Approaches to Mapping Laboratory Results in PCORnet**
M. Smerek, Duke Clinical Research Institute; E. Priest, Baylor Scott & White Health; S. Rosenbloom, Vanderbilt University Medical Center; J. Pura, P. Rivera, OCHIN, Inc.; S. Rusincovitch, Duke Translational Research Institute; R. Jain, Louisiana Public Health Institute; K. Marsolo, Cincinnati Children’s Hospital Medical Center

**Question Answering on Electronic Medical Records**
P. Raghavan, S. Patwardhan, IBM TJ Watson Research Center

**Data Café — A Platform for Creating Biomedical Data Lakes**
P. Kathiravelu, A. Sharma, Emory University

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10:30 a.m. – 3:00 p.m.  | Tutorial

### T03: Tutorial - Cancer Precision Medicine
L. Li, Z. Zhao, Vanderbilt University

Precision medicine is promising in both cancer research and clinical cancer care. However, precision medicine has many translational bioinformatics and medical informatics challenges. This tutorial aims to fill this much needed knowledge gap. We will introduce the analysis of DNA and RNA sequencing data generated by high throughput technologies and bioinformatics approaches to identify clinically relevant variants from large-scale cancer genomic data; review the cancer drug molecular pharmacology; illustrate the database integration for cancer drug targets and cancer drugs; demonstrate the operation of the cancer precision medicine clinics; and present challenges in the cancer precision medicine research. This tutorial is designed at the beginner’s level for the bioinformatics analysis of sequencing data and drug and target selections. We will focus more on the clinical applications of cancer precision medicine research.

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12:30 p.m. – 1:30 p.m.  | Lunch Break *(lunch on own)*

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

### II09: i2b2: Challenges and Solutions to Integrate FHIR and PCORI CDM
*Cyril Magnin III  #II09*

*For details see page 22.*
### S29: Papers/Podium Presentations - Data Standards, Terminologies, Ontologies

**An Ontology-supported OCR Error Correction Platform for Digitized Clinical Narratives Using Crowdsourced Responses**

*W. Zhu, H. Li, City of Hope*

**Ion Channel ElectroPhysiology Ontology (ICEPO) – A Case Study of Text Mining Assisted Ontology Development**

*R. Komandur Elayavilli, H. Liu, Mayo Clinic*

**Community-based Ontology Development, Annotation and Discussion with MediaWiki Extension Ontokiwi and Ontokiwi-based Ontobedia**

*E. Ong, Y. He, University of Michigan*

**CTOL2 Concept-based Search Using Natural Language Processing**

*W. Zhu, T. Kirkpatrick, J. Lin, A. Shah, J. Niland, City of Hope*

### S30: Podium Presentations - Machine Learning for Clinical Applications

**Session Chair: David Eichmann**

**Calibration Drift of Clinical Prediction Models Across Modeling Methods**

*S. Davis, T. Lasko, G. Chen, Vanderbilt University; M. Matheny, Vanderbilt University/VA Tennessee Valley Healthcare System*

**Modelling the Progression of CKD with EMR Data: a Partially Hidden Markov Approach**

*Z. Sun, Y. Cheng, A. Cahan, IBM T. J. Watson Research Center; F. Wang, University of Connecticut; J. Hu, IBM T. J. Watson Research Center*

**Identifying Subsets of “Big Data” Relevant for Hearing Loss Progression Research**

*T. Qian, A. Masino, The Children’s Hospital of Philadelphia*

**Automated Organization of Electronic Health Record Data by Probabilistic Topic Modeling to Inform Clinical Decision Making**

*J. Chen, M. Goldstein, S. Asch, Veteran Affairs/Stanford University; L. Mackey, R. Altman, Stanford University*

### S31: Podium Presentations - Ethical, Legal, and Social Issues

**Session Chair: Nicholas Anderson**

**On the Privacy Risks of Sharing Clinical Proteomics Data**

*S. Li, Indiana University; N. Bandeira, University of California; X. Wang, H. Tang, Indiana University*

**My Cancer Genome: Evaluating an Educational Model to Introduce Patients and Caregivers to Precision Medicine Information**

*S. Kusnoor, T. Koonce, Vanderbilt University Medical Center; M. Levy, C. Lovly, Vanderbilt University Medical Center/Vanderbilt University School of Medicine; H. Naylor, I. Anderson, Vanderbilt University Medical Center; C. Micheil, Vanderbilt University Medical Center/Vanderbilt University School of Medicine; S. Chen, F. Ye, Vanderbilt University School of Medicine; N. Giuse, Vanderbilt University Medical Center/Vanderbilt University Medical Center*

**A Pilot Study of the Integration of a Quantified-self Wearable Device with EMR Data in the Acute Postoperative Setting**

*J. Norden, T. Sweeney, A. Pavlovic, E. Ashley, N. Shah, C. Kin, A. Morgan, Stanford University School of Medicine*

**Caregivers Access to Patient Portal: A Retrospective Descriptive Analysis**

*S. He, Intermountain Healthcare; S. Thornton, Intermountain Healthcare/University of Utah*
### WEDNESDAY, MARCH 23
3:30 p.m. – 8:30 p.m.  | CONTINUED

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<tr>
<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>Plenary Session and Keynote Presentation</td>
<td>Cyril Magnin Ballroom</td>
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<td><strong>David Haussler, PhD</strong></td>
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<td></td>
<td>Investigator, Howard Hughes Medical Institute</td>
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<td>Distinguished Professor, Biomolecular Engineering, University of California, Santa Cruz</td>
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<td>Scientific Director, UC Santa Cruz Genomics Institute, University of California, Santa Cruz</td>
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<td>Director, UCSC Cancer Genomics Hub, University of California, Santa Cruz</td>
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<td>Scientific Co-Director, California Institute for Quantitative Biosciences (QB3)</td>
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<td>5:00 p.m. – 6:00 p.m.</td>
<td>Poster Session 2 and Reception</td>
<td>Cyril Magnin Foyer</td>
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<td><em>See page 57 for list of posters, listed alphabetically by the first author.</em></td>
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<td>6:30 p.m. – 8:30 p.m.</td>
<td>i2b2 Community Discussion and Tutorial</td>
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<td>6:30 p.m. – 8:30 p.m.</td>
<td>Social Event</td>
<td>Lobby Bar</td>
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<td>WINE - Women in Informatics Networking Event</td>
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**Thursday, March 24**

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<th>Facilitator/Details</th>
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<tr>
<td>7:00 a.m. – 8:15 a.m.</td>
<td>Birds-of-a-Feather Sessions</td>
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<td><strong>CRI-BOF01: The Role of the Chief Research Informatics Officer</strong>&lt;br&gt;<strong>Sponsored by AMIA Clinical Research Informatics Working Group</strong>&lt;br&gt;(not eligible for CME/CE)&lt;br&gt;Facilitators: Peter J. Embi, The Ohio State University Wexner Medical Center, and Umberto Tachinardi, University of Wisconsin School of Medicine and Public Health&lt;br&gt;The role of chief research informatics officer (CRI) is developing at academic institutions and has been the subject of active discussions at the Joint Conference. In 2012 and 2013, very popular panels discussed the CRI role as critical to managing the interface between clinical systems and research needs. In this Birds-of-a-Feather session, we will discuss the growing responsibilities of the CRI and how to better manage all these responsibilities for medical research. All joint conference participants welcome.</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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<td>7:00 a.m. – 3:30 p.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>II10: Supporting Research Using Mobile Platforms (Interactive Learning)</strong>&lt;br&gt;For details see page 23.</td>
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THURSDAY, MARCH 24
Scientific Sessions
8:30 a.m. – 10:00 a.m. | CONTINUED

**S32: Podium Presentations – Outcomes Research**
Session Chair: David Eichman

Analysis of Free-text Symptom Narratives to Enhance Functionality of the National Cancer Institute’s PRO-CTCAE System for Patient-reported Symptomatic Adverse Events in Clinical Trials
A. Chung, University of North Carolina at Chapel Hill School of Medicine; S. Mitchell, National Institutes of Health; R. Osborne, University of North Carolina at Chapel Hill School of Medicine; P. Baumgartner, Semantic Bits; L. Rogak, Memorial Sloan Kettering Cancer Center; E. Basch, University of North Carolina

A Systematic Review of Using Electronic Heath Records to Predict Clinical Events: Assessment of Opportunities and Challenges

Decrease in Inappropriate Vitamin D Testing Using Clinical Decision Support (CDS) Tools
A. Felcher, Kaiser Permanente NW; D. Mosen, KPCHR; R. Gold, KPCHR/OCHIN; A. Stoneburner, J. Pope, KPCHR

Seamless Integration of Patient Reported Outcomes Assessments into the EHR Workflow
J. Starren, Northwestern University/Northwestern University Feinberg School of Medicine; C. Bethman, F. Almaraz, R. Chmiel, Northwestern Memorial HealthCare; M. Bass, L. Rasmussen, Northwestern University Feinberg School of Medicine

**S33: Panel – Observational Health Data Sciences and Informatics (OHDSI): A Rapidly Growing International Network for Open Science and Data Analytics in Healthcare**
J. Duke, Regenstrief Institute; G. Hripcsak, Columbia University; N. Shah, Stanford University; P. Ryan, Janssen Research and Development; V. Huser, NIH

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 databases and providing a community where advanced analytic methods and interoperable software tools can be easily shared. This panel will discuss recent advances and opportunities for participation in the OHDSI collaborative, focusing on network science, data quality, evidence dissemination, and phenotype development. Ample time will be allotted for interactive discussion based on questions from the audience.

**S34: Podium Presentations – Clinical and Research Data Collection, Curation, Preservation, or Sharing**
Session Chair: Nicholas Anderson

Physician Perceptions of Performance Feedback
A. Bunce, Kaiser Permanente - Center for Health Research; R. Gold, Kaiser Permanente - Center for Health Research/OCHIN, Inc.; J. Davis, Kaiser Permanente - Center for Health Research; M. Mercer, Virginia Garcia Memorial Health Center; V. Jaworski, Multnomah County Health Department; C. Nelson, OCHIN, Inc.; C. Hollombe, Kaiser Permanente - Center for Health Research

Construction & Management of a Dynamic Quality Improvement Registry Using REDCap
K. Mittal, Northwestern University; A. Borders, Northwestern University/NorthShore University Health System/University of Chicago Pritzker School of Medicine; P. King, Northwestern University; K. Finnegan, NorthShore University Health System; P. Ittmann, Rockford Health System; A. Naguchi, Cardinal Glennon Children’s Medical Center; D. Rosenberg, University of Illinois at Chicago School of Public Health; A. Kho, S. Goel, Northwestern University

Watson Cognitive Computing for Electronic Medical Records
M. Devarakonda, IBM Research

Assessing Reproducible Research: A Common Biomedical Informatics Framework
C. Vitale, Washington University in St. Louis; L. McIntosh, Washington University School of Medicine; A. Juehne, R. Alcoser, A. Addison, B. Evanoff, Washington University in St. Louis
8:30 a.m. – 12:00 p.m.  Tutorial

**T04: Tutorial - Developing Executable Phenotype Algorithms Using the KNIME Analytics Platform**

*H. Mo, Vanderbilt University; W. Thompson, J. Pacheco, Northwestern University; R. Carroll, Vanderbilt University*

KNIME Analytics (www.knime.org) is an open source platform that integrates data access, data transformation, statistical analysis, data-mining tools, and snippets of different programming languages in a visual workbench. It is the sixth most popular data science tool in the 2015 KDNuggets poll. The Electronic Medical Records and Genomics (eMERGE) network has implemented more and more phenotype algorithms, such as colon polyps and type 2 diabetes mellitus (T2DM), as KNIME workflows to enhance their inter-institutional portability. The PhEMA group has also demonstrated an executable implementation of the NQF Quality Data Model (QDM) on KNIME. In addition to the applications that we will demonstrate in this tutorial, KNIME provides toolkits for Next Generation Sequencing (NGS) analyses, data mining, text processing, and social media research. It also provides support for integrating code written in SQL, Java, R, Python, and other programming languages.

Part one of the presentation will cover fundamental KNIME concepts and operations, the development of extract, transform, and load (ETL) workflows, algorithm implementation, and effective communication in KNIME. After introducing basic concepts, we will show how ETL workflows can facilitate intra- and inter-institutional collaboration and that these workflows are executable artifacts which enable reproducible research. We will then implement a phenotype algorithm, developed and validated by eMERGE, to demonstrate the value of KNIME in a more complex workflow. We will conclude this section by emphasizing collaboration as one of the core benefits of KNIME, dedicating time to discuss effective communication using KNIME. In the second part of the presentation, we will discuss how to leverage the extensibility of KNIME for more sophisticated applications, including phenome-wide association studies (PheWAS), natural language processing (NLP), XML processing, and incorporating RESTful web services.

10:00 a.m. – 10:30 a.m.  Coffee Break

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

II11: Creating Collaborative Opportunities in Research Data Management: Implementation and Impact of REDCAP in U.S. Department of Veterans Affairs

For details see page 23.

S35: Podium Presentations - Pharmacogenomics, Dosing, and Drug Interactions
Session Chair: Peggy Peisig

Developing Combination Cancer Therapy from Ontology Fingerprint Derived Gene Network
W. Zheng, G. Chen, University of Texas Health Science Center at Houston; L. Tsoi, T. Qin, University of Michigan; C. Chang, G. Bartholomeusz, UT-MD Anderson Cancer Center; H. Xu, University of Texas Health Science Center at Houston

An Automated System for Retrieving Herb-drug Interaction Related Articles from MEDLINE
K. Lin, C. Friedman, J. Finkelstein, Columbia University

The Clinical Pharmacogenetics Implementation Consortium (CPIC) Term Standardization for Clinical Pharmacogenetic Test Results: Alleles and Phenotypes
J. Hoffman, St. Jude Children’s Research Hospital; H. Dunnenberger, NorthShore Healthsystem; J. Burlison, St. Jude Children’s Research Hospital; M. Whirl-Carrillo, Stanford University; R. Freimuth, Mayo Clinic; M. Williams, Gesinger Health System; S. Scott, Icahn School of Medicine at Mount Sinai; J. Peterson, Vanderbilt University Medical Center; H. Rehm, Harvard Medical School; T. Klein, Stanford University; S. Murphy, Massachusetts General Hospital/Harvard University

Evaluating Physician Response to Pharmacogenomic-guided Warfarin Dosing in an Hospitalized Population
L. Wiley, Vanderbilt University; M. Beller, J. Field, J. Peterson, J. Denny, Vanderbilt University Medical Center

S36: Podium Presentations - Infrastructure for Data-driven Translational Science
Session Chair: Russ Waitman

Read only SMART on FHIR Façade for I2b2
K. Wagholikar, Massachusetts General Hospital/Harvard Medical School/Partners Healthcare; J. Mandel, Harvard Medical School/Children’s Hospital Boston; J. Klann, Massachusetts General Hospital/Harvard University; N. Wattanasin, M. Mendis, Partners Healthcare; C. Chute, Johns Hopkins University; K. Mandal, Children’s Hospital Boston; S. Murphy, Massachusetts General Hospital/Harvard University

Iterative Design and Modeling for the PCORnet Common Data Model v3.0
S. Rusincovitch, Duke Translational Research Institute; J. Brown, Harvard Medical School/Harvard Pilgrim Health Care Institute; K. Marsolo, Cincinnati Children’s Hospital Medical Center; J. Ibarra, Duke Clinical Research Institute; A. Kho, Northwestern University; D. Meeker, University of Southern California; L. Curtis, Duke University School of Medicine/Duke Clinical Research Institute

A Semantic Web RDF-based Approach for Modeling HL7 FHIR Profiles
E. Prud’hommeaux, MIT; H. Solbrig, D. Sharma, Mayo Clinic; C. Chute, Johns Hopkins University; G. Jiang, Mayo Clinic

Design and Architecture of a Distributed Network Pragmatic Clinical Trial: The PCORnet ADAPTABLE Study
S37: Papers - Machine Learning for Clinical Applications

**Session Chair:** Jihad Obeid

**Automated Summarization of Publications Associated with Adverse Drug Reactions from PubMed**

J. Finkelstein, Q. Chen, Columbia University; H. Adams, Stony Brook University; C. Friedman, Columbia University

**Identifying Family History and Substance Use Associations for Adult Epilepsy from the Electronic Health Record**

Y. Wang, University of Minnesota; E. Chen, Brown University; I. Leppik, S. Pakhomov, University of Minnesota; I. Sarkar, Brown University; G. Melton, University of Minnesota

**Exploring Gaps of Family History Documentation in EHR for Precision Medicine - A Case Study of Familial Hypercholesterolemia Ascertainment**

S. Mehrabi, Y. Wang, D. Ihrke, H. Liu, Mayo Clinic

**Regular Expression-based Learning for METs Value Extraction**

D. Redd, University of Utah/VA Salt Lake City Health Care System; J. Kuang, University of Utah; A. Mohanty, VA Salt Lake City Health Care System; B. Bray, Q. Zeng-Treitler, University of Utah/VA Salt Lake City Health Care System

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**12:15 p.m. – 1:15 p.m.**

TriNetX Lunch and Learn

(Not eligible for CME/CE)

**TriNetX: A Public/Private Network For Accelerating Clinical Trials**

*Michael Kamerick, VP Provider Acquisition, TriNetX*

The TriNetX mission is to help bring new therapies to market faster by enhancing clinical trial design and accelerating patient recruitment. TriNetX facilitates collaboration between healthcare providers, pharmaceutical companies and contract research organizations (CROs) through the creation of a global, federated clinical data network that connects researchers in real-time to the patient populations they are seeking to study. This session will include an update on the rapid growth of the network, an overview of the architecture, security policies, and governance principles, and a demonstration of the new capabilities of the TriNetX network.
Scientific Sessions
1:30 p.m. – 3:00 p.m.

II12: Informatics Landscape: How Your Work Matters and the Implementation of Research

For details see page 23.

S38: Panel - Advanced Machine Learning for Healthcare
J. Sun, J. Rehg, Georgia Institute of Technology; S. Saria, Johns Hopkins; H. Xu, UT Health; E. Xing, Carnegie Mellon

Due to the explosion of health-related “big data,” ranging from electronic health records and genomic sequencing to environmental and wearable sensor data, the healthcare industry is in desperate need of effective ways to utilize these complex and diverse data sources in order to simultaneously improve quality of care and reduce cost. Machine learning is playing a central role in data-driven healthcare applications such as clinical risk prediction, computational phenotyping, treatment recommendation, and disease progression modeling. However, most clinical informaticians have limited knowledge of or exposure to the latest developments in machine learning. This panel will discuss the latest advances in machine learning methods and models along with their applications to healthcare. In particular, we will describe scalable methods for clustering, mining, modeling, and predicting health states and treatment outcomes from diverse multimodal health datasets. The goal of this panel is to enable the exchange and collaboration between researchers and practitioners in the clinical informatics and machine learning communities.

S39: Panel - Completing the Learning Health Care System Cycle: Developing and Testing eCQM in pSCANNER, a PCORNet Research Network
L. Schilling, University of Colorado School of Medicine; E. Holve, AcademyHealth; J. Goldwater, National Quality Forum; P. Payne, The Ohio State University; D. Meeker, University of Southern California

The goal of this panel is to discuss the ways in which two historically independent data-driven communities key to the Learning Health System, researchers and quality measure developers, have come together to advance the work of both. Members of this panel are collaborating on a prototype infrastructure to advance the work of both communities. Measure developers often test measure feasibility with select health care organizations, but broad feasibility testing and the ability to assess a measure’s true predictive correlation with meaningful outcomes is difficult. The clinical research informatics community has made progress in technologies that support the reuse of EHR data however, both communities face challenges of EHR data quality, heterogeneity, timeliness, accessibility, and concomitant regulatory “hurdles”.

S40: Podium Presentations - Data Mining and Knowledge Discovery
Session Chair: David Eichmann

3D Motion Analysis of Clinical Performance: A New Big Data Opportunity
M. Hoffman, UMKC/Children’s Mercy Hospital; S. Siddicky, UMKC; B. Balakrishnan, University of Missouri - Columbia; G. King, UMKC

Using Karyotype Data for Automated Disease Classification: A Proof of Concept Demonstration
S. Raje, Z. Abrams, K. Coombes, P. Payne, The Ohio State University

Analytical Toolkits for University Healthcare Consortium’s Quality and Performance Dataset
N. Bahroos, X. Dong, P. Kanabar, M. Chukhman, K. Pradhan, University of Illinois at Chicago

The Applicability of an EHR Phenotype for Cohort Identification
N. Shang, G. Hripcsak, Columbia University; P. Ryan, Columbia University/Observational Health Data Sciences and Informatics/Janssen Research & Development, LLC; C. Weng, Columbia University
S41: Papers - Clinical and Research Data Collection, Curation, Preservation, or Sharing

Session Chair: Davera Gabriel

**Expanding Interprofessional EHR Data in i2b2**

B. Westra, University of Minnesota; B. Christie, Fairview Health System; S. Johnson, L. Pruinelli, University of Minnesota; A. LaFlamme, Fairview Health System; J. Park, University of Minnesota; S. Sherman, Fairview Health System; P. Ranallo, SixAims for Behavioral Health; M. Byrne, UnitedHealth Group; S. Speedie, University of Minnesota

**TRANSFoRm eHealth Solution for Quality of Life Monitoring**

S. Saganowski, A. Misiaszek, P. Brodka, Wrocław University of Technology; A. Andreasson, Karolinska Institutet; V. Curcin, King's College London; K. Fraczkowski, Wrocław University of Technology

**Semantic Web Ontology and Data Integration: a Case Study in Aiding Psychiatric Drug Repurposing**

C. Liang, J. Sun, C. Tao, University of Texas Health Science Center at Houston

**The Drug Data to Knowledge Pipeline: Large-scale Claims Data Classification for Pharmacologic Insight**

M. Homer, N. Palmer, Harvard Medical School/Boston Children’s Hospital; O. Bodenreider, National Library of Medicine; A. Cami, Harvard Medical School/Boston Children’s Hospital; L. Chadwick, Harvard Medical School/Boston Children’s Hospital/MCPHS University; K. Mandl, Harvard Medical School/Boston Children’s Hospital

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**Clinical Research Informatics Year-in-Review**

**Peter Embi, MD, MS, FACMI**

@embimd

Associate Professor and Vice Chair, Department of Biomedical Informatics, The Ohio State University; Chief Research Information Officer, The Ohio State University Medical Center; Physician, Department of Internal Medicine, Division of Rheumatology & Immunology

For details see page 17.

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# Poster Session 1 & 2

(Not eligible for CME/CE)

**Tuesday, March 22**

**5:00 p.m. – 6:00 p.m**

Cyril Magnin Foyer

All posters displayed.

TBI Authors present; CRI authors optional

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**Wednesday, March 23**

**5:00 p.m. – 6:00 p.m**

Cyril Magnin Foyer

All posters displayed.

CRI Authors present; TBI authors optional

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