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ABOUT THE JOINT SUMMITS ON TRANSLATIONAL SCIENCE

AMIA presents two essential back-to-back meetings for TBI and CRI scientists working throughout the spectrum of translational science. A 'Bridge Day' joins the two summit meetings for a day of shared sessions, a keynote, and informational exchange. The **AMIA Joint Summits on Translational Science** are a set of two joined conferences held annually with the Translational Bioinformatics Summit (TBI) immediately preceding the Clinical Research Informatics Summit (CRI). The Joint Summits provide a venue to gather translational bioinformatics and clinical research informatics professionals from academia, industry, government and non-profit sectors, along with those interested in the full translational science spectrum. The 2012 Joint Summits on Translational Science will be held March 19-23 at the Parc 55 Hotel in San Francisco. Registration is open and can be accessed at www.amia.org/jointsummits2012/registration

SCHEDULE AT-A-GLANCE

MONDAY, MARCH 19

7:30 – 8:30 am
Coffee and Pastries

7:30 am – 5:00 pm
Registration Open

8:30 am – 12:00 pm
Tutorials
(additional registration required)

10:00 – 10:30 am
Coffee Break

12:15 – 1:15 pm
Lunch & Learn

1:30 – 3:00 pm
Opening Session and Keynote
Address: Dr. Trey Ideker

3:00 – 3:30 pm
Coffee Break

3:30 – 5:00 pm
Scientific Sessions

5:00 – 6:00 pm
Reception

TUESDAY, MARCH 20

8:00 – 9:00 am
Coffee and Pastries

8:00 am – 5:00 pm
Registration Open

9:00 – 10:30 am
Scientific Sessions

10:30 – 11:00 am
Coffee Break

11:00 am – 12:00 pm
Keynote Presentation:
Dr. Howard Jacob

12:15 – 1:15 pm
Lunch & Learn - Apixio

1:30 – 3:00 pm
Scientific Sessions

3:00 – 3:30 pm
Coffee Break

3:30 – 5:00 pm
Scientific Sessions

5:00 – 6:00 pm
Poster Session and Reception

WEDNESDAY, MARCH 21

7:30 – 8:30 am
Coffee and Pastries

7:30 am – 5:00 pm
Registration Open

8:30 – 10:00 am
Keynote Presentation:
Dr. Robert M. Califf

10:00 – 10:30 am
Coffee Break

10:30 am – 12:00 pm
Scientific Sessions

12:15 – 1:15 pm
Lunch & Learn

1:30 – 3:00 pm
Scientific Sessions

3:30 – 5:00 pm
Closing Session and TBI Year in
Review: Dr. Russ Altman

5:00 – 6:00 pm
Joint Summits Reception -
sponsored by Booz Allen Hamilton

TRACK DESCRIPTIONS

TRACK 1: CONCEPTS, TOOLS AND TECHNIQUES FOR TRANSLATIONAL BIOINFORMATICS

Translational informatics research requires the co-ordinated analysis of molecular as well as clinical phenotypic information to understand the pathophysiology or disease as well as to predict responses to therapeutic interventions. This track will focus on methods, tools and techniques ranging from text-mining, cloud computing and Semantic Web Technologies as well as information integration and data warehousing. Presentations will demonstrate case studies, prototype implementations and mature, production grade tools and platforms.

TRACK 2: INTEGRATIVE ANALYSIS OF MULTI MODAL MEASUREMENTS

With over 30 different high-throughput measurement modalities for measuring the disease state at multiple levels, there is constant innovation for devising integrative analytic methods that relate molecular measurements to clinical phenotypes—particularly by identifying biomarkers for diagnosis, prognosis and personalization of care. This track will focus on systems approaches to integrate multiple kinds of data to facilitate drug discovery, drug repositioning and biomarker discovery.

TRACK 3: BASE PAIRS TO BEDSIDE

It is expected that 30,000 people will have whole genome sequenced just this year. Our current approaches to understand genetic information in the clinical setting need overhaul. With the increase in the ability to capture phenotypic information – both in the research and clinical settings – our capability to represent and relate phenotypes with genotypes to understand the natural history of diseases has become rate limiting. This track will focus on efforts to link phenotypes in clinical descriptions with the massive amounts of individual genomic information that will be available soon.

TRACK 4: INFORMATICS WITH BIG DATA

Given the rapid advances in natural language processing and access to vast computing infrastructure as well as sophisticated ontologies, data-mining and machine learning tools have converged in manner that allows us to perform “Big Data” analyses. Simultaneously, because of the changes in public policy, information technology, and electronic health record (EHR) adoption, large datasets are increasingly available in healthcare bringing us close to the “threshold of sufficient data Web-scale data mining efforts have shown that algorithms behave differently when applied to very large datasets and that with sufficient data simple approaches can work well. This track will focus on efforts that apply Web-scale data-mining methods on massive datasets.

LEARNING OBJECTIVES

- To present the latest progress on using informatics approaches to improve translational biomedical research
- To demonstrate how molecular bioinformatics can enhance clinical research, genetic medicine, and healthcare
- To demonstrate how clinical informatics deploying molecular data and knowledge can contribute to the delivery of molecular medicine and individualized health management
- To identify the current challenges of translational bioinformatics, articulate opportunities, and to define the future directions
- To identify areas of interaction among computational biology, genomics research, statistical genetics, electronic health records, health information exchanges, and public health
- To establish a framework for developing, deploying and assessing translational bioinformatics initiatives
- To provide a platform to share research-related issues among the nationwide initiatives on translational research informatics, such as CTAs, NCBCs, caBIG, etc.

KEYNOTE SPEAKERS

MONDAY, MARCH 19, 2012

1:30 – 3:00 pm



Trey Ideker, PhD

Division Chief of Medical Genetics at University of California San Diego School of Medicine

Dr. Ideker is Chief of Genetics at the UCSD School of Medicine. He also serves as Professor of Bioengineering, Adjunct Professor of Computer Science and Member of the Moores UCSD Cancer Center. Ideker received Bachelor's and Master's degrees from MIT in Electrical Engineering and Computer Science and his Ph.D. from the University of Washington in Molecular Biology under the supervision of Dr. Leroy Hood. He is a pioneer in using genome-scale measurements to construct network models of cellular processes and disease. His recent research activities include assembly of networks governing the response to DNA damage, development of software for protein network cross-species comparisons, and network-based diagnosis of disease. Ideker serves on the Editorial Boards for Bioinformatics and PLoS Computational Biology, Board of Directors for US-HUPO and the Cytoscape Consortium, and is a regular consultant for companies such as Monsanto, Genstruct, and Mendel Biotechnology. He was named one of the Top 10 Innovators of 2006 by Technology Review magazine and the 2009 Overton Prize recipient from the International Society for Computational Biology. His work has been featured in news outlets such as The Scientist, the San Diego Union Tribune, and Forbes magazine.

TUESDAY, MARCH 20, 2012

11:00 am – 12:00 pm



Howard J. Jacob

Warren P. Knowles Chair of Genetics
Director, Human and Molecular Genetics Center
Professor, Departments of Physiology and Pediatrics
Vice Chair of Research in Pediatrics
Medical College of Wisconsin

Professor Jacob received his Ph.D. in Pharmacology from the University of Iowa in 1989. He completed two parallel post-doctoral fellowships in functional genomics and molecular genetics/genomics at Harvard, Stanford and MIT with Victor J. Dzau, M.D. and Eric S. Lander, Ph.D. He was on the faculty at Massachusetts General Hospital and Harvard Medical School for nearly 4 years before moving to Milwaukee. He joined the Medical College of Wisconsin in 1996 as an Associate Professor, Department of Physiology with full Professorship and Tenure in 2001. He was appointed the Founding Director of the Human and Molecular Genetics Center (HMGC) and was awarded the Warren P. Knowles Chair of Genetics in 1999. He has published more than 200 peer reviewed articles.

In 2010 Dr. Jacob led a team of researchers at the Medical College who used an innovative DNA sequencing technique to unravel the medical mystery of Nicholas Volker, a young boy whose life-threatening disease had baffled his doctors and tested his family's faith. Working with Medical College scientists and physicians at the Children's Hospital of Wisconsin, Dr. Jacob's team used Nicholas' DNA to diagnose his disease and recommend a course of treatment. This treatment has so far been successful.

KEYNOTE SPEAKERS

WEDNESDAY, MARCH 21, 2012

8:30 – 10:00 am



Robert M. Califf, MD,
Vice Chancellor for Clinical Research
Professor of Medicine, Division of Cardiology
Duke University's Translational Medicine Institute

Vice Chancellor for Clinical Research, Director of the Duke Translational Medicine Institute (DTMI), and Professor of Medicine, Cardiology, Duke University Medical Center, Dr. Robert Califf leads a large, multifaceted organization focused on transforming the path for scientific discoveries into improved medical care. Prior to his role at DTMI, he was the founding Director, Duke Clinical Research Institute, an academic research organization. He is the editor-in-chief of American Heart Journal, and has authored more than 1000 peer-reviewed articles.

He has served on the Cardiorenal Advisory Panel of the U.S. Food and Drug Administration and the Pharmaceutical Roundtable of the Institute of Medicine (IOM). He co-chairs the Clinical Trials Transformation Initiative, a public private partnership focused on improving the clinical trials system, as is the Director of the Clinical Research Forum, an organization of academic health and science system leaders working to enhancing the effectiveness of the clinical research enterprise. A member of the Drug Discovery, Development, and Translation Forum of the IOM, Dr. Califf also participates as a member of the National Institute of Health Council on Aging, and President Obama's Council of Advisors on Science and Technology.

3:30 – 5:00 pm



Russ Altman, MD, PhD
Professor of Bioengineering, Genetics, and Medicine
(and Computer Science, by courtesy)
Chairman, Department of Bioengineering
Director, Biomedical Informatics Training Program
Stanford University

The importance of Translational Bioinformatics continues to grow in biomedical research, genetics, education, and diagnostic and therapeutic discovery. In the past year, we have seen continued progress in linking clinical data to molecular data, as we usher in a new era of molecular medicine. This session will review notable publications over the past twelve months, highlighting trends and milestones achieved in the past year. This is the fifth installment of this keynote talk by Dr. Altman.

TUTORIALS

T01: INTRODUCTION TO TRANSLATIONAL BIOINFORMATICS

Indra Neil Sarkar, University of Vermont and Jessica Tenenbaum, Duke University

In 2005, Dr. Elias Zerhouni, Director of the National Institutes of Health (NIH), wrote “It is the responsibility of those of us involved in today’s biomedical research enterprise to translate the remarkable scientific innovations we are witnessing into health gains for the nation... At no other time has the need for a robust, bidirectional information flow between basic and translational scientists been so necessary.” Clearly evident in Dr. Zerhouni’s quote is the role biomedical informatics needs to play in facilitating translational medicine. American Medical Informatics Association (AMIA) now hosts the Joint Summits on Translational Science of which the Summit on Translational Bioinformatics is one of the two components. This tutorial is designed to teach the basics of the various types of molecular data and methodologies currently used in bioinformatics and genomics research, and how these can interface with clinical data. This tutorial will address the hypotheses one can start with by integrating molecular biological data with clinical data, and will show how to implement systems to address these hypotheses. The tutorial will cover real-world case-studies of how genetic, genomics, and proteomic data has been integrated with clinical data.

By the end of the tutorial, participants will be able to:

- Understand why biologists and clinicians use each measurement technology, and the advantages of each.
- Appropriate for studying diseases.
- Be able to list high-level requirements for an infrastructure relating research and clinical genetic and genomic data.

Outline of Topics:

- Basic understanding of various genome-scale measurement modalities: sequencing, polymorphisms, haplotypes, proteomics, gene expression, metabolomics, and others
- Crucial difference between genetic and genomic data
- Nature and format of expression, polymorphism, proteomics, and sequencing data
- Overview of the most commonly used structured vocabularies, taxonomies, and ontologies used in genomics research
- Description of the most frequently used analysis and clustering techniques
- How the genetic predisposition to disease is studied
- Use of genetic information across medical specialties
- How to find clinical genetic tests
- Genomic and clinical data to study patient disease-free status and survival
- How informatics can be used to identify potential drug targets
- Types of biomarkers
- Parallels between research methods in medical informatics and bioinformatics
- Relating clinical measurements with molecular measurements

Intended Audience: Academic faculty or professionals setting up bioinformatics facilities and/or relating these to clinical data repositories, or to data from General Clinical Research Centers or Clinical and Translational Science Awards; health information professionals responsible for clinical databases or data warehouses and tying these to researchers; informaticians, clinicians, and scientists interested in genetics, functional genomics, and microarray analysis; physicians interested in how medicine is advancing through the use of genomics and genetics; and students.

Content level: 20% Basic, 50% Intermediate, 30% Advanced

TUTORIALS

T02: ONTOLOGY SERVICES FOR TRANSLATIONAL RESEARCH IN THE I2B2 WORKBENCH

Shawn Murphy, Massachusetts General Hospital and Ray Ferguson, Stanford University

The i2b2 platform uses vocabularies extensively in the querying and manipulation of patient data for translational and clinical research. The National Center for Biomedical Ontology offers an extensive range of Web services for accessing ontologies, generating value sets and lexicons, annotating data, and performing information retrieval that form key elements of software systems in informatics. Given the importance of the use of ontologies for data integration, NCBO and I2b2 have initiated a collaboration to provide access to cutting edge ontology services from within the i2b2 workbench to enable cross institution data transformation. This tutorial will review the drivers of this collaboration, provide experience in using the NCBO's resources, and will offer participants in-depth understanding of how ontologies and terminologies are used in biomedical informatics. This tutorial will review the use of ontologies in i2b2 and discuss their integration with the NCBO's Ontology Web Services infrastructure.

By the end of the tutorial, participants will be able to:

- Understand i2b2 ontology representation.
- Understand how i2b2 ontology's are manipulated in performing patient queries.
- Understand the biomedical ontology landscape.
- Understand the NCBO infrastructure available for data annotation and ontology access.
- Conceive workflows that utilize NCBO Web Services and i2b2 workbench to solve their own data entry and integration problems.

Outline of Topics:

- i2b2 ontology representation
- Diagnosis and procedures (items without associated values)
- Laboratories (items with associated values)
- Items with modifiers
- Use of i2b2 ontology representation in patient queries
- Overview of NCBO Web services
- Web-based tools for Ontology search, visualization and review
- Tools and Web Services for data annotation and semantic integration
- Design of custom workflows to utilize ontology-services

Intended Audience: Scientists, researchers, healthcare analysts, database programmers and informaticians seeking to understand how to optimally use ontologies for clinical data integration. Health IT System developers and CIOs seeking to understand how to leverage NIH-funded infrastructure for using Ontologies.

Content level: 50% basic; 30% intermediate; 20% advanced

TUTORIALS

T03: REUSING EHRs FOR CLINICAL, GENOMIC, AND PHARMACOGENOMIC DISCOVERY AT VANDERBILT AND WITHIN THE eMERGE NETWORK

Joshua Denny and Hua Xu Vanderbilt University

This tutorial will cover basic themes about use of EHRs for generating cohorts of patients to serve as cases and controls for given clinical phenotypes. EHRs can be used for many different types of research include disease-based, response to treatment, clinical biomarkers, redefining “normal”, and analysis of changes over time of clinical variables and parameters. Deriving such phenotypes from EHR data can be challenging. Methods typically involve use of billing data, medication records (often unstructured), laboratory data, and natural language processing. After derivation of these phenotypes, populations can be used for clinical research. Linkage to DNA biobanks also enables the possibility of genomic and pharmacogenomic associations. Research within the eMERGE network has demonstrated success with EHR-based genome-wide association studies (GWAS). In addition, use of EHR-linked genetic data uniquely enables phenome-wide associations studies (PheWAS), which allows an unbiased scan of what diseases may be associated with a given genotype.

This tutorial will review the design of EHR-linked biobanks; methods for creating phenotype algorithms with integrated use of NLP, billing codes, laboratory and test results, and medication records (with review of a number of case studies); basic principles of genetic analysis (candidate gene, GWAS, exome chips, and other platforms); use of standard vocabulary in representing and constructing phenotype algorithms; and application of PheWAS to further characterize clinical variants.

In addition to didactic portions of the tutorial, investigators will be encouraged to work through specific phenotypes of interest and begin discussion of phenotype algorithms as real-world examples. Several case-studies will be presented and worked through during the tutorial in an interactive fashion.

Topics to be covered:

- Design of EHR-linked DNA biobanks
 - Opt-in design
 - Opt-out design
 - De-identification
 - Overview of eMERGE I and II networks, composition, and goals
 - Introduction to genomewide association studies (GWAS)
 - Discussion of example primary GWAS from eMERGE
 - Examples of “GWAS” reuse for new phenotypes, with significant new findings
- Approaches
 - Types of data well represented in EHRs
 - When to use a fully-automated phenotyping approaches vs. “computer assisted” approach, and the importance of specific review interfaces (with demonstrations)
- Phenotyping algorithms
 - Case studies in several eMERGE algorithms: what has worked, and what hasn’t
 - Discussion of experiences with cross-institution implementation of phenotype
 - Examples of disease-based and pharmacogenetic algorithms
 - Classes of data available and strengths/weaknesses of each
 - Multimodal approaches
 - Experiments in transportability of phenotype algorithms across sites
 - Deterministic vs. machine learning approaches
 - Evaluation of the accuracy of different EMR categories of information for accurate phenotype algorithms
 - Development of sharable phenotype libraries available for public use
- NLP methods
 - Medication extraction
 - General NLP for conceptual elements
 - General NLP vs. specific NLP
 - Demonstration of some available tools
- Methods for evaluating the effectiveness (e.g., positive predictive value) of phenotyping algorithms
- Use of standard vocabularies for data dictionaries and phenotype algorithms
 - Demonstration of eleMAP, which allows efficient browsing of available structured representations of phenotype elements, demographics, and comorbidities
- Phenome-wide association studies (PheWAS) using EMR data for relevant genomic variants
 - Methodology and general validation
 - Case studies

Intended Audience: clinical and genetic researchers; providers interested in reuse of EHR data; translational bioinformaticians and medical informaticians.

Content level: 30% basic; 50% intermediate; 20% advanced

TUTORIALS

T04: INTRODUCTION TO R FOR BIOINFORMATICS AND BIOMEDICINE

David Ruau, Stanford University

To analyze multiple different genomic data types. Bioconductor, a package repository for bioinformatics, contains 467 packages in addition of the 3128 general-purpose packages from R. The wide array of possibility make R a platform particularly suited for translational bioinformatics research. However, like other statistical software, the learning curve can be steep for some of us less versed in computer science. This tutorial is based on the successful workshop “Introduction to R programming” taught at Stanford. Participants will be introduced to the basic of the R language through practical examples from real biomedical research projects. We will show advanced techniques on how different resources can be plugged into R to perform an analysis and produce-publication ready graphics.

At the end of this tutorial, participants will be able to:

- To import and export data from different resources, including databases.
- Use R to transform and manipulate their data and perform exploratory statistical graphs.
- Write small R functions and objects.
- Pre-process raw DNA microarray data and explore their gene lists.
- Interpret their results using metadata from KEGG database.
- How to perform classical statistical tests.
- Outline of topics:
 - Introduction to the R console and interactivity concept
 - How to write R code
 - Producing publication grade quality graphics easily
 - Directly downloading raw data from public microarray repositories
 - Clustering and graphical solutions available in R
 - Knowledge database and metadata accessible through R package repositories
 - Advance topics (GWAS, high level graphics, reproducible research...)

Intended Audience: Academics and professionals wanting to gain hands-on skills to analyze biomedical or clinical data as well as an overview of R possibilities. Translational scientists and students interested in analyzing their genomic data and to learn how to integrate them with external resources.

Content level: 30% Basic, 50% Intermediate, 20% Advanced

PANELS

Crossing the Omic Chasm: Integrating Omic Data into the EHR: For Personalized Genomic Medicine

J. Starren, Northwestern University; E. Bottinger, Mount Sinai School of Medicine; M. Dente, GE Healthcare; G. Wood, Intermountain Healthcare; J. Hoffman, St. Jude Children's Research Hospital

"Omic" data will need to be integrated into the Electronic Health Records (EHRs). This panel will present the perspective and approaches under use by the eMERGE Network, the Pharmacogenomics Research Network, the HL7 Clinical Genomics Workgroup and select EHR vendors.

Intellectual Property and Entrepreneurship in Translational Bioinformatics

A. Butte, Stanford University; W. Hogarth, Sequoia Capital; K. Ku, Stanford University

To realize the full benefit of translational bioinformatics, the scientific breakthroughs made in research laboratories need to be translated into commercially viable ventures. This panel will explore the milestones and challenges on that path as well as point out areas where there is market need but not enough research.

Big Data

Panelist: L. D'Avolio, VA Boston Healthcare System; P. Tonellato, Harvard Medical School; J. Hammerbacher, Cloudera, Inc.; D. Anderson, OptumInsight

Data can be "big" in terms of size (e.g. next gen sequencing data) or can be big in terms of the number of individuals on which there is some data collected. Increasingly we are moving towards generating data that is big along both these dimensions. This panel will explore the approaches to store, analyze and interpret Big Data.

Detection and Prediction of Adverse Drug Events in Clinical and Molecular Data

N. Tatonetti, R. Altman, Stanford University; I. Kohane, Harvard Medical School; A. Butte, Stanford University; C. Friedman, Columbia University; N. Shah, Stanford University

Adverse drug events (ADEs) are a leading cause of morbidity and mortality around the world, accounting for 100,000 deaths each year. This panel will explore the challenges of using large clinical data repositories for ADE discovery as well as the necessary methodological innovations that will be necessary to use clinical data in this manner.

SaaS-Based Translational Research

S. Granit, R. Winslow, The Johns Hopkins University; I. Foster, The University of Chicago; B. Athey, University of Michigan; D. Singh, Amazon Web Services

The Path to Reality for "Research in the Cloud": Cloud computing promises to alleviate some of the challenges associated with handling Big Data in biomedicine; however, concerns still exist around the questions of security, privacy and compliance. This panel will explore the requirements for a Software as a Service (SaaS) solution that can be used today to transform translational research.

Practical experience with Linked Open Biomedical Data

C. Torniai, Oregon Health & Science University; D. Bourges-Waldegg, Harvard University; C. Barnes, University of Florida; A. Ruttenberg, University of Buffalo; Y. Ding, Indiana University

State of the art and future directions -- A large portion of the valuable data produced in biomedical research remains inaccessible to the research community. Semantic Web technologies and the Linked Open Data initiative have gained traction for integrating, linking, and sharing biomedical data. This pane will explore the topics of i) Producing, maintaining, and consuming Linked Biomedical Data ii) Lessons learned in developing frameworks for large-scale sharing of biological information on the Web iii) Using clinical data sources in the context of Linked Data.

PANELS

Knowledge Synthesis for in silico Science: Lessons Learned and Future Directions

P. Payne, The Ohio State University; I. Sarkar, University of Vermont; P. Tarczy-Hornoch, University of Washington; P. Tonellato, Harvard Medical School

The ability to reason upon networks of biological and molecular markers, phenotypic variables, and available data sets, in order to learn biologically or clinically relevant interrelationships is a core activity in translational research. This panel will explore the state-of-the-art relative to evolving in silico knowledge synthesis techniques, intended to address the preceding gap in knowledge and practice.

transMART: An Open Source Analytical and Data Sharing Informatics Platform Enabling Translational Research

B. Athey, K. Smith, University of Michigan

This panel will explore tranSMART, an informatics platform developed by Johnson & Johnson (J&J) that has been placed in open source that enables translation research. The University of Michigan and key academic and industry partners are developing a next-generation analytical and data sharing informatics platform based on tranSMART 1.0. The platform will accelerate biomedical discovery by enabling collaboration among clinicians, researchers and informatics professionals, and will be sustained through an academic, government, and industry private-public partnership.

At the TBI Summit, there will be many paper and podium presentations of exciting scientific results. Here is a sample of some featured content:

The Role of Complementary Bipartite Visual Analytical Representations in the Analysis of SNPs: A Case Study in Ancestral Informative Markers

S. Bhavnani, University of Texas Medical Branch; G. Bellala, University of Michigan; S. Victor, University of Texas; M. Abbas, V. McMicken, J. Tupa, University Houston Clear Lake; S. Visweswaran, University of Pittsburgh

An Automated Bayesian Framework for Integrative Gene Expression Analysis and Predictive Medicine

A. Zollanvari, Harvard Medical School; N. Parikh, MIT; G. Alterovitz, Harvard Medical School

Stochastic Model Search with Binary Outcomes for Genome-wide Association Studies

A. Russu, G. Botta, A. Malovini, University of Pavia; F. Villa, A. Puca, IRCCS Multimedica; R. Bellazzi, University of Pavia

Towards an Oncology Database (ONCOD): a Case Study Using Data Warehousing Approach

X. Wang, L. Liui, J. Fackenthal, P. Chang, G. Newstead, S. Chmura, I. Foster O. Olopade, University of Chicago

Large-scale Prediction of Adverse Drug Reactions by Integrating Chemical, Biological, and Phenotypic Properties of Drugs

M. Liu, Y. Wu, Y. Chen, J. Sun, Z. Zhao, Vanderbilt University; X. Chen, University of Kansas; H. Xu, Vanderbilt University

Clinical Utility of Sequence-based Genotype Compared with that Derivable from Genotyping Arrays

A. Morgan, R. Chen, Rong, A. Butte, Stanford University

NEW THIS YEAR! BULLET PRESENTATIONS!

Poster authors will present a five minute "bullet presentation" of their poster to convey their innovative ideas! Don't miss this rare opportunity to learn about cutting edge ideas in the field. Bullet presentations will take place after paper and podium abstract presentations sessions.