American Medical Informatics Association

2009 Summit on Translational Bioinformatics Final Program

May 15-17, 2009 • Grand Hyatt San Francisco Union Square • San Francisco, California

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5:00 pm – 6:30 pm	**Poster Session 2**	Plaza Ballroom West
5:00 pm – 6:30 pm	**Reception**	Farallon

Tuesday, March 17

7:30 am – 8:30 am	**Continental Breakfast**	Farallon
7:30 am – 2:00 pm	**Registration open**	Ballroom Foyer West
8:30 am – 10:00 am	***Concurrent Sessions***	
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	(S20) Translational Research Support and Education: A Library-Based Approach	Plaza Ballroom East
	(S21) Informatics Concepts, Tools and Techniques to Enable Integrative Translational Research	Dolores
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10:00 am – 10:30 am	**Coffee Break**	Farallon
10:30 am – 12:00 pm	***Concurrent Sessions***	
	(S23) caBIG® Enterprise Support Network: Knowledge Centers	Merced AB
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	(S29) Methods in Translational Bioinformatics	Plaza Ballroom East
	(S30) Late Breaking Presentations	San Francisco ABC
3:00 pm – 3:30 pm	**Coffee Break**	Farallon
3:30 pm – 5:00 pm	***Closing Plenary Session***	Plaza Ballroom East

Scientific Program Committee

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Eric Neumann, Clinical Semantics Group
Lucila Ohno-Machado, Brigham and Women's Hospital
David States, University of Michigan

Track Descriptions

Track 1: Informatics Methods for the Analysis of Molecular and Clinical Measurements. Novel modalities for molecular measurements, including those for epigenetics, interactions, and proteins, continue to be introduced each year. This track will address the development of novel analytic methods for these molecular measurements as applied to disease, how molecular measurements can be stored and retrieved in electronic health records, and how existing analytic methods can now be applied to clinical measurements.

Track 2: Computational Approaches to Finding Molecular Mechanisms and Therapies for Disease. DNA sequencing, gene expression microarrays and other tools measuring outputs of the genome have been forecast to enable the discovery of biomarkers for disease and novel types of therapeutics. This track will focus on how data-driven, knowledge-driven, and physics-driven approaches can be applied to facilitate drug and biomarker discovery.

Track 3: Relating and Representing Phenotypes and Disease. Phenotypes broadly describe the unique traits of an organism, some of which are related to disease. Improved measurement technologies and ontologies have enabled investigators to obtain and represent large collections of phenotypes, but relating these to clinical and health remains a challenge. Though electronic health records are being increasingly adopted, much of the useful phenotypic and clinical descriptors remain in free-text. This track will address all of these challenges, with presentations geared towards enabling novel prognostic, diagnostic, and therapeutic applications.

Track 4: Dissecting Disease Through the Study of Organisms, Evolution, and Taxonomy. Over a quarter million different species have had some genetic sequence obtained. While animal and cellular models have long been studied as a proxy for human disease, this track will address the challenge of building informatics methods to relate experimental findings and phenotypes from models to human disease, and methods that take advantage of the evolutionary scale of sequenced genomes. This track will also cover modeling of the spread of infectious disease.

Track 5: Informatics Concepts, Tools, and Techniques to Enable Integrative Translational Research. Integrative translational research projects make coordinated use of molecular (genomic, epigenetic, proteomic, etc.) as well as clinical information (imaging, EMR, etc.) to understand pathophysiology and to understand and predict responses to therapeutic interventions. Studies of this kind are core components of many NIH Roadmap projects and aim to relate molecular and imaging parameters to the pathophysiology and clinical parameters. This interdisciplinary track will address informatics tools in the semantic modeling, grid, natural language processing, information integration and information warehouse areas that have the potential for facilitating integrative translational research. Presentations will demonstrate application case studies along with new concepts, prototypes and mature tools.

Track 6: Informatics Methods in Genetics Discoveries and Clinical Practice. In the past two years, over 250 disease genes have been discovered from genetic studies, the majority of which are associated with complex diseases such as diabetes, hypertension, cancer, etc. Consequently, molecular bioinformatics methods are increasingly considered for the identification of additional disease gene candidates. Further, with the reducing cost of genome-wide sequencing or assaying, new opportunities are emerging to provide personalized genome maps and their interpretation. This track focuses on the development of bioinformatics methods for disease gene discoveries in genetic studies and the integration of genetic data and knowledge in decision making and support, electronic records and other genetic applications to clinical practice and personal health management.

Board of Directors

Program Chronology

Sunday, March 15, 2009

7:30 am – 8:30 am: Continental Breakfast
Room: Farallon

7:30 am – 5:00 pm: Registration Open
Room: Ballroom Foyer West

8:30 am - 12:00 pm: Tutorials

(T01) Introduction to Translational Bioinformatics
Room: Dolores

Atul Butte, Stanford 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) recently added Translational Bioinformatics as one of its three major domains of informatics. This tutorial is designed around the successful curriculum used in Stanford's 2007 Translational Bioinformatics, one of the first courses to be offered in this field. 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.

(T02) Design & Conduct of Evaluation Studies in Translational Bioinformatics
Room: Merced A

Charles P. Friedman, Office of the National Coordinator, U.S. Department of Health and Human Services

It is now generally accepted that evaluation of information resources is one of the fundamental activities of biomedical and health informatics. Evaluation studies can address a wide range of questions using a wide range of methods. Studies are carried out before, during, and following the deployment of information resources. This tutorial is designed to support anyone designing, carrying out, or critically appraising an evaluative study of a biomedical information resource. The tutorial will offer an introduction to the rigorous scientific methods underlying evaluation, in such a manner that they are understandable and practical to apply. The tutorial starts by defining evaluation and describing why we do it, and then discusses alternative approaches and how to select between them. A case study focused on translational bioinformatics is used to introduce evaluation techniques and examine their strengths and weaknesses. The tutorial will also address how to formulate and include appropriate levels of evaluation in the context of projects whose primary focus is development of a new information resource.

(T03) geWorkbench: An Open-Source Platform for Integrated Genomics
Room: Merced B

Aris Floratos, Columbia University

A large number of bioinformatics techniques have been developed to serve the needs of biomedical research. The field is moving rapidly, with new and improved approaches appearing frequently. The fast pace of change and the technical sophistication of these approaches creates a barrier of adoption for ordinary biologists. The problem is exacerbated by the integrative nature of biomedical research which often requires combining data from multiple genomic/biomedical databases and using an array of advanced analysis techniques. geWorkbench, the bioinformatics platform of the Center for the Multi-scale Analysis of Genomic and Cellular Networks, MAGNet, http://magnet.c2b2.columbia.edu (a member of the NIH Roadmap funded National Centers for Biomedical Computing http://www.bisti.nih.gov/ncbc) is a Java application that provides users with access to an integrated suite of genomics tools. It is developed on top of an open-source, extensible component framework specifically designed to facilitate the rapid development of new modules and to support the easy integration of pre-existing tools. Indeed, many of the components in geWorkbench are the result of wrapping quality software from third parties.

10:00 am - 10:30 am: Coffee Break
Room: Farallon

1:30 pm - 3:00 pm: Plenary Session

(S01) Opening Session and Keynote Presentation
Room: Plaza Ballroom East

Lynn H. Vogel, University of Texas M.D. Anderson Cancer Center

Dr. Vogel is Vice President and Chief Information Officer at the University of Texas M.D. Anderson Cancer Center in Houston, Texas, a $2.3B+ clinical, research and teaching institution that is the world's largest and highest rated facility devoted to the care and cure of cancer. In 2006, M.D. Anderson was named to the CIO100 list of most innovative IT organizations, to the top 100 of InformationWeek's Top 500, and honored as one of the top 25 connected healthcare facilities by HealthImaging and IT. As the senior IT executive managing a 600+ person IT organization, Dr. Vogel is leading the in-house development of M.D. Anderson's Electronic Medical Record (EMR) with a major focus on the integration of research and clinical data. Dr. Vogel is also Adjunct Assistant Professor in the Department of Biomedical Informatics at Columbia University in New York City.

Previously, Dr. Vogel was Vice President, Healthlink, Inc., in Houston, Texas, where he was a leader on the Advisory Services team. He has also served as Vice-President, Information Services, NewYork-Presbyterian Healthcare System in New York City, responsible for coordinating information services planning and management for the more than thirty hospitals and other health care facilities which collectively form the nation's largest academic medical center-based health system. Dr. Vogel was previously Vice President and Chief Information Officer, Mount Sinai Medical Center, in New York City. He was also formerly at The University of Chicago Hospitals as Chief Information Officer, and as Director, Medical Center Information Services, as Associate Director in the Department of Finance, and as the Senior Executive responsible for Departments of Pharmacy, Clinical and Surgical Laboratories, Radiology and Medical Records.

3:00 pm – 3:30 pm: Coffee Break
Room: Farallon

3:30 pm – 5:00 pm: Concurrent Sessions

(S02) Late Breaking Presentations
Room: Merced AB

Comparative Analysis of Neurological Disorders Focuses Genome-wide Search for Autism Genes
D. Wall, F. Esteban, T. DeLuca, M. Huyck, T. Monaghan, N. Velez de Mendizabal, J. Goñí, I. Kohane, Harvard Medical School

Michigan Molecular Interactions r2: From Interacting Proteins to Pathways
V. G. Tarcea, T. Weymouth, A. Ade, A. Bookvich, J. Gao, V. Mahavisno, Z. Wright, A. Chapman, M. Jayapandian, A. Özgür, Y. Tian, J. Cavalcoli, B. Mirel, J. Patel, D. Radev, B. Athey, D. States and H. V. Jagadish, University of Michigan

Accurate Prediction of Secreted Substrates and Identification of a Conserved Putative Secretion Signal for Type III Secretion Systems
R. Samudrala, University of Washington; F. Heffron, Oregon Health & Science University; J. McDermott, Pacific Northwest National Laboratory

Application of the PORTAL-DOORS System for Use by Clinical Trial Registries
C. Taswell, Global TeleGenetics, Inc.

(S03) Proteins, Molecular Networks and Diseases
Room: Dolores
Track: Computational Approaches to Finding Molecular Mechanisms and Therapies for Disease

A Study on Frequent Co-Expression Networks in Cancers
Y. Xiang, Kent State University; J. Zhang, The Ohio State University; N. Ruan, R. Jin, Kent State University; K. Huang, The Ohio State University

Transcriptional Regulatory Networks Specify Clinical Outcome after Myocardial Infarction
F. Azuaje, Y. Devaux, C. Yvorra, M. Vausort, C. Jeanty, Centre de Recherche Public - Sante; D. Wagner, Centre Hospitalier

PGnet: A Novel Method for Predicting Epigenetic Regulatory Networks in Gene Expression Arrays of Acute Lymphoblastic Leukemia
X. Yang, University of Chicago; J. Xie, State Key Laboratory of Bioelectronics; X. Sun, State Key Laboratory of Bioelectronics; Y. Lussier, Center for Biomedical Informatics & Section of Genetic Medicine

(S04) Phenotypes and Diseases
Room: San Francisco ABC
Track: Relating and Representing Phenotypes and Disease

The Human Phenotype Ontology
S. Köhler, S. Bauer, D. Seelow, D. Horn, S. Mundlos, P. Robinson, Charité Universitätsmedizin Berlin

Carnitine Uptake Deficiency: An Integrated Genotype/Phenotype Database
D. Crockett, University of Utah; F. Calderon, R. Seamons, ARUP Institute for Clinical and Experimental Pathology; J. Mitchell, N. Longo, R. Mao, University of Utah

Effective EHR Phenotyping Strategies: The Importance of Mixed-mode Approaches
P. Peissig, L. Rasmussen, R. Berg, J. Linneman, C. McCarty, J. Starren, Marshfield Clinic Research Foundation

(S05) Methods in Cancer and Genetics
Room: Plaza Ballroom East
Track: Informatics Methods in Genetics Discoveries and Clinical Practice

Evaluating the Accuracy of a Functional SNP Annotation System
T. Shen, University of Washington; C. Carlson, Fred Hutchinson Cancer Research Center; P. Tarczy-Hornoch, University of Washington

A Tuned Cost-sensitive Learning Approach to Predict Breast Cancer Prognosis
A. Djebbari, C. Drummond, Institute for Information Technology, National Research Council Canada

Genomic-Scale Screening for Gene Fusions in Human Solid Tumors by Integrative Biomedical Informatics
X. Wang, National Center for Integrative Bioinformatics & Michigan Center for Translational Pathology, University of Michigan

Lessons Learned from Implementing Translational Research Systems in Breast Cancer, Multiple Myeloma and Acute Myeloid Leukemia
S. Beaulah, InforSense; M. Correll, InforSense; R. Munro, InforSense; J. Sheldon, InforSense

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5:00 pm - 6:30 pm: Poster Session 1
Room: Plaza Ballroom West

Poster titles and authors are listed on pages 22-24

5:00 pm - 6:30 pm: Reception
Room: Farallon

Monday, March 16, 2009

7:30 am - 8:30 am: Continental Breakfast
Room: Farallon

7:30 am - 5:00 pm: Registration Open
Room: Ballroom Foyer West

8:30 am - 10:00 am: Concurrent Sessions

(S06) Human Genetics, SNPs, and Pathways
Room: San Francisco ABC
Track: Informatics Methods in Genetics Discoveries and Clinical Practice

Identification of Novel Alternative Splice Isoforms using Proteomic Informatics with a Modified ECGene Database
R. Menon, D. States, G. Omenn, University of Michigan

The Multiplex Initiative: Developing a Computational Infrastructure for Studying the Impact of Personalized Genetic Testing
A. Baxevanis, M. Fredriksen, G. Gibney, D. Kanney, National Institutes of Health; N. Maddy, Henry Ford Health System; R. Pardee, E. Larson, R. Reid, Group Health Cooperative; S. Alford, Henry Ford Health System; C. McBride, L. Brody, National Institutes of Health

Computational Identification of Candidate Regulatory SNPs
V. Marinescu, University of Utah Medical Center; I. Kohane, Children's Hospital Boston; A. Riva, University of Florida

Powerful, Flexible, and Efficient Multilocus Genome-wide Association Testing Reveals Pathways Involved in Parkinson Disease
D. Shriner, National Institutes of Health; L. Vaughan, University of Alabama at Birmingham

(S07) Integrative Tools in Translational Research (Grid Focus)
Room: Plaza Ballroom East
Track: Informatics Concepts, Tools, and Techniques to Enable Integrative Translational Research

Adoption and Adaptation of caGrid for CTSA
S. Hastings, S. Oster, S. Langella, C. Melean, T. Borlawsky, R. Dhavel, P. Payne, The Ohio State University

Virtualizing XML Resources As caGrid Data Services
T. Pan, J. Permar, A. Sharma, D. Ervin, The Ohio State University; T. Kurc, J. Saltz, Emory University

Integrating Tools and Data using the NCIBI Suite of Tools
J. Cavalcoli, Y. Ikeda, B. Mirel, H. Jagadish, G. Omenn, B. Athey, University of Michigan

Agent Based Modeling Supporting the Migration of Registry Systems to Grid Based Architectures
M. Cryer, L. Frey, University of Utah

(S08) Understanding Diseases with Human or Animal Genomes
Room: Merced AB
Track: Dissecting Disease through the Study of Organisms, Evolution, and Taxonomy

ExpressionCombiner: A Web-based Tool for Cross-platform Analysis of Gene Expression Data
J. Kim, E. Pitzer, Brigham and Womens Hospital; P. Galante, Ludwig Institute for Cancer Research; C. Hinske, Brigham and Womens Hospital; W. Kuo, Harvard School of Dental Medicine; L. Ohno-Machado, Brigham and Womens Hospital

Patterns in the Human Genome: Discovery with a Highly Scalable and Flexible Suite of Tools
M. Ganapathiraju, A. Mitchell, T. Mohamed, University of Pittsburgh School of Medicine; K. Motwani, Indian Institute of Science

A Pharmacokinomics Study for Prediction of Molecular Mechanisms Underpinning the Side Effect of Kinase Inhibitors
Y. Huang, X. Yang, M. Crowson, J. Li, M. Maitland, Y. Lussier, University of Chicago

(S09) Featured Session: Developments in International and Domestic HICT Policy
Room: Dolores

Development of a Coordinated e-health Research Agenda- the UK Experience
Alan Doyle, The Wellcome Trust

This presentation will describe the efforts UK research funders are making to develop a common strategy to exploit the new research possibilities offered by the major e-Health investment in this country by the department of health. This covers issues from governance (access) to training/capacity building and will include examples of projects funded so far.

Update from the Office of the National Coordinator on the US Stimulus Bill (HR1)
Charles P. Friedman, Office of the National Coordinator for Health Information Technology, Department of Health and Human Services

President Barrack Obama recently signed HR1--The American Recovery and Reinvestment. HR1 will have significant implications on the profession/field of biomedical and health informatics including health research funding, health information technology (HIT) provisions and incentives, and new privacy requirements contained in the legislation. This session is designed to provide attendees with a late breaking update on federal policy activity from Charles P. Friedman, Deputy National Coordinator in the Office of the National Coordinator for Health Information Technology.

10:00 am - 10:30 am: Coffee Break
Room: Farallon

10:30 am - 12:00 pm: Concurrent Sessions

(S10) Electronic Health Information Exchange to Support Clinical Research Activities and Personalized Medicine
(Panel)
Room: San Francisco ABC
Track: Informatics Methods in Genetics Discoveries and Clinical Practice

G. Downing, Department of Health and Human Services
R. Kush, CDISC
K. Buetow, National Cancer Institute
A. Oliva, FDA Center for Drug Evaluation and Research

Frontiers of biomedical research are now dominated by the application of genomic sciences and technologies to understand the mechanisms of disease and support targeted approaches to interventions. Underpinning the pathway toward personalized medicine are electronic health information systems that connect the phenotypic and genotypic manifestations of disease and disease predisposition. Pharmacogenomics and genome-wide association studies represent the first wave of genetic information with relevance to clinical applications, but many other applications are anticipated to follow. The use of electronic health records and personal health records are critical assets in the clinical research enterprise in establishing meaningful understandings of the relations among biological measurements, disease pathways, processes, drug responses, and health outcomes. Many initiatives in clinical research are emerging to bring standards, systems architecture, and network data exchanges of the health care delivery system in alignment to support clinical research and establish a seamless continuum from clinical outcomes to molecular discovery to clinical research and back to clinical practice. While the ability to resolve the meaning of individual differences in health and disease is not yet at hand, strategic approaches are being taken to maximize the underutilized potential of patient information, both individually and in the aggregate, to achieve this goal.

(S11) GWAS to PheWAS: Using EMR-derived Phenotypes for Discovery of Relationships between Genotypes and Clinical Events (Panel)
Room: Dolores
Track: Informatics Methods in Genetics Discoveries and Clinical Practice

D. Masys, Vanderbilt University School of Medicine
J. Pulley, Vanderbilt University School of Medicine
J. Denny, Vanderbilt University School of Medicine
B. Malin, Vanderbilt University

Genetic variation contributes to phenomena of interest for personalized medicine, including disease susceptibility, therapy responses, and adverse events. High throughput approaches to measuring genetic variation have centered on the identification of a populations with clinical conditions, and use of Genome-wide Association Studies (GWAS) employing hundreds of thousands or millions of

measurements of single-nucleotide polymorphisms and copy number variations. However, electronic medical records may be viewed as a set of 'experiments of nature' that reveal the natural history of populations having particular genetic variants, enabling the possibility of 'Phenome-wide Association Studies' (PheWAS) based on measuring the frequency of all clinical conditions associated with a given genotype. This panel will provide a progress report on the Vanderbilt Genome Electronic Records Project (VGER), built on the nation's largest de-identified DNA biobank (currently containing more than 50,000 samples) and linked to de-identified clinical data on more than 1.6 million individuals. Topics to be addressed include management of the biobank, algorithmic approaches to phenotype identification, and minimizing the re-identification risk of de-identified samples and data. Data will be presented on genetic associations found for several common clinical conditions, and preliminary results from PheWAS analyses for several clinically relevant SNPs.

(S12) Molecular Networks, Proteomics, and Diseases
Room: Plaza Ballroom East
Track: Informatics Methods for the Analysis of Molecular and Clinical Measurements

Infection in the Intensive Care Unit Alters Physiological Networks
A. Grossman, Stanford University; M. Cohen, G. Manley, University of California, San Francisco; A. Butte, Stanford University School of Medicine

Analysis of AML Genes in Dysregulated Molecular Interaction Networks
E. Lee, KAIST; H. Jung, KAIST; P. Radivojac, Indiana University; J. Kim, Samsung Medical Center; D. Lee, KAIST

Towards Large-Scale Sample Annotation in Gene Expression Repositories
E. Pitzer, R. Lacson, C. Hinske, Brigham and Women's Hospital; J. Kim, Brigham and Women's Hospital; P. Galante, Ludwig Institute for Cancer Research; L. Ohno-Machado, Brigham and Women's Hospital

Knowledge Based Variable Selection for Rule Learning on Proteomic Data
J. Lustgarten, S. Visweswaran, W. Hogan, V. Gopalakrishnan, University of Pittsburgh

(S13) From Computational Biology Straight to the Drug? - A Scientific Session led by the International Society for Computational Biology (ISCB)
Room: Merced AB

B. Rost, Columbia University (Session Chair)

From Data to Networks and Understanding Disease in Functional Genomics
O. Troyanskaya, Princeton University

Integrating Diverse Data for Structure Determination of Macromolecular Assemblies
A. Sali, University of California, San Francisco

Augmented Browsing for the Life Scientists
R. Schneider, European Molecular Biology Laboratory

Every drug that comes on the market today received some input from resources developed by computational biology during its discovery and development. Olga Troyanskaya, Andrej Sali, and Reinhard Schneider will join in this session to bridge the gap between research and development as well as the widening cleft between the aspects pertaining to the coarse- grained analysis leading to discovery and the more detailed investigations leading on to the molecular details.

12:00 pm - 1:15 pm: Lunch Break and Sponsored Session

Informatics Tools to Enable Integrative Translational Research
Sponsored by GenoLogics
Room: Plaza Ballroom East

R. Mural, Windber Research Institute
E. Bernstam, School of Health Information Sciences at Houston, University of Texas
B. DiLaura, General Clinical Research Center, Case Western Reserve University

While a closer linkage between clinical and basic research domains will translate into scientific discoveries, there are a number of hurdles to implementing a translational research initiative. The panel of speakers will present their challenges and informatics approaches to deploying their translational research initiatives.

1:30 pm - 3:00 pm: Concurrent Sessions

(S14) Advanced Web Technologies for Translational Informatics across Different Biomedical Domains
(Panel)
Room: Merced AB
Track: Dissecting Disease through the Study of Organisms, Evolution, and Taxonomy

M. Scotch, Yale University
T. Clark, Massachusetts General Hospital
N. Shah, Stanford University
S. Stephens, Eli Lilly and Company
K. Cheung, Yale University

Advanced Web technologies including Semantic Web and Web 2.0, are being used for access, integration, and management of diverse content to support biomedical research. This panel will highlight how different types of advanced Web technologies can support various initiatives across a wide spectrum of biomedical fields. Dr. Scotch and Dr. Cheung will discuss "Advanced Web Technologies to Support Phylogeography for Public Health Research." This presentation will emphasize Web technologies for phylogeography and the integration of phylogenetic, geospatial, and surveillance data for public health research. Mr. Clark will present "Web 2.0 and 3.0 in Biomedical Informatics for Neurodegenerative Disorders." This presentation will highlight advanced Web technologies and the emerging role of scientific Web communities, amongst neurodegenerative researchers. Dr. Pritsker will present "Video-publication to increase efficiency and transparency in biological research." This talk will highlight the development of his online journal (JoVE), to support a video-based approach to scientific publishing to fully capture all dimensions of biomedical research. Dr. Stephens will present "Semantic Web to Support Pharmaceutical Research," and describe how Semantic Web approaches can be used to provide a flexible model for integrating and analyzing genotypic and phenotypic data to support pharmaceutical research.

(S15) Computations Underpinning Molecular Mechanisms of Diseases
Room: San Francisco ABC
Track: Computational Approaches to Finding Molecular Mechanisms and Therapies for Disease

Combined Knowledge-based and Physics-based Analysis to Identify Mutations Altering Influenza Host-receptor Binding
P. Kasson, V. Pande, Stanford University

PAPAyA: A Platform for Breast Cancer Biomarker Signature Discovery and Evaluation and Assessment
A. Janevski, S. Kamalakaran, N. Banerjee, V. Varadan, Y. alSafadi, N. Dimitrova, Philips Research NA

Mining to Find the Lipid Interaction Networks Involved in Ovarian Cancers
C. Baker, R. Kanagasabai, W. Ang, Institute for Infocomm Research; H. Low, M. Wenk, A. Fernandis, National University of Singapore; M. Choolani, K. Narasimhan, National University Health System

Automatically Classifying Sentences in Full-Text Biomedical Articles into Introduction, Methods, Results and Discussions
S. Agarwal, H. Yu, University of Wisconsin-Milwaukee

(S16) Text Mining and Ontology for Molecular and Clinical Discoveries
Room: Plaza Ballroom East
Track: Informatics Concepts, Tools, and Techniques to Enable Integrative Translational Research

PubAtlas: Literature Mapping with a "BLAST" for PubMed
D. Parker, W. Chu, F. Sabb, R. Bilder, UCLA

Prioritized Genes for Translational Research on Comorbidity of Bipolar Disorder with Substance Abuse
R. Isokpehi, Jackson State University; S. Lewis, Langston University; W. Ayensu, Jackson State University; T. Gerald, North Carolina Central University

Natural Language Query in the Biochemistry and Molecular Biology Domains Based on Cognition Search
E. Goldsmith, UTSW Medical Center at Dallas

Translational Systems Genomics: Ontology and Imaging
S. Chen, Partner Institute of Computational Biology; Y. Wang, University of Missouri-Kansas City

(S17) Integrative Tools in Translational Research
Room: Dolores
Track: Informatics Concepts, Tools, and Techniques to Enable Integrative Translational Research

The Open Biomedical Annotator
C. Jonquet, N. Shah, M. Musen, Stanford University

Structural Similarity Assessment for Drug Sensitivity Prediction in Cancer
P. Shivakumar, M. Krauthammer, Yale University

Conceptual Dissonance: Evaluating the Efficacy of Natural Language Processing Techniques for Validating Translational Knowledge Constructs
P. Payne, A. Kwok, R. Dhaval, T. Borlawsky, The Ohio State University

Empowering Knowledge Sharing on Betalactamases Research
L. Rodriguez-R, R. Mantilla Anaya, Universidad Nacional de Colombia; L. Falquet, Swiss Institute of Bioinformatics; M. Reguero-Reza, E. Barreto-Hernández, Universidad Nacional de Colombia

3:00 pm – 3:30 pm: Coffee Break
Room: Farallon

3:30 pm - 5:00 pm: Plenary Session

(S18) Keynote Presentation
Room: Plaza Ballroom East

Using Cancer Interactome for Therapeutic Target and Associated Biomarker Discovery

Andrea Califano, Columbia University

Dr. Andrea Califano received the Laurea in Physics (magna cum laude) on the study of the chaotic behavior in high-dimensional dynamical systems from the University of Florence, Italy, in 1985. He was first a Research Associate at the Istituto Nazionale di Ottica in Florence, Italy, and then a postdoc in the Information Mechanic Group at the Massachusetts Institute of Technology, Cambridge.

From 1986 to 1990, he was a Research Staff Member in the Exploratory Computer Vision Group at the IBM T.J. Watson Research Center. In 1990 Dr. Califano started the IBM research initiative in Computational Biology, which culminated with the creation of the IBM Computational Biology Center in 1997, a worldwide organization that he directed until his departure. The center's activities spanned bioinformatics, chemo informatics, protein structure prediction, and the modeling/simulation of complex biological system.

In 2000 he co-founded First Genetic Trust, Inc, a privately funded startup company, as Executive VP and Chief Technology Officer. Under his leadership, FGT built the first GxP compliant, integrated clinical-genomic trial management system and conducted several large scale Pharmacogenomic studies.

Finally, in 2003, he was appointed Professor of Biomedical Informatics at Columbia University, where he is currently Director of the Center for the Multiscale Analysis of Genetic Networks (MAGNet) – one of seven NIH-funded National Centers for Biomedical Computing, – Associate Director for Bioinformatics of the Herbert Irving Comprehensive Cancer Center (HICCC), and co-Director of the Center for Computational Biology and Bioinformatics (C2B2).

5:00 pm - 6:30 pm: Poster Session 2
Room: Plaza Ballroom West

Poster titles and authors are listed on pages 24-27

5:00 pm - 6:30 pm: Reception
Room: Farallon

Tuesday, March 17, 2009

7:30 am - 8:30 am: Continental Breakfast
Room: Farallon

7:30 am - 2:00 pm: Registration Open
Room: Ballroom Foyer West

8:30 am - 10:00 am: Concurrent Sessions

(S19) NLP and Ontology for Translational Research
Room: San Francisco ABC
Track: Relating and Representing Phenotypes and Disease

Toward an Ontological Treatment of the Initiation, Manifestation, Recognition and Representation of Disease
R. Scheuermann, U.T. Southwestern Medical Center; B. Smith, University at Buffalo

A Controlled Vocabulary to Represent Sonographic Features of the Thyroid and its application in a Bayesian Network to Predict Thyroid Nodule Malignancy
Y. Liu, A. Kamaya, T. Desser, D. Rubin, Stanford University

Applying NLP methods to Large Repositories of Electronic Clinical Documents to extract Phenotypic Information: Where Should We Start the Search?
B. South, University of Utah, Division of Clinical Epidemiology; S. Shen, M. Jones, University of Utah; J. Garvin, Philadelphia VA Medical Center; M. Samore, University of Utah; W. Chapman, University of Pittsburgh; A. Gundlapalli, University of Utah School of Medicine

Integrating Clinical Data into the i2b2 Repository
A. Abend, B. Johnson, D. Housman, Recombinant Data Corp

(S20) Translational Research Support and Education: A Library-Based Approach (Panel)
Room: Plaza Ballroom East
Track: Informatics Concepts, Tools, and Techniques to Enable Integrative Translational Research

I. Kohane, Harvard Medical School
K. Butter, University of California San Francisco
D. Osterbur, Harvard Medical School
J. Song, University of Michigan
K. Holmes, Washington University in St. Louis School of Medicine
Advancements in translational medicine have prompted a critical need for solutions which support information dissemination and facilitate a fluid exchange of data in a clinical research setting. Medical libraries provide information resources and technology in support of educational, research, and patient care objectives and are therefore particularly well-positioned to offer instructional resources and support services which enhance the flow of information in the translational research environment. This panel will highlight perspectives from two library directors as well as two bioinformationists to compare and contrast some of the successful strategies and partnerships enjoyed at different translational research centers. Topics to be addressed include a discussion of the role of libraries in meeting the changing information needs of clinical and research communities, examples of how new library-based education and support programs might be developed, and also the library's increasing role in fostering and supporting collaborative efforts on campus. Library directors will share their vision for library-based services and programming and discuss the details of their programs. Bioinformationists will discuss specific details about their varied roles at translational research centers and share their unique perspective about partnering with researchers and clinicians to bridge the gap between bench and bedside.

(S21) Informatics Concepts, Tools, and Techniques to Enable Integrative Translational Research
Room: Dolores
Track: Informatics Concepts, Tools, and Techniques to Enable Integrative Translational Research

Towards Interoperable Reporting Standards for Omics Data - Hopes and Hurdles
S. Sansone, EMBL-EBI; P. Rocca-Serra, EMBL-EBI, The European Bioinformatics Institute

Using Personal Health Records for Automated Clinical Trials Recruitment: the ePaIRing Model
A. Wilcox, K. Natarajan, C. Weng, Columbia University

Using the Weighted Keyword Model to Improve Information Retrieval for Answering Questions Posed by Physicians
H. Yu, Y. Cao, University of Wisconsin-Milwaukee

Consistent Visualizations of Changing Knowledge
H. Tipney, University of Colorado and Health Sciences Center; R. Schuyler, University of Colorado and Health Sciences Center; L. Hunter, University of Colorado and Health Sciences Center

(S22) Molecular Analyses and Translational Discoveries
Room: Merced AB
Track: Informatics Methods for the Analysis of Molecular and Clinical Measurements

An Information-theoretic Approach to the Phenome
D. Albers, G. Hripcsak, Columbia University

Prediction of Heart Failure after Myocardial Infarction through Integrative Bioinformatics
Y. Devaux, F. Azuaje, C. Yvorra, M. Vausort, C. Jeanty, Centre de Recherche Public - Sante; D. Wagner, Centre Hospitalier

Classification and Subspace Selection of Multiple Biomedical Time-Series via Ensemble Learning
P. Harrington, University of Michigan; A. Rao, Carnegie Mellon University; A. Hero, University of Michigan

Accelerating Translation Research with a Comprehensive Informatics Solution that Connects Discovery and Clinical Data
R. Mural, Windber Research Institute; J. DeGreef, GenoLogics Life Sciences

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10:00 am - 10:30 am: Coffee Break
Room: Farallon

10:30 am - 12:00 pm: Concurrent Sessions

(S23) caBIG® Enterprise Support Network: Knowledge Centers (Panel)
Room: Merced AB
Track: Dissecting Disease through the Study of Organisms, Evolution, and Taxonomy

J. Saltz, Emory University
J. Permar, The Ohio State University
R. Freimuth, Mayo Clinic; R. Annechiarico, Duke University
Z. Li, Columbia University; D. Mulvihill, Washington University
K. Smith, University of Michigan

The Cancer Biomedical Informatics Grid (caBIG®) is an NCI-sponsored initiative focused on supporting 21st century biomedical research. The program aims to create a voluntary network of cancer centers and other biomedical research institutions to facilitate information sharing and collaborative studies. As part of the evolution towards enterprise capability, the Enterprise Support Network has been established to help institutions adopt caBIG® tools and infrastructure. A key part of the ESN is knowledge centers aligned with specific domain areas. Presently, these domain areas and associated technologies are: 1) Grid computing and the caGrid middleware, 2) Controlled Vocabularies and related tools, 3) Clinical Trials Management Systems, 4) Molecular Analysis Tools, 5) Tissue/Biospecimen Banking and Technology Tools, and 6) Data Sharing and Intellectual Capital. The knowledge centers

offer expertise, knowledge resources, and tools in their respective areas. While the technologies and frameworks supported by the knowledge centers have been mainly motivated by use cases from the caBIG® community, they are applicable to other fields of biomedicine. The purpose of this panel is to introduce these frameworks and tools and discuss both how they can be used by the broader research community and how the knowledge centers can collaborate with the research community.

(S24) Personalized Clinical Practice and Genetic Knowledge
Room: Plaza Ballroom East
Track: Informatics Methods in Genetics Discoveries and Clinical Practice

Analysis of a Computerized Genealogy Linked to State-wide Cancer Data to Define Risks for Cancer Among Inbred Individuals
L. Cannon-Albright, University of Utah

Composite Patient Reports: A Laboratory Informatics Perspective and Pilot Project for Personalized Medicine and Translational Research
A. Gundlapalli, University of Utah School of Medicine; J. Delgado, B. Jackson, G. Tricot, H. Hill, University of Utah

Integrating Automated Workflows, Human Intelligence and Collaboration
B. Mirel, University of Michigan

An Approach to Question Answering in the Context of Genomic Medicine
C. Overby, P. Tarczy-Hornoch, University of Washington; D. Demner-Fushman, Lister Hill National Center for Biomedical Communications, National Library of Medicine, NIH, DHHS

(S25) Capturing Knowledge that Spans the Translational Gap: What is Needed and Why? (Panel)
Room: San Francisco ABC
Track: Dissecting Disease through the Study of Organisms, Evolution, and Taxonomy

L. Hirschman, The MITRE Corporation
L. Hunter, University of Colorado, Denver School of Medicine
Y. Lussier, University of Chicago; D. States, University of Michigan
C. Wu, Georgetown University Medical Center
The challenge of translational research is literally to translate between the world of cellular and molecular biology and the world of clinical medicine and public health. Translational research is by its nature multidisciplinary. As a result, translational research projects require a representation that captures all of the aspects of the project. Examples include linking the human microbiome to individuals' medical history, associating individual case histories with disease surveillance or translating from whole genome association to clinical disease risk. Much of the 'primary' information is captured in natural language, often in vocabularies specific to the subdiscipline. To link these disparate sources of information, there is a need for representations (ontologies and terminologies) that relate concepts across these disciplines. An important challenge is to maintain utility and usability while at the same time capturing the necessary breadth of representation. Often, individual scientists may be unfamiliar with some aspects of the overall problem, so the representational framework should be widely accepted and easily learned and communicated. Stability and standardization are also critical; individual scientists are often involved in multiple projects, and increasingly, projects involve pooling data collected across multiple sites.

(S26) Interpretation of Mutations with Semantic Support - A Scientific Session led by the International Society for Computational Biology (ISCB)
Room: Dolores

C. Baker, University of New Brunswick, Canada
Y. Lussier, University of Chicago
B. Rost, Columbia University

Description: Annotation of mutations with their impact on phenotypic expression is crucial to the understanding of genetic mechanisms, biological processes and complex diseases. Despite the proliferation of rich sources of literature and databases describing the impacts of mutations, association studies fail to deliver linkage to phenotypes, and contribute only weakly to generating novel hypotheses. This session will explore the status quo and overlap between (i) extraction, storage and reuse of genotype-phenotype information, (ii) semantic infrastructure for phenotype description and the application of phenotype ontologies, (iii) existing efforts to predict the impacts of un-annotated mutations.

12:00 pm - 1:30 pm: Lunch Break

1:30 pm - 3:00 pm: Concurrent Sessions

(S27) Biomolecular Network and Imaging for Translational Research
Room: Merced AB
Track: Computational Approaches to Finding Molecular Mechanisms and Therapies for Disease

A Systems Biology Approach to the Identification and Analysis of Transcriptional Regulatory Networks in Osteocytes
A. Dean, University of Texas at San Antonio; S. Harris, University of Texas Health Science Center at San Antonio; J. Ruan, University of Texas at San Antonio

Transcriptional Diagnosis by Bayesian Networks
H. Chang, M. Ramoni, Harvard Medical School

Feature Selection for fMRI-based Deception Detection
B. Jin, A. Strasburger, Medical University of South Carolina; S. Laken, Cephos Corp.; A. Kozel, University of Texas Southwestern Medical Center; K. Johnson, M. George, X. Lu, Medical University of South Carolina

Network Analysis of Genes Regulated in Renal Diseases: Implications for a Molecular-Based Classification
S. Bhavnani, F. Eichinger, S. Martini, P. Saxman, M. Kretzler, University of Michigan

A Comparative Study of Metabolic Network Topology between a Pathogenic and a Non-Pathogenic Bacterium for Potential Drug Target Identification
D. Perumal, Nanyang Technological University, Singapore

(S28) Semantics and Annotations in Translational Research
Room: Dolores
Track: Informatics Concepts, Tools, and Techniques to Enable Integrative Translational Research

MultiNets: A Web Server for Integrative Analysis of Multiple Networks from Multiple Datasets
S. Liang, M. Zhang, University of Cincinnati; B. Hu, J. Li, University of Wuhan; L. Lu, University of Cincinnati, Cincinnati Children's Hospital Medical Center

Comparing Concept Recognizers for Ontology-Based Indexing: MGREP vs. MetaMap
N. Bhatia, N. Shah, D. Rubin, A. Chiang, M. Musen, Stanford University

A Semantic Image Annotation Model to Enable Integrative Translational Research
D. Rubin, Stanford University; P. Mongkolwat, Northwestern University; D. Channin, Northwestern University

Evaluation of a Large-Scale Biomedical Data Annotation Initiative
R. Lacson, E. Pitzer, C. Hinske, Brigham and Women's Hospital; P. Galante, 2Ludwig Institute for Cancer Research; L. Ohno-Machado, Brigham and Women's Hospital

(S29) Methods in Translational Bioinformatics
Room: Plaza Ballroom East
Track: Relating and Representing Phenotypes and Disease

Extraction of Conditional Probabilities of the Relationships between Drugs, Diseases, and Genes from PubMed Guided by Relationships in PharmGKB
M. Theobald, N. Shah, J. Shrager, Stanford University

Characterizing Environmental and Phenotypic Associations using Information Theory and Electronic Health Records
X. Wang, G. Hripcsak, C. Friedman, Columbia University

Development of an Agile Knowledge Engineering Framework in Support of Multi-Disciplinary Translational Research
T. Borlawsky, R. Dhaval, S. Hastings, P. Payne, The Ohio State University

Multi-Criteria Decision Making Approaches for Quality Control of Genome-Wide Association Studies
A. Malovini, University of Pavia; C. Rognoni, University of Pavia; A. Puca, IRCCS Multimedica; R. Bellazzi, University of Pavia

(S30) Late Breaking Presentations
Room: San Francisco ABC

Estimation of the Warfarin Dose with Clinical and Pharmacogenetic Data
H. Sagreiya on behalf of The International Warfarin Pharmacogenetics Consortium, Stanford University

BioProspecting the Bibleome: Adding Evidence to Support the Inflammatory Basis of Cancer
P. Elkin, Mayo Clinic College of Medicine and Mount Sinai School of Medicine; A. Frankel, E. Liebow-Liebling, J. Elkin, M. Tuttle, B. Trusko, M. Pittelkow, Mayo Clinic College of Medicine; S. Brown, Vanderbilt University

Distributed XQuery-based Integration and Visualization of Multimodality Brain Mapping Data
L. Detwiler, D. Suciu, J. Franklin, E. Moore, A. Poliakov, E. Lee,University of Washington; D. Corina, University of California at Davis; G. Ojemann, J. Brinkley, University of Washington

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3:00 pm – 3:30 pm: Coffee Break
Room: Farallon

3:30 pm - 5:00 pm: Closing Plenary Session

(S31) Closing Session
Room: Plaza Ballroom East

Yves Lussier, University of Chicago

Translational Bioinformatics Year in Review
Russ Altman, Stanford University

Description: 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 the public-release of the first human diploid genome, as well as tens of thousands of individuals participating in genome-wide association studies. This session will review a sample of notable events that have occurred in the past twelve months. Included will be new findings from the published literature, achievements in the application of bioinformatics, changes in public policy and government, and emerging new methodologies. The implications of these events for the future of Translational Bioinformatics and clinical practice will be addressed.

Russ B. Altman is Professor of Bioengineering, Genetics, and Medicine (and Computer Science, by courtesy), Chairman, Department of Bioengineering, and Director, Biomedical Informatics Training Program at Stanford University. He is a Past-President of International Society of Computational Biology and a Fellow in the American College of Medical Informatics among his many honors.

Poster Session 1 (Sunday)

Track: Informatics Methods for the Analysis of Molecular and Clinical Measurements

Ontology-Based eXtensible Data Model (OBX) (Board #1)
M. Kong, UT Southwestern Medical Center; C. Dalke, Northrop Grumman IT; Y. Qian, J. Cai, UT Southwestern Medical Center; P. Dunn, J. Wiser, Northrop Grumman IT; D. Karp, R. Scheuermann, UT Southwestern Medical Center

Towards an Epistemological Model for Automated Reasoning Systems in Genome-wide Studies (Board #2)
A. Nuzzo, University of Pavia; A. Riva, University of Florida; M. Stefanelli, R. Bellazzi, Università di Pavia

Enterprise-wide Repurposing and Distribution of Medical Record Data Through the i2b2 Software Hive (Board #3)
L. Phillips, M. Mendis, V. Gainer, R. Kuttan, W. Pan, J. Glaser, Partners Healthcare Systems; H. Chueh, Massachusetts General Hospital; G. Weber, Harvard Medical School; I. Kohane, Children's Hospital; S. Murphy, Massachusetts General Hospital

Model of Glioblastoma Multiforme Survival Using Clinical and Somatic Mutation Data (Board #4)
S. Piccolo, L. Frey, University of Utah

The MURDOCK Study: Measurement to Understand Reclassification of Disease Of Cabarrus/Kannapolis (Board #5)
J. Tenenbaum, C. Blach, A. Dunham, S. Feng, M. Gardner, C. Haynes, D. Lobach, J. Lucas, B. McCourt, M. Nahm, J. McCarthy, R. Califf, Duke University School of Medicine

A Web-based System for Automated Identification and Reporting of Common Clinical Serotypes of Salmonella Enterica Utilizing Multiplex PCR Amplification Patterns (Board #6)
Q. Yi, University of Washington; B. Leader, Washington State Department of Health; D. Boyle, PATH; J. Wallace, University of Washington

Track: Computational Approaches to Finding Molecular Mechanisms and Therapies for Disease

Introduction of an Agent-based Framework for Ontology Integration: A Step in the Evolution of Executable Knowledge Representation (Board #7)
G. An, Northwestern University Feinberg School of Medicine; M. Parker, Metascape; S. Christley, University of California, Irvine

GeneSubspace: A Tool for Clustering the Gene Expression Profiles Using Mixture Linear Models (Board #8)
L. Cooper, The Ohio State University; J. Wright, University of Illinois at Urbana-Champaign; Y. Ma, University of Illinois at Urbana-Champaign; K. Huang, The Ohio State University

GenomeScape: A Universal 3D Visualization Tool for Genomic Data (Board #9)
K. Huang, J. Wu, T. Huang, J. Parvin, The Ohio State University

Compositional Data Mining of Complex Genetic Disease Data (Board #10)
B. Keller, Eastern Michigan University; C. Owens, T. Murali, N. Ramakrishnan, Virginia Tech; M. McInnis, University of Michigan

OmniBiomarker: A Translational Biomedical Informatics Application (Board #11)
J. Phan, R. Moffitt, T. Stokes, M. Wang, Georgia Institute of Technology and Emory University

Track: Relating and Representing Phenotypes and Disease

Safety Knowledge Base Integrates Multiple Data Sources (Board #12)
D. Chin, R. Varma, V. Mahuvakar, S. Connolly, J. Vig, J. Shon, Roche Palo Alto

PhenX: Consensus Measures to Facilitate Cross-Study Analyses for Genome-wide Association Studies (Board #13)
C. Hamilton, RTI International; E. Ramos, National Human Genome Research Institute; R. Kwok, D. Wagener, RTI International; W. Harlan, National Library of Medicine; J. Haines, Vanderbilt University

An OWL-based Virtual Medical Record to Support Translational Research (Board #14)
W. Lee, A. Das, S. Tu, Stanford University

An Ontology-Driven Bleeding History Phenotyping System to Pool Data Across Sites (Board #15)
A. Mauer, E. Barbour, N. Khazanov, N. Levenkova, B. Coller, Rockefeller University

Track: Dissecting Disease through the Study of Organisms, Evolution, and Taxonomy

Statistical N-gram Modeling of Genomes for Pattern Discovery (Board #16)
T. Mohamed, University of Pittsburgh; K. Motwani, Indian Institute of Science; A. Mitchell, University of Pittsburgh; M. Ganapathiraju, University of Pittsburgh School of Medicine

Track: Informatics Concepts, Tools and Techniques to Enable Integrative Translational Research

A Hybrid System Design Approach to Enable Translational Research (Board #17)
A. Alaoui, D. Kim, K. Cleary, B. Levine, Georgetown University; S. Byers, Georgetown University Medical Center; P. Shields, Georgetown University; L. Leondaridis, Georgetown University Medical Center

Bioinformatic Quantification of Noggin Inhibition of Osteogenic BMPs (Board #18)
K. Balch, R. Haydon, H. Luu, T. He, University of Chicago

Anvita eReference: Biomedical Knowledge Representation Integrating Science and Medicine (Board #19)
S. Ball, SafeMed; V. Mah, UCLA; A. Ghouri, SafeMed

Integrating Clinical, Mechanistic and Study Design Metadata for Public Sharing of Clinical Trial Results from the Immune Tolerance Network (Board #20)
K. Boyce, Immune Tolerance Network / UCSF

Evaluation of Cardiovascular Risk Assessment Models with Respect to the Clinical Interpretation of Atherosclerosis in a Different Type II Diabetes Cohort (Board #21)
L. Chan, Y. Sun, Hong Kong Polytechnic University

Natural Language Query in the Biochemistry and Molecular Biology Domains Based on Cognition Search (Board #22)
E. Goldsmith, UTSW Medical Center at Dallas

Network Modeling grounded on Information Theory Accurately Predicts Future Research Collaborators (Board #23)
Y. Lussier, University of Chicago

Implementing Metadata Standards in Public Health Information Systems (Board #24)
J. Reid, University of Utah; W. Xu, Utah Department of Health; S. Narus, M. Samore, University of Utah

Grid-Based Federation of Human Studies Data for Translational Research (Board #25)
I. Sim, University of California San Francisco; C. Chute, Mayo Clinic; M. Nahm, Duke Translational Medicine Institute; R. Nagarajan, Washington University, St. Louis; B. Pollock, University of Texas Health Science Center at San Antonio

Implementation of Prototype Biomedical Registries for PORTAL-DOORS (Board #26)
C. Taswell, Global TeleGenetics, Inc.

Patient Discovery with Clinical Specialty Ontologies (Board #27)
P. Tonellato, P. Kos, P. Patil, Harvard Medical School; M. Mullman-Cullere, Partners HealthCare

Finding Temporal Gene Expression Profiles for Exploratory Translational Analysis (Board #28)
G. Tusch, S. Malgi Reddy, Grand Valley State University; M. O'Connor, A. Das, Stanford University

Ontology Based Clinical Query Extraction (Board #29)
P. Wennerberg, Corporate Technology

Track: Informatics Methods in Genetics Discoveries and Clinical Practice

Detection of Multiple-way Epistatic Gene Effects in Affected Sibling Pairs (Board #30)
J. Hulet, K. Allen-Brady, J. Facelli, University of Utah

Design of Integrated Translational Bioinformatics Systems (Board #31)
B. Mirel, University of Michigan; B. Keller, Eastern Michigan University; M. Peleg, Stanford University; X. Cui, University of Alabama at Birmingham

Bayesian Combinatorial Partitioning For Detecting Interactions Among Genetic Variants (Board #32)
S. Visweswaran, A. Wong, University of Pittsburgh

Associations of Beta 2-Adrenergic Receptor Polymorphisms with Diseases: A Concept Proof for Phenome-Wide Association Studies (Board #33)
C. Weng, Columbia University; R. Smiley, Columbia University; P. Flood, Columbia University; G. Hripcsak, Columbia University

Poster Session 2 (Monday)

Track: Informatics Methods for the Analysis of Molecular and Clinical Measurements

Identification of Class II Human Leukocyte Antigen (HLA) Supertypes (Board #1)
J. Chung, C. Moore, J. Sidney, J. Greenbaum, A. Sette, B. Peters, The La Jolla Institute for Allergy and Immunology

A Visual Environment for Complex Computational Workflow Design for Molecular Biologists (Board #2)
M. Fursov, A. Varlamov, Center of Information Technologies "UniPro", Russia; O. Novikova, Institute of Cytology and Genetics, Russia

Bioinformatics Framework for the Analysis and Interpretation of Metabolomic Data (Board #3)
A. Karnovsky, University of Michigan; A. Ade, National Center for Integrative Biomedical Informatics; C. Beecher, University of Michigan

Deploying the Cancer Biomedical Informatics Grid (caBIG®): Taking More than a Village to Build a Network (Board #4)
M. Keller, Booz Allen Hamilton

Assembly and Visualization of Lymphoblast Transcriptome (Board #5)
R. Kramer, University of Missouri-Columbia; K. Taylor, H. Shi, C. Caldwell, D. Xu, University of Missouri

Track: Computational Approaches to Finding Molecular Mechanisms and Therapies for Disease

Pattern Discovery in Breast Cancer Specific Protein Interaction Network (Board #6)
J. Chen, Indiana University - Purdue University Indianapolis

Using Patient's Clinical Characteristics To Examine Functional Patterns In Regulatory Pathways (Board #7)
K. Ma, Purdue University; S. Ragg, Indiana University; G. Schadow, Indiana University; I. Ott, Technical University of Munich; O. Vitek, Purdue University

Combined Computational-Experimental Analyses of Selected Metabolic Enzymes in Pseudomonas Species (Board #8)
D. Perumal, Nanyang Technological University, Singapore

Knowledge Generation Using Informed Bioinformatic Workflows for Genome Wide Association Hits: Functional Discovery and Clinical Relevance (Board #9)
D. Ross, Celera

Modeling and Characterization of Disease Associated Sub-networks in the Human Interactome Using Machine Learning (Board #10)
L. Sam, G. Michailidis, University of Michigan

Track: Relating and Representing Phenotypes and Disease

Towards a Policy Framework for Supporting Inter-institutional Biorepository Data Sharing (Board #11)
N. Anderson, K. Fryer-Edwards, D. Freeman, S. Fullerton, University of Washington

Security Frameworks Protecting Clinical Data (Board #12)
M. Keller, D. Smith, Booz Allen Hamilton

Intelligent Character Recognition for Phenotyping Cataract Types (Board #13)
L. Rasmussen, R. Berg, J. Linneman, P. Peissig, C. McCarty, J. Starren, L. Chen, C. Waudby, Marshfield Clinic Research Foundation

Track: Dissecting Disease through the Study of Organisms, Evolution, and Taxonomy

Pattern Landscape of the Human Genome (Board #14)
A. Mitchell, University of Pittsburgh; M. Ganapathiraju, University of Pittsburgh School of Medicine; T. Mohamed, University of Pittsburgh; K. Motwani, Indian Institute of Science

Track: Informatics Concepts, Tools, and Techniques to Enable Integrative Translational Research

A Sophisticated Analysis Toolkit for Translational Oncology Xenograft Studies (Board #15)
B. Alicke, D. Caulder, S. Gould, B. Gunter, N. Lewin-Koh, S. Ross, V. Ramaswamy, J. Tien, K. Woods, Genentech

Clustering the Interacting Molecular and Clinical Atherosclerosis Risk Factors using Principal Components Analysis (Board #16)
L. Chan, Hong Kong Polytechnic University

Q-IHC: A Tissue Image Quantification Tool for Translational Cancer Research (Board #17)
Q. Chaudry, S. H. Raza, C. Jaybhaye, S. Kothari, Georgia Institute of Technology; R. M. Parry, M. Wang, Georgia Institute of Technology and Emory University

Resolving Terminology Issues for a Clinical Research Data Warehouse (Board #18)
J. Cimino, E. Ayres, L. Remennik, NIH Clinical Center

The Cancer Therapy Evaluation Program (CTEP) (Board #19)
S. Friedman, G. Redmond, S. Finnigan, Cancer Therapy Evaluation Program, NIH;
Sudhir Raju; Kumar Chandran, Capital Technology Information Services, Inc. (CTIS); Jeff Abrams, Cancer Therapy Evaluation Program, NIH

Building the Missing Link: Tissue and Clinical Data Integration (Board #20)
J. Kamal, J. Ding, F. Liu, S. Erdal, J. Ramaradjou, S. Jewell, The Ohio State University Medical Center

Genome Data into Cloned Whole Clinical Database -Quick and Safe Tool for Genomic Study (Board #21)
M. Kimura, T. Furuta, S. Tani, Hamamatsu University

The National Cancer Institute's Cancer Biomedical Informatics Grid® (caBIG®): Open Source Tools to Facilitate Integrative Cancer Research (Board #22)
J. Klemm, C. Andonyadis, A. Basu, I. Fore, National Cancer Institute; A. Floratos, Columbia University; S. Goldstein, Sapient; S. Madhavan, NCI Georgetown University; P. Covitz, NCIMDS Nordion; G. Komatsoulis, NCI

Catalyst Portal Architecture for Accelerating Translational Research (Board #23)
D. MacFadden, G. Weber, M. Palchuk, M. Cervone, A. McCray, Harvard Medical School; I. Kohane, Children's Hospital Boston

Rembrandt: An Integrative Translational Research Portal for Brain Tumor Studies (Board #24)
S. Madhavan, Lombardi Comprehensive Cancer Center; J. Zenklusen, Y. Kotliarov, NCI, Center for Cancer Research; H. Sahni, R. Landy, A. Jiang, H. Liu, Science Applications International Corporation (SAIC); S. Jacob, Enterprise Solutions and Consulting (ESAC); A. Basu, M. Heiskanen, K. Buetow, National Cancer Institute (NCI); H. Fine, NCI, Center for Cancer Research

The ABC and Ps of Biomedical Research and the Case for an Integrated Data Repository (Board #25)
K. Mobed, University of California, San Francisco

The Integrated Data Repository: Ontology Mapping and Data Discovery for the Translational Investigator (Board #26)
K. Mobed, University of California, San Francisco

BioInvestigation Index - Standards and Infrastructure for Omics Data at EBI (Board #27)
S. Sansone, EMBL-EBI; P. Rocca-Serra, M. Brandizi, N. Sklyar, E. Maguire, C. Taylor, EMBL-EBI, The European Bioinformatics Institute

A Modular Web Client Architecture for i2b2 (Board #28)
G. Weber, Harvard Medical School, IMBIO, Beth Israel Deaconess Medical Center; N. Benik, Harvard Medical School; D. Housman, P. Emerson, J. Liu, Recombinant Data

The Shared Health Research Information Network (SHRINE): A Prototype Federated Query Tool for Clinical and Translational Data Repositories (Board #29)
G. Weber, Harvard Medical School; S. Churchill, Partners HealthCare System; D. MacFadden, A. McMurry, Harvard Medical School; S. Murphy, Massachusetts General Hospital; D. Nigrin, Children's Hospital Boston; I. Kohane, Children's Hospital Boston

Are Figure Legends Sufficient? Evaluating the Contribution of Associated Text to Biomedical Figure Comprehension (Board #30)
H. Yu, S. Agarwal, University of Wisconsin-Milwaukee; M. Johnston, A. Cohen, Oregon Health & Science University

Variant Name Mapper: Mapping Gene Variant Common Names to RS Numbers (Board #31)
W. Yu, R. Ned, A. Wulf, T. Liu, M. Khoury, M. Gwinn, Centers for Disease Control and Prevention

Track: Informatics Methods in Genetics Discoveries and Clinical Practice

Artificial Neural Networks in Prediction of Secondary Protein Structure Using CB513 Database (Board #32)
Z. Avdagic, Faculty for Electrical Engineering; E. Purisevic, Elektroprivreda; S. Omanovic, Faculty of Electrical Engineering; Z. Coralic, University of California

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S. Devineni, University of Texas at San Antonio

Understanding and Accounting for Dependence in Microarray Gene Expression Data (Board #34)
A. Sinha, M. Markatou, Columbia University

Genomic-Scale Screening for Gene Fusions in Human Solid Tumors by Integrative Biomedical Informatics (Board #35)
X. Wang, National Center for Integrative Bioinformatics, University of Michigan

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