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Final Agenda

Cambridge Healthtech Institute's Seventh Annual

Bio·IT World

CONFERENCE & EXPO '09

April 27 – 29, 2009 • World Trade Center • Boston, MA

Enabling Technology. Leveraging Data. Transforming Medicine.

KEYNOTE PANEL:

The Future of Personal Genomics:

A special plenary panel discussion featuring...

Jorge Conde, Co-Founder & CEO, Knome, Inc.

Robert C. Green, M.D., M.P.H., Professor of Neurology, Genetics and Epidemiology, Boston University School of Medicine and Public Health

John Halamka, M.D., M.S., CIO, Harvard Medical School

Clifford Reid, Ph.D., Chief Executive Officer, Complete Genomics, Inc.

Philip Reilly, Third Rock Ventures

Dietrich Stephan, Ph.D., Co-founder and Chief Science Officer, Navigenics, Inc.

KEYNOTE PRESENTATIONS BY:

Chris Dagdigian, Founding Partner and Director of Technology, BioTeam, Inc.

Clifford Reid, Ph.D., Chief Executive Officer, Complete Genomics, Inc.

Eric E. Schadt, Ph.D., Executive Scientific Director, Genetics, Rosetta Inpharmatics/ Merck Research Labs; Vice President and Chief Scientific Officer, Sage

Event Features:

- Access All Six Tracks for One Price
- Network with 1,500+ Attendees
- Hear 100+ Technology and Scientific Presentations
- Choose from Multiple Pre-conference Workshops
- Attend Bio-IT World's Best Practices Awards
- Connect with Attendees Using CHI's Intro-Net
- Participate in the Poster Competition
- See the Winners of the following 2009 Awards:
  - Benjamin Franklin
  - Best of Show
  - Best Practices
- View Novel Technologies and Solutions in the Expansive Exhibit Hall
- And Much More!

CONCURRENT TRACKS:

Track 1: IT Infrastructure & Operations

Track 2: Informatics for Genomic Medicine

Track 3: Predictive and *in silico* Science

Track 4: Computational Chemistry

Track 5: Clinical and Medical Informatics

Track 6: eHealth Solutions ***NEW***

Featured Presentations by:

caBIG

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Keynote Speakers

Chris Dagdigian, Founding Partner and Director of Technology, BioTeam, Inc.
Formerly of Blackstone Computing and Genetics Institute,Dagdigian specializes in research computing and infrastructure technology issues in the life sciences. A supporter of free software and open standards for life science research, he is a founding member of the Bioperl Project, co-founder of the Bioclusters mailing list and serves on the board of directors as Treasurer of the Open Bioinformatics Foundation. While at Blackstone, Dagdigian was project manager and technical lead for the creation and integration of the Vertex Pharmaceutical VAMPIRE cluster, which replaced an existing Top 500 supercomputer used for cutting edge discovery research and informatics. Dagdigian received his bachelor's degree from Worcester Polytechnic Institute (WPI) in Biotechnology and occasionally finds the time to continue his graduate coursework at Harvard Extension School.

Clifford Reid, Ph.D., Chief Executive Officer, Complete Genomics, Inc.
Dr. Clifford Reid, Chairman and Chief Executive Officer of Complete Genomics, has 25 years of experience in startup and growth companies managing the commercialization of innovative biotechnology and data management technologies. Prior to founding Complete Genomics he founded two software companies, Verity and Eloquent, both of which went public and were subsequently acquired. Dr. Reid earned a B.S. in Physics from the Massachusetts Institute of Technology (MIT), an M.B.A. from the Harvard Business School and a Ph.D. in Management Science and Engineering (MSE) from Stanford University.

Eric E. Schadt, Ph.D., Executive Scientific Director, Genetics, Rosetta Inpharmatics/Merck Research Labs; Vice President and Chief Scientific Officer, Sage
Dr. Schadt joined Rosetta as Informatics Analysis Research Leader in November 1999. He founded Rosetta's Research Genetics department, whose primary mission is elucidating common human diseases using novel integrative genomics approaches based on genetic and molecular profiling data, and has helped define a new field in statistical genetics – the genetics of gene expression. Prior to joining Rosetta, Dr. Schadt was a Senior Research Scientist at Roche Bioscience. He received his B.A. in applied mathematics and computer science from California Polytechnic State University, his M.A. in pure mathematics from UCLA, and his Ph.D. in bio-mathematics from UCLA.

Keynote Panel

The Future of Personal Genomics
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Bio-IT After Dark

Just Added – Networking Event on Monday, April 27th

Since February 2002, BiotechTuesday (http://biotechtuesday.com/) has been bringing together participants in the Boston area biotechnology community each month to network and learn more about the industry. A variety of professionals attend these events, including entrepreneurs, investors, attorneys, scientists, and journalists. No lectures - no agenda. Some call it networking, others just good fun, and the event offers both. Following the close of the Bio-IT conference on Monday evening, be sure to come by and meet up with fellow conference attendees and members of the Boston biotech community for spirited conversation at the Atlantic Beer Garden next door to the convention center at 146 Northern Avenue. Tickets are $20 and can be purchased in advance by credit card at www.acteva.com/booking.cfm?bevaid=180896.

Please see page 16 for a detailed Schedule-at-a-Glance.

2009 Benjamin Franklin Award

The Benjamin Franklin Award for Open Access in the Life Sciences is a humanitarian/bioethics award presented annually by the Bioinformatics Organization to an individual who has, in his or her practice, promoted free and open access to the materials and methods used in the life sciences. Nominations are now being accepted! Full details including previous laureates and entry forms are available at www.bioinformatics.org/franklin/. The winner will be announced Tuesday, April 28.

Best of Show Awards

The Best of Show Awards offer exhibitors an opportunity to distinguish their products from the competition. Judged by a joint team of Bio-IT World magazine editors and leading industry experts in the Exhibit Hall, this Awards program will identify exceptional innovation in technologies used by life science professionals today. Deadline for entry is April 1st so reserve your booth space today! For more information and to download the entry form please visit www.bio-itworldexpo.com.

Best Practices Awards – Call for Entries!

Add value to your Conference & Expo attendance, sponsorship or exhibit package, and further heighten your visibility with the creative positioning offered as a Best Practices participant. The Best Practices Awards identify and showcase outstanding examples of innovative partnerships, technologies and strategies impacting research and drug development. Early bird deadline (no fee) for entry is December 18, 2008 and final deadline (fee) is January 21, 2009. Winners will be selected by a peer review expert panel in early 2009. Bio-IT World will present the Awards for its 2009 competition at a special gala dinner ceremony on April 28, 2009. Full details including previous winners and entry forms are available at www.bio-itworldexpo.com.

CHI's Intro-Net: Networking at its Best!

Maximize Your Experience Onsite at the Bio-IT World Conference & Expo!
The Intro-Net offers you the opportunity to set up meetings with selected attendees before, during and after this conference, allowing you to connect to the key people that you want to meet. This online system was designed with your privacy in mind and is only available to registered session attendees of this event. Registered conference attendees will receive more information on how to access the Intro-Net in the weeks leading up to the event!

Official Publication: Bio-IT World

Lead Sponsoring Publications:
eCliniqua, GEN Genetic Engineering & Biotechnology News, nature, Predictive Biomedicine, Science AAAS, The Scientist

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Assay and Drug Development Technologies, Bentham Science, BioPharm International, BioPhotonics International, Journal of Computational Biology, Current Bioinformatics, Current Computer-Aided Drug Design, ddn, Future Pharmaceuticals, HPCwire, Journal of Bioinformatics and Computational Biology, Mary Ann Liebert, Inc. publishers, MedAdNews, MHT, Molecular Diversity, OBBeC, On-Demand Enterprise, PharmaVOICE, Springer

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Half Day Workshops

Workshop 1: Application of Wikis by Lifescience Organizations (12:30-4:00pm)
Alan Ruttenberg, Principal Scientist, Science Commons
This workshop will explore how life science organizations are utilizing wikis. Participants will learn what has/has not worked, challenges faced, and best practices to help make data and technology integration more efficient.

Workshop 2: Advances in Drug Safety Informatics (12:30-4:00pm)
Albert Gough, Ph.D., Vice President, Discovery Technology, Cellumen, Inc.
Alex Tropsha, Ph.D., Chair, Department of Medicinal Chemistry and Natural Products, University of North Carolina School of Pharmacy
Nigel Greene, Ph.D., Senior Principle Scientist, Toxicoinformatics, Pfizer Global R&D
David Cook, Ph.D., Associate Director, Global Safety Assessment, AstraZeneca UK (tentative)
Kelley Moore, Division of Biostatistics, School of Public Health,University of California, Berkeley
Findings of unexpected toxicity during a clinical trial wrecks havoc on development schedules and budgets. Better approaches are needed to identify toxicity risk at earlier stages of drug development, and informatics can play a greater role than has traditionally been the case. The use of databases, toxicogenomics, text mining and interpretation of more informative *in vitro* assays are just some of the approaches that can with this issue. Informatics can be applied to avoid the inclusion of problematic structures, reduce the risk of continuing to invest in compounds that are likely to cause toxicity, or to help better understand the causes when toxicity appears in order to facilitate structural changes that could minimize the problem. The industry will continue to rely on empirical evidence for drug safety, but better use of informatics can improve results while reducing risks, time and costs.

Workshop 3: Visualization (8:00-11:30am)
Georges Grinstein, Ph.D., Professor & Director, Bioinformatics Program and the Center for Biomolecular and Medical Informatics, University of Massachusetts Lowell
Peter V. Henstock, Ph.D., Statistics & Visualization, Target & Mechanism Informatics, Pfizer Research Technology Center
Participants will learn how visualization techniques in bioinformatics and medical informatics can be applied to the drug discovery process. We will present a taxonomy of visualization, a variety of visualization techniques and tools, and their advantages and limitations. Additionally, we will discuss a number of different applications and software packages and provide live demos to show the capabilities of some of these systems.

Workshop 4: Recent Advances in Molecular Dynamics: Target Elucidation and Ligand Docking (12:30-4:00pm)
Ron Dror, Ph.D., Senior Research Scientist, D. E. Shaw Research
Roy Kimura, Ph.D., Senior Scientist, Computer Assisted Drug Design, Bristol-Myers Squibb
Dorothee Kern, Ph.D., Professor of Biochemistry, HHMI Investigator, Brandeis University
Molecular dynamics (MD) simulations provide a promising method to characterize the conformational changes that are critical to protein function, and may therefore facilitate target selection and ligand design. Thought leaders will present their latest work and challenges they face. Attendees will gain a better understanding of current capabilities and limitations of MD simulations and how they are being applied in practice.

Full Day Workshop

Workshop 5: High Performance Computing & Storage: Trends and Applications (8:00am-4:00pm)

Sponsored by

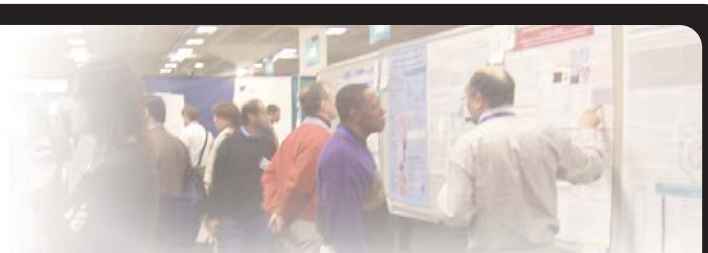
What are your storage and computing strategies during these tough economic times? How are you efficiently managing cost reductions, maximizing efficiencies and maintaining quality? Join thought leaders in this day long workshop to examine high performance computing trends and applications. The morning will discuss various computing technologies including grid, cloud and next generation sequencing. The afternoon will discuss practical applications of computing technologies with real world examples for efficient data storage and analysis.

- *John Halamaka, M.D., M.S., CIO, Harvard Medical School*
- *Jacob Farmer, Chief Technology Officer, Cambridge Computer*
- *John Dey, UNIX Operations Manager, Rosetta Inpharmatics, LLC*
- *Reece Hart, Scientific Manager, Research Computing, Genentech*
- *Rick Franckowiak, Information Technology Director, Johnson & Johnson*
- *Andrew Kaczorek, Eli Lilly and Company*
- *Giles Day, Senior Director BBC Informatics, Pfizer Biotherapeutics & Bioinnovation Center*
- *Stephan Bour, Ph.D., Chief Information Officer, Director, Center for Biomedical Informatics National Heart, Lung, and Blood Institute (NHLBI)*
- *Jason A. Stowe, Founder/CEO, Cycle Computing, LLC*
- *Carter George, Vice President Products, Ocarina Networks*
- *William Van Etten, Ph.D., Founding Partner and Director of Consulting Services, BioTeam, Inc.*
- *George Church, Ph.D., Professor of Genetics, Director of the Center for Computational Genetics, Harvard Medical School*
- *Matthew Trunnell, Manager, Research Computing, Broad Institute of MIT and Harvard*
- *Sujal Patel, Founder, President, CEO -- Isilon*
- *Moderator: Kevin Davies, Ph.D., Editor-in-Chief, Bio-IT World Magazine*

Gain Further Exposure
Present A Poster

7 Reasons Why You Should Present Your Research Poster at Bio-IT World Conference & Expo

- Available to over 1,500 delegates
- Will be seen by leaders from top pharmaceutical, biotech, academic, government institutes,and technology vendors
- Automatically entered in the Poster Competition, where two winners will each receive an American Express Gift Certificate
- Receive $50 off your registration fee
- Published on the event CD
- Displayed in the Exhibit Hall, which attracts the most number of the Event's delegates
- Dedicated poster hours



Poster authors will be available to talk about their research and answer questions during the following times:
Monday, April 27 | 5:00pm – 7:00pm
Tuesday, April 28 | 9:15am - 10:45am & 3:15pm - 3:45pm
Wednesday, April 29| 9:45am – 10:45am & 12:45pm – 2:00pm

Other Poster Viewing Hours Include:
Wednesday, April 29 | 9:45-10:45 am
Please visit www.bio-itworldexpo.com for poster instructions and deadlines.

Track 1:

IT Infrastructure & Operations

Efficiently prepare, acquire, manage, integrate, and analyze data and IT infrastructure/operation activities.

Monday, April 27

4:00 pm Event Chairperson's Opening Remarks

Cindy Crowninshield, Conference Director, Cambridge Healthtech Institute
Keynote Introduction: Rudy Potenzone, Ph.D., WW Industry Technology Strategist for Pharmaceuticals, Microsoft Corporation

4:15 PLENARY KEYNOTE

Research Computing and Infrastructure Technology

Chris Dagdigian, Founding Partner and Director of Technology, BioTeam, Inc.

5:00 Welcome Reception in the Exhibit Hall *Sponsored by* MERCK

Drop off a business card at the CHI Sales Booth for a chance to win 1 of 2 iPods ®!

7:00 Networking Event hosted by BiotechTuesday

Tuesday, April 28

7:30 am Registration and Morning Coffee

8:15 Event Chairperson's Opening Remarks

Phillips Kuhl, Co-founder and President, Cambridge Healthtech Institute
Keynote Introduction: Ken Buetow, Ph.D., Associate Director, Bioinformatics and Information Technology, National Cancer Institute

8:20 PLENARY KEYNOTE

Integrative Genomics

Eric E. Schadt, Ph.D., Executive Scientific Director, Genetics, Rosetta Inpharmatics/Merck Research Labs; Vice President and Chief Scientific Officer, Sage

9:00 Keynote Presentation & 2009 Benjamin Franklin Award

9:30 Coffee Break, Exhibit and Poster Viewing in the Exhibit Hall

Operations: Grids 'n Clouds

10:50 Track Chairperson's Remarks

Gerard Sample, Senior Product Marketing Manager, BlueArc Corporation

11:00 Panel Discussion: Cloud Computing

Chairperson: Jason A. Stowe, Founder/CEO, Cycle Computing, LLC

- *Chris Dagdigian, Founding Partner and Director of Technology, BioTeam, Inc.*
- *Rick Franckowiak, Information Technology Director, Johnson & Johnson*
- *Michael Daoust, Google*
- *David Powers, Associate Information Consultant, Eli Lilly and Company*
- *Deepak Singh, Ph.D., Business Development Manager, Amazon Web Services*

This talk will explore how life sciences is using cloud computing application, its challenges and effectiveness, how money can be saved by an organization, and regulatory compliance. Leading experts will discuss how cloud computing can be used effectively as an external IT service.

12:00 caBIG® in the Trenches - Deploying a Grid Infrastructure *Featured by* caBIG

George Komatsoulis, Ph.D., Deputy Director, Center for Bioinformatics and Information Technology, National Cancer Institute

This presentation will describe the deployment of caBIG® technology and standards at over 50 medical centers across the US. Attendees will learn technical details on how to develop tools that are interoperable with caBIG® and the lessons learned in connecting a wide variety of organizations with differing resources and needs.

12:30 Luncheon Presentation: Microsoft BioIT Alliance: An Update *Sponsored by* Microsoft

Rudy Potenzone, Ph.D., WW Industry Technology Strategist for Pharmaceuticals, Microsoft Corporation

This talk will present the latest activities of the BioIT Alliance, a cross-industry group working to further integrate science and technology as a first step toward making personalized medicine a reality.

1:40 Chairperson's Remarks

Gerard Sample, Senior Product Marketing Manager, BlueArc Corporation

1:45 Ramping Up Your Computational Science to a Global Scale on the Open Science Grid

John McGee, Manager, CI-Development, Renaissance Computing Institute, UNC Chapel Hill

The Open Science Grid (OSG) is the US contribution to the worldwide compute/data infrastructure servicing the needs of High Energy Physicists working on the Large Hadron Collider experiments at CERN. Attendees will gain a perspective of life scientists who have integrated the Open Science Grid into their research and the makeup of a highly functional distributed compute/data infrastructure involving more than 80 sites from across the US.

Operations: Sourcing

2:15 Creating a Global Development Factory to Reduce the Costs of Pharma IT Design and Development for R&D

Robert Maguire, Senior Director MRL-IT Solutions Delivery, MRL-IT Solutions Delivery, Merck

This presentation will explore the sigma approach applied to develop an in- and out-sourcing with in-and off-shorting capabilities, the lessons learned, and the significant benefits and ongoing challenges we face.

2:45 Adjusting Information Flow from In-house HTS to Global Outsourcing Partners

Brian Bissett, Staff Scientist, Molecular Properties, Pfizer

This talk will describe the benefits and pitfalls of working with a single supplier for screening services, methods for determining if reliable data is being generated by an outsourcing partner, and various mechanisms of action for manipulating, transferring, and integrating data into the corporate environment from a foreign entity.

3:15 Refreshment Break, Exhibits and Poster Viewing in the Exhibit Hall

Operations: Sequencing

3:45 Next Generation Sequencing Data Management & Analysis (Panel discussion *Sponsored by* BLUEARC

Moderator : Gerard Sample, Senior Product Marketing Manager, BlueArc Corporation

- *Bruce Martin, Vice President Software, Complete Genomics, Inc.*
- *Melissa Kramer, Scientific Informatics Analyst I, Woodbury Genome Research Center, Cold Spring Harbor Laboratory*
- *Lincoln Stein, Cold Spring Harbor Laboratory (invited)*
- *Matthew Trunnell, Manager, Research Computing, Broad Institute of MIT and Harvard*

You'll get practical information about the analysis, assessment, design, implementation, testing, and support needed to bring a research organization from technology adoption to publication in the next-gen world.

4:45 Storage for Science – Maximizing the Value of Unprecedented Data Growth *Sponsored by* ISILON SYSTEMS

Chris Dwan, Director of Products and Principal Investigator, The BioTeam

This session will focus on advances in DNA sequencing and other bioinformatics-related technologies driving unprecedented data growth; the implications of this data growth for researchers and scientists, as well as its potential to transform modern medicine, and scale-out, file-based storage

architectures as the most compelling solution for maximizing the potential of bioinformatics data.

5:15 **2009 Best of Show Awards in Exhibit Hall**

6:30 **2009 Bio-IT World's Best Practices Awards/Dinner**

6:15 **Exhibit Hall Closes**

Wednesday, April 29

7:00am **HP Petabyte-Scale Storage Solutions for Life Sciences: Mastering the Data Challenge in Life Sciences** *Sponsored by*

Les Fox, Ph.D., Distinguished Technologist
Scalable Computing and Infrastructure, Hewlett Packard Corporation

HP's innovative solutions for management and storage of peta-byte scale data enables researchers to focus on what matters to them - science. Learn about HP innovations including the massively-scalable HP StorageWorks 9100 Extreme Data Storage system, which provides researchers with the storage volume required for instruments that generate terabytes of data per run.

7:30 am **Registration and Morning Coffee**

8:00 **Event Chairperson's Opening Remarks**

Kevin Davies, Ph.D., Editor-in-Chief, Bio-IT World

8:05 **PLENARY KEYNOTE**

Personalized Genomics – The Impact of Large-Scale Human Sequencing Projects

Clifford Reid, Ph.D., Chief Executive Officer, Complete Genomics, Inc.

8:45 **KEYNOTE PANEL**

The Future of Personal Genomics

A special plenary panel discussion featuring:

- *Jorge Conde, Co-Founder & CEO, Knome, Inc.*
- *Robert C. Green, M.D., M.P.H. Professor of Neurology, Genetics and Epidemiology, Boston University School of Medicine and Public Health*
- *John Halamka, M.D., M.S., CIO, Harvard Medical School*
- *Clifford Reid, Ph.D., Chief Executive Officer, Complete Genomics, Inc.*
- *Philip Reilly, Third Rock Ventures*
- *Dietrich Stephan, Ph.D., Co-founder and Chief Science Officer, Navigenics, Inc.*

9:45 **Coffee Break, Exhibit Viewing, Vendor Theater Presentations, and Poster Competition in the Exhibit Hall**

Infrastructure: Collaborations & Social Networking

10:50 **Track Chairperson's Remarks**

Carter George, Vice President Products, Ocarina Networks

11:00 **ELN and Decision Support Informatics Enabling Enterprise, Partnership and CRO R&D Collaboration**

John McCarthy, Vice President, Product Management & Strategy, Symyx Technologies, Inc. *Sponsored by* Symyx

Economic pressures and the need for R&D agility are generating a large industry shift to partnership and outsource strategies with Contract Research Organizations (CRO). These initiatives drive new challenges in scientific information management where scientific workflows extend not only over scientific disciplines and geographical boundaries but also between research organizations. This session highlights some of the primary challenges for deploying electronic notebooks and decision support software across an enterprise with geographic and business partnership boundaries, and how these challenges can be addressed in the new economic climate.

11:30 **Research Informatics a Productivity Booster: The SGC – A Case Study**

Johanna Sagemark, Head of Research Informatics, Structural Genomics Consortium, Karolinska Institute

The workflow implemented at the Structural Genomics Consortium comprising high throughput protein production and crystallization generates vast amounts of data. To keep track of the research pipeline and the status of all projects, an electronic laboratory notebook system (ELN) has been implemented together with a laboratory information management system (LIMS). The latter is configured with a user-friendly GUI that enables fast and intuitive data mining. These tools will be presented together with reflections on productivity benefits, data capture and issues such as intellectual property protection, compliance, long term storage as well as perspectives on system integration.

12:00 **Leveraging Web2.0 Social Networks for Collaborative Drug Discovery**

Barry A. Bunin, Ph.D., Chief Executive Officer and President, Collaborative Drug Discovery, Inc.

Collaborative Drug Discovery (CDD) has created a community based platform that combines traditional drug discovery informatics with Web2.0 features to provide the best of both worlds. These combined capabilities promote inter-group collaborations for open access drug discovery in areas like neglected infectious disease and also facilitate intra-group collaboration in more traditional commercial therapeutic areas like cancer. Four case studies will be used to highlight how community based drug discovery informatics capabilities are transforming academic, and increasingly industrial science in today's more collaborative pharmaceutical research environment.

12:30 **Luncheon in the Exhibit Hall**

2:00 **Exhibit Hall Closes**

1:55 **Chairperson's Remarks**

Carter George, Vice President Products, Ocarina Networks

Infrastructure: Collaborations & Social Networking *(continued)*

2:00 **Deploying Enterprise 2.0 Solutions: Case Studies & Business Challenges**

David Hodgson, Site Head, Research Informatics & Global Head, Group Knowledge Exchange, Roche Pharmaceuticals

Deploying Enterprise 2.0 and search capability into a large life sciences company presents many challenges. Although much of the technology exists already, and results from social network based business models on the internet are compelling, ensuring a positive ROI in the corporate environment can be difficult. Short case studies will be presented that illustrate the provision of workspaces for team collaboration, the use of idea management software for innovation and the prototype of a guided navigation system for domain-based search.

Operations: Data Management and Storage

2:30 **When Science Becomes Business: Visualizing Risk in R&D**

Angela Shen-Hsieh, President and Chief Executive Officer, Visual i|o

Attend this session to learn how interactive reporting systems and data visualization are tools for helping teams and decision-makers evaluate the risks of R&D, and see a demonstration of how different kinds of risk can be visualized.

3:00 **Scientific Intelligence in R&D - Knowledge Integration across Discovery, Pre-clinical, and Clinical Development** *(Joint with Informatics for Genomic Medicine & Clinical and Medical Informatics Tracks)*

John Apathy, Assistant Vice President, Business Systems and Processes - Discovery, PreClinical, and Vaccines, Wyeth

Investments in information systems within Pharmaceutical R&D organizations tend to be made by individual departments or functional units and serve the local purpose of those units. Over time these silo-based approaches lead to real challenges in enabling the exchange of data, information, and knowledge across the various Discovery, Pre-clinical, and Clinical Development domains. At Wyeth, we have been purposefully developing solutions that cut across organizational boundaries and have developed a set of Knowledge Integration solutions that allow senior scientists, study directors, and functional management to find, access, and manage disparate R&D data, information, and knowledge assets. This presentation will provide an overview of the journey undertaken to ensure the right information is available to researchers and management within Wyeth Pre-clinical Research and Development organization at the right time to enable faster decision-making.

3:30 **Service Oriented Architecture – A New Data Sharing Architecture** *(Joint w/Clinical and Medical Informatics & eHealth Solutions Tracks)*

Robert Lundsten, Director of Biorepository, Feinstein Institute for Medical Research

The ability to integrate data from multiple independent data repositories across the North Shore Long Island Jewish Health System's (NSLIJHS) 15 hospitals and many outpatient care centers into a specialized data warehouse environment for analysis and data mining is a daunting process for many reasons. Creating the scaffolding to facilitate data transfers requires many components including a mediating registry and meta data repository, a data warehouse, a federated identity manager, a standards based methods(s), a web-based portal or user interface, and the services management layer. This talk will describe how the North Shore Informatics Group (NSIG) created a pilot framework of a Service Oriented Architecture that integrated and shared data between different data management groups.

4:00 **Conference Adjourns**

Track 2:

Informatics for Genomic Medicine

Apply informatics tools, science and statistics to extract the most knowledge from medical and clinical data for genome analysis, biomarker detection, and target discovery.

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Cindy Crowninshield, Conference Director, Cambridge Healthtech Institute
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9:30 Coffee Break, Exhibit and Poster Viewing in the Exhibit Hall

Biological Data: Modeling & Imaging for Gene Expression

10:50 Track Chairperson's Remarks
Colin Williams, Product Manager, Biology & Bioinformatics and Product Management, PharmaChem, Thomson Reuters

11:00 Going Beyond Genome-Wide Association Studies
Andrew Kasarskis, Ph.D., Scientific Director, Genetics, Merck Research Laboratories
This talk provides an overview of Merck's current approaches to translating genome-wide association studies (GWAS) into clinical practice. GWAS have provided a robust set of replicated associations between DNA variation and clinical traits. However, understanding the mechanism by which DNA variation affects disease is often not straightforward. Adding genetics of gene expression study results into the interpretation of clinical GWAS provides mechanistic insight that can be interpreted in the context of network models, with the goal of building predictive models of disease processes. These models then form the basis for informed selection of new biomarkers and drug targets. Construction of effective models based on high-dimensional biological data places introduces unique problems in computing that demand innovation in hardware, algorithms, and software development processes.

11:30 BORA: Biologically Oriented Repository Architecture for Genomic Medicine
Hugues Sicotte, Ph.D., Assistant Professor of Medical Informatics, Biomedical Statistics and Informatics, Mayo Clinic
The Biologically Oriented Repository Architecture (BORA) mines multiple types of genomics data in the context of clinical information and bioinformatics annotation. Unlike other genomics data mart systems, the BORA system allows arbitrary questions to be asked of the data and goes well beyond the "genome browser"-style of integration that is limited to correlating elements at the same genomics position. The BORA system enables a more mechanistic understanding of complex data sets and can enable the study of the relationships between any genomics data elements, clinical variables, and known or predicted biological relationships.

12:00 Assessment of the Function and Potential Clinical Relevance of Gene Variants from Genome Wide Association Studies Using Workflow-Driven Bioinformatics
David Ross, Ph.D., Director, Computational Biology, Celera

12:30 Making the Most of Your GWAS Data *Sponsored by* ROSETTA BIOSOFTWARE
Michael Rosenberg, Ph.D., Senior Director Professional Services, Rosetta Biosoftware
A growing number of comprehensive genome-wide association (GWAS) data sets is being generated by academic and publicly-funded consortia. Notable examples are the Framingham Heart Study and data released by the Wellcome Trust Case Control Consortium. This abundance of data is creating new opportunities for academic researchers,, and pharmaceutical, biotech and emerging direct-to-consumer diagnostics companies to expand the context and increase the power of their own genetics association research efforts. Organizations are tasked with the formidable challenge of how to make the best use of these data sets, implementing approaches to effectively bring them in-house and integrate with proprietary data. We will address the various opportunities and challenges R&D organizations face when working with public GWAS data. We will discuss how existing and emerging commercial software solutions can help eliminate barriers to extracting scientific value from these data sets and provide examples of data mining approaches.

Biological Data: Modeling & Imaging for Gene Expression *(continued)*

1:40 Chairperson's Remarks
Stuart Tugendreich, Director, Product Management New Solution, Ingenuity Systems

1:45 Cancer Epigenomics: A Systematic Approach to Biomarker Discovery and Computational Optimization
Christoph Bock, Department of Computational Biology, Max Planck Institute for Informatics
The demand for computational support and bioinformatics tools in cancer epigenetics is rapidly increasing, due to complex experimental methods, increasingly genome-wide analysis and the pressure to translate scientific results into clinical practice. Our goal is to develop bioinformatics methodology for addressing these issues, and to implement a set of web services that make powerful algorithms available to typical bench scientists. Recent work on computational epigenetics (performed in conjunction with The Broad Institute) will be presented, highlighting a systematic workflow for optimizing epigenetic biomarker candidates for clinical applications.

2:15 Computational Approaches in Biological Imaging
Jean-Christophe Olivo-Marin, Ph.D., Group Leader, Quantitative Image
We will present the latest innovative tools in computer aided biological imagery and exemplify them on successful projects from different areas of biology like cell biology, infectious diseases, development biology and immunology.

Technology Highlights

2:45 Connecting Public and Internal Data using a Gene- and Sequence-Centric Semantic Integration Framework *Sponsored by* NEXTBIO
Ilya Kupershmidt, Co-founder and Vice President Products, NextBio
Organizations are increasingly looking for ways to leverage combined public and internal data (legacy, current and future) to improve their basic and clinical research programs. NextBio has developed a scientific platform that brings together and correlates large quantities of data from microarray and next-generation sequencing platforms to enable comprehensive and efficient discovery and testing of new hypotheses. In this session we will describe how a semantic integration framework, public and internal gene- and sequence-centric data and a large number of pre-computations enable real time knowledge discovery within NextBio.

3:00 Putting It All Together: The Acceleration of Biomarker Qualification in Drug Discovery *Sponsored by* accelrys®
Jonathan Usuka, Ph.D., M.B.A., Senior Director, Life Sciences, Accelrys, Inc.

3:15 Refreshment Break, Exhibits and Poster Viewing in the Exhibit Hall

Discovery Informatics and Platforms

3:45 You're Using Your Computer Wrong: Semantics in Pharma R&D

Ted Slater, Senior Manager, Pfizer Worldwide Technologies

Most informatics efforts are aimed at data integration, but data integration is insufficient to enhance our ability to accurately predict drug efficacy and safety. To reach the next level in R&D, we must move beyond data integration to the point where computers generate hypotheses. This talk will provide a view of a practical, semantics-based solution which provides for automated reasoning over pharmaceutical knowledge bases, and which has useful emergent properties such as streamlined data interoperability and a universal platform for knowledge management.

4:15 CBIP: Successfully Implementing a Large-Scale Automation and Informatics Platform for Academic Probe Discovery

David DeCaprio, Associate Platform Director for Chemical Biology and Novel Therapeutics, The Broad Institute

Raza Shaikh, Associate Director of Informatics, Chemical Biology Platform, The Broad Institute

Over the past two years, The Broad Institute set out to completely rebuild its high throughput screening and probe discovery platform using state of the art automation and informatics tools. The platform uses an electronic notebook as the rich front-end for recording chemical and biological information integrated with a web-based LIMS system. Our innovative approach to engineering the solution included informatics participating in Factory Acceptance Tests (FAT) and building functionality to align with Site Acceptance Tests (SAT). This approach coupled with just-in-time approach to software engineering has allowed us to build a comprehensive platform. Attendees will learn the issues and decisions involved in building an informatics platform that caters to the needs for a diverse set of processes.

4:45 RISe – Research Informatics System at Elan

Ajay Shah, Ph.D., MBA, PMP, Director of Research Informatics, Elan Pharmaceuticals Inc.

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Research Informatics at Elan has embarked upon the design and implementation of data and application integration platform - RISe. This platform seeks to integrate experimental chemistry and biology databases, computational tools, workflow systems, and knowledge management tools from various in-house and commercial sources. Using agile development methodology, and a blended resource model involving FTEs, contractors and offshore vendor resources, we have been able to rapidly develop a proof of concept & deploy it into production. These systems include biology registration, workflow and inventory management systems for plasmid, antibody and cell lines. We have also implemented a customized compound registration system and an innovative integration of chemistry and biology data. These scientific systems are augmented by a new collaborative environment for research, enriched with research analytics tools.

5:15 2009 Best of Show Awards in Exhibit Hall

6:30 2009 Bio-IT World's Best Practices Awards/Dinner

6:15 Exhibit Hall Closes

Wednesday, April 29

7:30 am Registration and Morning Coffee

8:00 Event Chairperson's Opening Remarks

Kevin Davies, Ph.D., Editor-in-Chief, Bio-IT World

8:05 PLENARY KEYNOTE

Personalized Genomics – The Impact of Large-Scale Human Sequencing Projects

Clifford Reid, Ph.D., Chief Executive Officer, Complete Genomics, Inc.

8:45 KEYNOTE PANEL

The Future of Personal Genomics

A special plenary panel discussion featuring:

- *Jorge Conde, Co-Founder & CEO, Knome, Inc.*
- *Robert C. Green, M.D., M.P.H. Professor of Neurology, Genetics and Epidemiology, Boston University School of Medicine and Public Health*
- *John Halamka, M.D., M.S., CIO, Harvard Medical School*
- *Clifford Reid, Ph.D., Chief Executive Officer, Complete Genomics, Inc.*
- *Philip Reilly, Third Rock Ventures*
- *Dietrich Stephan, Ph.D., Co-founder and Chief Science Officer, Navigenics, Inc.*

9:45 Coffee Break, Exhibit Viewing, Vendor Theater Presentations, and Poster Competition in the Exhibit Hall

Disease Pathway Solutions

10:55 Track Chairperson's Remarks

Yaron Turpaz, Ph.D., Director of Integrative Computational Sciences, Lilly Singapore Centre for Drug Discovery

11:00 Use of Pathways Solutions to Gain Extensive Domain Knowledge of Disease Related Pathways and Targets

Sponsored by INGENUITY® SYSTEMS

Stuart Tugendreich, Director, Product Management New Solution, Ingenuity Systems

Cellular behavior in health and disease is controlled by the events such as activation, repression and interaction of signal transduction pathways. This presentation will demonstrate how IPA can be used to identify molecular pathways and individual proteins that regulate disease-related processes.

11:30 Applied Diseaseomics: A Generalized Approach for Assembling Gene and Disease-Related Feature Networks to Enable Disease-Specific Inferential Reasoning for Causal Factors and Candidate Therapeutics

Bruce Aronow, Ph.D., Professor of Pediatrics; Scientific Director, Center for Computational Medicine, Biomedical Informatics, Cincinnati Children's Hospital Medical Center, University of Cincinnati

This talk will outline methods for rapid aggregation of prior knowledge associated with specific diseases and groups of diseases; aggregating known, associated genes; and undertaking a variety of feature enrichment, network aggregation, and network extension analyses that can potentially be used to shed light into operative underlying disease processes and how these might be modified.

12:00

Mark van der Laan, Ph.D., Professor of Biostatistics and Statistics, UC Berkeley

We present a general targeted maximum likelihood statistical methodology that targets a user supplied variable importance or causal effect of a variable/treatment on an outcome. This method provides an optimal way in extracting the relevant information and dealing with the curse of dimensionality, while preserving the maximum likelihood principle. We illustrate this method for the purpose of assessing the effect of mutations in the HIV virus that cause resistance to a particular drug, and for assessing a causal effect of a treatment in a clinical trial and survival outcome, in the presence of informative censoring. We also apply the targeted maximum likelihood methodology to case control data providing a new way of assessing causal effects of single nucleotide mutations on phenotypes of interest.

12:30 Luncheon in the Exhibit Hall

2:00 Exhibit Hall Closes

Leveraging Data and Standards

1:55 Chairperson's Remarks

2:00 Pharma's Role and Possible Approaches to Driving Data Standards for Early Stage Research

Martin D. Leach, Ph.D., Executive Director, MRL IT Basic Research & Biomarkers, Merck & Co.

An increasing trend across the pharmaceutical and biotechnology industry is an increase in the leverage of external research organizations and integrating these 'virtual sites' into the overall research pipelines. To accomplish this, there needs to be a standardization of the methods and data formats for biology and chemistry. There is consensus for the need and development of data standards for early stage research and some specific successes, such as those around the transmission and management of gene expression data. Overall progress, however, has been poor in the development and adoption of additional standards. There are lessons to be gained from the clinical data standard realm and there needs to be a call to arms to apply these lessons to needs of early research.

2:30 The Neurodegeneration Knowledge Sphere: Integrated Software for Preclinical Drug Development

Steven Perrin, Ph.D., Chief Scientific Officer, ALS Therapy Development Institute

This presentation will examine how to design and implement the informatics infrastructure to track all aspects of preclinical drug development from discovery to in vivo testing. Additionally, attendees will learn how data visualization tools can assist scientific groups in the organization to leverage the data for portfolio prioritization and management.

3:00 Scientific Intelligence in R&D - Knowledge Integration across Discovery, Pre-clinical, and Clinical Development *(Joint with IT Infrastructure and Operations & Clinical and Medical Informatics Tracks)*

John Apathy, Assistant Vice President, Business Systems and Processes - Discovery, PreClinical, and Vaccines, Wyeth

3:30 Service Oriented Architecture – A New Data Sharing Architecture *(Joint w/IT Infrastructure and Operations, Clinical and Medical Informatics, & eHealth Solutions Tracks)*

Robert Lundsten, Director of Biorepository, Feinstein Institute for Medical Research

4:00 Conference Adjourns

Track 3:

Predictive and *in silico* Science

Use of model-simulated therapeutics, in silico tools, drug discovery and development, and predictive bio-simulations & models to explore and understand chemical and biological systems.

Monday, April 27

4:00 pm Event Chairperson's Opening Remarks
Cindy Crowninshield, Conference Director, Cambridge Healthtech Institute
Keynote Introduction: Rudy Potenzone, Ph.D., WW Industry Technology Strategist for Pharmaceuticals, Microsoft Corporation

4:15 PLENARY KEYNOTE

Research Computing and Infrastructure Technology
Chris Dagdigian, Founding Partner and Director of Technology, BioTeam, Inc.

5:00 Welcome Reception in the Exhibit Hall *Sponsored by* MERCK

Drop off a business card at the CHI Sales Booth for a chance to win 1 of 2 iPods ®!

7:00 Networking Event hosted by BiotechTuesday

Tuesday, April 28

7:30 am Registration and Morning Coffee

8:15 Event Chairperson's Opening Remarks
Phillips Kuhl, Co-founder and President, Cambridge Healthtech Institute
Keynote Introduction: Ken Buetow, Ph.D., Associate Director, Bioinformatics and Information Technology, National Cancer Institute

8:20 PLENARY KEYNOTE

Integrative Genomics
Eric E. Schadt, Ph.D., Executive Scientific Director, Genetics, Rosetta Inpharmatics/Merck Research Labs; Vice President and Chief Scientific Officer, Sage

9:00 Keynote Presentation & 2009 Benjamin Franklin Award

9:30 Coffee Break, Exhibit and Poster Viewing in the Exhibit Hall

in silico Modeling and Simulation Tools

10:50 Track Chairperson's Remarks
John Russell, Executive Editor, Bio-IT World

11:00 Drug Salvaging with Optimata Virtual Patient
Mark Tepper, Ph.D., Chief Executive Officer, Optimata
We have developed *in silico* models of drug-patient dynamic interactions to optimize the clinical development of oncology compounds. Using the Optimata Virtual Patient (OVP) technology, we have been able to accurately predict the optimal match between clinical indication, patient sub-population and drug schedule for a previously discontinued oncology compound. We will present a case study in which the OVP technology successfully salvaged a previously discontinued prostate cancer drug by identifying a new dosing regimen and drug combination. This new drug treatment protocol is predicted to extend the survival of prostate cancer patients by over 3 fold over five years.

11:30 Utilizing Virtual Populations to Reduce Risk in Clinical Studies
Alex L. Bangs, Co-Founder & CTO, Entelos, Inc.
New methods and technologies have been developed to analyze existing clinical data sets and create virtual populations - large sets of individual mechanistically simulated virtual patients that statistically mirror clinical populations. These virtual populations have been used to simulate clinical trials on novel therapeutics and analyze simulated trial results for potential biomarkers. The methods and technology will be discussed as well as specific examples from completed research projects.

12:00 *in silico* Modeling and Simulation Using Automated Fitting Algorithms to Optimize Antibody Study Design
Serge Guzy, Ph.D., Principal Scientist, Business Development, XOMA
Few companies use automated processes to optimize trial design. In addition, non optimal algorithms are used for that purpose. The main objective of our work is to provide the optimal trial design for future oncology experiments by running one series of simple scripts that would generate automatically output files with the optimal information for decision making. This talk will discuss the special tools developed that address statistical optimization challenges, save time and money, increases the probability of detecting true positives, and affords improved decision making.

12:30 Luncheon Presentation
(Sponsorship Opportunity Available)

in silico Modeling and Simulation Tools *(continued)*

1:40 Chairperson's Remarks
John Russell, Executive Editor, Bio-IT World

1:45 Modeling and Simulation: Taking the Clinic into the Lab and Back Again
Michael N. Liebman, Ph.D., Managing Director, Strategic Medicine, Inc
There is a significant opportunity to apply modeling and simulation into clinical application which goes Beyond its use in biomedical/translational research. We have focused on identifying critical clinical issues That directly impact patient treatment, i.e. clinical decision support, and have developed and applied these Modeling methods in the diagnosis and treatment of breast cancer, coagulation disorders and cardiac transplant matching, utilizing pathway-based approaches and both neural networks and Bayesian analysis to analyze pathology data as well as SNP's, all integrated with clinical data and outcomes and will present several case studies.

2:15 Talk X: Computational Architecture for Modeling the Cell
Shiva Ayyadurai, Ph.D., Fulbright Scholar & Faculty Lecturer, M.I.T.; Executive Director, International Center for Integrative Systems Research
A grand challenge of predictive and *in silico* Medicine is to create a model of the whole cell. Over the past decade, the description of biomolecular pathways is rapidly moving from simple diagrammatic representations to detailed mathematical models. This trend provides the opportunity to create a model of the cell by integrating the individual biological pathway models. Current approaches to modeling the whole cell are not scalable to integrate the large number of pathway models, each of which may be in different formats and under constant change. In this talk, we present CytoSolve a new approach that provides a scalable computational platform for integrating multiple biological pathway models.

2:45 Virtual Screening for R-Groups *Sponsored by* Tripos, A Certara Company
Richard Cramer, Ph.D., Senior Vice President, Science & Chief Scientific Officer, Tripos
Success in lead optimization requires discovery of one or more R-groups that confer the desired set of properties on a clinical candidate. Large compound collections implicitly describe a larger variety of R-group candidates, all presumably synthesizable. R-Group Virtual Screening in SYBYL provides a unique means of selecting the most promising of these, based on objective and relatively accurate pIC50 predictions using Topomer CoMFA, with remarkable ease and speed. Validation studies continue to strongly confirm these apparent benefits.

3:15 Refreshment Break, Exhibits and Poster Viewing in the Exhibit Hall

Modeling Toxicity Data

3:45 Unlocking Toxicity Data for Structure-Activity Modeling By Semi-Automated Extraction from Study Reports
Nigel Greene, Ph.D., Associate Research Fellow & Head of Computational Toxicology, Pfizer
David Milward, Ph.D., Chief Technology Officer, Linguamatics
Many of the results obtained from toxicity tests are stored in study report documents that cannot be easily interrogated to allow toxicity modeling, such as the creation of structure-activity relationships. Fully manual extraction of structured data, including numerical values, is time consuming and expensive. This collaboration between Pfizer, Linguamatics and Lhasa has resulted in a semi-automated method which involves text mining based on natural language processing (NLP), followed by interactive curation. This talk will provide attendees an understanding of how NLP-based text mining can unlock value in legacy safety studies to support current decision-making.

4:15 Cheminformatics Approaches for Toxicity Predictions in

Drug Discovery

Florian Nigsch, Ph.D., University of Cambridge and Novartis Institutes for BioMedical Research

Our work combines data and methods from different areas—cheminformatics, toxicology, pharmacology—to gain new insights into (un)desired actions of small molecule modulators of biological pathways. Developing models for the prediction of toxicological outcomes is vital due to changing legislation regarding drug safety as well as reduction in the use of laboratory animals. We will show the limitations inherent in such computational approaches and highlight the benefits and relevance to drug discovery projects. Attendees will understand the: development process and what can be learned from target prediction models in a toxicological context, limitations in the underlying data, overview of data integration required in order to build and use such models, presentation of the methodology that was used and how it can be extended.

4:45 Causal Network Modeling in Drug Toxicity: Predicting the Risk of Idiosyncratic DILI and Hemangiosarcoma in Animal Models

Keith O. Elliston, Ph.D., Co-Founder, President and Chief Executive Officer, Genstruct, Inc.

The ability to correctly predict in preclinical settings the potential of a drug to be toxic to humans is crucial for successful and rapid drug development. This talk will discuss an innovative Causal NetworkTM Modeling (CNM) platform for systems biology that has been successfully applied to drug safety assessment, as well as to molecular mechanism of action characterization, and biomarker discovery.

5:15 2009 Best of Show Awards in Exhibit Hall

6:30 2009 Bio-IT World's Best Practices Awards/Dinner

6:15 Exhibit Hall Closes

Wednesday, April 29

7:30 am Registration and Morning Coffee

8:00 Event Chairperson's Opening Remarks

Kevin Davies, Ph.D., Editor-in-Chief, Bio-IT World

8:05 PLENARY KEYNOTE

Personalized Genomics – The Impact of Large-Scale Human Sequencing Projects

Clifford Reid, Ph.D., Chief Executive Officer, Complete Genomics, Inc.

8:45 KEYNOTE PANEL

The Future of Personal Genomics

A special plenary panel discussion featuring:

- *Jorge Conde, Co-Founder & CEO, Knome, Inc.*
- *Robert C. Green, M.D., M.P.H. Professor of Neurology, Genetics and Epidemiology, Boston University School of Medicine and Public Health*
- *John Halamka, M.D., M.S., CIO, Harvard Medical School*
- *Clifford Reid, Ph.D., Chief Executive Officer, Complete Genomics, Inc.*
- *Philip Reilly, Third Rock Ventures*
- *Dietrich Stephan, Ph.D., Co-founder and Chief Science Officer, Navigenics, Inc.*

9:45 Coffee Break, Exhibit Viewing, Vendor Theater Presentations, and Poster Competition in the Exhibit Hall

Systems Biology, Systems Integration & LIMS

10:45 Track Chairperson's Remarks

11:00 A Chemical Systems Biology to Drug Discovery: Side-Effect Engineering and Drug Repurposing

Lei Xie, Ph.D., Principal Scientist, San Diego Supercomputer Center, University of California, San Diego

Attendees will learn how our methods will help shift one-drug-one-target drug discovery process to a new paradigm of network pharmacology. We have developed a chemical systems biology approach to reconstructing and simulating protein-ligand interaction networks on a genome scale and applied it to elucidating molecular mechanisms of drug side-effects and repurposing pharmaceuticals to target different pathways. Attendees will learn how systems biology can play key roles in the future of drug discovery, side-effects can be modulated by the fine-tuning of the off-target binding network, and drug repurposing can be explored systematically and efficiently using chemical systems biology approaches.

11:30 Clotting, Cascades, and Computers - Systems Biology in Personalized Medicine

Michael H. Roehrl, M.D., Ph.D., Pathology and Laboratory Medicine, Massachusetts General Hospital

The human blood clotting system is a complex and highly regulated network of biomolecular interactions. This talk demonstrates how data from careful biochemical measurements can be integrated into quantitative and predictive computational models of blood coagulation. Pharmacological manipulation of blood clotting has tremendous medical and pharmaceutical ramifications. Millions of patients receive the oral anticoagulant Coumadin to prevent fatal thromboembolic events. Yet personalized Coumadin dosing is both cumbersome and expensive and potentially dangerous. Coumadin is among the top 10 drugs with the largest number of serious adverse event reports submitted to the FDA. We show how a novel Systems Biological approach can be used in the clinical setting to personalize Coumadin dosing and to achieve safe therapeutic goals. Additional specific examples of optimized clinical management using Systems Biology in clinical medicine will be discussed.

12:00 Achieving the Success of Genomics Research: Standardized & Compliant BioBanking for Today's Biorepositories

Jody Sylvia, Senior Bionformatics Project Manager, Harvard Channing Laboratory

This talk will share an insightful "use case" for a centralized, standardized biobanking solution for its Respiratory Epidemiology Genotyping Laboratory to maintain controlled access to biomaterials and correlative date, including critical genomic, proteomic, and phenotypic information across multiple facilities.

12:30 Luncheon in the Exhibit Hall

2:00 Exhibit Hall Closes

Case Studies and Lessons Learned from Your Peers (Joint with Track 4: Computational Chemistry)

1:55 Chairperson's Remarks

Jeremy L. Jenkins, Ph.D., Research Investigator, Lead Discovery Informatics, Novartis Institutes for BioMedical Research

2:00 Power to the People: Integrating Data and Analysis in One Easy Application

Derek Debe, Ph.D., Senior Group Leader, Scientific Informatics and Automation, Abbott Laboratories

This talk discusses the successful development and deployment of a Drug Discovery data integration and analysis platform at Abbott Laboratories. Specific use case examples will be presented, including functionality useful for Hit-to-Lead analysis and Lead Optimization efforts.

2:30 Automated Compound Submission and Active Learning Using HT-ADME in silico Models

Rishi Gupta, Ph.D., Senior Scientist, Computational Sciences Center of Emphasis, Pfizer

We present herein the status of our work towards automated compound submission and active learning. We introduce the concept of "automated submissions", that is, a mechanism that uses in-silico models and sends only those compounds for screening which it cannot predict with a high level of confidence. This mechanism not only decreases the number of compounds being screened but, also, allows a model to iteratively expand its chemical space where it has limited prediction scope. Co-authors of this work include Stefan J. Steyn of PDM Therapeutic Areas and Eric Gifford of CS CoE.

3:00 Predictive *In-Silico* Science: Shifting the Discovery Paradigm

Yossi Cohen, M.D., VP R&D, Compugen

We share insights into how new in silico predictive approaches differ from the traditional discovery approaches, and why it has the potential to predict high-quality candidates in a much more efficient and cost-effective manner. Through examples of some of Compugen's successes in drug candidate discoveries, this talk will demonstrate how the predictive in silico approach is steadily revolutionizing the R&D paradigm of the industry. We will highlight the potential of in silico science to increase success rates in the preclinical stages of drug development and how collaborative efforts can help stem clinical stage attrition.

3:30 "Virtual Fragment Linking": An Approach to Identify Potent Binders from Low Affinity Fragment Hits

Meir Glick, Ph.D., Research Investigator II, Lead Discovery Informatics, Novartis Institutes for BioMedical Research

We explore the possibilities of using fragment-based screening data to prioritize compounds from a full HTS library, a method we call virtual fragment linking (VFL). The ability of VFL to identify compounds of nanomolar potency based on micromolar fragment binding data was tested on 75 target classes from the WOMBAT database and succeeded in 57 cases. Further, the method was demonstrated for seven drug targets from in-house screening programs that performed both FBS of 8800 fragments and screens ofthe full library. VFL captured between 28% and 67% of the hits (IC50 < 10?M) in the top 5% of the ranked library for four of the targets (enrichment between 5-fold and 13-fold).

4:00 Conference Adjourns

Track 4:

Computational Chemistry

Enabling discovery and improving knowledge management through access to public and commercial science, tools and databases and through the integration of chemical and biological data.

Monday, April 27

4:00 pm **Event Chairperson's Opening Remarks**
Cindy Crowninshield, Conference Director, Cambridge Healthtech Institute
Keynote Introduction: Microsoft, speaker to be Announced

4:15 **PLENARY KEYNOTE**

Research Computing and Infrastructure Technology
Chris Dagdigian, Founding Partner and Director of Technology, BioTeam, Inc.

5:00 **Welcome Reception in the Exhibit Hall** *Sponsored by* MERCK
Drop off a business card at the CHI Sales Booth for a chance to win 1 of 2 iPods ®!

7:00 **Networking Event hosted by BiotechTuesday**

Tuesday, April 28

7:30 am **Registration and Morning Coffee**

8:15 **Event Chairperson's Opening Remarks**
Phillips Kuhl, Co-founder and President, Cambridge Healthtech Institute
Keynote Introduction: caBIG

8:20 **PLENARY KEYNOTE**

Integrative Genomics
Eric E. Schadt, Ph.D., Executive Scientific Director, Genetics, Rosetta Inpharmatics/Merck Research Labs; Vice President and Chief Scientific Officer, Sage

9:00 **Keynote Presentation & 2009 Benjamin Franklin Award**

9:30 **Coffee Break, Exhibit and Poster Viewing in the Exhibit Hall**

ACCESS: Enabling Discovery through Access to 'Open Source' Science, Databases and Software Tools

10:50 **Track Chairperson's Remarks**
Christopher Southan, Ph.D., EMBL European Bioinformatics Institute (EBI)

11:00 **Chemical Biology Databases: Going Beyond Lists of Compounds**
David DeCaprio, Ph.D., Associate Platform Director for Chemical Biology and Novel Therapeutics, Broad Institute
This talk will describe efforts underway at the Broad Institute to improve the consistency, quality, and transparency of stored experimental and other biological data of each compound as well as improved tools to enable more effective access.

11:30 **Crowdsourcing, Collaborations and Text-Mining in a World of Open Chemistry**
Antony Williams, Ph.D., Founder, ChemZoo, Inc.; Host, ChemSpider
This presentation will provide an overview of the issue of quality in many chemistry-related databases, approaches to cleaning up the data, and how a curated platform can become the centralized hub for resourcing information about chemical entities.

12:00 **Tapping Into the Custom Chemistry Space of Chemical Suppliers** *Sponsored by* omixon
Attila Bérces, Ph.D., CEO, Omixon Kft.
Lutz Weber, Ph.D., CEO, OntoChem GmbH
The custom chemistry space of synthetically feasible compounds of chemical suppliers is orders of magnitudes larger than what they offer off the shelf. This talk will present a database and search solution that enables pharmaceutical companies to enrich their compound archive by maximizing its diversity and fill gaps in their chemical space by adding uniquely selected custom synthetic compounds.

12:15 **PSILO: A Repository for Protein Structural Information**
Howard Feldman, Ph.D., Research Scientist, Research & Development, Chemical Computing Group *Sponsored by* CHEMICAL COMPUTING GROUP INC.
PSILO® is a database system that provides an easily accessible, consolidated repository for macromolecular structures, protein-ligand, electron density and related information. It offers research organizations a means to systematically track, register and search both experimental and computational macromolecular structural data. A web-based interface facilitates the searching and accessing of public and private data. Attendees will learn the benefits of a comprehensive data management solution for structural data, the benefits of mmCIF data representation, how RCSB's ligand dictionary can be used to correct ligand structures, and the importance of version control.

12:30 **Luncheon Presentation** *Sponsored by* Tripos A Certara Company
Pantheon: An Open Platform for Cheminformatics and CADD
Greg Smith, CTO, Tripos International
Pantheon is an affordable, extendable cheminformatics solution that enables discovery scientists to organize, analyze, and visualize chemical and biological data and make better decisions faster. Pantheon addresses many basic cheminformatics workflows and capabilities. It can act as a standalone software application or as a platform for drug discovery workflows, offering easy integration with 3rd party or in-house tools. Attendees will learn about cheminformatics workflows and user scenarios addressed by Pantheon as well as case studies illustrating Pantheon as a platform for drug discovery. Co-authors of this work include Greg Smith and Stephan Nagy of Tripos International.

SCREEN: Screening and Modelling: Success Stories and the Challenges that Remain

1:40 **Chairperson's Remarks**
Andreas Bender, Ph.D., Assistant Professor, Medicinal Chemistry Division, Leiden / Amsterdam Center for Drug Research

1:45 **Proteochemometrics Modeling: A Technique to Predict Activities Simultaneously Against Multiple Receptors / Mutants and Applications to Non-Nucleoside Reverse Transcriptase Inhibitors**
Andreas Bender, Ph.D., Assistant Professor, Medicinal Chemistry Division, Leiden / Amsterdam Center for Drug Research
Proteochemometrics Modeling involves ligand- as well as target-features for generating activity models. This talk will provide insight into a novel modeling method which can be applied also to in-house datasets.

2:15 **Virtual Screening at the Fragment Level**
Zenon Konteatis, Ph.D., Senior Scientist, Computational Chemistry, Locus Pharmaceuticals, Inc.
Virtual screening at the fragment level instead of the molecule level has the same advantages as its experimental counterpart. This talk will present a computational method that addresses each of these key elements and show case studies that demonstrate their overall efficacy in virtual fragment screening and the subsequent *de novo* design of molecules from the screening results.

2:45 **Findings and Discussion of the Challenge to Predict Aqueous Solubility Held by the Journal of Chemical Information and Modeling**
Anton Hopfinger, Ph.D., Professor, University of New Mexico, Editor, Journal of Chemical Information and Modeling
Recently the Journal of Chemical Information and Modeling (JCIM), held a Challenge to predict the aqueous solubility of 32 structurally diverse compounds based upon a training set of 100 compounds and any additional information contestants wished to employ. The entries have been scored and the findings are posted on the JCIM website. This presentation will further report findings from the Challenge, comments regarding the findings from contestants and preliminary thoughts of Journal editors regarding the Challenge and possible future prediction challenges.

3:15 **Refreshment Break, Exhibits and Poster Viewing in the Exhibit Hall**

MANAGE: Coping with the Volume of Data and Transforming it into Knowledge

3:45 Gaining Efficiencies through Open Innovation

Susie Stephens, Ph.D., Principal Research Scientist, Eli Lilly & Co.

This talk will examine how the industry can benefit from enabled decision making through open innovation, as well benefiting from data explosion, mining and linking knowledge, increasing uptake of new ideas, and easing barriers to collaboration.

4:15 Implementation and Uses of a Next Generation Discovery Informatics System

David Nunn, Ph.D., Principal Research Scientist, ChemInformatics, Wyeth Research

The NextGen project at Wyeth has been a large scale reinventing of our Discovery informatics data access and analytics capabilities. This presentation discusses how Wyeth scientists have worked closely with IS staff and external partners Tripos and Accenture to achieve these goals.

4:45 Leveraging Data Pipelining for On-the-Fly Data Integration of Multiple Experiments

Jeremy L. Jenkins, Ph.D., Research Investigator, Lead Discovery Informatics, Novartis Institutes for BioMedical Research

Data generated by project teams in the pharmaceutical industry is often held in data silos with the single-minded purpose of supporting one project. However, with even basic semantic standardizations in place, prospective lead finding may be driven by integrating historical data collected across multiple experiments as well as combining internal and external data sources to train probabilistic models and make new predictions.

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6:30 2009 Bio-IT World's Best Practices Awards/Dinner

6:15 Exhibit Hall Closes

Wednesday, April 29

7:30 am Registration and Morning Coffee

8:00 Event Chairperson's Opening Remarks

Kevin Davies, Ph.D., Editor-in-Chief, Bio-IT World

8:05 PLENARY KEYNOTE

Personalized Genomics – The Impact of Large-Scale Human Sequencing Projects

Clifford Reid, Ph.D., Chief Executive Officer, Complete Genomics, Inc.

8:45 Keynote Panel

The Future of Personal Genomics

A special plenary panel discussion featuring:

- *Jorge Conde, Co-Founder & CEO, Knome, Inc.*
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- *Clifford Reid, Ph.D., Chief Executive Officer, Complete Genomics, Inc.*
- *Philip Reilly, Third Rock Ventures*
- *Dietrich Stephan, Ph.D., Co-founder and Chief Science Officer, Navigenics, Inc.*

9:45 Coffee Break, Exhibit Viewing, Vendor Theater Presentations, and Poster Competition in the Exhibit Hall

INTEGRATE: Integrative Approaches for Chemical and Biological Data and Knowledge Management

10:45 Chairperson's Remarks

Richard Cramer, Ph.D., Senior Vice President, Science & Chief Scientific Officer, Tripos

11:00 Comparing Public and Commercial Databases of Bioactive Chemicals by Content and Compound-to-Protein Mappings

Christopher Southan, Ph.D., EMBL European Bioinformatics Institute (EBI)

This talk compares content from selected public and commercial databases and reviews the different strategies used for extracting unstructured data from documents describing bioactive compounds and transferring them to structured relational databases for high value data mining.

11:30 Open Semantic Data in Science

Peter Murray-Rust, Ph.D., Professor, Chemistry and Molecular Informatics, University of Cambridge, Senior Research Fellow, Churchill College

Science is increasingly dependent on data and Bioscience has led the world in exposing its data in Open Semantic form (genomes, sequences, proteins, etc.). This allows the power of the Semantic Web (Berners-Lee 2001) to use ontologies and inference to support scientific discovery and reasoning. In contrast much chemistry is hidden behind commercial firewalls or proprietary formats which prohibit their integration into the Semantic Web. I shall show what needs to be done to make chemical data (structures, reactions) fully available to bioscience; when this is done we can expect a major increase in our understanding of biology at the molecular level.

12:00 pm Open Source Cheminformatics: Tools and Data

Rajarshi Guha, Ph.D., Visiting Assistant Professor, Informatics, Indiana University

This talk highlights the current options for open source cheminformatics software, focusing more on toolkits (CDK and OpenBabel) and platforms (such as Bioclipse and R). Issues to be addressed include what they provide, problems with their usage, and support infrastructure.

12:30 Luncheon in the Exhibit Hall

2:00 Exhibit Hall Closes

EXECUTE: Case Studies and Lessons Learned from Your Peers (Joint with Track 3: Predictive and *in silico* Science)

1:55 Chairperson's Remarks

Jeremy L. Jenkins, Ph.D., Research Investigator, Lead Discovery Informatics, Novartis Institutes for BioMedical Research

2:00 Power to the People: Integrating Data and Analysis in One Easy Application

Derek Debe, Ph.D., Senior Group Leader, Scientific Informatics and Automation, Abbott Laboratories

This talk discusses the successful development and deployment of a Drug Discovery data integration and analysis platform at Abbott Laboratories. Specific use case examples will be presented, including functionality useful for Hit-to-Lead analysis and Lead Optimization efforts.

2:30 Automated Compound Submission and Active Learning Using HT-ADME in silico Models

Rishi Gupta, Ph.D., Senior Scientist, Computational Sciences Center of Emphasis, Pfizer

We present herein the status of our work towards automated compound submission and active learning. We introduce the concept of "automated submissions", that is, a mechanism that uses in-silico models and sends only those compounds for screening which it cannot predict with a high level of confidence. This mechanism not only decreases the number of compounds being screened but, also, allows a model to iteratively expand its chemical space where it has limited prediction scope. Co-authors of this work include Stefan J. Steyn of PDM Therapeutic Areas and Eric Gifford of CS CoE.

3:00 Predictive *In-Silico* Science: Shifting the Discovery Paradigm

Yossi Cohen, M.D., VP R&D, Compugen

We share insights into how new in silico predictive approaches differ from the traditional discovery approaches, and why it has the potential to predict high-quality candidates in a much more efficient and cost-effective manner. Through examples of some of Compugen's successes in drug candidate discoveries, this talk will demonstrate how the predictive in silico approach is steadily revolutionizing the R&D paradigm of the industry. We will highlight the potential of in silico science to increase success rates in the preclinical stages of drug development and how collaborative efforts can help stem clinical stage attrition.

3:30 "Virtual Fragment Linking": An Approach to Identify Potent Binders from Low Affinity Fragment Hits

Meir Glick, Ph.D., Research Investigator II, Lead Discovery Informatics, Novartis Institutes for BioMedical Research

We explore the possibilities of using fragment-based screening data to prioritize compounds from a full HTS library, a method we call virtual fragment linking (VFL). The ability of VFL to identify compounds of nanomolar potency based on micromolar fragment binding data was tested on 75 target classes from the WOMBAT database and succeeded in 57 cases. Further, the method was demonstrated for seven drug targets from in-house screening programs that performed both FBS of 8800 fragments and screens ofthe full library. VFL captured between 28% and 67% of the hits (IC50 < 10?M) in the top 5% of the ranked library for four of the targets (enrichment between 5-fold and 13-fold).

4:00 Conference Adjourns

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Track 5:

Clinical and Medical Informatics

Role IT solutions, theoretical knowledge and social infrastructure have in allowing for efficient collecting and integrating of clinical data and developing models.

Monday, April 27

4:00 pm Event Chairperson's Opening Remarks
Cindy Crowninshield, Conference Director, Cambridge Healthtech Institute
Keynote Introduction: Microsoft

4:15 PLENARY KEYNOTE

Research Computing and Infrastructure Technology
Chris Dagdigian, Founding Partner and Director of Technology, BioTeam, Inc.

5:00 Welcome Reception in the Exhibit Hall *Sponsored by* MERCK

Drop off a business card at the CHI Sales Booth for a chance to win 1 of 2 iPods ®!

7:00 Networking Event hosted by BiotechTuesday

Tuesday, April 28

7:30 am Registration and Morning Coffee

8:15 Event Chairperson's Opening Remarks
Phillips Kuhl, Co-founder and President, Cambridge Healthtech Institute
Keynote Introduction: Ken Buetow, Ph.D., Associate Director, Bioinformatics and Information Technology, National Cancer Institute

8:20 PLENARY KEYNOTE

Integrative Genomics
Eric E. Schadt, Ph.D., Executive Scientific Director, Genetics, Rosetta Inpharmatics/Merck Research Labs; Vice President and Chief Scientific Officer, Sage

9:00 Keynote Presentation & 2009 Benjamin Franklin Award

9:30 Coffee Break, Exhibit and Poster Viewing in the Exhibit Hall

EDC

10:50 Track Chairperson's Remarks
Joan Chambers, Senior Director of Marketing & Operations, Publications, Cambridge Healthtech Institute (CHI)

11:00 The Journey towards an Integrated Clinical Data Management Platform: Challenges and Potential
Jennifer Teta, Director, Clinical Research Information Services, Merck & Co., Inc.
A patient data management platform was implemented with 100% of late stage trials using EDC and a Janus-based clinical data warehouse based on external standards. Lessons learned from this work will be discussed including the challenges and potential of a clinical data warehouse for integrating data, thoughts on the advantages of implementing standards early in the patient data flow process, and the implication of various architectures on the ability to effectively partner with others.

11:30 How a New IT Specification Will Help Clinical Investigators Reduce Their Paperwork and Get Back To Their Real Work
Rich Furr, Head, Global Regulatory Affairs and Chief Compliance Officer, SAFE-BioPharma Association
Use of the IHE Retrieve Form for Data Capture allows creation of electronic case report forms and individual case safety reports by parsing electronic health records to identify and retrieve data directly to EDC systems based on specified values. This presentation will report on the problem faced by clinical investigators and the results of the joint initiative to address it. Understand the technology, procedures and policies that support the use of digital identities and digital signatures across the clinical trial space.

12:00 eSubmissions: What AstraZeneca Learned
Richard Ware, Senior Principal Business Partner, Regulatory Affairs, Global Drug Development Information Systems, AstraZeneca Pharmaceuticals
On September 18, 2006, AstraZeneca (AZ) U.S. Regulatory Affairs submitted the first electronic original 356h form to the FDA. AstraZeneca received *BIO-IT World* magazine's 2008 Best Practices Grand Prize for its pioneering accomplishment. This presentation will explain how AstraZeneca implemented eSubmissions and the internal process that resulted in achieving this industry milestone.

12:30 Luncheon Presentation *Sponsored by* GENERAL DYNAMICS
Visual Decision Support for Clinical Trial Management
Jason Neiss, Product Manager, Life Sciences, Viz | General Dynamics
Better tools are needed to help people interpret and act on integrated clinical trials data. Data capture or workflow-centric tools are inadequate for distributed managers, sponsors, and regulators who need both summary and detailed information to support study and portfolio decisions. Visualization tools should help reveal answers to known questions, but they should also allow non-programmers to pose and collaboratively answer new questions they didn't know theycould ask. This session will feature a case study of how a major biopharma uses collaborative visualization software to give managers and analysts topsight to more easily analyze data, detect problems, and plan solutions.

EDC *(continued)*

1:40 Chairperson's Remarks
Joan Chambers, Senior Director of Marketing & Operations, Publications, Cambridge Healthtech Institute (CHI)

1:45 Standards-Based Reference Architecture for Advanced Clinical Research Informatics and Patient Care
Jomol Mathew, Ph.D., Director, Clinical Research Information Technology, Dana-Farber Cancer Institute
Kevin Coonan, M.D., Clinical Research Information Technology, Dana-Farber Cancer Institute
We present a standards-based reference architecture for semantic interoperability between Clinical Information Systems (CIS)/Electronic Health Records (EHRs) and Clinical Trial Management Systems (CTMS). This is based upon the HL7 version 3.1 standards architecture using clinical terminologies designed as part of the Federal Health Architecture/Consolidated Health Informatics (FHA/CHI) to provide a ubiquitous and unambiguous framework. We discuss the design process and rationale, requirements for reference implementation, imperatives to HITSP and CCHIT, as well as required additional research and development.

Clinical Informatics Applied

Session Chair: Ken Buetow, Ph.D. Associate Director for Bioinformatics and Information Technology, National Cancer Institute

2:15 The Cancer Biomedical Informatics Grid (caBIG®) Clinical Trials Suite: A Standardized, Integrated Approach to Clinical Trials Management and Linking Research to Care *Featured by* caBIG

John Speakman, Associate Director, Clinical Products and Programs, Center for Bioinformatics and Information Technology, National Cancer Institute (NCI)
William Dyer, CRI, Principal Consultant, Bioinformatics, National Cancer Institute
The caBIG® vision is a virtual network of interconnected data, individuals, and organizations whose goal is to redefine how research is conducted, care is provided, and patients/participants interact with the biomedical research enterprise. The caBIG® Clinical Trials Suite is a comprehensive set of modular, interoperable and standards-based tools designed to meet the diverse clinical trials management needs across the clinical research community. Learn how caBIG® Clinical Trials Workspace and suite of applications achieves interoperability and data sharing across clinical research and translational medicine.

2:45 Knowledege Based Approach to Design and Visualization of Clinical Trial Operations
Dave Parrish, M.S., Director Informatics, Immune Tolerance Network
This presentation will demonstrate a visualization framework based on the Co-Motion visualization environment integrated with the ontology based trial design application (Trial-Designer). We will demonstrate how the integration of these two applications will allow an end user to define and interact with information generated in diverse trials from a single user interface

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and drive a common ontology based framework.

3:15 Extending Clinical IT to Support Adaptive Clinical Trials

Tom Parke, BSc, Head of Clinical Trial Solutions, Tessella Inc *Sponsored by*

Adaptive Clinical trials are a key part of the solution to the problems of drug development in pharmaceutical companies.

Particularly when considered at the program level and not simply the trial level, adaptive designs offer a number of ways to significantly improve the science and efficiency of drug development. At the same time, however, they set a number of challenges to the conventional clinical trial operation. This talk will discuss how can clinical IT can help meet these challenges.

3:30 Refreshment Break, Exhibits and Poster Viewing in the Exhibit Hall

Clinical Outcomes and Standards

3:45 caBIG®: An Interoperable IT Framework for Personalized Medicine *Featured by*
(Joint w/eHealth Solutions Track)

Ken Buetow, Ph.D. Associate Director for Bioinformatics and Information Technology, National Cancer Institute

Personalized approaches to drug discovery, development and clinical care promise a new generation of preventive and preemptive health care. Countless data "disconnects" continue to afflict these biomedical "pillars", though, resulting in delays, dysfunction, and poor clinical outcomes. The prerequisite to overcome these hurdles is broad IT interoperability within and across institutions. Many of these challenges are addressed by caBIG® (cancer Biomedical Informatics Grid®). This session will showcase case studies in discovery research, biobanking, imaging, and clinical research; new models of connectivity; and a new ecosystem to drive continuous learning from bench to bedside and back.

4:45 Do Healthcare IT Standards Hamper the Advance of Science? *(Joint with eHealth Solutions Track)*

Werner Ceusters, M.D., Director, Ontology Research Group, NYS Center of Excellence in Bioinformatics & Life Sciences

Standards are an absolute requirement to make semantic interoperability in healthcare informatics a reality. To achieve the goals of translational medicine, a variety of heterogeneous systems containing data at various levels of granularity need to be made interoperable. This talk will present an analysis of a number of adopted standards and highlight a number of problematic issues and propose directions for solutions.

5:15 2009 Best of Show Awards in Exhibit Hall

6:30 2009 Bio-IT World's Best Practices Awards/Dinner

6:15 Exhibit Hall Closes

Wednesday, April 29

7:30 am Registration and Morning Coffee

8:00 Event Chairperson's Opening Remarks

Kevin Davies, Ph.D., Editor-in-Chief, Bio-IT World

8:05 PLENARY KEYNOTE

Personalized Genomics – The Impact of Large-Scale Human Sequencing Projects

Clifford Reid, Ph.D., Chief Executive Officer, Complete Genomics, Inc.

8:45 Keynote Panel
The Future of Personal Genomics
A special plenary panel discussion featuring:

- *Jorge Conde, Co-Founder & CEO, Knome, Inc.*
- *Robert C. Green, M.D., M.P.H. Professor of Neurology, Genetics and Epidemiology, Boston University School of Medicine and Public Health*
- *John Halamka, M.D., M.S., CIO, Harvard Medical School*
- *Clifford Reid, Ph.D., Chief Executive Officer, Complete Genomics, Inc.*
- *Philip Reilly, Third Rock Ventures*
- *Dietrich Stephan, Ph.D., Co-founder and Chief Science Officer, Navigenics, Inc.*

9:45 Coffee Break, Exhibit Viewing, Vendor Theater Presentations, and Poster Competition in the Exhibit Hall

Clinical Application of Personalized Medicine

10:45 Track Chairperson's Remarks

Joan Chambers, Senior Director of Marketing & Operations, Publications, Cambridge Healthtech Institute (CHI)

11:00 Enabling a Collaborative, Informative, and Compliant Biobanking Environment

Kevin L. Swank, Lead Analyst/Programmer – RLIMS, Mayo Clinic

Organizations in today's economy are facing unprecedented pressures to ensure research success, while at the same time, maximizing operational efficiency and achieving the best return on investment (ROI). In addition, the complexity of managing the dramatically increased number of specimens throughout the organization compels them to replace their existing processes and ad-hoc systems with enterprise solutions. This talk will examine the critical biorepository management requirements for biospecimen accessioning laboratories at Mayo and share experiences in deploying a multi-phase, enterprise biorepository management solution that include ad hoc point system vs. enterprise solution, configurability to fulfill local and enterprise requirements, and truly compliant and secured operational environment.

11:30 Operationalizing Research in Clinical Application of Personalized Medicine

Moderator: Ronald Waife, MPH, President, Waife & Associates, Inc. and Ben Zeskind, Ph.D., M.B.A., Founder and Chief Executive Officer, Immuneering Corporation

This session will feature industry observers' current predictions on issues and solutions for how to design and conduct the first trials with personalized medicines and how to set up in advance an environment for rapid sharing of lessons learned for industry and regulatory authorities.

12:30 Luncheon in the Exhibit Hall

2:00 Exhibit Hall Closes

Clinical Data Management

1:55 Chairperson's Remarks

Joan Chambers, Senior Director of Marketing & Operations, Publications, Cambridge Healthtech Institute (CHI)

2:00 Collaborative Translational Research in the Public Sector

Kyle Brown, President, Innolyst

The public sector funds as much research as all pharmaceutical companies combined - with no common infrastructure. Learn how foundations and academia use technology to implement translational research programs. Shared target validation, screening, project management, and patient registries enable public organizations to manage research programs across an array of geographically dispersed vendors and researchers.

2:30 Molecular Considerations in Clinical Decisions: Aromatase Inhibitors in Breast Cancer

Michael N. Liebman, Ph.D., Managing Director, Strategic Medicine, Inc.

Aromatase inhibitors have become a significant treatment option for post-menopausal breast cancer patients because of their efficacy and limited profile of side-effects. Understand how this option better stratifies the patient and the disease to provide optimal decision support through molecular diagnostics and analysis.

3:00 Scientific Intelligence in R&D - Knowledge Integration across Discovery, Pre-clinical, and Clinical Development *(Joint with IT Infrastructure and Operations & Informatics for Genomic Medicine Tracks)*

John Apathy, Assistant Vice President, Business Systems and Processes - Discovery, PreClinical, and Vaccines, Wyeth

Investments in information systems within Pharmaceutical R&D organizations tend to be made by individual departments or functional units and serve the local purpose of those units. Over time these silo-based approaches lead to challenges in enabling the exchange of data, information, and knowledge across the various Discovery, Pre-clinical, and Clinical Development domains. At Wyeth, we are developing solutions that cut across organizational boundaries and have developed a set of Knowledge Integration solutions allowing senior scientists, study directors, and functional management to find, access, and manage disparate R&D data, information, and knowledge assets. This presentation provides an overview of the journey undertaken to ensure the right information is available to researchers and management within Wyeth Preclinical R&D organization at the right time to enable faster decision-making.

3:30 Service Oriented Architecture – A New Data Sharing Architecture for the Feinstein Institute for Medical Research *(Joint with IT Infrastructure & Operations and Informatics for Genomic Medicine Tracks)*

Robert Lundsten, Director of Biorepository, Feinstein Institute for Medical Research

The ability to integrate data from multiple independent data repositories across the North Shore Long Island Jewish Health System's (NSLIJHS) 15 hospitals and many outpatient care centers into a specialized data warehouse environment for analysis and data mining is a daunting process for many reasons. Creating the scaffolding to facilitate data transfers requires many components including a mediating registry and meta data repository, a data warehouse, a federated identity manager, a standards based methods(s), a web-based portal or user interface, and the services management layer. This talk will describe how the North Shore Informatics Group (NSIG) created a pilot framework of a Service Oriented Architecture that integrated and shared data between different data management groups.

4:00 Conference Adjourns

Track 6:

eHealth Solutions

NEW

Integrating life sciences, IT and general healthcare to support the care delivery process, clinical decision support, patient-delivery, and innovative R&D of next generation health IT and personalized medicine solutions.

Monday, April 27

4:00 pm Event Chairperson's Opening Remarks
Cindy Crowninshield, Conference Director, Cambridge Healthtech Institute
Keynote Introduction: Rudy Potenzone, Ph.D., WW Industry Technology Strategist for Pharmaceuticals, Microsoft Corporation

4:15 PLENARY KEYNOTE

Research Computing and Infrastructure Technology
Chris Dagdigian, Founding Partner and Director of Technology, BioTeam, Inc.

5:00 Welcome Reception in the Exhibit Hall *Sponsored by* MERCK

Drop off a business card at the CHI Sales Booth for a chance to win 1 of 2 iPods ®!

7:00 Networking Event hosted by BiotechTuesday

Tuesday, April 28

7:30 am Registration and Morning Coffee

8:15 Event Chairperson's Opening Remarks
Phillips Kuhl, Co-founder and President, Cambridge Healthtech Institute
Keynote Introduction: Ken Buetow, Ph.D., Associate Director, Bioinformatics and Information Technology, National Cancer Institute

8:20 PLENARY KEYNOTE

Integrative Genomics
Eric E. Schadt, Ph.D., Executive Scientific Director, Genetics, Rosetta Inpharmatics/Merck Research Labs; Vice President and Chief Scientific Officer, Sage

9:00 Keynote Presentation & 2009 Benjamin Franklin Award

9:30 Coffee Break, Exhibit and Poster Viewing in the Exhibit Hall

EHR

10:50 Track Chairperson's Remarks
Brent Gendleman, CEO, 5AM Solutions

11:00 Global Trends in Convergence of Electronic Health Records and Clinical Trials
Sujith Eramangalath, M.Sc, Senior Analyst & Team Lead, Healthcare, Frost & Sullivan
This talk will expose the global trends and the potential benefits of convergence of electronic health records and clinical trials. The presentation will provide valuable insight to potential in the market in terms of products and revenues. This would be a stepping stone in providing alliance across the lifescience and healthcare information technology spectrum.

11:30 Scalable Architecture for Genetics Enabling Electronic Health Records
Samuel (Sandy) Aronson, Executive Director of IT, Center for Personalized Genetic Medicine, Partners HealthCare
Personalized medicine cannot reach its full potential without robust genetic infrastructure in the electronic health record (EHR). Partners HealthCare is enhancing its support for Genetics in its EHR. We will discuss the new genetics aware components that we are adding to our infrastructure and how we envision these components supporting new forms of clinical decision support going forward.

12:00 Tools and Techniques for Integration of Healthcare, Insurance, Social, Service, Research and Clinical Information
Bernard Wess, MA, CSP, CDP, President, PERSEID Software Ltd.
It is extremely difficult to design the integrated solutions for eHealth requiring decades of experience in insurance, healthcare delivery and clinical medicine. Our presentation will outline how two of the world's largest healthcare enterprises in defense and insurance are using new integrated systems integration tools and software to develop advanced applications that integrate healthcare, insurance, social, service, research and clinical information into a uniform architecture that is enabled for the Internet and Oracle 11G.

12:30 Luncheon Presentation *(Sponsorship Opportunity Available)*

Online Consumer Health

1:40 Chairperson's Remarks

1:45 Online Health Information Retrieval by Consumers and the Challenge of Personal Genomics
Mark Boguski, M.D., Ph.D., Founder, Resounding Health Incorporated

Technology Highlights

2:15 Increase the pace of R&D Innovation with Google
Paul Souza, Enterprise Sales Manager, Google Inc. *Sponsored by* Google
As the leader in search technology, Google has developed universal search for enterprises, which provides the ability to search all enterprise content – including intranets, file shares, databases, real-time business data, and content management systems –through one simple search box. Additionally, Google Apps is a collaboration suite that lets researchers collaborate in real-time, enhancing time to market. This talk will discuss Google's tools to increase researcher productivity and how life sciences companies have benefited from the use of these tools.

2:30 The Logistics of Adaptive Trial Design for Biomarker Discovery and Validation *Sponsored by* ALMAC
Austin Tanney, Ph.D., Scientific Liaison Manager, Almac Diagnostics
In the drive towards personalized medicine, the application of genomics in healthcare is increasingly relevant, particularly in cancer treatment. The development of molecular companion diagnostics will be the key in stratification of patients for targeted drug therapy. There are, however, many challenges in the development of clinically relevant companion diagnostics, for example, ensuring that sufficient patients are identified that respond appropriately to a treatment to allow for generation of a stable signature of response. The use of an adaptive trial design can address this issue although this requires sophisticated informatics infrastructures. This talk will discuss Almac's approach to biomarker discovery and validation and the informatics solutions offered for adaptive trial designs.

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Compliance, Security and Standards

2:45 Secure Digital Identities for Authentication & Signing in an Electronic Healthcare Community

John Hendrix, Program Director, SAFE-BioPharma Association

3:15 Refreshment Break, Exhibits and Poster Viewing in the Exhibit Hall

3:45 caBIG®: An *Interoperable IT Framework for Personalized Medicine* *Featured by* caBIG
(Joint w/Clinical and Medical Informatics Track)

Ken Buetow, Ph.D. Associate Director for Bioinformatics and Information Technology, National Cancer Institute

Personalized approaches to drug discovery, development and clinical care promise a new generation of preventive and preemptive health care. Countless data "disconnects" continue to afflict these biomedical "pillars", though, resulting in delays, dysfunction, and poor clinical outcomes. The prerequisite to overcome these hurdles is broad IT interoperability within and across institutions. Many of these challenges are addressed by caBIG® (cancer Biomedical Informatics Grid®). This session will showcase case studies in discovery research, biobanking, imaging, and clinical research; new models of connectivity; and a new ecosystem to drive continuous learning from bench to bedside and back.

4:45 Do Healthcare IT Standards Hamper the Advance of Science? *(Joint w/Clinical and Medical Informatics Track)*

Werner Ceusters, M.D., Director, Ontology Research Group, NYS Center of Excellence in Bioinformatics & Life Sciences

Standards are an absolute requirement to make semantic interoperability in healthcare informatics a reality. To achieve the goals of translational medicine, a variety of heterogeneous systems containing data at various levels of granularity need to be made interoperable. This talk will present an analysis of a number of adopted standards and highlight a number of problematic issues and propose directions for solutions.

5:15 2009 Best of Show Awards in Exhibit Hall

6:15 Exhibit Hall Closes

6:30-10:00 2009 Bio-IT World's Best Practices Awards/Dinner
(see page 2 for details)

Wednesday, April 29

7:30 am Registration and Morning Coffee

8:00 Event Chairperson's Opening Remarks

Kevin Davies, Ph.D., Editor-in-Chief, Bio-IT World

8:05 PLENARY KEYNOTE

Personalized Genomics – The Impact of Large-Scale Human Sequencing Projects

Clifford Reid, Ph.D., Chief Executive Officer, Complete Genomics, Inc.

8:45 KEYNOTE PANEL

The Future of Personal Genomics

A special plenary panel discussion featuring:

- *Jorge Conde, Co-Founder & CEO, Knome, Inc.*
- *Robert C. Green, M.D., M.P.H. Professor of Neurology, Genetics and Epidemiology, Boston University School of Medicine and Public Health*
- *John Halamka, M.D., M.S., CIO, Harvard Medical School*
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- *Dietrich Stephan, Ph.D., Co-founder and Chief Science Officer, Navigenics, Inc.*

9:45 Coffee Break, Exhibit Viewing, Vendor Theater Presentations, and Poster Competition in the Exhibit Hall

Novel Patient Treatments

10:45 Track Chairperson's Remarks

Ken Buetow, Ph.D. Associate Director for Bioinformatics and Information Technology, National Cancer Institute

11:00 Optimizing Patient Care by Incorporating PGx into the Clinic: Testing and Guidance

Tibor van Rooij, Bioinformatics Director, Génome Québec & Montreal Heart Institute Pharmacogenomics Centre

Prescribing medication is still largely experimental. It is impossible to accurately predict what benefit or harm a patient may gain as a result of taking a particular medication. This presentation will describe a project utilizing translational pharmacogenomics in prescribing medications. The project created a prototype informatics pipeline to inform doctors of an available pharmacogenomic test while prescribing a specific medication in a specific clinic. Physicians could then opt to receive test results and guidance and incorporate into the patient's Electronic Health Record (EHR) in a timely and useful manner.

11:30 Elevating the Research Enterprise - Overcoming the Challenges to Discoverability in Healthcare and Life Science Research *Sponsored by* Microsoft

Paul Mattes, M.B.A., Director, Life Sciences, Health Solutions Group, Microsoft Corporation

This session will examine the challenges to the discoverability of novel treatments for personalized medicine. Participants will learn about a scalable and customizable environment to design, manage, monitor, and execute the key processes of scientific inquiry. Additionally, participants will learn the importance of bringing together structured and unstructured data (eg., text/literature) and how translational medicine connects basic research directly to patient care.

12:00 Integrating Personal Genomics into Medical Practice

Dietrich Stephan, Ph.D., Co-founder and Chief Science Officer of Navigenics

Navigenics uses microarray technology to perform genome-wide scans for approximately one million DNA markers in order to offer individuals and their healthcare providers personalized risk assessments based on relative disease risks for a variety of health conditions. Navigenics services are part of several studies, including those being performed by Mayo Clinic and Scripps, and are being integrated into medical practices around the country. Attendees will understand the technology and markers used in disease risk assessment; criteria for culling published clinical and medical studies on genetic risk factors; relative disease risk as a basis for preventive health care; and changes in the medical paradigm.

12:30 Luncheon in the Exhibit Hall

2:00 Exhibit Hall Closes

Data Access and Application to Improve Patient Health

1:55 Chairperson's Remarks

2:00 The Pediatric Knowledgebase -- A Hospital-based, Decision Support System to Guide Pharmacotherapy

Jeffrey S. Barrett, Ph.D., FCP, Director, Laboratory for Applied PK/PD, The Children's Hospital of Philadelphia; Research Associate Professor, Pediatrics, University of Pennsylvania Medical School

The Pediatric Knowledgebase being developed at The Children's Hospital of Philadelphia attempts to address many of the difficulties with managing pediatric pharmacotherapy. Attendees will learn how real-time decision support to guide individual patient decisions is accomplished in our PKB platform and how the broader adoption of similar systems can improve clinical outcomes for children and reduce patient costs.

2:30 G-DOC: A Framework for Personalized Medicine

Subha Madhavan, Ph.D., Director, Clinical Research Informatics, Lombardi Cancer Center, Georgetown University

This talk will present The Georgetown Database of Cancer (G-DOC), a project that creates a rich repository of clinical and molecular information that permits oncologists to personalize therapy for cancer patients. The G-DOC tests the concept that "knowledge is power" by obtaining all possible information about an individual's cancer to develop an evidence-based treatment plan. Through the G-DOC effort, The Lombardi Comprehensive Cancer Center at Georgetown University Medical Center will revolutionize the treatment of cancer through a Systems Medicine approach.

3:00 Establishing the Collaboration Center of Health Information Application (CCHIA) to Enable Public Health Policy Making

Belinda Chen, Ph.D., Deputy Director, IDEAS, Institute for Information Industry

As 98% of Taiwanese citizens are covered by the government's national health insurance, the Bureau of National Health Insurance in Taiwan contains a wealth of clinical/health information that could be leveraged by public healthcare researchers to drive innovation and improve quality of life. This talk will describe how the Department of Health initiated a project that links four nationwide databases (health insurance, cancer registration, household registration, and death registration) to establish CCHIA. We will describe the IT architecture and system implemented to construct the centralized data warehouse at the national level, as well as the ROI that can be achieved in terms of biomedical research, public health policy making and cost.

3:30 Service Oriented Architecture – A New Data Sharing Architecture *(Joint w/IT Infrastructure & Operations and Clinical and Medical Informatics Tracks)*

Robert Lundsten, Director of Biorepository, Feinstein Institute for Medical Research

The ability to integrate data from multiple independent data repositories across the North Shore Long Island Jewish Health System's (NSLIJHS) 15 hospitals and many outpatient care centers into a specialized data warehouse environment for analysis and data mining is a daunting process for many reasons. Creating the scaffolding to facilitate data transfers requires many components including a mediating registry and meta data repository, a data warehouse, a federated identity manager, a standards based methods(s), a web-based portal or user interface, and the services management layer. This talk will describe how the North Shore Informatics Group (NSIG) created a pilot framework of a Service Oriented Architecture that integrated and shared data between different data management groups.

4:00 Conference Adjourns

Schedule-at-a-Glance

Monday, April 27	Pre-Conference Events *(Separate Registration Required)*					
7:00 - 8:00	Pre-Conference Registration and Morning Coffee					
8:00-11:30	(W3) Visualization					
8:00-4:00	(W5) High Performance Computing: Trends and Applications					
12:30-4:00	(W1) Application of Wikis by Lifescience Organizations, (W2) Advances in Drug Safety Informatics, (W4) Recent Advances in Molecular Dynamics					
2:00-6:00	Main Conference Registration					
4:00-5:00	Plenary Keynote: Chris Dagdigian, Founding Partner and Director of Technology, BioTeam, Inc.					
5:00-7:00	Welcome Reception in Exhibit Hall - chance to win 1 of 2 iPods®!					
7:00	Networking Event hosted by BiotechTuesday (see page 2 for more details)					
Tuesday, April 28	**Main Conference**					
7:30-6:00	Registration					
7:30-8:15	Morning Coffee					
8:15-9:00	Plenary Keynote: Eric E. Schadt, Ph.D., Executive Scientific Director, Genetics, Rosetta Inpharmatics/Merck Research Labs					
9:00-9:30	Keynote Presentation & 2009 Benjamin Franklin Award (see page 2 for details)					
9:30	Exhibit Hall Opens (until 7:15p)					
9:30-10:50	Coffee Break, Exhibits and Poster Viewing in the Exhibit Hall-Start playing our "Game Card"					
	Track 1	**Track 2**	**Track 3**	**Track 4**	**Track 5**	**Track 6**
Concurrent Tracks	IT Infrastructure & Operations	Informatics for Genomic Medicine	Predictive and *in silico* Science	Computational Chemistry	Clinical and Medical Informatics	eHealth Solutions
10:50-12:30	Operations: Grids 'n Clouds	Biological Data: Modeling & Imaging for Gene Expression	*in silico* Modeling and Simulation Tools	Enabling Discovery through Access to 'Open Source' Science, Databases and Software Tools	EDC	EHR
12:30-1:40	Luncheon Workshop sponsored by Microsoft	Lunch (on own / workshop luncheon sponsorships available)		Luncheon Workshop sponsored by Tripos	Lunch (on own / workshop luncheon sponsorships available)	
1:45-3:15	Operations: Grids 'n Clouds & Sourcing	Biological Data: Modeling & Imaging for Gene Expression & Technology Highlights	*in silico* Modeling and Simulation Tools	Screening and Modeling: Success Stories and the Challenges that Remain	Clinical Trial Operations and Management	Online Consumer Health & Technology Highlights & Compliance, Security and Standards
3:15-3:45	Refreshment Break, Exhibit and Poster Viewing **Continue to play "Game Card"!					
3:45-5:15	Operations: Sequencing	Discovery Informatics and Platforms	Modeling Toxicity Data	Managing the Volume of Data and Transforming it into Knowledge	Clinical Outcomes and Standards	Compliance, Security and Standards
5:15	2009 Best of Show Awards in Exhibit Hall (see page 2 for details)					
6:15	Exhibit Hall Closes					
6:30-10:00	2009 Bio-IT World's Best Practices Awards/Dinner (see page 2 for details)					
Wednesday, April 29	**Main Conference**					
7:30-2:30	Registration					
7:30-8:00	Morning Coffee					
8:00-8:55	Plenary Keynote: Clifford Reid, Ph.D., Chief Executive Officer, Complete Genomics, Inc.					
8:55-9:45	Plenary Keynote Panel: The Future of Personal Genomics Robert C. Green, M.D. (Boston University School of Medicine and Public Health), John Halamka, M.D., M.S. (Harvard Medical School), Clifford Reid, Ph.D. (Complete Genomics, Inc.), Dietrich Stephan, Ph.D. (Navigenics, Inc.) Jorge Conde (Knome, Inc.) and Philip Reilly (Third Rock Ventures)					
9:45	Exhibit Hall Opens (until 2:00pm) **Continue to play "Game Card"!					
9:45-10:50	Coffee Break and Exhibit Viewing and Poster Competition					
	Track 1	**Track 2**	**Track 3**	**Track 4**	**Track 5**	**Track 6**
Concurrent Tracks	IT Infrastructure & Operations	Informatics for Genomic Medicine	Predictive and *in silico* Science	Computational Chemistry	Clinical and Medical Informatics	eHealth Solutions
10:50-12:30	Infrastructure: Collaborations & Social Networking	Disease Pathway Solutions	Systems Biology & Systems Integration	Integrative Approaches for Chemical and Biological Data and Knowledge Management	Clinical Application of Personalized Medicine	Novel Patient Treatments
12:30-1:45	Luncheon in Exhibit Hall **Last chance to play the Game Card, turn in your Game Card at the CHI Resign Sales Booth# 4 ~ 2 iPods® and 2 Nintendo® Wii™ Systems will be raffled! ~ Drawing at 1:30pm at the Vendor Theatre.					
1:55-4:00	Operations: Data Management and Storage	Leveraging Data and Standards	Session Theme TBD	Case Studies and Lessons Learned from Your Peers	Clinical Data Management	Data Access and Application to Improve Patient Health
2:00	Exhibit Hall closes					
4:00	Conference Adjourns					

Apple® is not a sponsor or participant in this program.

For detailed abstracts please visit:

www.Bio-ITWorldExpo.com

Sponsorship & Exhibit Information:

Your sponsorship provides you with the opportunity to promote your company's solutions to this targeted and hard to reach audience. Custom designed sponsorship programs enable you to competitively position your company as a thought leader in biotech and pharma industries, while collecting quality leads in formal and informal settings. CHI sales managers work with you to shape a Sponsorship program that suits your company's strategic sales and business development objectives.

Benefits of Exhibiting & Sponsoring

- Bio-IT World is the only life sciences conference that focuses on enabling technologies for predictive biology.
- Access to highly influential audience consisting of senior level scientists, IT professionals and executives from organizations across the life sciences industry including pharmaceutical, biotechnology, health systems, academia, government, and national laboratories.
- The Best of Show Award offers exhibitors an opportunity to distinguish their products from the competition. Judged by a joint team of Bio-IT World magazine editors and leading industry experts in the Exhibit Hall, this awards program will identify exceptional innovation in technologies used by life science professionals today. Deadline for entry is April 1st so reserve your booth space today!
- Benefit from dedicated exhibit hours designed to promote traffic in the exhibit hall.
- Enhance your company's marketing and branding efforts by participating in CHI's Co-Operative Marketing Program.

Other Promotional Opportunities Include:

- Hospitality Suite Reception
- Exhibit Hall Reception
- Tote Bags
- Tote Bag Inserts
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- And more!

Sponsorship Opportunities Include:

Sponsored Presentations
Select a conference program and present your latest technologies or solutions to qualified end-users for 15-30 minutes. Presentations are given during the scientific agenda, ensuring your audience is seated and ready to listen.

Luncheon Workshops
Whether you are ready to present an exciting new technology, preparing for a new product launch or need feedback on a specific idea, this is the perfect platform for you to present in front of your target audience. Sponsors will give a 30-minute presentation while lunch is served on your company's behalf.

Focus Groups
CHI will deliver 7-10 pre-qualified participants and provide the venue for your market research focus group

Invitation-Only VIP Dinner
Networking at its best! You hand pick your top prospects for an elegant evening at a premier local restaurant. Establish lasting relationships and create qualified business leads with this exclusive program.

Vendor Theatre Presentations
Deliver your message with a 20-minute presentation to delegates in the exhibit hall during session breaks. The theatre is equipped with AV and seating for 25-30. In addition, CHI will promote your presence on the event website, program and exhibit guide, through signage and with announcements at the event.

User Group Meetings
CHI provides integrated services to help you design, promote and execute your conference, user group meeting or custom event, nationally or internationally. You can select those capabilities for which you want assistance, or work with a CHI comprehensive solution. With over 16 years experience organizing and administering events worldwide, we can help enhance your existing event, provide audience development expertise, as well as design and tailor an event to meet your needs and secure your target market.

CHI's Co-Operative Marketing Program
CHI is pleased to help you market to your prospect list at a shared cost. We will offer your prospects a discounted rate to attend the conference on your behalf via mailing or email campaigns. CHI's Marketing Managers will customize a specific message to your target audience.

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Katelin Fitzgerald
Manager, Business Development
781.972.5458 • kfitzgerald@healthtech.com
or
Ilana Schwartz
Manager, Business Development
781.972.5457 • ischwartz@healthtech.com

HOTEL & TRAVEL

Conference Venue:
Seaport World Trade Center
200 Seaport Boulevard
Boston, MA 02210
T: 617-385-5049

Host Hotel:
Seaport Hotel (located directly across the street)
One Seaport Lane
Boston, MA 02210
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Discounted Room Rate: $249 s/d
Discounted Room Rate Cut-off Date: April 8, 2009

To make reservations please visit www.seaportboston.com and enter Group Code: BIOIT9. You may also call the hotel directly to reserve your sleeping accommodations. Identify yourself as a Cambridge Healthtech Institute conference attendee to receive the discounted room rate. Reservations made after the cut-off date or after the group room block has been filled (whichever comes first) will be accepted on a space-and-rate-availability basis. Rooms are limited, so please book early.

Flight Discounts:
To receive a 5% or greater discount on all American Airline flights please use one of the following methods: Call 1-800-433-1790 (authorization code A4819SS). Go online at www.aa.com (enter A4819SS in promotion discount box). Contact our designated travel agent, Wendy Levine, at 1-800-336-5248 ext. 137.

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REGISTER 3 — 4th IS FREE: Individuals must register for the same conference or conference combination and submit completed registration forms together for discount to apply. Please reproduce this registration form as needed.

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*Email is not a mandatory field. However, by excluding your email you will not receive notification about online access to pre-conference presenter materials, conference updates and networking opportunities.

How would you prefer to receive notices from CHI: EMAIL: ❒ Yes ❒ No FAX: ❒ Yes ❒ No

2. PRICING INFORMATION

PRE-CONFERENCE WORKSHOPS

Choose 1 Half Day Workshop	**Choose 2 Half Day Workshops or 1 All Day Workshop** BEST VALUE
❒ $595 Commercial	❒ $895 Commercial
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Half Day Workshops

❒ (W1) Application of Wikis by Lifescience Organizations (Afternoon)
❒ (W2) Advances in Drug Safety Informatics (Afternoon)
❒ (W3) Visualization (Morning)
❒ (W4) Recent Advances in Molecular Dynamics: Target Elucidation and Ligand Docking (Afternoon)

All Day Workshop (check one box only)

❒ (W5) High Performance Computing: Trends and Applications

MAIN CONFERENCE	COMMERCIAL	ACADEMIC, GOVERNMENT, HOSP. AFFILIATED
Early Registration (until January 23, 2009)	❒ $1,345	❒ $675
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Registration after March 13, 2009 and onsite	❒ $1,845	❒ $925
DISCOUNTS*		
❒ Poster Discount	❒ $50 Off	❒ $50 Off

TRACK SELECTION: *(Please Indicate the One Track You Are Most Likely To Attend)*

Conference Tracks

❒ Track 1: IT Infrastructure & Operations
❒ Track 2: Informatics for Genomic Medicine
❒ Track 3: Predictive and *in silico* Science
❒ Track 4: Computational Chemistry
❒ Track 5: Clinical and Medical Informatics
❒ Track 6: eHealth Solutions

Bio-IT World's Best Practices Awards Dinner (April 28, 2009) ❒ $105

❒ I cannot attend but would like to purchase The Bio-IT World Conference & Expo conference CD for $750 (plus shipping). Massachusetts delivery will include 5% sales tax.
❒ Please send information on exhibiting and opportunities to present workshops.

3. PAYMENT INFORMATION

❒ Enclosed is a check or money order payable to Cambridge Healthtech Institute, drawn on a U.S. bank, in U.S. currency.
❒ Invoice me, but reserve my space with credit card information listed below. Invoices unpaid two weeks prior to conference will be billed to credit card at full registration rate. Invoices must be paid in full and checks received by the deadline date to retain registration discount. If you plan to register on site, please check with CHI beforehand for space availability.

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Present a Poster and Save $50!

Cambridge Healthtech Institute encourages attendees to gain further exposure by presenting their work in the poster sessions.
To secure a poster board and inclusion in the conference CD, your abstract must be submitted, accepted and registration paid in full by March 16, 2009. Register online to use the Poster Abstract Submission form or, if you register by phone, fax, or mail, you will receive Poster Abstract Submission guidelines Via email.
I am interested in presenting a poster at
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Title

CHI Insight Pharma Reports

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Additional Registration Details

Each registration includes all conference sessions, posters and exhibits, food functions, and a copy of the conference CD.

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- Request a refund minus a $100 processing fee per conference
- Request a refund minus the cost ($750) of ordering a copy of the CD

NOTE: Cancellations will only be accepted up to two weeks prior to the conference.

Program and speakers are subject to change.

Video and or audio recording of any kind is prohibited onsite at all CHI events.

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250 First Avenue, Suite 300, Needham, Massachusetts 02494
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