Celebrating 10 YEARS OF Innovation

Final Agenda

Cambridge Healthtech Institute's Tenth Annual

Bio·IT World CONFERENCE & EXPO '11

April 12-14, 2011
World Trade Center
Boston, MA

Enabling Technology. Leveraging Data. Transforming Medicine.

Featured Presentations by:

caBIG cancer Biomedical Informatics Grid®

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Official Publication:

Bio·IT World

Organized & Managed by:

CONCURRENT TRACKS:

1. IT Infrastructure – Hardware
2. IT Infrastructure – Software
3. Cloud Computing NEW!
4. Bioinformatics
5. Next-Generation Sequencing Informatics NEW!
6. Systems & Predictive Medicine
7. eClinical Solutions for Clinical Trials and Clinical Operations
8. eHealth and HIT Solutions for Personalized Medicine
9. Drug Discovery Informatics NEW!

EVENT FEATURES:

- Access All Nine Tracks for One Price
- Network with 1,700+ Global Attendees
- Hear 125+ Technology and Scientific Presentations
- Attend *Bio-IT World*'s Best Practices Awards
- Connect with Attendees Using CHI's Intro-Net
- Participate in the Poster Competition
- Choose from 13 Pre-Conference Workshops
- See the Winners of the following 2011 Awards:
  - Benjamin Franklin
  - Best of Show
  - Best Practices
- View Novel Technologies and Solutions in the Expansive Exhibit Hall
- And Much More!

KEYNOTE PRESENTATIONS BY:

Stephen Wolfram, Ph.D., CEO, Wolfram Research; Creator of Wolfram|Alpha

Bryn Roberts, Ph.D., Global Head, Informatics, Pharma Research and Early Development, F. Hoffmann-La Roche Ltd.

KEYNOTE PANEL:

A special plenary session featuring a series of succinct, forward-looking presentations by:

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

Martin D. Leach, Ph.D., Executive Director, MRL IT for Discovery & Pre-Clinical Sciences, Merck & Co.

Mark Boguski, M.D., Ph.D., Founder, Resounding Health Incorporated

Jamie Heywood, Co-founder and Chairman, PatientsLikeMe

Debra Goldfarb, Senior Director, Strategy, Microsoft

Yury Rozenman, Global Head of Marketing, Pharmaceutical and Life Sciences Sector, BT Global Services

Cambridge Healthtech Institute, 250 First Avenue, Suite 300, Needham, MA 02494
Phone: 781-972-5400 • Toll-free in the U.S. 888-999-6288 • Fax: 781-972-5425

Bio-ITWorldExpo.com

SCHEDULE-AT-A-GLANCE

Tuesday, April 12, 2011	
8:00am – 4:00pm	Pre-Conference Workshops* **Separate Registration Required*
4:00pm – 5:00pm	Keynotes
5:00pm	Exhibit Hall Open
5:00pm – 7:00pm	Welcome Reception in the Exhibit Hall with Poster Viewing
Wednesday, April 13, 2011	
7:55am - 9:45am	Keynote & Awards Program
9:45am	Exhibit Hall Opens
9:45am-10:50am	Coffee Break in the Exhibit Hall with Poster Viewing
10:50am – 12:30pm	Tracks 1-9
12:30pm – 1:40pm	Luncheon Presentations
1:40pm – 3:15pm	Tracks 1-9
3:15pm - 3:45pm	Refreshment Break in Exhibit Hall with Poster Viewing
3:45pm – 5:15pm	Tracks 1-9
5:15pm – 6:15pm	Best of Show Awards in the Exhibit Hall
Thursday, April 14, 2011	
8:45am - 10:30am	Keynote Panel
10:30am	Exhibit Hall Opens
10:30am – 10:55am	Coffee Break in the Exhibit Hall with Poster Viewing
10:55am – 12:30pm	Tracks 1-9
12:30pm – 2:00pm	Lunch in the Exhibit Hall with Poster Viewing
2:00pm – 4:00pm	Tracks 1-9

KEYNOTE PRESENTATIONS BY:

Making the World's Knowledge Computable

Stephen Wolfram, Ph.D., CEO, Wolfram Research; Creator of Wolfram|Alpha

Stephen Wolfram is the founder and CEO of Wolfram Research, the creator of Mathematica and Wolfram|Alpha, and the author of *A New Kind of Science*. His career has been characterized by a sequence of original and significant achievements, including the recent launch of the computational knowledge engine Wolfram|Alpha. As an academic, he made various contributions to particle physics, cosmology, and computer science, and played a founding role in the development of complexity theory.

Interacting with Complex Information Landscapes: Integration and Next Generation User Interfaces

Bryn Roberts, Ph.D., Global Head, Informatics, Pharma Research and Early Development, F. Hoffmann-La Roche Ltd.

Bryn gained his BSc and PhD in pharmacology from the University of Bristol, UK. Following post-doctoral work in neuropharmacology, he joined Organon as Senior Scientist in 1996. A number of roles followed with Zeneca and AstraZeneca, including team and project leader roles in high throughput screening and lead discovery informatics. In 2004 he became head of Discovery Informatics at the AstraZeneca sites in Cheshire, UK. Bryn moved to Basel in 2006 to join Roche, where he is currently Global Head of Informatics in Pharma Research and Early Development.

KEYNOTE PANEL:

As a change-up to one of the usual keynotes at the Expo, we're offering a session that will feature a series of succinct, forward-looking plenary presentations. Five special guests have been invited to share their unique perspectives on the future challenges facing the research, pharma, and medical communities. Views expressed are not necessarily those of their employers.

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

Debra Goldfarb, Senior Director, Strategy, Microsoft

Martin D. Leach, Ph.D., Executive Director, MRL IT for Discovery & Preclinical Sciences, Merck & Co.

Mark Boguski, M.D., Ph.D., Founder, Resounding Health Incorporated

Jamie Heywood, Co-founder and Chairman, PatientsLikeMe

Yury Rozenman, Global Head of Marketing, Pharmaceutical and Life Sciences Sector, BT Global Services

AWARDS PROGRAMS

Cambridge Healthtech Institute and *Bio-IT World* will again be recognizing and celebrating leaders in innovation through the "Best of Show Award" and "Best Practices Award" Programs. Finalists in the Best of Show Awards will be recognized on-site, and winners will be honored in a ceremony on the exhibit hall floor. The Best Practices Awards Program will take place in the Ampitheater on Wednesday morning April 13, 2011.

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, this awards program will identify exceptional innovation in technologies used by life sciences professionals today. Judging and the announcement of winners is conducted live in the Exhibit Hall. To learn more about this program and submission deadlines, please contact Demetrios Louloudes at 781-972-5445 or email dlouloudes@healthtech.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. Winners will be selected by a peer review expert panel in early 2011. Bio-IT World will present the Awards in the Ampitheatre at 9:10am on April 13, 2011. Early bird deadline (no fee) for entry is December 19, 2010 and final deadline (fee) is January 14, 2011. Full details including previous winners and entry forms are available at www.Bio-ITWorldExpo.com.

2011 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 Wednesday, April 13, 2011.

Morning Workshops 8:00–11:30am

(W2) Pathway-Based Analysis: A Systematic Approach to Biomarker Discovery

Edward Khokhlovich, Technical Scientific Leader, Biomarker Development, Novartis Institutes for Biological Research, Cambridge, MA
Jeffrey Tsao, Ph.D., Associate Director, Oncology Translational Medicine, Novartis Institutes for Biomedical Research, Cambridge, MA
Lellean JeBailey, Ph.D., Application Scientist, Thomson Reuters

(W4) Creating a Best of Breed Informatics Environment for Your Organization

Jonas Almeida, Abell-Hanger Distinguished Professor, Department of Bioinformatics and Computational Biology, University of Texas MD Anderson Cancer Center
Gregg TeHennepe, Senior Manager, Research Liaison, Information Technology, The Jackson Laboratory
Jonas Almeida, Professor and Director, Division of Informatics, Department of Pathology, University of Alabama at Birmingham

(W5) Building and Using an Ontological Framework for Drug Discovery to Clinical Data

Elgar Pichler, Ph.D., Computational Biologist, Boston

(W6) Tools and Methods for RNA-seq Analysis

Michael Reich, Director of Cancer Informatics Development, Broad Institute of MIT and Harvard
Jim Robinson, Ph.D., Senior Software Engineer, Broad Institute of Harvard and MIT
Helga Thorvaldsdottir, Senior Engineering Project Manager, Cancer Informatics, Broad Institute of Harvard and MIT

(W9) Utilization of EHRs/EMRs to Further Drug and Disease Related Research

Zhaohui (John) Cai, Ph.D., Director, Biomedical Informatics, Clinical Information Science, AstraZeneca Pharmaceuticals, Inc.
Werner Ceusters, Ph.D., Director, Ontology Research Group, NYS Center of Excellence in Bioinformatics & Life Sciences
Kaushal Desai, Global Informatics Lead, Real World Evidence Program, AstraZeneca Pharmaceuticals, Inc.
William Hogan, M.D., Associate Professor and Chief, Biomedical Informatics, University of Arkansas for Medical Sciences
Richard Scheuermann, Ph.D., Professor, Director, Division of Biomedical Informatics, University of Texas Southwestern Medical Center
Matthew Samore, M.D., VA Salt Lake City Health Care System; Professor, Division of Epidemiology, University of Utah; Linked Health Data Foundation Board of Directors

(W10) Imaging Informatics: Data Management and Annotation for the Life Sciences

Stefan Baumann, Head of Imaging Infrastructure, Biomarker Development / Clinical Imaging, Novartis Pharma AG
Baek Hwan (BK) Cho, Ph.D., Postdoctoral Fellow, Murphy Lab, Lane Center for Computational Biology, Carnegie Mellon University
Chinh Dang, Ph.D., Senior Director of Technology, Allen Institute for Brain Science
Kevin Eliceiri, Ph.D., Director, Laboratory for Optical and Computational Instrumentation, College of Engineering, University of Wisconsin-Madison
David Orloff, MBA, Manager, Image Library, ASCB - American Society for Cell Biology
Lydia Ng, Ph.D., Director of Atlas Development, Allen Institute for Brain Science

Afternoon Workshops 12:30–4:00pm

(W3) Conquering the Complexity of Protein Data: Genes are Easy

Florian Nigsch, Ph.D., Presidential Postdoctoral Fellow, Novartis Institutes for BioMedical Research

Nurit Haspel, Assistant Professor, University of Massachusetts, Boston

Sanguthevar Rajasekaran, Ph.D., Chair and Professor, Computer Science and Engineering, University of Connecticut

Rafael Bruschweiler, Ph.D., George M. Edgar Professor of Chemistry and Biochemistry; Chemical Sciences Laboratory & National High Magnetic Field Laboratory, Florida State University

C. James McKnight, Associate Professor of Physiology & Biophysics, Boston University School of Medicine

(W7) Visualization of Large-Scale Biological Data

Nils Gehlenborg, Ph.D., Research Associate, Center for Biomedical Informatics, Harvard Medical School

Miriah Meyer, Ph.D., Scientist, School of Engineering and Applied Science, Harvard University

(W11) Cloud Computing: Applications and Advances

Sponsored by:

SAVVIS

Richard Wellner, President, Object Environments

Reed Smith, Director of Cloud Product Management, Savvis

Ravi K. Madduri, Fellow, Computation Institute, University of Chicago; Project Manager, Mathematics and Computer Science Division, Argonne National Laboratory

Neil Bahroos, Director, Initiative in Biomedical Informatics, University of Chicago

(W12) Advancing Personalized Cancer Medicine through IT Innovation

Sharon Marsh, Ph.D., Assistant Professor, Pharmacy and Pharmaceutical Sciences, University of Alberta

Tibor van Rooij, Ph.D. Candidate, Pharmacy and Pharmaceutical Sciences, University of Alberta; former Director of Bioinformatics, Génome Québec and Montreal Heart Institute Pharmacogenomics Centre

(W13) Next Generation Sequencing: From Data to Discovery - "I Have My Data, Now What?"

Joseph D. Szustakowski, Ph.D., Senior Group Head, Novartis Institutes for BioMedical Research, Cambridge, MA

Robert Bruccoleri, Ph.D., President, Congenomics LLC

Jadwiga Bienkowska, Principal Scientist, Head of Computational Biology Group, Genetics and Genomics, BiogenIdec

Steve Lincoln, Ph.D., Vice President, Scientific Applications, Complete Genomics

Full Day 8:00am–4:00pm

(W1) Current Methods for Computational Toxicology and Chemogenomics

Jeremy Jenkins, Ph.D., Senior Investigator I, Developmental & Molecular Pathways, Quantitative Biology, Novartis Institutes for BioMedical Research

Josef Scheiber, Ph.D., Pharma Research & Early Development Informatics, F. Hoffmann-La Roche Ltd.

Christopher Southan, Ph.D., ChrisDS Consulting

Luis Tari, Ph.D., Postdoctoral Research Fellow, Biomedical Informatics, F. Hoffmann-La Roche Ltd.

Patrick Walters, Ph.D., Senior Research Fellow, Computational Chemistry & Molecular Modeling, Vertex Pharmaceuticals

Antony Williams, Ph.D., Vice President, Strategic Development, ChemSpider, Royal Society of Chemistry

Yuriy Gankin, Ph.D., Co-Founder and Chief Scientific Officer, GGA Software Services

Barry Hardy, OpenTox Project Coordinator, Douglas Connect, Switzerland

IT Infrastructure – Hardware

TUESDAY, APRIL 12

7:00 am Workshop Registration and Morning Coffee

8:00 - 4:00 pm Pre-Conference Workshops*

**Separate Registration Required. See page 3 for details.*

2:00 - 6:00 Main Conference Registration

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

4:05 Keynote Introduction
Chris Blessington, Life Sciences Solutions Architect, Isilon

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PLENARY KEYNOTE

4:15 Making the World's Knowledge Computable
Stephen Wolfram, Ph.D., CEO, Wolfram Research; Creator of Wolfram|Alpha

5:00 Welcome Reception in the Exhibit Hall and Poster Viewing

Sponsored by BLUE ARC

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WEDNESDAY, APRIL 13

7:00 am Registration and Morning Coffee

8:00 Event Chairperson's Opening Remarks
Phillips Kuhl, Co-Founder and President, Cambridge Healthtech Institute

8:05 Keynote Introduction
Grant Stephen, CEO, Tessella, Inc.

Sponsored by Tessella Technology & Consulting

PLENARY KEYNOTE

8:15 Interacting with Complex Information Landscapes: Integration and Next Generation User Interfaces
Bryn Roberts, Ph.D., Global Head, Informatics, Pharma Research and Early Development, F. Hoffmann-La Roche Ltd.

8:45 Benjamin Franklin Award/Presentation:
Jonathan Eisen, Ph.D., Professor, Genome Center, University of California, Davis

9:10 Best Practices Awards Program

9:45 Coffee Break in the Exhibit Hall and Poster Viewing

Sponsored by SCYNEXIS

IT INFRASTRUCTURE TRENDS AND PROJECTIONS

10:50 Chairperson's Remarks
Barbara Murphy, CMO, Panasas, Inc.

Sponsored by panasas

11:00 FEATURED PRESENTATION
HPC Trends from the Trenches *(Joint with Tracks 1 - 3)*
Chris Dagdigian, Founding Partner and Director of Technology, BioTeam, Inc.
This talk will review some of the BioTeam's recent work with biotech, pharmaceutical, government and enterprise clients. As an independent consulting firm, the BioTeam is able to see how HPC problems in life science informatics have been approached by organizations of varying type and size. We will address common problems and observed trends in computing, workflows and data movement, along with details on particularly clever solutions observed in production environments around the world.

11:30 Strategic Planning for IT Infrastructure in Support of Data-Intensive Science
Gregg TeHennepe, Senior Manager, Research Liaison, Information Technology, The Jackson Laboratory
In 2010, Jackson produced a whitepaper surveying the IT infrastructure needed to support the biological and genetic research projected over the next five years. This talk will review those projections, survey the key issues facing the institution, and cover the actions and efforts that have been undertaken to meet these needs.

12:00 pm Redefining Storage in the Era of Big Data: An End-User Roundtable Discussion

Sponsored by ISILON SYSTEMS

Stuart Glenn, Software Engineer, Oklahoma Medical Research Center
Yate-Ching Yuan, Director, Biomedical Informatics, City of Hope
James Lowey, IT Manager, Translational Genomics Research Institute
With the onset of the latest generation of DNA sequencing technologies, scientists and IT pros are challenged with how to best store and manage this tsunami of data, with few answers from traditional storage systems. Bioinformaticists, researchers, scientists and IT staff will discuss these changes and how they impede the next generation of discovery. Through real-world experience and first-hand perspectives, end-users will share the strategies and technologies they've deployed to overcome these challenges and drive new breakthroughs in scientific understanding.

12:30 Luncheon Presentation
Solving Data Management Challenges in Genome Sequencing Research

Sponsored by hp

Peter Brey, Worldwide Business Development Manager, HP Storage
Research organizations are faced with rapidly exploding amounts of data. Analyzing, storing, and managing this data is becoming particularly challenging. Learn how HP's Converged Infrastructure Strategy can provide an innovate solution for data management.

1:40 Chairperson's Remarks
Barbara Murphy, CMO, Panasas, Inc.

1:45 Comprehensive Picture of Biopharma IT & Knowledge Management
John Keilty, Vice President, Informatics, Infinity Pharmaceuticals

DATA CENTERS: TECHNOLOGIES, APPLICATIONS AND REDESIGN

2:15 Data Warehousing to Enable Superior Decision Support across the R&D Process
Eric Perakslis, Ph.D., Vice President, Research & Development IT, Johnson & Johnson Pharmaceuticals Research and Development

2:45 Fast Access to Terascale Data – Large Memory x86 Servers Speed Bioscience Research

Sponsored by sgi

Jill Matzke, Ph.D., Director, Server Marketing, SGI
In the dynamic world of bioscience, one constant is data explosion. New servers with terabytes of memory drive huge performance gains in computational chemistry, genomics and system biology. This means not only great ROI, but entirely new modes of discovery.

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

Track 1 explores high performance computing technologies and techniques (traditional and accelerated technologies), architecture to handle data in a concise fashion, transferring data across networks (storage, management, safety, visualization), and open source support.

3:45 Biogen Idec's Data Center Redesign
Mike Russo, Information Technology Director, Global Infrastructure and Operations, Biogen Idec

4:15 Unifying Networking Technologies in Data Centers
Vijay Samalam, Senior Director, IT and Scientific Computing, Janelia Farm Research Campus, Howard Hughes Medical Institute
This presentation will detail some of our attempts to use 10G Ethernet as a single unifying networking technology in our data center. We will describe our experiences installing and running one of the largest 10G Ethernet networked high performance computing commodity cluster in our data center. Co-collaborators of this work include Goran Ceric, Manager, Scientific Computing Systems and Spartaco Cicerchia, Manager, Networking.

4:45 Sponsored Presentation *Sponsored by*
Jacob Farmer, CTO, Cambridge Computer

5:15 Best of Show Awards in the Exhibit Hall

6:15 Exhibit Hall Closes

THURSDAY, APRIL 14

8:45 Event Chairperson's Opening Remarks
Kevin Davies, Ph.D., Editor-in-Chief, Bio-IT World

8:50 KEYNOTE PANEL:
KEYNOTE INTRODUCTION *Sponsored by* BT
A special plenary session featuring a series of succinct, forward-looking presentations by:
Ken Buetow, Ph.D., Associate Director, Bioinformatics and Information Technology, National Cancer Institute
Debra Goldfarb, Senior Director, Strategy, Microsoft
Martin D. Leach, Ph.D., Executive Director, MRL IT for Discovery & Pre-Clinical Sciences, Merck & Co.
Mark Boguski, M.D., Ph.D., Founder, Resounding Health Incorporated
Jamie Heywood, Co-founder and Chairman, PatientsLikeMe
Yury Rozenman, Global Head of Marketing, Pharmaceutical and Life Sciences Sector, BT Global Services

10:30 Coffee Break in the Exhibit Hall with Poster Competition

INVESTMENT IN VIRTUALIZED AND NETWORK STORAGE INFRASTRUCTURE: END-USER PERSPECTIVES

10:55 Chairperson's Remarks

11:00 End-User Value of Virtualized and Network Storage Infrastructure Investment
Jeff Pennington, Director, Translational Informatics, Center for Biomedical Informatics, The Children's Hospital Of Philadelphia Research Institute
This presentation will explore the key role that virtualization and flexible, multifaceted storage infrastructure plays in an academic R&D environment. The perspective of this talk arises from the hospital's NIH-funded projects. Multiple case studies will highlight the payoff in grant competitiveness, speed of innovation, support for large-scale studies, data sharing, collaboration, and FISMA compliance an institution realizes from investment in advanced computing infrastructure.

11:30 Proposed Virtual BioRepository Platform for Distributed Research Networks: Case Study in ALS
Alexander Sherman, Director, Strategic Development and Systems, Neurology, Massachusetts General Hospital

12:00 pm Scaling File Storage To Keep Up With Science *Sponsored by* BLUE ARC
Bjorn Andersson, Director, Product Marketing, Blue Arc Corporation
New and more affordable instruments are driving an ever increasing flow of data to be analyzed and managed. Meanwhile, advances in science and the increasing use of application mash-ups create more mixed and unpredictable workloads for shared storage solutions. It's essential to be able to scale to independently meet performance and capacity demands as well as optimize operations. pNFS is the new industry standard that addresses these scalability requirements.

12:30 Luncheon in the Exhibit Hall and Poster Viewing

2:00 Exhibit Hall Closes

1:55 Chairperson's Remarks

2:00 Requirements for a Successful Electronic Lab Notebook Deployment: Eli Lilly and Company Case Study
Michael E. Kopach, Ph.D., Research Advisor, Eli Lilly and Co.
Since 2003 Eli Lilly and Company has steadily broadened its adoption of Electronic Lab Notebook (ELN) across multiple business unit and geographic areas including at select contract manufacturing organizations. While positive efficiency gains are achieved by deployment of an ELN, the transition from the main-stay paper laboratory notebook involves challenges on many levels for an organization including data management and network storage. This presentation will discuss deployment of a "fully electronic" ELN at Eli Lilly and Company and present lessons learned after seven years of operation.

2:30 Applying Lean Information Flow Principles to Biological Informatics within R&D
Gemma Satterthwaite, Ph.D, EMBA, Global Lead, Biological Informatics, Astrazeneca
Patrik Holmqvist, MSc, Computer Science & Engineering, Head of Information Management & Continuous Improvement, AstraZeneca
With the current R&D productivity challenges faced by Pharmaceutical companies, improving the quality and speed of decision making is a key driver. This presentation will describe Astra Zeneca's response to this challenge, focusing on the biological informatics. We will describe how we bring Lean Information Management to life within a scientific environment bridging the gap between science.

3:00 Talk Title to be Announced
Speaker to be Announced

3:30 The Atlas Cloud Computing Infrastructure for Organizing and Querying Multiomics Data *(Joint with Tracks 1-5)*
Misha Kapushesky, Ph.D., Functional Genomics Team Leader, EBI, Cambridge UK
The Expression Atlas is a cloud computing based distributed infrastructure for organizing and querying multiomics data. Built upon the open-source Expression Atlas project at the EBI in partnership with the pharmaceutical industry, the Atlas provides a scalable solution that can be easily deployed on in-house servers or accessed remotely in the cloud. Learn how the Atlas deals with secure processing and combined analysis and integration of public/private transcriptomic and proteomic data, with an emphasis on our novel pipeline for next-generation sequencing data processing and reporting.

4:00 Conference Adjourns

IT Infrastructure – Software

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TECHNOLOGIES AND APPLICATIONS FOR MANAGING, SHARING, PUBLISHING, AND PRESERVING DATA

10:50 Chairperson's Remarks

11:00 FEATURED PRESENTATION
HPC Trends from the Trenches *(Joint with Tracks 1 - 3)*
Chris Dagdigian, Founding Partner and Director of Technology, BioTeam, Inc.
This talk will review some of the BioTeam's recent work with biotech, pharmaceutical, government and enterprise clients. As an independent consulting firm, the BioTeam is able to see how HPC problems in life science informatics have been approached by organizations of varying type and size. We will address common problems and observed trends in computing, workflows and data movement, along with details on particularly clever solutions observed in production environments around the world.

11:30 Translational Research Bandwidth: The Value of Integrative Informatics Platforms

Presented by caBIG

Philip Payne, Ph.D., Associate Professor and Chair, Biomedical Informatics, The Ohio State University
This session will describe how caBIG®-interoperable infrastructure may be deployed to simplify data management and information exchange, thereby supporting collaborative research in cancer and other diseases. Approaches to link robust middleware developed by the NCI with clinical and translational research use cases at the local, community, and national levels will be discussed.

12:00 pm Ultra High-Speed Transport of Life Sciences Data over Global Networks

Sponsored by aspera

Diego Dugatkin, Ph.D., Vice President, Product Management, Aspera, Inc
Collaborative research teams need to efficiently exchange, process and analyze gigabytes of data in a sequence run. Traditional data transport methods are unable to manage this volume of data. This session focuses on now-generation transport technologies used in genomic research that achieves up to 1000x the throughput of standard file transfer protocols. A case study of global researchers participating in the 1000 Genomes Project showcases how they have been able to exchange sequencing data at 1 Gbps.

12:30 The Role of Standards in Discovery

Sponsored by Microsoft

Les Jordan, Industry Technology Strategist, Life Sciences, Microsoft Corporation
Drug discovery has traditionally had a lack of integration and interoperability between systems. Now there are a couple emerging standards and companies that are starting to focus on integration and interop. This session will discuss those standards, architectures for their implementation and a vision for the future of interoperability that crosses all sectors of Health.

1:40 Chairperson's Remarks

1:45 A Unifying Platform for Integrative Informatics
Victor Lobanov, Director, Informatics & Pharmaceutical R&D, Johnson & Johnson Pharmaceutical
With more than 2,000 users around the world, the ABCD informatics platform has now been firmly established as an indispensible tool for pharmaceutical research at Johnson & Johnson Pharmaceutical Research & Development. This talk will provide an overview of the current capabilities of the platform and a perspective on its future direction.

2:15 Agile BI & Agile Data Services: A Perfect Fit
Murtaza Cherawala, Senior Information Technology Architect, Enterprise Applications Group, Biogen Idec
To improve business processes for customer interactions, financial performance management, operational BI, and strategic intelligence, an agile BI is needed. This includes a data service infrastructure that leverages virtualization, data integration, data quality and other existing tools that deliver reusable information-as-a-service across disparate, historical and real-time, internal and external "big data" with increased flexibility. This case study presentation will demonstrate the use of data virtualization and data warehouse as an extension to increase project completion time and reduce costs.

2:45 Enabling Informatics and Enterprise Search in Drug Discovery

Sponsored by THOMSON REUTERS

Andreas Matern, Vice President, Technical Sales, Thomson Reuters
As technological advances change how users interact with web based data, researchers in pharma R&D are eager to adopt technologies which allow them to search and perform analysis on proprietary and public data sets in easy to use systems. The development of APIs (application programming interfaces) to web based databases enables the construction of novel user interfaces through a variety of end user applications. This talk will focus on accessing public and proprietary data with an emphasis on a competitive intelligence work stream.

Track 2 explores data handling and integration activities. Themes covered include technologies and applications for managing/sharing/publishing/preserving data, software tools, open source solutions, collaborative web technologies, and advances & trends.

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

3:45 Data Warehouses for Pharma Development: A Stepwise and Lean Approach
Norbert Fritz, Ph.D., Development Leader, Product Development - Information Management, F. Hoffmann-La Roche Ltd.
Data integration, the core element of any Data Warehouse, can be accomplished to different degrees: technical, structural and semantic. Whereas it is generally desirable to achieve the highest level of data integration (semantic), this might not always be feasible due to many factors including constraints of data sources, limited data quality, and budgets. This presentation will describe a stepwise approach for different levels of data integration in the context of clinical data and analyze its impact on data processing and usage.

4:15 Deployment of iRODs for Large Scale Genomics Archive
Chris Smith, Co-founder and Technical Director, Distributed Bio LLC
This presentation will describe how we implemented an iRODs virtual file system to replace an existing file based archive system.

4:45 Surfing the Rich Data Deluge Steps Toward Developing an Effective IT Strategy
Sponsored by Tessella
John Whittle, Vice President, Tessella, Inc.
Today's pharmaceutical and biotech companies are drowning under a tsunami of digital images and other types of rich data. From NextGen DNA sequencing to high content screening to whole animal imaging, these complex and rapidly evolving technologies open new avenues of scientific exploration across drug discovery and development. But these advances present IT organizations with the challenge of managing large, diverse data sets generated by research scientists who are frequently geographically dispersed. There is no "one size fits all" approach IT organizations can follow to overcome these challenges. In this session, Scott Shepard, Senior Vice President at Tessella examines these IT challenges and presents practical approaches to developing an IT strategy tailored to your organization's needs.

5:15 Best of Show Awards in the Exhibit Hall

6:15 Exhibit Hall Closes

THURSDAY, APRIL 14

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Martin D. Leach, Ph.D., Executive Director, MRL IT for Discovery & Pre-Clinical Sciences, Merck & Co.
Mark Boguski, M.D., Ph.D., Founder, Resounding Health Incorporated
Jamie Heywood, Co-founder and Chairman, PatientsLikeMe
Yury Rozenman, Global Head of Marketing, Pharmaceutical and Life Sciences Sector, BT Global Services

10:30 Coffee Break in the Exhibit Hall with Poster Competition

SOFTWARE TOOLS, OPEN SOURCE SOLUTIONS, AND COLLABORATIVE WEB TECHNOLOGIES

10:55 Chairperson's Remarks

11:00 Data Analytics of Strategic Information Technology Asset Reviews
Brian Bissett, M.B.A., M.S.E.E., Staff Analyst, Office of the CIO, Social Security Administration
The Social Security Administration (SSA) has recently been tasked with legislative mandates to take on more Health Care IT programs. To ensure a uniform process is utilized in selecting the best health care efforts for the agency to start or continue funding, the SSA created the Strategic IT Asset Review (SITAR) process to evaluate the programmatic costs and benefits of proposed IT programs. A case study will be presented of software tools and collaborative web technologies that show how data collected, integrated, and automated from data analysis of healthcare proposals can determine initiatives costs, benefits, and Return on Investment (ROI).

11:30 Integrated Decision Support for Drug Safety Assessment
Ola Spjuth, Ph.D., Researcher, Pharmaceutical Biosciences, Uppsala University; Project Leader, Bioclipse
Lars Carlsson, Ph.D., Global Safety Assessment, AstraZeneca R&D, Mölndal, Sweden
The Bioclipse Decision Support system is a free and open source solution developed as a collaboration between the Department of Pharmaceutical Biosciences at Uppsala University, Sweden, and the Computational Toxicology group at AstraZeneca R&D, Mölndal, Sweden. This talk presents a general framework for building and deploying predictive ***in silico*** models, demonstrated on drug safety data. The result is a decision support system capable of running local and remote models with interpretable results.

12:00 pm Sponsored Presentation
To Be Announced

12:30 Luncheon in the Exhibit Hall and Poster Viewing

2:00 Exhibit Hall Closes

ADVANCES AND TRENDS

1:55 Chairperson's Remarks

2:00 Investing in Translational Medicine: Analysis of the Impact of Information Systems
Jonathan Usuka, Ph.D., M.B.A., Director, Global Business Partnering, Celgene Corporation
This presentation explores the cost/benefit analysis of pharmaceutical industry spending in translational therapies, survey of novel vendor solutions that have impacted translational approaches, and success scenarios for bringing diagnostic information into therapy development.

2:30 Semantic Computing and Biomedicine
Phillip Sheu, Ph.D., Professor, Electrical Engineering and Computer Science and Biomedical Engineering, University of California, Irvine
Semantic computing is in line with Web 3.0, the next generation of Web that is characterized by semantic Web and the Internet of 'things,' and may be even broader as it also includes computing driven by natural language and all computational content such as software, devices, and processes. This presentation addresses the applications of Semantic Computing in biomedicine.

3:00 Cyber Infrastructures for Synthetic Genomics: The Emergence of Genetic Design Automation
Jean Peccoud, Ph.D., Associate Professor, Bioinformatics, Virginia Tech
Chemically synthesizing DNA molecules the size of bacterial genomes should now lead to the development of a new generation of software infrastructures to automate the design, fabrication, and characterization of synthetic DNA molecules. A challenge is how specialists who work in different branches of the organization can contribute to the project without needing to know the entire project plan. Learn the support needed to develop a synthetic biology project of this kind including open source applications and how to engage different stakeholders in an organization.

3:30 The Atlas Cloud Computing Infrastructure for Organizing and Querying Multiomics Data *(Joint with Tracks 1-5)*
Misha Kapushesky, Ph.D., Functional Genomics Team Leader, EBI, Cambridge UK
The Expression Atlas is a cloud computing based distributed infrastructure for organizing and querying multiomics data. Built upon the open-source Expression Atlas project at the EBI in partnership with the pharmaceutical industry, the Atlas provides a scalable solution that can be easily deployed on in-house servers or accessed remotely in the cloud. Learn how the Atlas deals with secure processing and combined analysis and integration of public/private transcriptomic and proteomic data, with an emphasis on our novel pipeline for next-generation sequencing data processing and reporting.

4:00 Conference Adjourns

Cloud Computing

TUESDAY, APRIL 12

7:00 am Workshop Registration and Morning Coffee

8:00 - 4:00 pm Pre-Conference Workshops*
Recommended workshop: (W11) Cloud Computing
**Separate Registration Required. See page 3 for details.*

2:00 - 6:00 Main Conference Registration

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

4:05 Keynote Introduction
Chris Blessington, Life Sciences Solutions Architect, Isilon

Sponsored by ISILON SYSTEMS

PLENARY KEYNOTE

4:15 Making the World's Knowledge Computable
Stephen Wolfram, Ph.D., CEO, Wolfram Research; Creator of Wolfram|Alpha

5:00 Welcome Reception in the Exhibit Hall and Poster Viewing
***Drop off a business card at the CHI Sales booth for a chance to win 1 of 2 iPod®s! **Apple® is not a sponsor in the program.*

Sponsored by BLUE ARC

Wednesday, April 13

7:00 am Registration and Morning Coffee

8:00 Event Chairperson's Opening Remarks
Phillips Kuhl, Co-Founder and President, Cambridge Healthtech Institute

8:05 Keynote Introduction
Grant Stephen, CEO, Tessella, Inc.

Sponsored by Tessella Technology & Consulting

PLENARY KEYNOTE

8:15 Interacting with Complex Information Landscapes: Integration and Next Generation User Interfaces
Bryn Roberts, Ph.D., Global Head, Informatics, Pharma Research and Early Development, F. Hoffmann-La Roche Ltd.

8:45 Benjamin Franklin Award/Presentation:
Jonathan Eisen, Ph.D., Professor, Genome Center, University of California, Davis

9:10 Best Practices Awards Program

9:45 Coffee Break in the Exhibit Hall and Poster Viewing

Sponsored by SCYNEXIS

HIGH PERFORMANCE COMPUTING AND DATA ANALYSIS PIPELINE

10:50 Chairperson's Remarks
Jason Hanley, Director, Life Sciences, Model Metrics Inc.

Sponsored by model metrics

11:00 FEATURED PRESENTATION
HPC Trends from the Trenches *(Joint with Tracks 1 - 3)*
Chris Dagdigian, Founding Partner, Director, Technology, BioTeam, Inc.
This talk will review some of the BioTeam's recent work with biotech, pharmaceutical, government and enterprise clients. As an independent consulting firm, the BioTeam is able to see how HPC problems in life science informatics have been approached by organizations of varying type and size. We will address common problems and observed trends in computing, workflows and data movement, along with details on particularly clever solutions observed in production environments around the world.

11:30 High-Throughput Analysis Pipelines on the Cloud
Toby Bloom, Ph.D., Director , Informatics, Genome Sequencing, Broad Institute
Cloud computing is often suggested as a solution to the next-gen sequencing data deluge. Running high-throughput pipelines on very large volumes of data introduces some interesting challenges not seen in smaller applications on the cloud. The Broad production sequencing analysis pipeline is an example of such a high-throughput application. We discuss our experiences porting that pipeline to the Amazon cloud, the challenges we encountered, and the solutions we utilized. We will also compare the requirements of this application, designed to process large numbers of runs concurrently, with the requirements of many next-gen users to process a single run at a time on the cloud.

12:00 pm Easy-to-Use, Customized Next-Generation Sequencing Data Pipelines on Cloud Computing
Attila Berces, Ph.D., CEO, Omixon
We demonstrate Omixon's fully automated, easy-to-use, custom built data analysis pipelines to solve customers' problems on Amazon Web Services. We demonstrate applications in genome variant analysis and human exome analysis.

Sponsored by omixon BIOCOMPUTING SOLUTIONS

12:15 A Viable Alternative to In-House Compute Clusters: Real Results from Life Science Use Cases in the Cloud
Jason Stowe, Founder and CEO, Cycle Computing, LLC

Sponsored by CYCLE COMPUTING

12:30 Experiencing LifeScope™ Genomic Analysis Software through the Cloud
Nicholas D. Socci, Ph.D., Assistant Director, Bioinformatic Core, Computational Biology Center, Memorial Sloan Kettering Cancer Center
LifeScope™ Cloud offers customers an alternative to buying and maintaining the computer infrastructure typically required for second-generation sequencing data analysis. Dr. Socci will describe his experience of using LifeScope™ Genomic Analysis Software through the Cloud, and will focus on how LifeScope™ can be used for analyzing targeted resequencing data generated from AB SOLiD™ Sequencing instruments from Life Technologies.

Sponsored by life technologies

NEXT-GENERATION SEQUENCING ON THE CLOUD

1:40 Chairperson's Remarks
Andrew Su, Ph.D., Associate Director of Bioinformatics, Genomics Institute of the Novartis Research Foundation

1:45 Critical Components for Cloud-Computing
Angel Pizarro, Director, ITMAT Bioinformatics Facility, Institute for Translational Medicine & Therapeutics, University of Pennsylvania
To facilitate using second generation sequencing for interrogating diseases, cloud computing providers promise instant access to vast amounts of computational resources on a pay-as-you-go basis. However, orchestrating loosely coupled system components into a cohesive high-throughput computational resource is a challenge. This talk will cover the critical components that need to be in place to be successful on the cloud.

2:15 Scalability of Genome Assemblers for Cloud and HPC Computing Environments
C. Victor Jongeneel, Ph.D., Director, Bioinformatics & Biomedical Informatics, Natl. Center for Supercomputing Applications, Inst. for Genomic Biology, University of Illinois at Urbana-Champaign
While cloud computing is gaining acceptance in the biological community, high-end HPC has not yet been fully embraced. This presentation will demonstrate the applicability of a diversity of computational fabrics (cloud, HPC, and HPC in a cloud) for *de novo* genome assembly using Velvet and

Track 3 provides focused research presentations, real world use cases and individual experiences with cloud computing. Themes include HPC in the Cloud, value of cloud computing studies, cloud vendors/providers, non cloud solutions that provide what the cloud does, performance benchmarking, security models, and tools and frameworks for data analysis.

ABySS, two applications with widely different characteristics. It will be based on real use cases and performance benchmarks.

2:45 Cloud Computing: Beyond the Hype and Headlines
Neil Lock, IT Services Program Director, BT Global Services
Sponsored by BT
This presentation explores what lies beyond the cloud. As so much of the debate, hype and headlines about cloud computing has focused on technology, we will look rather at why pharma organisations should focus on the benefits of cloud services and how it can drive performance in R&D. We will discuss what organisations need to do to make cloud solutions work for them along with the how and why.

3:15 Refreshment Break in the Exhibit Hall with Poster Viewing

3:45 BioGPS – Crowdsourcing the Development of a Gene Annotation Portal
Andrew Su, Ph.D., Associate Director of Bioinformatics, Genomics Institute of the Novartis Research Foundation
The landscape of online, gene-centric annotation databases is highly fragmented, spanning hundreds or thousands of individual web sites. To better navigate and organize these resources, we developed BioGPS (http://biogps.gnf.org), a gene annotation portal that aggregates gene annotation data within a single framework. BioGPS focuses on two key concepts: user customizability and community extensibility. To maximize the addition of new functionality and the efficiency of our development, we currently host significant sections of our data and application in the cloud.

4:15 Dynamically Scalable, Accessible Analysis for High-Throughput Sequence Data
Enis Afgan, Ph.D., Postdoctoral Researcher, Departments of Biology and Math & Computer Science, Emory University
High-throughput sequencing has transformed biomedical research, however making sense of this resource requires sophisticated computational tools. The Galaxy project seeks to make these tools available to a wide audience of researchers, while ensuring that analyses are reproducible and can be communicated transparently. The Galaxy framework provides a consistent accessible user interface for complex tools; however, many such tools require significant computational resources. Here we describe Galaxy cloud, which allows researchers to instantiate an analysis environment which can be scaled up and down on demand as needed, using nothing more than a web browser.

4:45 Understand How your Workloads can Leverage a Trusted Cloud Environment
John Hanrahan, Director, EMC Consulting Life Science & Healthcare Practice
Sponsored by EMC² where information lives
Cloud computing allows life sciences business and IT leaders to build a trusted, secure, reliable and cost effective IT environment. We will provide a unique perspective on how to determine what data workloads can and should be moved to the cloud, protocols on how to control "acceptable use" and how to ensure secure information-sharing practices are in place with applicable controls. This session will discuss how we analyze your collaboration, high performance and other workloads and our approach to defining a cloud strategy.

5:00 Cloud Computing in Support of Biomedical Research and Clinical Care
Mark Adams, Ph.D., Principal, Booz Allen Hamilton
Sponsored by Booz | Allen | Hamilton
This talk will present how Booz Allen has worked with a range of clients in the biomedical research and care spaces to leverage cloud computing as a key part of implementing solutions for a variety of challenging problems. We will present how Booz Allen has developed and implemented a private cloud infrastructure, secured and validated for identifiable health data. We will then present how the team has developed an open source set of tools which provide for semantically-enabled query and analysis in Hadoop databases. We will finally discuss how these components have been used to rapidly and cost-effectively carry out significant clinical and biomedical research activities for several clients.

5:15 Best of Show Awards in the Exhibit Hall
6:15 Exhibit Hall Closes

Thursday, April 14

8:45 Event Chairperson's Opening Remarks
Kevin Davies, Ph.D., Editor-in-Chief, Bio-IT World

8:50 KEYNOTE PANEL:
KEYNOTE INTRODUCTION Sponsored by BT
A special plenary session featuring a series of succinct, forward-looking presentations by:
Ken Buetow, Ph.D., Associate Director, Bioinformatics and Information Technology, National Cancer Institute
Debra Goldfarb, Senior Director, Strategy, Microsoft
Martin D. Leach, Ph.D., Executive Director, MRL IT for Discovery & Pre-Clinical Sciences, Merck & Co.
Mark Boguski, M.D., Ph.D., Founder, Resounding Health Incorporated
Jamie Heywood, Co-founder and Chairman, PatientsLikeMe
Yury Rozenman, Global Head of Marketing, Pharmaceutical and Life Sciences Sector, BT Global Services

10:30 Coffee Break in the Exhibit Hall with Poster Competition

PHARMA & HEALTHCARE: PERSPECTIVE ON THE CLOUD

10:55 Chairperson's Remarks
David Medina, Worldwide Life Science and Pharma Segment Executive, HP Enterprise Business
Sponsored by hp

11:00 Cloud Computing Concepts Applied in Pharma R&D
Rick Franckowiak, IT Director, Johnson and Johnson Pharmaceutical Research and Development
Thomas Messina, IT Manager, Johnson and Johnson Global R&D Delivery Services
A session to share lessons learned and approaches in applying cloud computing concepts in a pharmaceutical research and development environment. Specific real world use cases will be highlighted. There will be discussion on future opportunities as well as current challenges in reaching further adoption including strategic issues such as security, technical integration, platform readiness, cost and service support.

11:30 Genome Era Medicine and HealthCare Disruptive Technology
Dennis P. Wall, Ph.D., Assistant Professor of Pathology, Beth Israel Deaconess Medical Center & Director, Computational Biology Initiative, Center for Biomedical Informatics, Harvard Medical School
Using a novel translational and clinical science 'cloud' computing platform, we created mathematical models that reflect patient populations and the use of personalized medicine by testing preventative health care for individuals based on their specific medical, family, and genetic characteristics. This presentation will discuss the objectives, serious medical practice barriers, outcomes and future effort of a series of pilot projects.

12:00 pm Applying Technologies Designed for the Cloud to Transform Pharma and Healthcare
Steven Kludt, Vice President Marketing, Cambridge Semantics
Sponsored by CAMBRIDGE SEMANTICS
By applying Semantic technologies designed from the ground up for the cloud, computational capabilities of the cloud can be combined with next generation data management in the cloud. Current processes become radically cheaper and faster to implement while new solutions and levels of collaboration are being developed that were not possible before. This session will present new ways of thinking about leveraging data in the cloud and the architectural and governance challenges they present. Use cases will be presented in pharma with discussions of next steps being explored.

12:15 Scale-Out Storage for High Performance Bioinformatics in the Cloud
Sponsored by GLUSTER
Anand Babu Periasamy, CTO & Co-Founder, Gluster
Gluster and RightScale Cloud Management enable bioinformatics companies to focus on research and forget about IT by leveraging the automation and massive scalability capabilities of the Amazon public cloud. Best practices, recommendations, and use cases on managing research data in the cloud will be discussed.

12:30 Luncheon in the Exhibit Hall with Poster Viewing

2:00 Exhibit Hall Closes

COLLABORATION AND SECURITY ON THE CLOUD

1:55 Chairperson's Remarks
William Tulskie, CEO and CTO, Healthcare IT, Inc.

2:00 Research Collaboration in the Cloud: How NCI and Research Partners are Using Digital Identities to Accelerate Medical Advances
Cindy Cullen, SSBB, CISM, CISSP, CTO, SAFE BioPharma Association
The National Cancer Institute, the private sectors [Bristol-Myers Squibb & Sanofi Aventis], and SAFE BioPharma Association are piloting a process to use federated trust to access, digitally sign and exchange documents, eliminating use of paper-based forms in research projects associated with oncology drug development and clinical trials. The goal is faster, lower cost delivery of medical advances to patients.

2:30 Elastic-R, a Ubiquitous Data Analysis Workbench for IaaS-Style Clouds
Karim Chine, Director, Cloud Era Ltd., Cambridge, UK
The success of EC2 announces the emergence of a new era in scientific computing and data analysis. Bringing that era for research still requires new software that would bridge the gap between the cloud and the scientists' tools. Elastic-R enables anyone, using a standard Web browser, to work virtually and collaboratively with mainstream scientific computing environments without memory or computing constraints.

3:00 caBIG® in the Cloud
Presented by caBIG
William Tulskie, CEO and CTO, Healthcare IT, Inc.
Access to applications for collecting patient outcomes and related research data is enabling innovations in personalized healthcare. As cloud-based offerings mature, these data and applications are becoming easier and more economical to implement. The Support Service Provider program within caBIG® offers a fully functional enterprise class cloud environment tuned to the specialized security and availability requirements for healthcare and clinical research applications and data. This session will present case study examples of current implementations that demonstrate innovative cloud-based support for biomedical research.

3:30 The Atlas Cloud Computing Infrastructure for Organizing and Querying Multiomics Data *(Joint with Tracks 1-5)*
Misha Kapushesky, Ph.D., Functional Genomics Team Leader, EBI, Cambridge, UK
The Expression Atlas is a cloud computing based distributed infrastructure for organizing and querying multiomics data. Built upon the open-source Expression Atlas project at the EBI in partnership with the pharmaceutical industry, the Atlas provides a scalable solution that can be easily deployed on in-house servers or accessed remotely in the cloud. Learn how the Atlas deals with secure processing and combined analysis and integration of public/private transcriptomic and proteomic data, with an emphasis on our novel pipeline for next-generation sequencing data processing and reporting.

4:00 Conference Adjourns

Bioinformatics

TUESDAY, APRIL 12

7:00 am Workshop Registration and Morning Coffee

8:00 - 4:00 pm Pre-Conference Workshops*

**Separate Registration Required. See page 3 for details.*

2:00 - 6:00 Main Conference Registration

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

4:05 Keynote Introduction
Chris Blessington, Life Sciences Solutions Architect, Isilon

Sponsored by ISILON SYSTEMS

PLENARY KEYNOTE

4:15 Making the World's Knowledge Computable
Stephen Wolfram, Ph.D., CEO, Wolfram Research; Creator of Wolfram|Alpha

5:00 Welcome Reception in the Exhibit Hall and Poster Viewing
***Drop off a business card at the CHI Sales booth for a chance to win 1 of 2 iPod®s! **Apple® is not a sponsor in the program.*

Sponsored by BLUE ARC

WEDNESDAY, APRIL 13

7:00 am Registration and Morning Coffee

8:00 Event Chairperson's Opening Remarks
Phillips Kuhl, Co-Founder and President, Cambridge Healthtech Institute

8:05 Keynote Introduction
Grant Stephen, CEO, Tessella, Inc.

Sponsored by Tessella Technology & Consulting

PLENARY KEYNOTE

8:15 Interacting with Complex Information Landscapes: Integration and Next Generation User Interfaces
Bryn Roberts, Ph.D., Global Head, Informatics, Pharma Research and Early Development, F. Hoffmann-La Roche Ltd.

8:45 Benjamin Franklin Award/Presentation:
Jonathan Eisen, Ph.D., Professor, Genome Center, University of California, Davis

9:10 Best Practices Awards Program

9:45 Coffee Break in the Exhibit Hall and Poster Viewing

Sponsored by SCYNEXIS

BIOINFORMATICS & CANCER

10:50 Chairperson's Remarks
Eitan Gross, Ph.D., Assistant Professor, Physics, University of Arkansas

11:00 Web Portal for Integrated Analysis of Radiation Responsive Cancer Gene Expression Profiles
Uma Shankavaram, Ph.D., Staff Scientist, National Cancer Institute/National Institutes of Health
The abundance of cancer research is evident from a PubMed search. However, studies focusing strictly on Radiation effects on cancer are rare and, to our knowledge, there are no web portals dedicated to this topic. This presentation will describe a web portal called MAQuery we have created that would house cancer related microarray expression data focusing primarily on radiation oncology data. Attendees will learn how MAQuery will help in the search for genes with particular expression profiles in cancers.

11:30 Lung Genomics Research Consortium: Building a Translational Research Portal to Improve the Molecular Understanding of Lung Disease
Mick Correll, Associate Director, Center for Cancer Computational Biology, Dana-Farber Cancer Institute
The LGRC portal represents a revolutionary new way to support collaborative research in the genetics of chronic lung disease. The portal addresses many needs, from supporting uploading of large experimental data seta, assessment of available samples and their characteristics, sample and data tracking capabilities across a distributed consortium, and the availability of sophisticated, automated analytical tools. Learn about the project requirements, solution design, and commercial and open source tools that were utilized to construct the system.

12:00 pm Enhancing Cancer Biobanks through Novel IT: The BioGeoBank
Janet M. Hock, B.D.S., Ph.D., Senior Investigator & Founding Director, Maine Institute of Human Genetics and Health; Professor, Tufts University School of Dental Medicine

12:30 pm Luncheon Presentation
Data Exploration as an Integral Component of Data Cleaning and Standardization in Translational Informatics

Sponsored by BioFortis

Mark Brocato, Director, Software Engineering, BioFortis, Inc.
Traditionally, data cleaning and standardization must happen first before meaningful queries and reports can be generated in clinical and translational research. In this presentation, we will describe a new paradigm that allows data cleaning and standardization to be an iterative process enabling scientific value to be derived every step of the way.

NEXT-GENERATION SEQUENCING AND NOVEL BIOINFORMATIC AND DATA INTEGRATION APPROACHES

1:40 Chairperson's Remarks
Eitan Gross, Ph.D., Assistant Professor, Physics, University of Arkansas

1:45 Leveraging caBIG®: New Collaborative Models in Science and Business

Presented by caBIG

Brent Gendleman, President and CEO, 5AM Solutions
Joel Saltz, M.D., Ph.D., Director, Center for Comprehensive Informatics, Emory University
Vast amounts of data generated by sophisticated research techniques and millions of clinical interactions represent an un-mined opportunity for advancing collaborative research and discovery at a 21st century pace. Realization of this potential is predicated upon an interoperable IT

environment to facilitate data integration and exchange in support of a wide variety of basic, clinical and translational research efforts. The caBIG® principles of open access, open source, open development, and federation drive unique opportunities for business, academic, and research enterprises to solve research challenges that translate into viable results.

2:15 Broad-Scale Next-Generation Sequencingin Marine Metagenomics - Novel Applications and Future Prospects
Hanno Teeling, Ph.D., Scientist, Department of Molecular Ecology/Microbial Genomics & Bioinformatics Group, Max Planck Institute for Marine Microbiology
This talk will demonstrate by means of the German research project MIMAS (Microbial Interactions in Marine Systems) and the European project MAMBA (Marine Metagenomics for New Biotechnological Applications) how next-generation sequencing in combination with novel bioinformatic and data integration approaches can be used to link biodiversity and functional information, and thus turn the data deluge from broad-scale environmental sequencing into meaningful biological knowledge.

2:45 Democratizing Large-Scale Genomic Data for Basic and Clinical Researchers
Sponsored by NEXTBIO
Ilya Kupershmidt, Co-Founder and Vice President, Products, NextBio
Evolution of array and next-generation sequencing technologies is driving exponential growth of data in the public domain, as well as private data generated by individual labs and organizations. In order to truly make use of this information, data-driven understanding of disease by different types of researchers is required. In this talk I will describe how NextBio platform is enabling scientific groups with diverse backgrounds to utilize massive quantities of genomic information across basic and clinical research initiatives.

3:00 Drug Discovery Optimization in the Teradata Agile Analytics Cloud
Sponsored by TERADATA Raising Intelligence
Ed Acker, Senior Consultant, Life Sciences Industry, Teradata
Scientists can optimize discovery/replication analyses of gene to protein experiment data using Teradata's Agile Analytics Cloud to quickly create/combine/share and analyze customizied private virtual data marts without IT participation.

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

DATA MINING AND MODELING

3:45 Data Mining & Synthetic Biology: A Tool for Knowledge Discovery
Merridee Wouters, Ph.D., Group Leader, Structural & Computational Biology, Victor Chang Cardiac Research Institute
As a relatively new field, bioinformatics is still in the process of defining itself and demonstrating its usefulness to biological and medical research. The large amount of publicly available data is a rich source of biological systems knowledge which is currently underutilized. Effective data mining programs can maximize the potential of acquired data and are a cost effective solution for knowledge discovery. Learn the importance of data mining and its relationship to other areas of bioinformatics.

4:15 A Data Warehouse for Translational Research
Hai Hu, Ph.D., Deputy CSO, Senior Director, Biomedical Informatics, Windber Research Institute
We have developed an extensible data warehouse, the Data Warehouse for Translational Research (DW4TR), based on a novel patient-centric modularly-structured clinical data model and a specimen-centric molecular data model. Learn how we conceived and developed the model, how temporal relationships are modeled and incorporated, how the DW4TR is used as a research environment for clinicopathologic risk factor analysis and for virtual experiments, and how the DW4TR can be used as the basis for the development of a physician decision-support system.

4:45 Clustering Algorithms in Gene Expression Analysis
Eitan Gross, Ph.D., Assistant Professor, Physics, University of Arkansas
The exponential growth in gene expression data in recent years, due to the introduction of fast sequencing technologies, calls for fast, reliable and automatic clustering algorithms that can assist in analyzing and extracting valuable information that is potentially embedded in the ever growing gene expression data banks. This talk will discuss the various methods and approaches (parametric, non-parametric, etc.) used to cluster gene expression data.

5:15 Best of Show Awards in the Exhibit Hall

6:15 Exhibit Hall Closes

THURSDAY, APRIL 14

8:45 am Event Chairperson's Opening Remarks
Kevin Davies, Ph.D., Editor-in-Chief, Bio-IT World

8:50 KEYNOTE PANEL:
KEYNOTE INTRODUCTION *Sponsored by* BT
A special plenary session featuring a series of succinct, forward-looking presentations by:
Ken Buetow, Ph.D., Associate Director, Bioinformatics and Information Technology, National Cancer Institute
Debra Goldfarb, Senior Director, Strategy, Microsoft
Martin D. Leach, Ph.D., Executive Director, MRL IT for Discovery & Pre-Clinical Sciences, Merck & Co.
Mark Boguski, M.D., Ph.D., Founder, Resounding Health Incorporated
Jamie Heywood, Co-founder and Chairman, PatientsLikeMe
Yury Rozenman, Global Head of Marketing, Pharmaceutical and Life Sciences Sector, BT Global Services

10:30 Coffee Break in the Exhibit Hall with Poster Competition

DATA MODELING & COMPUTATIONAL INTEGRATIVE TOOLS

10:55 Chairperson's Remarks
Rong Chen, Ph.D., Bioinformatics Scientist, Division of Systems Medicine, Department of Pediatrics, Stanford University School of Medicine

11:00 Affordable Departmental Supercomputer Facilitates the Conformational Modeling and Simulation of Protein Dynamics
Nurit Haspel, Ph.D., Assistant Professor, Computer Science, University of Massachusetts, Boston
Through academic and industry research collaborations, we have developed a computational, theoretical and experimental framework to rationally design nano- and micro-structures made of amphiphilic hybrid materials which combine peptides used in the formation of amyloids with polyesters. This work was made possible through the use of a NAMD molecular dynamics software installed on a supercomputer. This presentation will describe our work and how the supercomputer helps us to perform research more efficiently than any other locally or nationally available resource.

11:30 Using Public Molecular Measurements to Drive Discovery of Biomarkers and Therapeutics
Rong Chen, Ph.D., Bioinformatics Scientist, Division of Systems Medicine, Department of Pediatrics, Stanford University School of Medicine
The measurement of most molecular states is now a commoditized service on well established platforms. Funding agency and journal mandates have led to the deposition of billions of data elements into international repositories, while the lay public and press have demanded more clinical translation from these data. This presentation will describe how computational integrative tools can be used to convert more than 15 billion points of molecular, clinical, and epidemiological data measured by researchers and clinicians over the past decade into novel diagnostics, therapeutics, and insights into disease. The presentation will end with six important lessons learned from using public molecular measurements.

12:00 pm Inspire: Novartis Translational Science Data Warehouse
Philippe Marc, Ph.D., Safety Knowledge Management Expert, Translational Science, Novartis Institute for Biomedical Research
The Novartis Institutes for Biomedical Research (NIBR) are composed of approximately 6 000 scientists and physicians located in various locations worldwide. We are known for our robust pipeline and our track record of innovation. One of the keys to such success is to have a proper flow of ideas and information across the organization. This talk will illustrate a successful project – the creation and use of Inspire, our translational data warehouse. Inspire is aggregating data from fifty internal and external sources in a single place, including data from clinical trials, preclinical studies, drugs and targets. We will discuss agile programming, business and IT communication, ETL, service orientation, use of master data, and ontologies.

12:30 Luncheon in the Exhibit Hall and Poster Viewing

2:00 Exhibit Hall Closes

BIOINFORMATICS IN THE CLOUD: AN AFFORDABLE ALTERNATIVE

1:55 Chairperson's Remarks
William Frezza, Venture Partner, Adams Capital Management

2:00 Bioinformatics in the Cloud
Giles Day, Managing Director, Distributed Bio, LLC
This talk will describe how to implement a complete sequence annotation pipeline on Amazon, including maintaing databases, using queuing systems and interacting with relational databases.

2:30 Translational Bioinformatics: A Multidisciplinary Approach to Biomedical Research
Yate-Ching Yuan, Ph.D., Director, Bioinformatics Core Facility, Molecular Medicine, Beckman Research Institute, City of Hope
This presentation will describe our use of cloud computing to help streamline our data analysis pipelines. We have been able to provide cost-effective translational bioinformatics platforms using an integrated cyber-infrastructure to support high-throughput data analysis, management, and integration in order to advance research on predictive, preventive, personalized and participatory medicine.

3:00 Bioinformatics on Cloud Cyberinfrastructure
Geoffrey Fox, Ph.D., Professor, Informatics and Computing; Director, Community Grids Laboratory, School of Informatics and Computing, Indiana University, Bloomington
Clouds offer computing on demand plus important platforms capabilities including MapReduce and Data Parallel File systems. This talk will look at public and private clouds for large scale sequence processing characterizing performance and usability, as well as FutureGrid, an N SF facility supporting such studies.

3:30 The Atlas Cloud Computing Infrastructure for Organizing and Querying Multiomics Data *(Joint with Tracks 1-5)*
Misha Kapushesky, Ph.D., Functional Genomics Team Leader, EBI, Cambridge UK
The Expression Atlas is a cloud computing based distributed infrastructure for organizing and querying multiomics data. Built upon the open-source Expression Atlas project at the EBI in partnership with the pharmaceutical industry, the Atlas provides a scalable solution that can be easily deployed on in-house servers or accessed remotely in the cloud. Learn how the Atlas deals with secure processing and combined analysis and integration of public/private transcriptomic and proteomic data, with an emphasis on our novel pipeline for next-generation sequencing data processing and reporting.

4:00 Conference Adjourns

Next-Generation Sequencing Informatics

TUESDAY, APRIL 12

7:00 am Workshop Registration and Morning Coffee

8:00 - 4:00 pm Pre-Conference Workshops*
Recommended workshop: (W13) Next-Generation Sequencing: from Data to Discovery

**Separate Registration Required. See page 3 for details.*

2:00 - 6:00 Main Conference Registration

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

4:05 Keynote Introduction
Chris Blessington, Life Sciences Solutions Architect, Isilon

Sponsored by ISILON SYSTEMS

PLENARY KEYNOTE

4:15 Making the World's Knowledge Computable
Stephen Wolfram, Ph.D., CEO, Wolfram Research; Creator of Wolfram|Alpha

5:00 Welcome Reception in the Exhibit Hall and Poster Viewing

Sponsored by BLUEARC

***Drop off a business card at the CHI Sales booth for a chance to win 1 of 2 iPod®s! **Apple® is not a sponsor in the program.*

WEDNESDAY, APRIL 13

7:00 am Registration and Morning Coffee

8:00 Event Chairperson's Opening Remarks
Phillips Kuhl, Co-Founder and President, Cambridge Healthtech Institute

8:05 Keynote Introduction
Grant Stephen, CEO, Tessella, Inc.

Sponsored by Tessella Technology & Consulting

PLENARY KEYNOTE

8:15 Interacting with Complex Information Landscapes: Integration and Next Generation User Interfaces
Bryn Roberts, Ph.D., Global Head, Informatics, Pharma Research and Early Development, F. Hoffmann-La Roche Ltd.

8:45 Benjamin Franklin Award/Presentation:
Jonathan Eisen, Ph.D., Professor, Genome Center, University of California, Davis

9:10 Best Practices Awards Program

9:45 Coffee Break in the Exhibit Hall and Poster Viewing

Sponsored by SCYNEXIS

DATA MINING, ANALYSIS AND FLOW

10:50 Chairperson's Remarks
David J. Dooling, Ph.D., Assistant Director, The Genome Center, Washington University, St. Louis

11:00 From Data to Discovery: Case Studies, Lessons Learned, and Next Steps
Joseph Szustakowski, Ph.D., Senior Group Head, Bioinformatics, Biomarker Discovery, Novartis
This presentation will describe several case studies to highlight the bioinformatics challenges we face when analyzing NGS data, the computational infrastructure required to enable such analyses, and the analysis algorithms and strategies used to solve the problems at hand. From our early successes (and failures) we have already learned crucial lessons that will help to maximize the impact of future NGS projects, and to prepare for third generation sequencing technologies.

11:30 Extremely Fast Queuing and Sorting for Next-Gen Sequencing Data Flow and Data Mining
Jochen Kumm, Ph.D., Director, Biomathematics; Head, IT, Stanford Genome Technology Center, Stanford University
The Stanford Genome Technology Center is a world leading genomics facility bridging the gap between genomics and medical care. Our data flow and analysis pipelines are integrated to deliver high-throughput with simultaneous analysis. We see a five-fold increase in throughput and significant reduction in cost for IT infrastructure linking queuing theory and sorting algorithms. This case study discusses the next gen sequencing pipeline and illustrates the algorithms and software used for significant performance gain cost savings.

12:00 pm Identification and Modeling of Gene-Environment Interactions: A Data Intensive Discovery Initiative Case Study with Netezza

Sponsored by NETEZZA an IBM Company

Murali Ramanathan, Director of Graduate Studies, Pharmaceutical Sciences and Neurology, State University of New York
The risk of developing of many complex diseases is related to the interactions of environmental factors with genes. Effective and efficient methods for identifying and modeling gene-environment interactions (GEI) are critical for medical discovery from next generation sequencing studies. However, GEI analysis is a combinatorially explosive problem. I will describe AMBIENCE and related GEI analysis algorithms that use novel information theoretic search metrics to search combinatorial space. I will also demonstrate how novel data intensive supercomputing architectures are capable of enhancing computational efficiency in these applications.

12:30 Luncheon Presentation
Selecting A LIMS for Next Generation Sequencing Research

Sponsored by GLS GenoLogics

Michael Kuzyk, Ph.D., Product Manager, Omics Labs, GenoLogics Life Sciences Software
Bruce Pharr, VP Products, Marketing and Business Development, GenoLogics Life Sciences Software
No other industry has seen processing speeds rise and costs drop as dramatically as genomics. Modern genomics labs are now struggling to manage the data these techniques generate. A recent survey cites data storage, data management, and informatics as the biggest hurdle to expanding next gen sequencing (NGS). Moreover, analysis costs for sequencing remain high, spotlighting the need for better ways to centralize information and track sample information across experiments. This talk reviews the informatics challenges presented by NGS and proposes three criteria that labs should assess when selecting an NGS lab information management system (LIMS).

1:40 Chairperson's Remarks
David J. Dooling, Ph.D., Assistant Director, The Genome Center, Washington University, St. Louis

1:45 Assessing Next-Gen Data Quality in Production Analysis
Tim Fennell, Senior Developer, Broad Institute

Track 5 explores sequencing platforms and managing the instruments, data mining, analysis tools and workflows, sequencing informatics and cancer, and trends and new applications.

2:15 Data Driven Sequence Analysis
David J. Dooling, Ph.D., Assistant Director, The Genome Center, Washington University, St. Louis
The massive scale of next-generation sequence data forces analysts to often make compromises between sensitivity and specificity, accuracy and speed, etc. How can an analyst be certain that they are making the right choices? This presentation will discuss a combined computational and laboratory framework that allows for unprecedented exploration of the computational variable (tools and their parameters) space, ensuring optimal analysis pipelines are employed for each data set.

2:45 How Many Indels Are You Missing? Highly Accurate Variant Analysis in Diagnostic Applications with Omixon Variant Toolkit
Sponsored by Omixon
Attila Berces, Ph.D., CEO, Omixon
This presentation shows case studies applying the Omixon Variant Toolkit, a highly sensitive tool to find variants and small indels. The cases range from pathogen strain identification to human exome study. Results are compared to Bowtie, BFAST, SHRiMP, and Bioscope results.

3:00 Complete Human Genome Sequencing of More than 60 Samples Across 9 Different Populations
Sponsored by Complete genomics
Steve Lincoln, Vice President of Scientific Applications, Complete Genomics

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

3:45 Genome Sequencing in Support of Translational Research
Sandor Szalma, Ph.D., Head, Oncology Informatics, Oncology Biomarkers, Centocor R&D, Inc.
We have implemented a BioIT World award winning knowledge management platform - tranSMART - supporting translational research. The initial focus was to combine clinical, genomics and proteomics data from clinical and non-clinical studies. We now are extending the system to support biomarker discovery using genetics data - in particular SNP chips and next-generation sequencing. In this talk we will present how this open source system is being extended and initial success will be highlighted.

4:15 A Bi-Asymmetric-Laplace Model (BALM) to Analyze ChIP-seq and MBD-seq Data
Victor Jin, Ph.D., Assistant Professor, Department of Biomedical Informatics, The Ohio State University
This talk presents a novel algorithm based on a bi-asymmetric-Laplace model (BALM) to analyze both ChIP-seq and MBD-seq data. The algorithm was not only tested to achieve better accuracy on publicly available TF ChIP-seq data compared to other tools, but also applied to analyze MBD-seq data from breast cancer MCF7 cells. The results demonstrate the algorithm's ability to distinguish closely positioned target sites and to accurately predict DNA methylation regions. This study demonstrates BALM may provide another useful tool for the sequencing user community.

4:45 The Pipeline Pilot NGS Collection: A New Approach to the Challenges of NGS Data Analysis
Sponsored by accelrys
Clifford Baron, Product Marketing Director, Accelrys
In repeated surveys, scientists using next generation sequencing technologies report that data analysis is their greatest challenge, and the most significant impediment to continued market growth. This is so despite the availability of over a dozen commercial software offerings and literally hundreds of public domain NGS algorithms, with more appearing weekly. The most frequently discussed factor contributing to the data analysis challenge is the sheer volume of data generated. But as significant though less frequently acknowledged is the rapid evolution of available algorithms and attendant computational best practices, and the need for techniques tailored to specific research goals. We discuss how Pipeline Pilot, a widely used commercial software system for the rapid development and deployment of computational pipelines, can be used along with a newly released collection of NGS analysis components to address these fundamental challenges.

5:15 Best of Show Awards in the Exhibit Hall

6:15 Exhibit Hall Closes

THURSDAY, APRIL 14

8:45 am Event Chairperson's Opening Remarks
Kevin Davies, Ph.D., Editor-in-Chief, Bio-IT World

8:50 KEYNOTE PANEL:
KEYNOTE INTRODUCTION *Sponsored by* BT
A special plenary session featuring a series of succinct, forward-looking presentations by:
Ken Buetow, Ph.D., Associate Director, Bioinformatics and Information Technology, National Cancer Institute
Debra Goldfarb, Senior Director, Strategy, Microsoft
Martin D. Leach, Ph.D., Executive Director, MRL IT for Discovery & Pre-Clinical Sciences, Merck & Co.
Mark Boguski, M.D., Ph.D., Founder, Resounding Health Incorporated
Jamie Heywood, Co-founder and Chairman, PatientsLikeMe
Yury Rozenman, Global Head of Marketing, Pharmaceutical and Life Sciences Sector, BT Global Services

10:30 Coffee Break in the Exhibit Hall with Poster Competition

SEQUENCING INFORMATICS A ND CANCER

10:55 Chairperson's Remarks
Tim Harris, DSc., Chief Technology Officer and Director of the Advanced Technology Program, SAIC Frederick

11:00 Does the Sequencing Data Tsunami Mean that People and Projects Are Going to be Left High and Dry? *(60 min session)*
Tim Harris, Ph.D., CTO and Director, Advanced Technology Program, SAIC-Frederick
Ewen Kirkness, Ph.D., Professor, The J. Craig Venter Institute
Robert Stephens, Ph.D., Director, Bioinformatics Support Group, Advanced Biomedical Computing Center, Information Systems Program, SAIC-Frederick/NCI-Frederick
There is an increasing disconnect between the ability to generate sequence data by using second and third generation methods and the ability to interpret what the sequence data means. In tumor DNA sequencing, for example, there are many common mutations being found in cancers but there are also mutations that are being found in the same cancers by some sequencing techniques but not by others. This presentation will explore why this is and what it means.

12:00 pm Dell Next Generation Bioinformatics and Research Computing Solutions: The Power to do more Science
Sponsored by DELL The power to do more
Jose Alvarez, Business Development Manager, HPC Solutions, Dell
Utilizing High Performance purpose build building blocks, Dell is simplifying research computing. Dell have created an ecosystem that is helping research groups accelerate their time to results and enhanced the user interaction by simplifying reference architecture, deployment and integration. Dell also have partner with Next Generation Sequencing (NGS) industry leaders and instrument vendors to deliver an array of solutions that facilitates the collection and analysis of NGS data. With an array of high performance storage and archival solutions Dell also have simplified the retention and management of the NGS data life cycle. In this short presentation the Dell Life Sciences Research Computing team will give a snapshot of the ecosystem that give researchers the power to do more Science.

12:15 pm From NexGen Sequencing Data Management to 4'th Generation Sequencing
Sponsored by IBM
Michael Hehenberger, Ph.D., IBM, T.J. Watson Research Center
IBM is currently working with leading Sequencing Centers on data

management challenges posed by whole genome sequencing activities. It is shown how leading edge hardware and software solutions can be used to address the related extreme requirements. In addition, IBM Research has partnered with Roche 454 to develop a new "DNA Transistor" based sequencing technology. While the technical challenges are significant, the partners are optimistic about being able to succeed with this exciting project.

12:30 Luncheon in the Exhibit Hall and Poster Viewing

2:00 Exhibit Hall Closes

1:55 Chairperson's Remarks
Kevin Davies, Ph.D., Editor-in-Chief, Bio-IT World

2:00 Using Next-Gen Analysis to Improve Cancer Treatment Decisions
Paul Aldridge, CIO, Genomic Health
This presentation will cover various use cases for next generation sequencing data and analysis for research into cancer treatment efficacy. Attendees will gain a broader knowledge of costs and other considerations when using various approaches to enable R&D researchers to get more discoveries done.

SEQUENCING INFORMATICS TRENDS AND NEW APPLICATIONS

2:30 NGS-AaaS: Next Generation Sequencing-Annotation as a Service
Robert Haines, University of Manchester, UK
Next Generation Sequencing technologies bring genome-wide sequencing within the reach of a greater number of research labs. The $1000 genome, however, is accompanied by the $100,000 analysis. How do we keep down the cost of analytics? How do we enable labs with limited bioinformatics capability or local compute provision to benefit from NGS? Scientific workflow systems can be used for assembly and annotation pipelines. Focusing on the latter, Manchester, together with partners in Liverpool and Eagle Genomics Ltd, are using the commercial Amazon EC2 cloud and the open source Taverna workflow system to operate an on-demand, low cost, on-line analytics service for DNA analysis. As a case study we will present an AaaS application for understanding genetic variation between cattle breeds.

3:00 Sequencing without a Sequencer: How Buying Lanes Can Beat Buying a Machine
Keith Robison, Ph.D., Lead Senior Scientist, Informatics, Infinity Pharmaceuticals, Inc.
What are the economics of buying sequencing services vs. owning your own lab? How can you mix internal operations with contracted ones? What are potential issues in vendor performance? What are the trade-offs of accessing multiple sequencing platforms through vendors? This talk will focus on the economic & operational issues around contracting for sequencing & analysis services including vendor selection issues, vendor experiences, and opportunities.

3:30 The Atlas Cloud Computing Infrastructure for Organizing and Querying Multiomics Data *(Joint with Tracks 1-5)*
Misha Kapushesky, Ph.D., Functional Genomics Team Leader, EBI, Cambridge UK
The Expression Atlas is a cloud computing based distributed infrastructure for organizing and querying multiomics data. Built upon the open-source Expression Atlas project at the EBI in partnership with the pharmaceutical industry, the Atlas provides a scalable solution that can be easily deployed on in-house servers or accessed remotely in the cloud. Learn how the Atlas deals with secure processing and combined analysis and integration of public/private transcriptomic and proteomic data, with an emphasis on our novel pipeline for next-generation sequencing data processing and reporting.

4:00 Conference Adjourns

caBIG®
cancer Biomedical Informatics Grid®

http://cabig.cancer.gov
caBIG® is a virtual network of interconnected data, individuals, and organizations that is redefining how research is conducted, care is provided, and patients and consumers interact with the biomedical research enterprise. caBIG® capabilities enable all stakeholders along the spectrum of research and care to connect for data exchange, collaborations, and achieving personalized medicine.

Systems & Predictive Medicine

TUESDAY, APRIL 12

7:00 am Workshop Registration and Morning Coffee

8:00 - 4:00 pm Pre-Conference Workshops*

**Separate Registration Required. See page 3 for details.*

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8:45 Benjamin Franklin Award/Presentation:
Jonathan Eisen, Ph.D., Professor, Genome Center, University of California, Davis

9:10 Best Practices Awards Program

9:45 Coffee Break in the Exhibit Hall and Poster Viewing

Sponsored by SCYNEXIS

SYSTEMS MEDICINE

10:50 Chairperson's Remarks
Mary Ann Brown, Executive Director, Conferences, Cambridge Healthtech Institute

11:00 FEATURED PRESENTATION
Systems Medicine - Where East Meets West: The Future of Personalized Health
V.A. Shiva Ayyadurai, Ph.D., Fulbright Scholar & Faculty Lecturer, Department of Biological Engineering, Massachusetts Institute of Technology
Modern medicine has provided great discoveries and tools for humanity over the past several decades, particular in the biomolecular sciences. Traditional and ancient systems of medicine, developed over 5,000 years, offer an interconnected approach to understanding the whole human physiome and its interrelationships to the ecosystem. Systems Medicine provides an integrative platform, for bridging ancient and modern, East and West, science and tradition to deliver a personalized health, as never before, to each one of us.

11:30 Bridging the Gap between Systems Biology and Medicine
Gilles Clermont, Department of Critical Care Medicine, University of Pittsburgh School of Medicine

12:00 pm Linking Disease Genetics to Future Therapeutics through Disease Allele/Drug Interaction Screens
Stanley Y. Shaw, M.D., Ph.D., Co-Director, Chemical Biology, Center for Systems Biology, Massachusetts General Hospital; Assistant Professor, Medicine, Harvard Medical School
Translating discoveries in disease genetics into functional insights and therapies has proven challenging. We performed a synthetic interaction screen in human patient-derived cells, and identified genes and small molecules that interact with a monogenic diabetes mutation. This approach applies the logic of model organism genetic interaction screens to study pathway interactions in patient cells, and may help assign function to disease mutations of unclear mechanism, and suggest novel therapeutic approaches.

12:30 Luncheon Presentation *(Sponsorship Opportunity Available)* **or Lunch on Your Own**

DATA GENERATION

1:40 Chairperson's Remarks
V.A. Shiva Ayyadurai, Ph.D., Fulbright Scholar & Faculty Lecturer, Department of Biological Engineering, Massachusetts Institute of Technology

1:45 FEATURED PRESENTATION
The Role of Variation in Cell Fate Determination
John Quackenbush, Ph.D., Professor, Biostatistics and Computational Biology, Cancer Biology Center for Cancer Computational Biology, Dana-Farber Cancer Institute
The history of biomedical research has been driven by one basic and extraordinarily successful question: Given a measurement for an experimental and a control group, is the average difference between groups large relative to the variance? While this has allowed us to discover elements that are activated or deactivated during development, disease progression, and in different tissues and organs, it fails to capture the entire spectrum of changes that occur as cells change from one state to another. There is a second, equally important question one might ask: For a biologically relevant pathway or mechanism, is there a large difference in the variance exhibited by different phenotypic groups?

Track 6 provides in-depth modeling approaches from *in silico* to *in vivo* with an emphasis on drug discovery, ADME predictions, and systems medicine leading to effective translation into the clinic.

2:15 Single Molecules Meet Systems Biology - Quantifying the *E. coli* Proteome and Transcriptome with Single-Molecule Sensitivity in Single Cells
Yuichi Taniguchi, Ph.D., Postdoctoral Fellow, Chemistry and Chemical Biology, Harvard University
System-wide measurements of protein and mRNA copy numbers with single molecule sensitivity in single cells are carried out for the model organism of *Escherichia coli*. The results provide a comprehensive and quantitative description of stochastic gene expression, and of cell-to-cell variation in protein and mRNA production in isogenic bacterial populations.

2:45 Screening for Novel Chemical and Genetics Regulators of the Wnt/Wingless Signaling Pathway
Ramanuj DasGupta, Ph.D., Assistant Professor, Pharmacology, Director, RNAi-Screening Facility, NYU School of Medicine/ Cancer Institute
We have designed an RNAi-based chemical genetic screen to identify novel small molecule modulators of the Wnt signaling pathway. Our screen has identified 3 compounds, that we call "inhibitors of ß-catenin-responsive transcription" or iCRTs, that specifically and potently inhibit the activity of the Wnt pathway in a variety of Wnt-responsive and disease relevant cell lines. Importantly, these novel Wnt inhibitors are specifically cytotoxic to human colon tumor biopsy cultures as well as colon cancer cell lines that exhibit deregulated Wnt signaling.

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

DATA INTEGRATION

3:45 Physiological and Pathological Population Dynamics of Circulating Human Red Blood Cells
John Higgins, M.D., Assistant Professor of Systems Biology, Harvard Medical School, Assistant Pathologist, Massachusetts General Hospital

4:15 Discovering Copy Number Variations in Cancer Genomes by Data Integration
Peter J. Park, Ph.D., Assistant Professor, Harvard Medical School Center for Biomedical Informatics
We have collected and analyzed thousands of DNA copy number profiles of tumor genomes from public databases. Our analysis reveals a spectrum of common and tissue type-specific aberrations, correlations among the observed aberrations, and potential molecular mechanisms. I will also describe some of our efforts in using next-generation sequencing to better characterize structural variations in cancer genomes.

4:45 Sponsored Presentation *(Opportunity Available)*

5:15 Best of Show Awards in the Exhibit Hall

6:15 Exhibit Hall Closes

Thursday, April 14

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

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Mark Boguski, M.D., Ph.D., Founder, Resounding Health Incorporated
Jamie Heywood, Co-founder and Chairman, PatientsLikeMe
Yury Rozenman, Global Head of Marketing, Pharmaceutical and Life Sciences Sector, BT Global Services

10:30 Coffee Break in the Exhibit Hall with Poster Competition

DATA MODELING

10:55 Chairperson's Remarks
Zhaohui Cai, M.D., Ph.D., Director, Biomedical Informatics, AstraZeneca

11:00 Computational Models for Human Drug Induced Liver Injury
Sean Ekins, Ph.D., D.Sc., Senior Consultant, Collaborations in Chemistry
Drug-induced liver injury (DILI) is one of the most important reasons for drug development failure at both pre-approval and post-approval stages. I will describe machine learning models for DILI and their large scale validation. These computational models may represent a cost effective selection criteria prior to *in vitro* or *in vivo* experimental studies.

11:30 Model-Based Drug Development: How *in silico* Approaches Are Reshaping the Clinical Enterprise
Zhaohui Cai, M.D., Ph.D., Director, Biomedical Informatics, AstraZeneca
This presentation will demonstrate how the application of advanced in-silico methods for predictive modeling look set to change the way that clinical trials are conducted in the future. Specifically, it will cover different applications of predictive modeling in drug development and demonstrate how disciplines like Biomedical and Health Informatics can help address the gaps in drug development through real case scenarios. It will end with a discussion on the successes and challenges surrounding how to implement modeling as a routine way of working in biopharmaceutical drug development.

12:00 pm Understanding the Human Microbiome through Data Integration
Curtis Huttenhower, Ph.D., Assistant Professor, Department of Biostatistics, Harvard School of Public Health
In order to interpret the biological activity of our microbial communities, it is necessary to harness a wide range of experimental results generated by decades of work on model organisms in the laboratory. I will discuss work that my lab has done integrating such data in order to characterize individual microbes and assembling it to better understand microbial communities. I will conclude with an overview of the functional genomics involved in the Human Microbiome Project and their potential for future cohort studies of the microbiota for disease diagnosis and treatment.

12:30 Luncheon in the Exhibit Hall and Poster Viewing

2:00 Exhibit Hall Closes

THE 4 D'S: DATA, DRUG DISCOVERY & DEVELOPMENT

1:55 Chairperson's Remarks

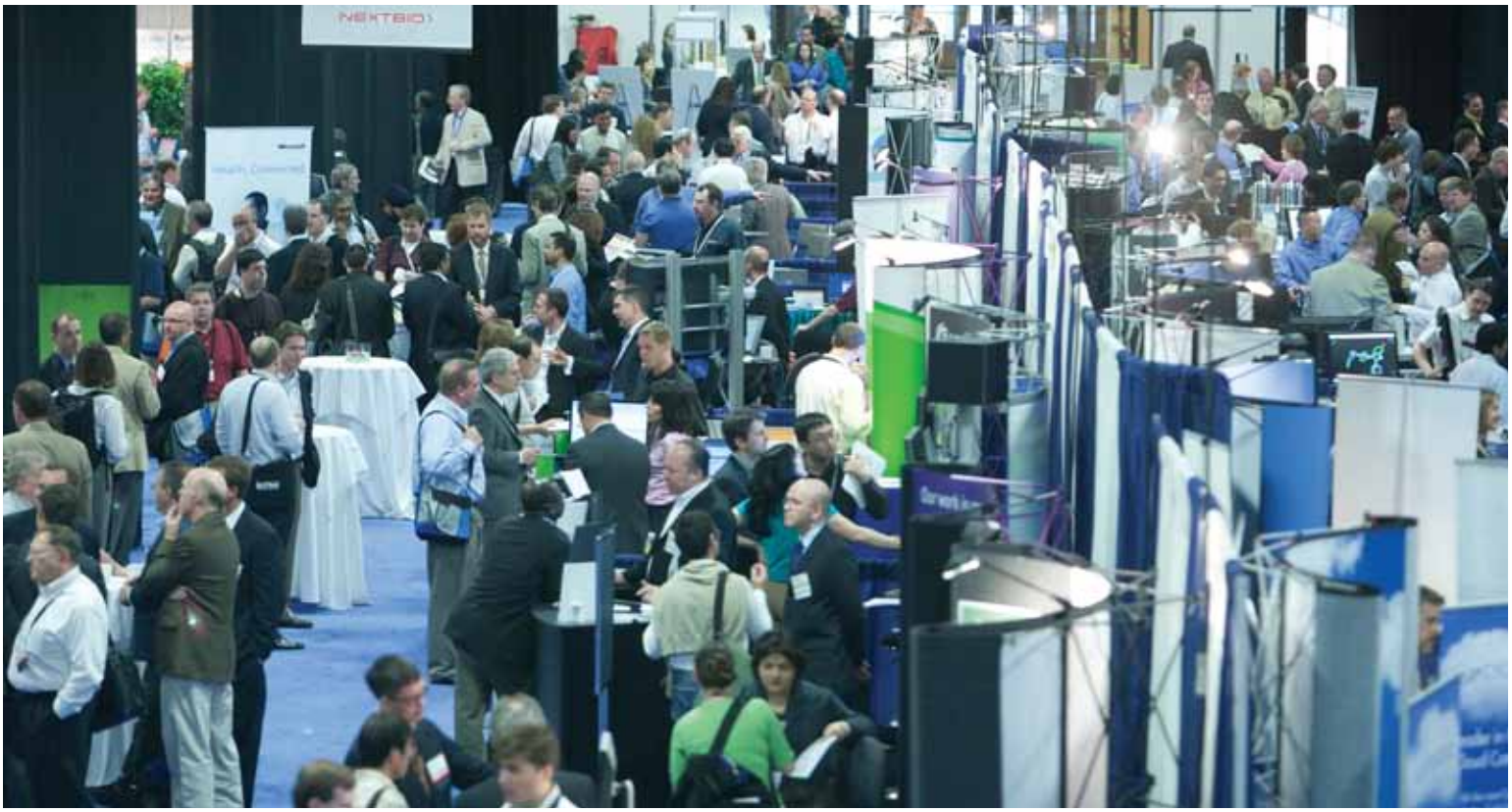
2:00 Re-Engineering CNS Drug R&D Using Computer-Based Mechanistic Modeling and Simulation
Hugo Geerts, Ph.D., CSO, Computational Neuropharmacology, In Silico Biosciences; Adjunct Associate Professor, School of Medicine, University of Pennsylvania
A major difference between the pharmaceutical industry and other successful industries is the lack of integrated computer simulation. Computer-based mechanistic modeling based upon the physiology of brain networks and the pharmacology of drug-receptor interaction, based upon pre-clinical and clinical data for schizophrenia and cognitive disorders is a powerful tool to support a variety of decision processes in pre-clinical and clinical CNS R&D, especially when validated by correlations with clinical outcomes.

2:30 Drugable.com -- Drug Discovery in the Systems Biology Era Meets the Web
James Swetnam, Lead Scientific Programmer, Pharmacology, New York University Langone Medical Center
Drugable.com is an NLM stimulus-funded venture that maintains a comprehensive, clean, and intuitive index of drugable targets, druglike chemistry, experimental activity, crystallographic structures, and *in silico* docking predictions. This talk will show how drugable.com can be used to diversify lead portfolios, explore off-target activity, and accelerate drug discovery. Broader emerging concepts in drug discovery informatics will also be discussed.

3:00 Practical Applications of Systems Biology in the Pharmaceutical Industry
Bruce Gomes, Ph.D., Head, Mathematical Modeling, Systems Biology, Research Technology Center, Pfizer, Inc.
At one end of the R&D spectrum, modeling and simulation of therapeutics is applied in clinical trial design and patient stratification. At the other end of the discovery pipeline, Systems Biology is used to objectively define therapeutic product profiles. In addition, the combination of text mining and modeling is being effectively deployed for target generation from the combination of disease, therapeutic modality, and pathway modeling. This talk will trace some of the practical applications of Systems Biology that have been used to speed discovery, increase its success rate, improve safety of biotherapeutic drug candidates and deliver these drugs to the correct patient populations.

3:30 A Systems Approach to Drug Discovery
Ulrik Nielsen, Ph.D., Senior Vice President & CSO, Merrimack Pharmaceuticals
Merrimack has built a pharmaceutical organization designed to drive innovation through a systems approach to therapeutic research and development. Insights from multidisciplinary teams working on drug design and diagnostics have led to a pipeline of novel experimental cancer therapies. We will discuss our experience based on several programs that are now in clinical trials.

4:00 Conference Adjourns



eClinical Solutions for Clinical Trials and Clinical Operations

TUESDAY, APRIL 12

7:00 am Workshop Registration and Morning Coffee

8:00 - 4:00 pm Pre-Conference Workshops*
**Separate Registration Required. See page 3 for details.*

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4:00 Event Chairperson's Opening Remarks
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Stephen Wolfram, Ph.D., CEO, Wolfram Research; Creator of Wolfram|Alpha

5:00 Welcome Reception in the Exhibit Hall and Poster Viewing

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Wednesday, April 13

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PLENARY KEYNOTE

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9:10 Best Practices Awards Program

9:45 Coffee Break in the Exhibit Hall and Poster Viewing

Sponsored by SCYNEXIS

CLINICAL TRIAL DATA INTEGRATION

10:50 Chairperson's Remarks
James Weatherall, Ph.D., Global Director, Biomedical Informatics, Clinical Information Management, AstraZeneca

11:00 Efficient Integration and Analysis of Clinical Trial Data
Steve Sweeney, Head, Clinical Operations, Infinity Pharmaceuticals
Co-Developed with John Keilty, Vice President, Informatics, Infinity Pharmaceuticals
Infinity's integrated clinical systems, consisting of custom CTMS, Pharmacovigilance, EDC and a CDISC-compliant data warehouse enables the timely analysis of clinical data to meet strategic and tactical needs. The platform's automated reporting and a progressive approach to data visualization and analysis has led to broad and effective use throughout the company. The team utilizes a variety of mechanism for data review, transforming all aspects of clinical operations and medical review. This approach to data integration and reporting has increased company-wide productivity while dramatically reducing the dependency on traditional programming efforts.

11:30 Merck/Schering-Plough Merger: R&D Master Data Harmonizing Program
Speaker to be Announced
As Merck and Schering-Plough move forward to create one combined company, we are focusing on rationalizing the complex R&D Application Landscape to define and implement the New Merck Application Roadmap. Foundational to that roadmap is defining and implementing master data that will be utilized across research and research systems. This session will outline the approach utilized to assess, rationalize, define and, as necessary, implement Reference Data and Vocabularies in support of the New Merck Clinical environment. Topics to be covered include: Clinical Master Data Information Architecture and Modeling; Information and Program Governance & Stewardship; Solution Architecture and Planning; and Reference Data solution and Application Transition Planning.

12:00 pm Leveraging Integrated Clinical Research Data
Sponsored by ICON A Symbol of Excellence
Adrian Pencak, Vice President Data & Technology Services, ICON Clinical Research
In this presentation we ask the question; are we leveraging our safety and clinical data to get the most out of it? This presentation will describe the benefits of using a central warehouse for all clinical data. The central data warehouse can enable the integration, management, reporting, visualisation and analysis of that data. The concept will be explained and how it can provide; intelligence to support more timely decision making, more transparency to the sponsor and improved chain of custody for clinical data.

12:30 Luncheon Presentation *(Sponsorship Opportunity Available)* **or Lunch on Your Own**

EDC IMPLEMENTATION ACROSS VENDOR AND INTERNAL SYSTEMS

1:40 Chairperson's Remarks
Joan Chambers, COO, CenterWatch

1:45 Case Study: Data Integration across Multiple Vendor and Internal Platforms in Support of eClinical Trial Setup
Ramzi Najm, Vice President, R&D Information and Technology Management, Allergan
SOA integration of internal systems can be a challenge. When eClinical operations are distributed across multiple vendors' SaaS platforms as well as internally managed applications, integration can present unique challenges. This discussion will review our unique SOA integration approach for internal and multiple external environments and share a case of collaboration across multiple stakeholders.

2:15 Case Study: Lessons Learned from EDC Implementation at the Dana Farber Cancer Institute
Marina Nillni, EDC Program Manager, Dana Farber Cancer Institute
This presentation will share the story of EDC implementation at the Cancer Center. Details to be shared include how the journey started and where we are today. Lastly, the presentation will summarize what we consider to be the key challenges and benefits.

2:45 Emerging Clinical Trial Data Integration Requirements and Technologies
Sponsored by LIAISON
Bruce Chen, M.Sc., CTO, Liaison Technologies
In many industries integration services and solutions have reached maturity, though incremental improvement and evolution does occur. Recent developments in eClinical data integration have generated a higher order of requirements that are unique to the pharmaceutical industry.

Track 7 explores how to leverage technology to optimize speed, quality and cost of clinical trials. Themes covered include best practices in data collection and analysis, systems integration across multiple vendor and internal platforms, clinical imaging, utilization of informatics for drug safety surveillance, and utilization of EHRs to accelerate patient recruitment.

In this session Bruce Chen will describe emerging technologies and trends that will define integration for clinical trials over the next several years including semantic integration, expert matching, pattern recognition, and the combination of health care and pharmaceutical data.

3:00 Utilizing SaaS-based Clinical Trial Operations Software to Optimize Clinical Development
Sponsored by CLEAR TRIAL
Andrew Grygiel, Vice President, Marketing and Product Management, ClearTrial
Biopharmaceutical and medical device companies are turning to new types of software to accelerate clinical development while reducing IT infrastructure costs. Attendees will discover how Clinical Trial Operations (CTO) software delivered as Software-as-a-Service (SaaS) is enabling study sponsors to reduce study cycle-times and costs—while maintaining study feasibility.

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

ETRIAL DATA INTEGRATION AND IMPLEMENTATION

3:45 ImagEDC - Clinical Trial Imaging Integration Using Service-Oriented Architecture, Grid Computing and Open Source
Josh C. Snyder, Imaging Infrastructure Expert, Biomarker Development/Clinical Imaging & Thierry Cladé, Solution Architect, IT & Automation, Novartis Pharma AG
Co-Developed with Stefan Baumann, Head, Imaging Infrastructure, Biomarker Development/Clinical Imaging, Novartis Pharma AG
Novartis has released ImagEDC, an open source tool based on the National Cancer Institute's grid computing platform "caGrid". The software enables machine-to-machine integration between partners involved in a Clinical Imaging Trial. As a reference implementation for service-oriented architecture (SOA), and being free from license costs, ImagEDC can help to integrate both academic and commercial partners using a shared communication standard. Key advantages of the proposed SOA standard include archive federation to avoid large bulk data transfers.

4:15 Sorting Out eTrial Solutions for the Clinical Operations Professional: Which is Right for You?
Adam Ruskin, Ph.D., D.V.M., M.P.H., Director, Clinical Affairs, Gentura, Inc.
With many eTrial solutions for various tasks now on the market, how does the Clinical Trial Manager decide what they really need for their trial? How does a company decide what technologies are needed to optimize their overall efficiency? With so many choices, decision points based on cost, performance and efficiencies need to be made. This presentation will help to sort out the ever growing variety of eSolutions for the Clinical Operations professionals who use these systems to help make informed technology-based decisions.

4:45 Bridging Patient Care and Clinical Research through Biomedical Informatics
Aaron Kamauu, M.D., M.S., M.P.H., Head of Healthcare Data Strategy, Genentech
Massive amounts of rich patient-level clinical data is generated by electronic health information systems (including EHR/EMR) as they are increasingly used to assist healthcare providers in providing quality patient care. At the same time these data sources are also increasing in both depth and breadth of clinical information collected. This change in the healthcare environment provides new opportunities in how these data can be used to support a variety of drug development activities. I will present some unique ways we have leveraged these healthcare data to support clinical research and clinical trials in Roche and Genentech, focusing on examples that have strengthened assumptions in clinical trial strategy, protocol design and site identification.

5:15 Best of Show Awards in the Exhibit Hall

6:15 Exhibit Hall Closes

Thursday, April 14

8:45 am Event Chairperson's Opening Remarks
Kevin Davies, Ph.D., Editor-in-Chief, Bio-IT World

8:50 KEYNOTE PANEL:
KEYNOTE INTRODUCTION *Sponsored by* BT
A special plenary session featuring a series of succinct, forward-looking presentations by:
Ken Buetow, Ph.D., Associate Director, Bioinformatics and Information Technology, National Cancer Institute
Debra Goldfarb, Senior Director, Strategy, Microsoft
Martin D. Leach, Ph.D., Executive Director, MRL IT for Discovery & Pre-Clinical Sciences, Merck & Co.
Mark Boguski, M.D., Ph.D., Founder, Resounding Health Incorporated
Jamie Heywood, Co-founder and Chairman, PatientsLikeMe
Yury Rozenman, Global Head of Marketing, Pharmaceutical and Life Sciences Sector, BT Global Services

10:30 Coffee Break in the Exhibit Hall with Poster Competition

LEVERAGING TECHNOLOGY TO OVERCOME TRIAL COMPLEXITY AND IMPROVE EFFICIENCY

10:55 Chairperson's Remarks
Aaron Kamauu, M.D., M.S., M.P.H., Head of Healthcare Data Strategy, Genentech

11:00 Rising Protocol Design Complexity and Its Impact on Clinical Trial Performance
Ken Getz, Senior Research Fellow, Assistant Professor, Tufts Center for the Study of Drug Development, Tufts University Medical School
This session explores how protocol designs have changed during the past decade and discusses the dramatic negative impact that rising protocol complexity has on clinical trial cycle time, cost and efficiency. Variability by phase and therapeutic area will be presented with insights into targeted areas where protocol complexity is the highest and where it has grown the fastest. Sponsor approaches and technology solutions used to simplify and streamline protocol designs will also be discussed.

11:30 Case Study: Approach and Experiences Implementing Structured Protocol Authoring at Genzyme
A. Brooke Hinkson, Associate Director Program Management, Global Biomedical Informatics, Genzyme
There is significant pressure to streamline business processes, increase reuse of clinical information, produce high quality clinical documentation and decrease overall development timelines. This presentation will share the approach and experiences to date implementing topic-based structured content at Genzyme.

12:00 pm The Application of Text Analytics to Drug Safety Surveillance
James Weatherall, Ph.D., Global Director, Biomedical Informatics, Clinical Information Management, AstraZeneca
This presentation will: Outline the fundamental challenges of conducting routine post-marketing surveillance on the published literature; Explain why the utilization of informatics approaches such as text analytics potentially addresses some of these challenges; Describe how an agile internal project succeeded in delivering a system to employ such an approach within 6 months; Report on the business impact of the new system so far; Look ahead to possible future enhancements, and alternative applications of the approach.

12:30 Luncheon in the Exhibit Hall and Poster Viewing

2:00 Exhibit Hall Closes

CASE STUDIES IN HIT AND eCLINICAL FROM THE caBIG PERSPECTIVE

Solutions for Personalized Medicine and eClinical Solutions

(shared session between Tracks 7 and 8)

1:55 Chairperson's Remarks

2:00 Creating a Research Infrastructure to Support Cancer Personalized Medicine

Presented by caBIG

Gregory C. Bloom, Ph.D., Assistant Professor, Biomedical Informatics, H. Lee Moffitt Cancer Center and Research Institute
Sorena Nadaf, Director, Translational and Biomedical Informatics and CIO, Helen Diller Family Comprehensive Cancer Center Translational Informatics, University of California, San Francisco
Kenneth Buetow, Ph.D., Associate Director for Bioinformatics and Information Technology, National Cancer Institute

The personalized medicine paradigm requires data liquidity so that information and knowledge can be freely exchanged among stakeholders at all stages of the bench-to-bedside continuum. In this approach to biomedicine, research and clinical care are seamlessly linked in a virtuous circle that enables the collection and analysis of information on clinical outcomes of large populations. This session will discuss how caBIG® technology is being leveraged to build and extend capabilities that will support a rapid learning system of healthcare.

USING HEALTH RECORDS AND POINT-OF-CARE DATA TO ACCELERATE PATIENT RECRUITMENT

3:00 Interactive Presentations and Panel Discussion

David A. Krusch, M.D., Chief Medical Information Officer, University of Rochester Medical Center
Kathy Ciccone, Executive Director, Quality Institute, The Healthcare Association of New York State
David Leventhal, Director, Healthcare Informatics, Pfizer
Jeff Kraut, Senior Vice President, Strategic Planning and Marketing, North Shore-LIJ Health System
John Murphy, Dr.P.H., Head, Clinical Analytics, Quintiles

4:00 Conference Adjourns

CHI's INTRONET Networking at its Best

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!

eHealth and HIT Solutions for Personalized Medicine

TUESDAY, APRIL 12

7:00 am Workshop Registration and Morning Coffee

8:00 - 4:00 pm Pre-Conference Workshops*

**Separate Registration Required. See page 3 for details.*

2:00 - 6:00 Main Conference Registration

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

4:05 Keynote Introduction
Chris Blessington, Life Sciences Solutions Architect, Isilon

Sponsored by ISILON SYSTEMS

PLENARY KEYNOTE

4:15 Making the World's Knowledge Computable
Stephen Wolfram, Ph.D., CEO, Wolfram Research; Creator of Wolfram|Alpha

5:00 Welcome Reception in the Exhibit Hall and Poster Viewing
***Drop off a business card at the CHI Sales booth for a chance to win 1 of 2 iPod®s! **Apple® is not a sponsor in the program.*

Sponsored by BLUE ARC

Wednesday, April 13

7:00 am Registration and Morning Coffee

8:00 Event Chairperson's Opening Remarks
Phillips Kuhl, Co-Founder and President, Cambridge Healthtech Institute

8:05 Keynote Introduction
Grant Stephen, CEO, Tessella, Inc.

Sponsored by Tessella Technology & Consulting

PLENARY KEYNOTE

8:15 Interacting with Complex Information Landscapes: Integration and Next Generation User Interfaces
Bryn Roberts, Ph.D., Global Head, Informatics, Pharma Research and Early Development, F. Hoffmann-La Roche Ltd.

8:45 Benjamin Franklin Award/Presentation:
Jonathan Eisen, Ph.D., Professor, Genome Center, University of California, Davis

9:10 Best Practices Awards Program

9:45 Coffee Break in the Exhibit Hall and Poster Viewing

Sponsored by SCYNEXIS

DELIVERING CLINICALLY ACTIONABLE DATA TO THE PHYSICIAN AND BACK

10:50 Chairperson's Remarks
David Medina, Worldwide Life Science and Pharma Segment Executive, HP Enterprise Business

Sponsored by hp

11:00 Connecting Patients, Providers and Payers
John D. Halamka, M.D., M.S., CIO, Harvard Medical School; CIO, Beth Israel Deaconess Medical Center; CIO, Harvard Clinical Research Institute

Patient engagement provisions in recent federal regulations are encouraging patients to collect and manage their own healthcare data from clinicians offices, personal health records, and home devices. In this presentation, we'll examine the emergence of novel patient sourced data sources and their implications for research and clinical trials.

1:30 ATHENA Breast Health Network: A Model Learning System to Improve Clinical Care and Research
Subha Madhavan, M.D., Director, Clinical Research Informatics, Oncology, Georgetown University
The ATHENA Breast Health Network (ATHENA) is a unique collaboration among the five University of California (UC) medical centers that will revolutionize the delivery of care by integrating research and clinical care in prevention, screening, treatment and management of breast cancer. Critical to the success of this program is a technology roadmap that is adapting and extending current open source and commercial tools to collect, aggregate and report patient reported data, point-of-care clinical data, pathologic and molecular data, and clinical decisions, and provide the engine for comparative effectiveness and integration of optimal practices into clinical care.

Sponsored by hp

12:00 pm "Seeded" Cloud Computing Transformation in Cancer Research– A Case Study
Krishna Sankhavaram, Director, Research IS & Technology Development, University of Texas, MD Anderson Cancer Center
Srikanth Venkata Seshu, Worldwide Solutions Marketing Manager, HP StorageWorks
Learn how MD Anderson has strategically built one of the largest supercomputing centers of its kind in an academic research setting to service several next-generation sequencing laboratories in a centralized and virtualized private cloud environment.

12:30 Luncheon Presentation *(Sponsorship Opportunity Available)* **or Lunch on Your Own**

1:40 Chairperson's Remarks
Samuel J. Aronson, Executive Director, IT, Harvard Medical School & Partners Healthcare for Genetics and Genomics

1:45 Delivering Scalable IT Support to Clinicians Practicing Personalized Medicine *(60 min session)*
Samuel J. Aronson, Executive Director, IT, Harvard Medical School & Partners Healthcare for Genetics and Genomics
Heidi Rehm, Ph.D., FACMG, Laboratory Director, Molecular Medicine, Assistant Professor of Pathology, Harvard Medical School
The value of personalized medicine rests on enabling clinicians to use genetics to make better decisions. In practice, as genetic testing becomes more complex and widespread, it will become increasingly difficult for clinicians to track which variants have been found in each of their patients and how these variants should impact the clinical decisions they make. Information technology can help solve this problem, but to be effective applications must enable new forms of integration between laboratories and treating clinicians. In effect, genetic testing laboratories, clinical end users and IT need to work together to create support for new clinical processes and workflows that cannot exist without substantial IT support. In this presentation, we will discuss our experience designing, building and deploying these types of applications.

2:45 Sponsored Presentation *(Opportunity Available)*
3:15 Refreshment Break in the Exhibit Hall and Poster Viewing
3:45 Synergistic Patient and Research Knowledge Systems—An Enterprise Data Integration and Analysis Platform
Jomol Mathew, Ph.D., Director, Clinical and Translational Informatics, IS, Dana-Farber Cancer Institute
The Synergistic Patient and Research Knowledge System (SPARKS) establishes an enterprise informatics framework designed to accelerate scientific discoveries, and their translation into personalized medicine and clinical practice. SPARKS implements the policies, standards, systems, and tools that facilitate the collection, integration, mining, analysis, and interpretation of biomedical data.

Track 8 explores the integration of life sciences, IT and general healthcare to support the care delivery process and innovative R&D of next generation health IT and personalized medicine solutions. Themes covered include EHRs and their impact on R&D, translational medicine, the development of companion diagnostics, integrating clinical data with genomic data, and technology tools to support the care delivery process.

4:15 Exploring Risk/Benefit Profiles of Medicines through Mining of Observational Data
Victor Lobanov, Director, Informatics & Pharmaceutical R&D, Johnson & Johnson Pharmaceutical
Observational healthcare databases, such as administrative claims and electronic health records, offer a wealth of information for analysis of natural history of diseases, effectiveness of treatments, safety profiles of medications, and drug utilization trends. Several open-source analytics tools to perform such analyses have been created and are under investigation as part of the Observational Medical Outcomes Partnership, a public-private partnership between the pharmaceutical industry, academic institutions, non-profit organizations, and federal agencies.

4:45 Why Actions Speak Louder than Words: Early Case Studies in Personalized Medicine
Tibor van Rooij, Ph.D. Candidate, Pharmacy and Pharmaceutical Sciences, University of Alberta; former Director of Bioinformatics, Génome Québec and Montreal Heart Institute Pharmacogenomics Centre

5:15 Best of Show Awards in the Exhibit Hall

6:15 Exhibit Hall Closes

Thursday, April 14

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10:30 Coffee Break in the Exhibit Hall with Poster Competition

HEALTHCARE INFORMATICS AND PERSONALIZED MEDICINE FROM THE PHARMACEUTICAL PERSPECTIVE

10:55 Chairperson's Remarks

11:00 eHealth: A Transformative Opportunity for Pharma
Chris L. Waller, Ph.D., Senior Director, HealthCare Informatics, Medical Business Technology, Pfizer, Inc.
Advances in health information technology (HIT) present the pharmaceutical industry with many innovative opportunities that promise to transform business processes across the research, development, commercial, and medical continuum. For over a decade, Pfizer has recognized the potential of, and supported advances in, HIT. At Pfizer, a cross-disciplinary eHealth team comprising representatives from Corporate Strategy and Innovation, Business Technology, Business Development, and Policy has been created to identify, evaluate, and implement HIT-enabled business changes.

11:20 Using HIT Health IT to Breakdown Geographic and Social Barriers and Advance Personalized Medicine and Drug R&D
Eric D. Perakslis, Ph.D., Vice President, Research & Development IT, Johnson & Johnson Pharmaceuticals Research and Development
Despite years of technological progress and an unprecedented push for EMRs via government stimulus, few successful examples of eHealth business models exist. The basic abilities to reach wider patient audiences, aggregate medical data, identify patient populations at need/risk and to provide a healthcare collaboration platform across public, private and NGO boundaries are within reach and must be realized.

11:40 Healthcare Technologies to Enable Health@Home
Adel Laoui, Ph.D., M.B.A., Director, Healthcare Technologies, Aging Therapeutic Strategic Unit, Sanofi-Aventis U.S.
This presentation will address the new opportunities arising for the aging business, ranging from solutions for drug administration to ensure treatment adherence, to diagnostics & labs "@ home" to minimize travel to the medical facility, to telemedicine for prevention, and to "smart homes" integrating all these technologies. All of these needed healthcare technology solutions require an unprecedented effort to consolidated a much segmented market and develop a vision of a true integrated and diversified healthcare system.

12:00 Enabling Secondary Uses of EMR: The Quality Stack
Gary Keith Mallow, Ph.D., Director, Health Information Technology, Merck & Co., Inc.

12:30 Luncheon in the Exhibit Hall and Poster Viewing

2:00 Exhibit Hall Closes

CASE STUDIES IN HIT AND eCLINICAL FROM THE caBIG PERSPECTIVE
Solutions for Personalized Medicine and eClinical Solutions
(shared session between tracks 7 and 8)

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Presented by caBIG

2:00 Creating a Research Infrastructure to Support Cancer Personalized Medicine
Gregory C. Bloom, Ph.D., Assistant Professor, Biomedical Informatics, H. Lee Moffitt Cancer Center and Research Institute
Sorena Nadaf, Director, Translational and Biomedical Informatics and CIO, Helen Diller Family Comprehensive Cancer Center Translational Informatics, University of California, San Francisco
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USING HEATH RECORDS AND POINT-OF-CARE DATA TO ACCELERATE PATIENT RECRUITMENT

3:00 Interactive Presentations and Panel Discussion
The Partnership to Advance Clinical electronic Research (PACeR) is a broad-based health care collaborative that is led by the Healthcare Association of New York and comprised of New York State hospitals, healthcare providers, patients and pharmaceutical and technology companies. Since its inception in early 2010, PACeR has been working to identify new approaches for the collection and use of clinical information to accelerate evidence-based medical research. Its long-range goal is to improve the delivery and outcomes of patient care by effectively and efficiently leveraging electronic clinical data for research-related activities through a sustainable model.

David A. Krusch, M.D., Chief Medical Information Officer, University of Rochester Medical Center
Terri Straub, Consultant, Healthcare Association of New York State
David Leventhal, Director, Healthcare Informatics, Pfizer
Jeff Kraut, Senior Vice President, Strategic Planning and Marketing, North Shore-LIJ Health System
John Murphy, Dr.P.H., Head, Clinical Analytics, Quintiles

4:00 Conference Adjourns

Drug Discovery Informatics

TUESDAY, APRIL 12

7:00 am Workshop Registration and Morning Coffee

8:00 - 4:00 pm Pre-Conference Workshops*

**Separate Registration Required. See page 3 for details.*

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Cindy Crowninshield, Conference Director, Cambridge Healthtech Institute

4:05 Keynote Introduction
Chris Blessington, Life Sciences Solutions Architect, Isilon

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PLENARY KEYNOTE

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Stephen Wolfram, Ph.D., CEO, Wolfram Research; Creator of Wolfram|Alpha

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8:05 Keynote Introduction
Grant Stephen, CEO, Tessella, Inc.

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8:15 Interacting with Complex Information Landscapes: Integration and Next Generation User Interfaces
Bryn Roberts, Ph.D., Global Head, Informatics, Pharma Research and Early Development, F. Hoffmann-La Roche Ltd.

8:45 Benjamin Franklin Award/Presentation:
Jonathan Eisen, Ph.D., Professor, Genome Center, University of California, Davis

9:10 Best Practices Awards Program

9:45 Coffee Break in the Exhibit Hall and Poster Viewing

Sponsored by SCYNEXIS

COLLABORATIVE DRUG DISCOVERY

10:50 Chairperson's Remarks
Yuriy Gankin, Ph.D., Co-Founder, CSO, GGA Software Services

Sponsored by GGA Software Services LLC

11:00 The Pistoia Alliance: Pre-Competitive Collaborations in Research Informatics
Ramesh Durvasula, Ph.D., Director, Chemistry Informatics, Bristol-Myers Squibb, and Board Member, Pistoia Alliance
The Pistoia Alliance has been working hard to establish several standards in areas as diverse as e-notebooks, scientific literature, and sequence services. This presentation will provide an update on the progress of Pistoia, and highlight opportunities for attendees to participate in current and emerging standardization efforts.

11:30 Collaborative Virtual Organization & Infrastructure for Anti-Malarial Drug Design
Barry Hardy, Ph.D., Project Coordinator, Scientists Against Malaria and SYNERGY
The Scientists Against Malaria consortium is a virtual drug discovery organization collaborating on target selection and modeling, protein expression and assay development, computational drug design, and screening. Supported by developments on the EU FP7 funded SYNERGY and OpenTox projects, a combination of interoperable information systems, ontologies and web services were designed and deployed to manage the data, documents, computational and assay results, activity and toxicology predictions, as well as dashboards to track project progress and to support decision making.

12:00 Data Management and Informatics Platform for Enhancing Research and Development Productivity and Innovation

Sponsored by accelrys

Robert Brown, Ph.D., Senior Director Life Sciences, Accelrys, Inc.
Dominic John, Product Marketing Director, Accelrys, Inc.
This talk will discuss the use of the Accelrys data management and informatics platform, one of the pillars of its Enterprise R&D architecture, to enhance research and development productivity and innovation for small molecules and biotherapeutics. Managing end-to-end scientific workflows in a unified informatics platform allows research and development organizations to:

- streamline their operations and reduce operating costs
- increase the potential for innovation through timely capture of information, enhanced collaboration and informed decision making

12:30 Luncheon Presentation

Sponsored by OpenEye Scientific Software

FastROCS: Revolutionizing Drug Discovery on the GPU
Robert W. Tolbert, Ph.D., Vice President, Development, OpenEye Scientific Software
Shape has become a standard tool in the drug discovery process finding utility in virtual screening, lead optimization, library design, pose prediction, and active site comparison. Leveraging the power of GPU technology, FastROCS is capable of matching over 2 million conformations per second which means that corporate collections can be searched in seconds instead of hours or days.

1:40 Multi-User/Multi-Touch Real-Time Collaboration Tools for Drug Discovery Scientists
Steve Guise, Global Head Scientific I.S. & Center Head Basel, Pharma Research & Early Development Informatics, Roche
Roche has developed multi-user, real-time collaboration tools using Perceptive Pixel's innovative multi-touch technology to support decision making within drug discovery project team. The first application allows for the visualization of chemical and biological data in novel ways facilitating real-time decision capture. A second proof-of-concept application enables multiple users to simultaneously visualize and interact with networks of semantically integrated data. Both applications represent a new way of working that can be best described as "Team Computing".

Track 9 will explore innovative methods, approaches and technologies that pharmaceutical and biotechnology organizations are utilizing for collaborative drug design, knowledge management and translational medicine. New paradigms in drug discovery will also be addressed.

TRANSLATIONAL INFORMATICS AND KNOWLEDGE MANAGEMENT

2:10 Chairperson's Remarks
Paul Denny-Gouldson, Ph.D., Vice President, Translational Medicine, Head Global Healthcare Group, IDBS

2:15 The Translational Medicine Ontology: Driving Personalized Medicine by Bridging the Gap from Bedside to Bench
Susie Stephens, Ph.D., Director, In Silico Immunology, Centocor Research & Development
The Translational Medicine Ontology provides terminology that bridges diverse areas of translational medicine from bedside to bench. An overview of the ontology will be provided along with a demonstration of its utility through question answering over a prototype knowledge base composed of sample patient data integrated with linked open data.

2:45 pm Converting Data Overload into Data Assets: The Enabling Role of High Context Data Management for R&D *Sponsored by* idbs
Paul Denny-Gouldson, Ph.D., Vice President, Translational Medicine, Head Global Healthcare Group, IDBS
Clinical, 'omic, CRO and validated data are true capital assets of pharmaceuticals R&D. Agile progression from target to candidate requires the orchestration of diverse scientific disciplines, each generators and consumers of data. Instant access across this entire data landscape is now a must-have capability for speeding innovative products to market.

3:00 Driving a Linked Data Framework with Semantic Wikis
Laurent Alquier, Ph.D., Project Lead, Pharma R&D Informatics, Johnson & Johnson Pharmaceutical Research & Development
Semantic Wikis have matured to become much more than wikis. Recent advances in Semantic MediaWiki make it an ideal, low cost platform for data integration and authoring of Linked Data. A practical example applied to translational research will be provided.

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

3:45 SEEK and You Will Find …
Bo Yang, Senior Manager, Knowledge Management Program, Global Manufacturing Business Technology, Pfizer, Inc.
A tremendous amount of experimental information and scientific knowledge has been locked or lost in semi-structured and unstructured data silos in today's pharmaceutical industry. Enterprise search engines do not understand scientific terms and objects embedded in the contents. This presentation will discuss a scientifically aware search implementation at Pfizer leveraging enterprise search platform. The scope of the document indexing process is expanded to cover embedded chemistry objects and terms such as common chemical names, corporate IDs, SMILES, and InChIs from unstructured content repositories.

4:15 PharmaConnect: Connecting Knowledge from the Lab, Literature and Clinic
Bryan Takasaki, Ph.D., IS Informatics Science Director, AstraZeneca
The Knowledge Engineering initiative within AstraZeneca has recently delivered the first version of a platform and interface (PharmaConnect) that integrates internal and external evidence for connections between key concepts such as targets, pathways, compounds, diseases and clinical outcome. This talk will describe the impact of this new platform and lessons learned during its development.

4:45 Accelerating Competitive Velocity through Licensing
Sanjeev Wadhwa, Partner, WW Director Life Sciences R&D, Life Sciences, CSC
Pharma companies would take numerous bets with greater coverage to determine the landscape of technologies and people, influential innovators, IP sources and capabilities and competitor portfolios. Leveraging Innovation Networks and Connecting the Dots through Semantic Intelligence will help researchers make discoveries across and among information sources which previously had no connectivity. This new "semantic engine" can organize and present information in a visually appealing manner, highlighting connections, and helping scientists rapidly find correlations between previously unavailable data.

5:15 Best of Show Awards in the Exhibit Hall

6:15 Exhibit Hall Closes

Thursday, April 14

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Jamie Heywood, Co-founder and Chairman, PatientsLikeMe
Yury Rozenman, Global Head of Marketing, Pharmaceutical

10:30 Coffee Break in the Exhibit Hall with Poster Competition

INFORMATION SHARING PLATFORM

10:55 Chairperson's Remarks
Kenneth Buetow, Ph.D., Associate Director for Bioinformatics and Information Technology, National Cancer Institute

11:00 How to Turn a Model-T eLabNotebook into a Sleek Tesla
Martin D. Leach, Ph.D., Executive Director, IT for Discovery & Pre-Clinical Sciences (DPS), Merck & Co.
The prevailing model in large pharmaceutical companies to drive down cost and leverage external innovation is to use COTS software platforms. Without heavy customization, you are at the mercy of the underlying software and database architecture that comes with these products. With increased deployment of our chosen eLabNotebook we hit a performance wall due to the underlying structure of the software. To overcome performance issues we leveraged a third party platform that supercharged the transactional system and transformed this platform into an information sharing environment.

11:30 NCI and Novartis Collaboration: Developing a Network to Support Image Data Exchange in Pharma-Driven Clinical Research *Presented by* caBIG
Kenneth Buetow, Ph.D., Associate Director for Bioinformatics and Information Technology, National Cancer Institute
Stefan Baumann, Head of Imaging Infrastructure, Novartis Institutes for BioMedical Research, Inc.
Novartis has released ImagEDC—an open source tool based on caGrid, the National Cancer Institute's grid computing platform—a proof-of-concept tool to enable machine-to-machine integration between partners in Clinical Imaging Trials. This session will discuss program level aspects of this public-private collaboration, as well as efforts to provide other pharmaceutical partners with access to the software through the Pharma Image Exchange Consortium. The process and requirements to migrate the software from a pilot to production system will also be discussed.

Sponsored by

12:00 pm The Emerging Role of Translational Science in the Development of New Drugs
Daniel Weiner, Ph.D., Senior Vice President and General Manager, Tripos and Pharsight – Certara Companies
Drug development is a process that is heavily and equally dependent on two main areas: vertical domains of individual expertise, and the transfer of knowledge between those domains. However, one of the classic challenges in drug development is the lack of attention paid to sharing data from one domain to another. Translational science strives to overcome this challenge by emphasizing more collaboration between domains. This presentation will outline why translational science is important, the status of its implementation in the industry, and a vision for its future.

12:30 Luncheon in the Exhibit Hall and Poster Viewing

2:00 Exhibit Hall Closes

NEW PARADIGM IN DRUG DISCOVERY

1:55 Chairperson's Remarks
Nathan Walsh, Ph.D., Director, Informatics and IT, Ensemble Therapeutics Corporation"

2:00 "Bioactivity Profile" Prediction - From Single to Multiple Targets Using Computational Supporting Methods
Andreas Bender, Ph.D., Lecturer for Molecular Informatics, Department of Chemistry, University of Cambridge
The prevalent paradigm that drugs should be selective has been changed recently to the 'selective promiscuity' approach - that the right combination of targets hit is most promising. In this talk we present proteochemometrics' methods which consider data from both the ligand and target side to predict bioactivity profiles of compounds across sets of targets. In addition, prospective validations on NNRTI and GPCR datasets will be presented.

2:30 Chemical and Biological Features of Polypharmacology and Promiscuity
Florian Nigsch, Ph.D., Presidential Postdoctoral Fellow, Novartis Institutes for BioMedical Research
The idiosyncratic use of "polypharmacology" and "promiscuity" incited us to analyze a vast number of compound–protein relations and corresponding target families. A forcefully simplistic model was able to reasonably accurately attribute compounds to either group. Moreover, we analyzed the differences in cellular responses (mRNA levels) to compounds in each group to further delineate the two.

3:00 Identifying Macrocycles as Protein-Protein Inhibitors Using Bioinformatic Analysis of DNA Programmed Chemistry (DPC) Libraries
Nathan Walsh, Ph.D., Director, Informatics and IT, Ensemble Therapeutics Corporation
This talk will focus on the processing and interpretation of the data generated using DPC libraries of synthetic macrocycle drugs, called Ensemblins™. Ensemblins, with their unique chemical and biological properties, are a new class of drugs in the emerging therapeutic space between small molecules and biologics. As a therapeutic discovery company we are interested in disease pathways where the targets are considered undruggable with current small molecules.

3:30 The Resurgence of Covalent Drugs and Their Potential as Novel Targeted Therapies
Russell C. Petter, Ph.D., Vice President of Drug Discovery, Avila Therapeutics, Inc.
Targeted therapies have revolutionized cancer treatment. Despite this, there is significant need for further chemical and computational innovation to improve potency, selectivity and drug resistance profiles for targeted therapies to make them more effective. This talk will review the potential for computationally designed targeted covalent drugs to overcome these limitations to current therapies.

4:00 Conference Adjourns

HOTEL & TRAVEL

Conference Venue:

Seaport World Trade Center

200 Seaport Boulevard, Boston, MA 02210

Host Hotel:

Seaport Hotel (Located directly across the street)

One Seaport Lane, Boston, MA 02210
T: 617-385-4000 • F: 617-385-4001

Discounted Room Rate: $234 s/d
Discounted Room Rate Cut-off Date: March 18, 2011

CAR RENTAL DISCOUNTS:

Special discount rentals have been established with Hertz for this conference. Call Hertz directly at 800-654-3131 and reference our Discount Number 04KL0002.

Please visit our website to make your reservations online or 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. For information on parking, directions to the Seaport World Trade Center, airport transportation, and visiting Boston and New England, visit www.Bio-ITWorldExpo.com.

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 use Conference code 8941AV
- Go to www.aa.com enter Conference code 8941AV in promotion discount box
- Contact Wendy Levine, Great International Travel 1-800-336-5248 ext. 137

MEDIA PARTNERS

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nature

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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, national laboratories, and niche service providers.
- The Best of Show offers exhibitors an exclusive opportunity to distinguish their new 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 new product technologies used by life science professionals today. Deadline for entry is February 18, 2011 so reserve your booth space today!
- Benefit from dedicated exhibit hours designed to promote traffic in the exhibit hall.

BEST PRACTICES AWARDS SPONSOR

- Increase your company's presence at Bio-IT World's premier awards event.
- Collect qualified sales leads.
- Position your company with the best practices in the industry.
- Develop relationships with key organizations and life science professionals involved in clinical trials and research, IT and Informatics, as well as drug discovery and development.

BEST OF SHOW AWARDS

The Best of Show Awards offer exhibitors an exclusive opportunity to distinguish their new products from the competition. Judged by a joint team of *Bio-IT World* magazine editors and leading industry experts, this awards program will identify exceptional innovation in new product technologies used by life sciences professionals today. Judging and the announcement of winners is conducted live in the Exhibit Hall. To learn more about this program and submission deadlines, please contact Demetrios Loulloudes at 781-972-5445 or email dlouloudes@healthtech.com.

SPONSORSHIP OPPORTUNITIES INCLUDE:

Bio-IT World delivers a focused and progressive audience consisting of IT professionals and executives from major pharmaceutical and biotechnology companies responsible for identifying and implementing the strategies and technologies that drive their business. Bio-IT World Conference & Expo is the only major event that focuses on the integration of technology for research, drug discovery and clinical trials. Participating as a sponsor provides your company with the opportunity to demonstrate your products and services to this targeted and otherwise hard to reach market.

SPONSORED PRESENTATIONS

Whether you are presenting an exciting new technology, preparing for a new product launch, or requesting feedback on a specific idea, this conference offers the perfect platform for you to present in front of your target audience. Podium presentations during the main conference program allow you to present for 15-30 minutes and ensure your audience is seated and ready to hear your talk.

LUNCHEON PRESENTATIONS

Perfect for product launches, luncheon workshops allow you to present your latest technology or solution for 30 minutes while session attendees enjoy lunch provided on your company's behalf. Your talk is concluded with 15 minutes of Q&A.

FOCUS GROUPS

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

KEYNOTE INTRODUCTIONS & CHAIR DROPS

A 10-minute corporate introduction immediately precedes a major keynote presentation, plus your company literature will be distributed on all chairs in the keynote room. A sure way to deliver your message and make a lasting impression!

USER GROUP MEETINGS

Co-locate your user group meeting with Bio-IT World Conference & Expo. CHI will help market the event, manage logistical operations, develop the agenda, and more. CHI can handle the entirety of the meeting, or aspects of your choosing.

OTHER PROMOTIONAL OPPORTUNITIES INCLUDE:

- Exhibit Hall Reception
- Hotel Room Drop
- Internet & Message Center Sponsor
- Keynote Sponsorship
- Registration Area Sponsor
- Show Guide Advertising
- Show Guide – Bottom Stripe
- Tote Bag Insert
- Chair Drop in Session Room

NEW FOR 2011

For the first time ever, the BioIT World Conference & Expo will feature a New Product Pavilion. The New Product Pavilion is the place for exhibitors to introduce and promote your new product to conference attendees. CHI will promote the New Product Pavilion in our pre-show promotions, on our website, as well as on on-site. The Pavilion is complimentary to all exhibitors. Paticipants in the New Product Pavilion will automatically be entered in the Best of Show Awards program. **For more information please contact Demetrios Loulloudes at 781-972-5445 or dlouloudes@healthtech.com**

2011 EXHIBITORS (As of December 1, 2010)

Accelerated Technology Laboratories, Inc.
Accelrys
Accunet Solutions, Inc.
Aspera, Inc.
Bioinformatics.org
BIOTEAM
Blue Arc Corporation
BT Global Services
caBIG
Cambridge Semantics
CambridgeSoft
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International Society for Computational Biology (ISCB)
Isilon Systems
Japan Bioinformatics KK
LabAnswer
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Linguamatics
MassBio
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Microsoft
Microway, Inc.
Molecular Connections Pvt Ltd
NextBio
Omixon
Openeye
Optibrium Ltd
Partek, Inc.
Parthys Reverse Informatics
Perceptive Informatics
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For Sponsorship and Exhibit Information, please contact:
Angela Parsons, Vice President, Business Development: 781-972-5467 • aparsons@healthtech.com

Celebrating 10 Years of Innovation

Cambridge Healthtech Institute's Tenth Annual

Bio·IT World CONFERENCE & EXPO '11

April 12-14, 2011
World Trade Center
Boston, MA

Key Code 1120 F

1. REGISTRATION INFORMATION

Bring your Team!

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.

❒ Mr. ❒ Ms. ❒ Mrs. ❒ Dr. ❒ Prof.

Name

Job Title Div./Dept.

Company

Address

City/State/Postal Code

Country

Telephone

Fax

Email*

*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
❒ $595 Commercial
❒ $295 Academic, Government, Hospital-Affiliated

Choose 2 Half-Day Workshops or 1 Full Day Workshop BEST VALUE
❒ $895 Commercial
❒ $495 Academic, Government, Hospital-Affiliated

Half-Day Workshops

Morning Workshops
❒ (W4) Best of Breed Informatics
❒ (W2) Pathway-based Analysis
❒ (W5) Ontology Building
❒ (W6) RNA-seq Analysis
❒ (W9) EHRs/EMRs
❒ (W10) Imaging

Afternoon Workshops
❒ (W3) Complexity of Protein Data
❒ (W7) Visualization
❒ (W11) Cloud Computing
❒ (W12) Personalized Cancer Medicine
❒ (W13) NGS Data to Discovery

Full Day Workshop
❒ (W1) Chemogenomics

MAIN CONFERENCE

Registrations after March 11, 2011 and onsite

Commercial ❒ $1,945

Academic, Government, Hosp. Affiliated ❒ $925

DISCOUNTS
❒ Poster Discount ($50 off)
❒ International Society for Computational Biology (ISCB) Member Discount (10% off)

TRACK SELECTION: (PLEASE INDICATE THE ONE TRACK YOU ARE MOST LIKELY TO ATTEND)

Conference Tracks
❒ Track 1: IT Infrastructure - Hardware
❒ Track 2: IT Infrastructure - Software
❒ Track 3: Cloud Computing
❒ Track 4: Bioinformatics
❒ Track 5: Next-Gen Sequencing Informatics
❒ Track 6: Systems & Predictive Medicine
❒ Track 7: eClinical Solutions for Clinical Trials and Clinical Operations
❒ Track 8: eHealth and HIT Solutions for Personalized Medicine
❒ Track 9: Drug Discovery Informatics

❒ I cannot attend but would like to purchase the Bio-IT World Conference & Expo conference CD for $750 (plus shipping). Massachusetts delivery will include 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.

❒ Please charge: ❒ AMEX (15 digits) ❒ Visa (13-16 digits) ❒ MasterCard (16 digits)

Card # Exp. Date

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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 materials, your abstract must be submitted, approved and your registration paid in full by **March 4, 2011.** Register online, or by phone, fax or mail. Indicate that you would like to present a poster and you will receive abstract submission instructions via email.

I am interested in presenting a poster at: ❒ **Bio-IT World Conference & Expo 2011**
Title

To Register...

Web: www.Bio-ITWorldExpo.com
Fax: 781-972-5425
Phone: 781-972-5400 or toll-free in the U.S.:888-999-6288
Mail: 250 First Avenue, Suite 300, Needham, MA, USA 02494

Additional Registration Details
Each registration includes all conference sessions, posters and exhibits, food functions, and access to the conference proceedings link.

Group Discounts
Special rates are available for multiple attendees from the same organization. **Contact David Cunningham at 781-972-5472** to discuss youroptions and take advantage of the savings.

Handicapped Equal Access
In accordance with the ADA, Cambridge Healthtech Institute is pleased to arrange special accommodations for attendees with special needs. All requests for such assistance must be submitted in writing to CHI at least 30 days prior to the start of the meeting.

Substitution/Cancellation Policy
In the event that you need to cancel a registration, you may:
- Transfer your registration to a colleague within your organization.
- Credit your registration to another Cambridge Healthtech Institute program.
- 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.