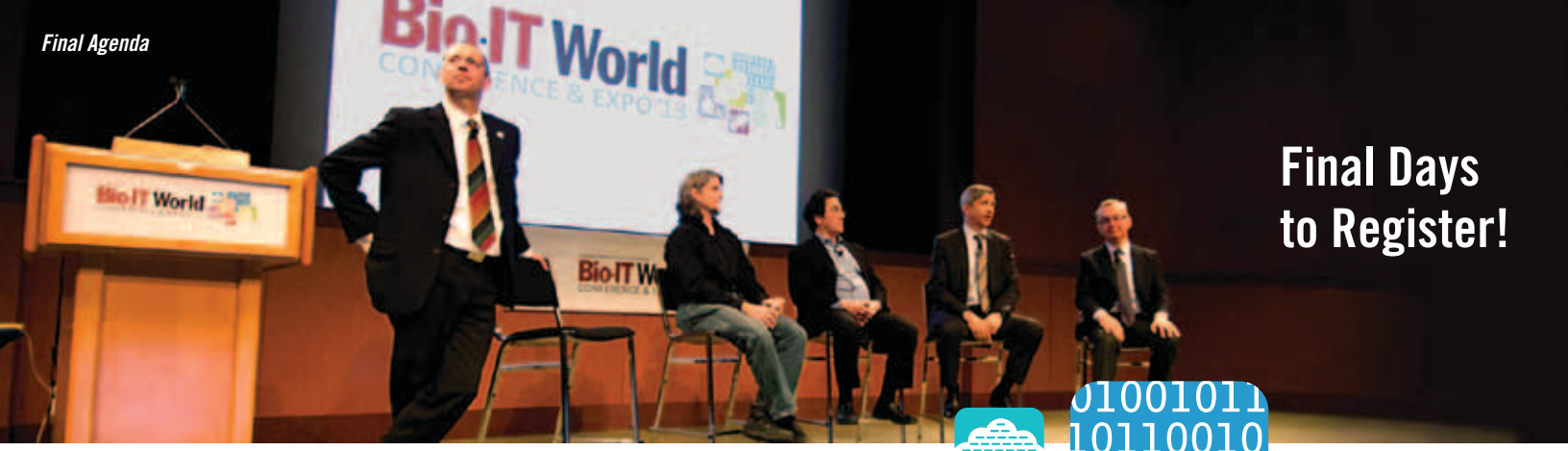

Cambridge Healthtech Institute's Twelfth Annual

Bio-IT World CONFERENCE & EXPO '13

April 9 – 11, 2013 • World Trade Center • Boston, MA

Enabling Technology. Leveraging Data. Transforming Medicine.

CONFERENCE TRACKS:

1. IT Infrastructure – Hardware
2. Software Development
3. Cloud Computing
4. Bioinformatics
5. Next-Gen Sequencing Informatics
6. Systems Pharmacology
7. eClinical Trials Solutions
8. Data Visualization **NEW!**
9. Drug Discovery Informatics
10. Clinical Omics **NEW!**
11. Collaborations and Open Access Innovations
12. Cancer Informatics

EVENT FEATURES:

- Access All 12 Tracks for One Price
- Network with 2,500+ Global Attendees
- Hear 150+ Technology and Scientific Presentations
- Connect with Attendees Using CHI's Intro-Net
- Choose from 16 Pre-Conference Workshops
- See the Winners of the following 2013 Awards: Benjamin Franklin, Best of Show, and Best Practices
- View Novel Technologies and Solutions in the Expansive Exhibit Hall
- And Much More!

KEYNOTE PRESENTERS:

Atul Butte, M.D., Ph.D., Division Chief and Associate Professor, Stanford University School of Medicine; Director, Center for Pediatric Bioinformatics, Lucile Packard Children's Hospital; Co-founder, Personalis and Numedii

Andrew L. Hopkins, D.Phil, FRSC, FSB, Division of Biological Chemistry and Drug Design, College of Life Sciences, University of Dundee

PLENARY SESSION:

The Life Sciences CIO Panel

From managing big data and cloud computing capabilities to building virtual communities and optimizing drug development, the life sciences CIO has to be a firefighter, evangelist, visionary. In this special plenary roundtable, Bio-IT World invites a select group of CIOs from big pharma, academia and government to discuss the major issues facing today's biosciences organization and the prospects for future growth and organizational success.

Special guests:

Remy Evard – CIO, Novartis Institutes for BioMedical Research

Martin Leach – VP, Biogen Idec

Andrea T. Norris – Director, Center for Information Technology (CIT) and CIO, NIH

Gunaretnam Rajagopal – VP & CIO, Janssen Pharmaceuticals

Cris Ross – CIO, Mayo Clinic

Matthew Trunnell –CIO, Broad Institute of MIT and Harvard

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Held in Conjunction with

Medical Informatics World Conference 2013

April 8 - 9, 2013 • Boston, MA

Organized by:
Cambridge Healthtech Institute

Bio-ITWorldExpo.com

SCHEDULE-AT-A-GLANCE

Tuesday, April 9, 2013

8:00am – 4:00pm	Pre-Conference Workshops
4:00 – 5:00pm	Plenary Keynote
5:00 – 7:00pm	Exhibit Hall Open
5:00 – 7:00pm	Welcome Reception in the Exhibit Hall with Poster Viewing

Wednesday, April 10, 2013

8:00 – 9:45am	Plenary Keynote, Benjamin Franklin Awards Presentation, and Best Practices Awards Program
9:45am – 6:15pm	Exhibit Hall Open
9:45 – 10:50am	Coffee Break in the Exhibit Hall with Poster Viewing
10:50am – 12:30pm	Tracks 1-12
12:30 – 1:30pm	Luncheon Presentations
1:40 – 3:15pm	Tracks 1-12
3:15 – 3:45pm	Refreshment Break in Exhibit Hall with Poster Viewing
3:45 – 5:15pm	Tracks 1-12
5:15 – 6:15pm	Best of Show Awards Reception in the Exhibit Hall

Thursday, April 11, 2013

7:00 – 8:00am	Breakfast Sponsored Presentations (Opportunities Available)
8:00 – 8:40am	Featured Presentation Tracks 1-3
8:45 – 10:20am	Tracks 1-12
10:20am – 1:55pm	Exhibit Hall Open
10:20 – 10:45am	Coffee Break in the Exhibit Hall and Poster Competition Winners Announced
10:45am – 12:15pm	Plenary Keynote
12:15 – 1:55pm	Lunch in the Exhibit Hall with Poster Viewing
1:55 – 4:05pm	Tracks 1-12

FEATURED SESSIONS

Managing Big Data: The Genome Center Perspective

Genome centers not only have the challenge of managing petabytes of data but the implied responsibility of sharing their hard-fought solutions and best practices with the multitude of organizations lacking their IT resources. This special session draws together the IT directors of various world-class genomics institutes to discuss their technological and organizational strategies for managing big data.

Panelists Include:

Matthew Trunnell (Broad Institute)
Guy Coates (The Wellcome Trust Sanger Institute)

Building the IT Architecture of the New York Genome Center

In 2011, a consortium of 11 major academic and medical organizations in and around New York announced the creation of the New York Genome Center (NYGC). Under the direction of Nancy Kelley, the NYGC aspires to be a world-class genomics and medical research center, and is currently undergoing construction in the heart of Manhattan. NYGC management has the opportunity to design and create a state-of-the-art IT and data management infrastructure to handle, store and share the output from what will rapidly become one of the world's foremost genome sequencing facilities. This series of talks will describe the thinking that went into the design, creation and construction of the NYGC's IT infrastructure and entire data management strategy.

Christopher Dwan, Acting Senior Vice President, IT, New York Genome Center
Kevin Shianna, Senior Vice President, Sequencing Operations, New York Genome Center
Additional Speakers to be Announced

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PRE-CONFERENCE WORKSHOPS* Tuesday, April 9, 2013

Morning Workshops

Integrated Research Data Management for Next Gen Sequencing Analysis Using Galaxy and Globus Online Software-as-a-Service
Ravi K. Madduri, Fellow, Computation Institute, University of Chicago; Project Manager, Mathematics and Computer Science Division, Argonne National Laboratory
Alex R. Paciorkowski, M.D., Senior Instructor, Department of Neurology, Child Neurology (SMD), University of Rochester Medical Center, School of Medicine and Dentistry
Vas Vasiliadis, Director, Products, Computation Institute, University of Chicago

Quality Practices for R&D Informatics Platform Selection and Solution Development
Richard Lysakowski, Ph.D., Director, R&D; Advisor, The Collaborative Electronic Notebook Systems Association (CENSA)
Jeff Spitzner, Ph.D., Founder, President and Chief Scientific Officer, Amperand

Beyond the Cloud: Improving the R&D Innovation Process through Cloud Services
Sponsored by BT
David Brown, CTO, BT Life Sciences, BT Global Services
Yury Rozenman, Business Development Director, Life Sciences Solutions, BT Global Services
Zheng Yang, Ph.D., Associate Director, R&D Informatics, Boehringer Ingelheim

IT & Informatics in Support of Collaboration and Externalization
Sponsored by accelrys® AnnaiSystems
Workshop & Discussion Forum
Chairperson: Martin Leach, Ph.D., Vice President, R&D IT, Biogen Idec
Panelists: Art Morales, Ph.D., Informatics Systems Lead, Novartis
David Sedlock, Ph.D., Senior Director, R&D Systems at Millennium Pharmaceuticals, Inc.
Michael H. Elliott, CEO, Atrium Research & Consulting LLC
Mary Bradley, Ph.D. M.B.A., CollaborationFinder
Frederic Bost, Director, Product Management, Accelrys
Sergey Krymgold, Ph.D., Associate Director, Information Technology, Discovery & Preclinical, Biogen Idec
Tom Arneman, President, Ceiba Solutions

Updates from the tranSMART Open-Source Community
Sponsored by tranSMART Foundation
Brian Athey, Ph.D., Co-CEO, tranSMART Foundation
Michael Braxenthaler, Ph.D., Co-CEO, tranSMART Foundation
Ian Dix, Ph.D., Coordinator, eTRIKS Consortium
Gerrit A. Meijer, M.D., Ph.D., Principal Investigator, CTMM Translational Research IT (TraIT) Project
Robert Boland, Directing Senior Manager, External Innovation R&D IT, Janssen, Pharmaceutical Companies of Johnson & Johnson

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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 Amphitheater on Wednesday morning April 10, during the Plenary Keynote and Awards Program.

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 Julie DiGiovine at 781-972-5445 or email jdigiovine@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. Winners will be selected by a peer review expert panel in early 2013. Bio-IT World will present the Awards in the Amphitheater at 9:10am on Wednesday, April 10 during the Plenary Keynote and Awards Program. Early bird deadline (no fee) for entry is December 21, 2012 and final deadline (fee) is January 14, 2013. Full details including previous winners and entry forms are available at Bio-ITWorldExpo.com.

2013 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 10, 2013.

CHI's INTRO-NET 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!

Held in Conjunction with

Medical Informatics World Conference 2013

April 8 - 9, 2013
World Trade Center • Boston, MA

MedicalInformaticsWorld.com

Exclusive Offer to Attend Medical Informatics World Conference

Bio-IT World and Cambridge Healthtech Institute are proud to announce the launch of their inaugural Medical Informatics World Conference, to be held immediately prior to Bio-IT World Conference & Expo. The two-day conference is designed to answer the rising need for collaboration between healthcare and life science teams, around the theme, "Deploying Information Technology to Sustain Innovation within the Rapidly Changing Care Delivery Models: ACOs, Meaningful Use, Bundles, Medicaid and Personalized Care." The agenda will include three major tracks on: 1) Provider-Payer-Pharma Cross-Industry Data Collaboration, 2) Coordinated Patient Care, Engagement and Empowerment and 3) Population Health Management, Segmentation and Stratification.

Medical Informatics World and Bio-IT World Expo are being held back-to-back to complete the week of scientific content by bridging the healthcare and life science worlds. Paid attendees of Bio-IT World Conference & Expo can attend Medical Informatics World Conference (April 8-9) for a special discounted rate. See the registration page for details.

PRE-CONFERENCE WORKSHOPS* Tuesday, April 9, 2013

Afternoon Workshops

Advancing the Use of EHR/EMR for Clinical Research and Drug Development: Breaking Down Barriers & Building Up Bridges
Aaron Kamauu, M.D., CEO, Healthcare Data Analytics, Anolinx LLC; former Head, Healthcare Data Strategy, Roche and Genentech
Dipak Kalra, Professor, Health Informatics, University College London
Andreas Schmidt, Senior Healthcare Data Scientist, Pharma Development, F. Hoffmann–La Roche AG

Cloud Computing in Hospital Data Management and Integration
Andrew Litt, M.D., CMO, Healthcare and Life Sciences, Dell
Carrick Carpenter, Delivery Director, Healthcare Cloud Computing, Healthcare and Life Sciences, Dell

Data Visualization in Biology: From the Basics to Big Data
Nils Gehlenborg, Ph.D., Research Associate, Center for Biomedical Informatics, Harvard Medical School

Software for Clinical Genomics
Ronald Ranauro, Founder and Managing Partner, Incite Advisors
Joel Dudley, Ph.D., Assistant Professor, Genetics and Genomic Sciences; Director, Biomedical Informatics, Mount Sinai School of Medicine
Nazneen Aziz, Ph.D., Director of Molecular Medicine, Transformation Program Office, College of American Pathologists
Konrad J. Karczewski, Ph.D. Candidate, Biomedical Informatics, Stanford University
Matthew Lebo, Ph.D., Instructor, Pathology, Brigham & Women's Hospital and Harvard Medical School; Assistant Laboratory Director, Senior IS Domain Specialist, Laboratory for Molecular Medicine
Matthew McCarty, M.D., CEO and Founder, Genotox Laboratories; President and Founder, Balcones Pain Consultants

IT Project Planning and Implementation
Gurpreet Kanwar, Senior Project Manager, Information Management, Nav Canada

Avoiding Intellectual Property Problems in Research Collaborations Using Information Technology
John L. Marquardt, Jr., J.D., M.B.A., Ph.D., Attorney at Law, Marquardt Law
N. Scott Pierce, Esq., Partner, Hamilton, Brook, Smith & Reynolds, P.C.
David Yeary, M.B.A., Vice President, Merrill DataSite - LIfe Sciences

The Next Cloud Phase: Hybrid Cloud Sick of a One Size Fits All Cloud? Look for the Flexibility of a Hybrid Cloud.
Sponsored by SAVVIS
Reed Smith, Director, Cloud Product Management, Savvis

**Separate Registration Required*

Track 1
IT Infrastructure – Hardware
Big Data Solutions and End-User Perspectives

Track 1 explores networking infrastructure and compute management solutions to support big data. Topics to be covered include storage, management, security, regulatory, HPC technologies and techniques, and FPGA and GPU cards to reduce the need for large compute clusters.

TUESDAY, APRIL 9

7:00 am Workshop Registration and Morning Coffee

8:00 Pre-Conference Workshops*
**Separate Registration Required*

2:00 - 7:00 pm Main Conference Registration

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

4:05 Keynote Introduction
Kevin Brode, Senior Director, Health & Life Sciences, Americas Hitachi Data Systems

» 4:15 PLENARY KEYNOTE
Do Network Pharmacologists Need Robot Chemists?
Andrew L. Hopkins, DPhil, FRSC, FSB, Division of Biological Chemistry and Drug Design, College of Life Sciences, University of Dundee

5:00 Welcome Reception in the Exhibit Hall with Poster Viewing
*Drop off a business card at the CHI Sales booth for a chance to win 1 of 2 iPads® or 1 of 2 Kindle Fires®!**
**Apple ® and Amazon are not sponsors or participants in this program*

WEDNESDAY, APRIL 10

7:00 am Registration and Morning Coffee

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

8:05 Keynote Introduction
Sanjay Joshi, CTO, Life Sciences, EMC Isilon

» 8:15 PLENARY KEYNOTE
Atul Butte, M.D., Ph.D., Division Chief and Associate Professor, Stanford University School of Medicine; Director, Center for Pediatric Bioinformatics, Lucile Packard Children's Hospital; Co-founder, Personalis and Numedii

8:55 Benjamin Franklin Award & Laureate Presentation

9:15 Best Practices Award Program

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

Best Practices for Building and Managing Data Center & Research Programs

10:50 Chairperson's Remarks
Brian Bissett, Program Manager, Office of Systems, Social Security Administration

11:00 Best Practices for Building and Managing Multi-Tenant Research Clusters
Chris Dagdigian, Founding Partner and Director of Technology, BioTeam, Inc.
A case study exploring the real world implementation of a shared HPC environment for scientific computing. Topics will include architecting for scalability and efficiency, accommodating different scientific disciplines and workflows in a common platform, building consensus amongst competing interests, and the importance of a user driven governance structure.

11:30 Multi-Million Dollar Data Center Program Management
Brian Bissett, Program Manager, Office of Systems, Social Security Administration
This presentation will detail the program management strategy of the Social Security Administration's Data Center Program, a $407.4 million dollar program, which processes over 140 million transactions daily, and stores nearly 250 million medical records, with an additional 2 million medical records added every week. Learn best practices to utilize when managing similar programs of this size.

12:00 pm Compute for Personalized Medicine *Sponsored by* intel
Ketan Paranjape, Global Director, Healthcare and Life Sciences, Intel Corp.
As we arrive at the $1000 genome, we find the fundamental problems have shifted... it is no longer about shrinking the cost of sequencing but the explosive growth of big data: the downstream analytics with rapidly evolving parameters, data sources and formats; the storage, movement and management of massive datasets and workloads; and perhaps most paradoxical of all, the challenge of articulating the results and translating the latest findings directly into improving patient outcomes using newer, smaller form factor mobile devices. Indeed, as we approach the scale of "impossibly small" for both technology and disease management, the complexity of problems grows by orders of magnitude.

12:30 Luncheon Presentation I: Big Data and Scaling Biosciences Research *Sponsored by* ARISTA
Chris Bellmare, Director, Arista Networks
The increased use of common database sources with petabytes of stored data is driving new computing cluster architectures - EMR meets genomic and genetic data. Can your network keep up with increased CPU density bursts to 40GB or 100GB? How are you managing the growth of unstructured data? Do you have fast access to petabytes of processed data, Parallelization of the data, storage, and analysis algorithms? Arista is the leader in Life Sciences Data Center design, and attendees will learn about intelligent placement of compute to storage, as well as how to scale to meet the research needs while keeping the performance up and costs down.

1:00 Luncheon Presentation II: Life Science Computing *Sponsored by* hp
Etzard Stolte, Ph.D., CTO, HP Life Sciences
Health and Life Sciences continue to evolve as Information Technology provides new breakthroughs to make R&D more effective and accessible. Application Specific Computing, Big Analytics, Meaning Based Computing and Science Clouds

are quickly changing how and where science is done. In this talk, we will present trends and examples leading to the advent of "Information Driven Medicine."

Storage Management & Platforms for Big Data

1:40 Chairperson's Remarks

1:45 Storing Really Big Data with Fast Access Economically
Robert Cecil, Ph.D., Professional Staff, The Cleveland Clinic Foundation, Imaging Institute, The Cleveland Clinic Foundation
The Cleveland Clinic Foundation hosts and engineers one of the largest and fastest growing medical archives in the world. This archive is optimized for large file sizes and high bandwidth with requirements for permanent data retention. The extension to genomics and utilization in a cloud computing environment are straight forward. Learn about our storage and data retention evolution.

2:15 Building Bridges: Evolving High Performance Computing in the Life Sciences *Sponsored by* CRAY THE SUPERCOMPUTER COMPANY
Carlos P. Sosa, Manager, Chemistry and Life Sciences Segment, Cray, Inc.; Biomedical Informatics and Computational Biology, University of Minnesota Rochester
As the life sciences community enters the age of data intensive science, knowledge discovery rests upon analyzing massive amounts of data. Cray is evolving the role of supercomputing by developing highly integrated computing and storage solutions that provide unique advantages to enable data-driven approaches. Cray is also actively engaged with the life sciences community to develop these next generation applications.

2:30 Accelerating Bioscience and Technology with Titan, the World's Fastest Supercomputer
Jack C. Wells, Director of Science, Oak Ridge Leadership Computing Facility, Oak Ridge National Laboratory
Modeling and simulation with petascale computing has supercharged the process of innovation and understanding, dramatically accelerating time-to-insight and time-to-discovery. From petascale acceleration of drug discovery, to designing bio-inspired catalysts for renewable energy, to exploring complex disease mechanisms, petascale computing is delivering high impact results that are transforming bioscience and technology. This presentation will focus on early outcomes from Titan, the world's fastest supercomputer. We will showcase results from early science applications ready to use Titan's GPU-accelerated architecture. Preliminary Early Science results from users running on Titan will be discussed, including, for example, applications in organic photovoltaic materials and liquid-crystal biosensors. Lastly, details about Titan system setup, OLCF resources, and how to apply for time on Titan's 18,688 GPU accelerated nodes will be shared.

3:00 Fun with Metadata: Solving Age-Old Storage Management Problems *Sponsored by* CAMBRIDGE Computer ARTISTS IN DATA STORAGE
Jacob Farmer, CTO, Cambridge Computer
Starfish is commercial grade software that allows users (via GUI) and applications (via API) to associate metadata with files and directories in conventional file systems, tape archives, disk-based object stores, and cloud storage services. Cambridge Computer is partnering with a number of thought-leading research institutions to define and refine the next generation of best practices for storage management. We are solving problems related to data protection, life cycle management across disparate storage devices, chargebacks, curation, and collaboration within and across institutional boundaries. Oh, by the way, we do all of this at scale.

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

3:45 Looking Behind the Curtain of Your Data Center *Sponsored by* MARKLEY ONE SUMMER STREET
Christopher McLean, Director, Design, Markley Group
Key areas to focus on when choosing a location, and key "due diligence" questions inside of a Data Center.

4:00 Life Science "Big Data" Analytics Appliance – Hadoop Simplicity for the Enterprise *Sponsored by* DataDirect NETWORKS INFORMATION IN MOTION
Rajiv Garg, Hadoop/Big Data Product Manager, DataDirect Networks
Simplify Hadoop and deploy an analytics infrastructutre in hours, not months. Accelerates your time-to-insight by running Hadoop up to 7X faster. Eliminate programming requirements with a built-in ETL engine. Enable Hadoop-based bioinformatics applications like CloudBLAST and Crossbow. Up to 700% higher efficiency when compared to commodity to truly lower your TCO.

4:15 How to Break the Storage Bottleneck: A New Paradigm is Required to Meet Today's Data Performance Demands *Sponsored by* xyratex
Eric Lomascolo, Director, Solutions Marketing, Xyratex
ClusterStor™ scale-out file system solutions break the storage bottleneck and help you manage petascale capacities for high performance application needs. As life sciences demand higher resolutions of acquisition and analysis to achieve greater accuracy and insight, so too does the need for faster data throughput. Achieving efficiencies in higher data capacities and performance requires a different approach. Find out how ClusterStor's new scale-out HPC data storage solution delivers.

4:30 Life Sciences on Amazon Web Services *Sponsored by* amazon web services
Jafar Shameem, Business Development, Life Sciences, Amazon Web Services
The availability of utility computing is significantly accelerating life sciences in both academia and industry. Join Jafar Shameem to discuss how customers such as Illumina, Unilever, DNA Nexus and Spiral Genomics are removing the constraints of static IT to deliver new secure services to market more quickly and at scale.

4:45 Accelerating Life Sciences Workloads with Hybrid SSD/SATA Scale-Out NAS Storage *Sponsored by* panasas
Geoffrey Noer, Senior Director, Product Marketing, Panasas
File systems used for life sciences workloads share a number of characteristics that are quite different from what is typical in other industries using scale-out storage. This talk will cover the research Panasas recently conducted with customers to understand how real-world file systems are actually used. As a result, Panasas created ActiveStor 14, a scale-out NAS solution featuring a hybrid SSD/SATA architecture ideally suited for meeting the demanding I/O requirements of NGS and other prominent BioIT applications.

5:15 Best of Show Awards Reception in the Exhibit Hall

6:15 Exhibit Hall Closes

THURSDAY, APRIL 11

7:00 am Breakfast Presentation Panel: Enabling Technology. Leveraging Data. Transforming Medicine. *Sponsored by* intel
Panelists:
Samuel Aronson, Executive Director, IT, Partners HealthCare Center for Personalized Genetic Medicine
Sanjay Joshi, CTO, Life Sciences, EMC Isilon
Glen Otero, Life Sciences HPC Solution Architect, Dell
Ketan Paranjape, Global Director, Healthcare & Life Sciences, Intel Corp.
Toby Bloom, Director, Informatics, Genomics Platform at Broad Institute
As we arrive at the $1000 genome, we find the fundamental problems have shifted... it is no longer about shrinking the cost of sequencing but the explosive growth of big data: the downstream analytics with rapidly evolving parameters, data sources and formats; the storage, movement and management of massive datasets and workloads; and perhaps most paradoxical of all, the challenge of articulating the results and translating the latest findings directly into improving patient outcomes. Please join Intel and our distinguished panel to discuss how collaborating with a broad

range of ecosystem partners to develop innovative solutions to seemingly intractable problems emerging in healthcare and life sciences today is driving us towards the vision of personalized medicine.

» FEATURED PRESENTATION

8:00 Featured Presentation Introduction
Geoffrey Noer, Senior Director, Product Marketing, Panasas

8:10 Trends in the Trenches 2013
Chris Dagdigian, Founding Partner and Director of Technology, BioTeam, Inc.
HPC Trends in the Trenches is one of the most popular presentations of the Expo! This talk will present how common HPC problems in life science informatics have been approached by organizations of varying type and size. We will discuss observed trends in computing, workflows and data movement, along with details on particularly clever solutions observed in production environments around the world.

Managing Big Data: Genome Center Perspectives

8:45 Chairperson's Opening Remarks

8:50 Managing Big Data: The Genome Center Perspective
Moderator: Kevin Davies, Ph.D., Editor-in-Chief, Bio-IT World
Guy Coates, Ph.D., Informatics Systems Group, The Wellcome Trust Sanger Institute
Alexander (Sasha) Wait Zaranek, Ph.D., Director, Informatics, Personal Genome Project, Harvard Medical School; Scientific Director, Clinical Future, Inc.
Xing Xu, Ph.D., Director, Cloud Computing Product, BGI Americas Corporation
Eric Jones, Manager, Research Computing, Broad Institute
Genome centers not only have the challenge of managing petabytes of data but the implied responsibility of sharing their hard-fought solutions and best practices with the multitude of organizations lacking their IT resources. This special session draws together the IT directors of various world-class genomics institutes to discuss their technological and organizational strategies for managing big data.

9:50 Big Data: The Challenges Around the 4 Vs
Kevin Brode, Senior Director, Health & Life Sciences, Americas Hitachi Data Systems10:20 Coffee Break in the Exhibit Hall and Poster Competition Winners Announced

10:45 Plenary Keynote Panel Chairperson's Remarks
Kevin Davies, Ph.D., Editor-in-Chief, Bio-IT World

10:50 Plenary Keynote Panel Introduction
Yury Rozenman, Head of BT for Life Sciences, BT Global Services
Niven R. Narain, President & CTO, Berg Pharma

» PLENARY KEYNOTE PANEL

11:05 The Life Sciences CIO Panel
Panelists:
Remy Evard, CIO, Novartis Institutes for BioMedical Research
Martin Leach, Ph.D., Vice President, R&D IT, Biogen Idec
Andrea T. Norris, Director, Center for Information Technology (CIT) and Chief Information Officer, NIH
Gunaretnam (Guna) Rajagopal, Ph.D., VP & CIO - R&D IT, Research, Bioinformatics & External Innovation, Janssen Pharmaceuticals
Cris Ross, Chief Information Officer, Mayo Clinic
Matthew Trunnell, CIO, Broad Institute of MIT and Harvard

12:15 Luncheon in the Exhibit Hall with Poster Viewing

Panel Session:Building the IT Architecture of the New York Genome Center

2:00 Panel Session: Building the IT Architecture of the New York Genome Center
Moderator: Kevin Davies, Ph.D., Editor-in-Chief, Bio-IT World
Christopher Dwan, Acting Senior Vice President, IT, New York Genome Center
Kevin Shianna, Senior Vice President, Sequencing Operations, New York Genome Center
Jim Harding, CTO, Sabey Corporation
Sanjay Joshi, CTO, Life Sciences, EMC Isilon Storage Division
Robert B. Darnell, M.D., Ph.D., President & Scientific Director, New York Genome Center
George Gosselin, CTO, Computer Design & Integration LLC
In 2011, a consortium of 11 major academic and medical organizations in and around New York announced the creation of the New York Genome Center (NYGC). Under the direction of Nancy Kelley, the NYGC aspires to be a world-class genomics and medical research center, and is currently undergoing construction in the heart of Manhattan. NYGC management has the opportunity to design and create a state-of-the-art IT and data management infrastructure to handle, store and share the output from what will rapidly become one of the world's foremost genome sequencing facilities. This series of talks will describe the thinking that went into the design, creation and construction of the NYGC's IT infrastructure and entire data management strategy.

4:00 Conference Adjourns

Track 2
Software Development
Technologies and Applications for Managing and Sharing Data

Track 2 explores data handling and integration activities. Themes covered include technologies and applications for managing/sharing/publishing/preserving data, software tools, open source software, grid engines, Hadoop, compute job management, and advances & trends.

TUESDAY, APRIL 9

7:00 am Workshop Registration and Morning Coffee

8:00 Pre-Conference Workshops*
**Separate Registration Required*

2:00 - 7:00 pm Main Conference Registration

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

4:05 Keynote Introduction
Kevin Brode, Senior Director, Health & Life Sciences, Americas Hitachi Data Systems

» 4:15 PLENARY KEYNOTE
Do Network Pharmacologists Need Robot Chemists?
Andrew L. Hopkins, DPhil, FRSC, FSB, Division of Biological Chemistry and Drug Design, College of Life Sciences, University of Dundee

5:00 Welcome Reception in the Exhibit Hall with Poster Viewing
*Drop off a business card at the CHI Sales booth for a chance to win 1 of 2 iPads® or 1 of 2 Kindle Fires®!**
**Apple ® and Amazon are not sponsors or participants in this program*

WEDNESDAY, APRIL 10

7:00 am Registration and Morning Coffee

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

8:05 Keynote Introduction
Sanjay Joshi, CTO, Life Sciences, EMC Isilon

» 8:15 PLENARY KEYNOTE
Atul Butte, M.D., Ph.D., Division Chief and Associate Professor, Stanford University School of Medicine; Director, Center for Pediatric Bioinformatics, Lucile Packard Children's Hospital; Co-founder, Personalis and Numedii

8:55 Benjamin Franklin Award & Laureate Presentation

9:15 Best Practices Award Program

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

Technologies and Applications for Data Handling and Integration

10:50 Chairperson's Remarks
Will McGrath, Strategic Marketing Manager, Big Data Product Division, Quantum

11:00 Bringing Disaster Recovery to a Peta-Scale Archive. Cost Effectively
Brant Kelley, Director, IT Services, The Scripps Research Institute
The Scripps Research Institute, one of the largest non-profit biomedical research organizations in the world, faced a NAS environment limited in scale and sharing within its research community. The speaker discusses his experience bringing in disaster recovery capabilities to a complex IT storage environment that manages large-scale next generation data, spanning across two sites and impacting over 270 scientific labs.

11:30 Developing Scalable Production Software for a Clinical Molecular Diagnostics Lab: A Case Study
Marcia Nizzari, Director of Informatics, Informatics & High Performance Computing/IT, Good Start Genetics, Inc.
This case study discusses many problems in our clinical laboratory business – data visualization, managing huge data loads, and creating a malleable system that is nimble. Learn about integration of different types of assay data, build versus buy tradeoffs, design considerations, and how a system built for a startup company is scaleable for handling large volumes in a commercial setting.

12:00 pm Technologies and Applications for Managing and Sharing Data *Sponsored by* IBM*
Janis E. Landry-Lane, Program Director, World Wide Deep Computing, Life Sciences/Higher Education Segments, IBM
Large data analytics poses several challenges: 1. How can I afford to keep all of this data on-line? Discussions will center around cost effective architectures for long-term data archive and use. Additionally, 2. Where is the data? Is it in an online file system, near-line tapes, relational databases, sensor data streams or on the web? There are proven technologies that allow for the lifecycle management of data as well as schema that allow users to access data without worrying about where it is located, what protocol to use to connect and access the system and without establishing a separate account or password/certificate to each of the underlying computer systems to gain access, etc. Genomic information is one of the newest sources of insight. Learn how to integrate data and perform the analysis.

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

1:40 Chairperson's Remarks
Brian Bissett, Program Manager, Office of Systems, Social Security Administration

1:45 Talk Title to be Announced
Brian Bissett, Program Manager, Office of Systems, Social Security Administration

2:15 Integration of High Throughput Omics Data Sets Using the Hadoop/HBase Platform
Ronald Taylor, Ph.D., Research Scientist, Computational Biology & Bioinformatics Group, Pacific Northwest National Laboratory
The scalable biological data warehouse system being built at the U.S. Department of Energy's Environmental Molecular Sciences Laboratory (EMSL) using Hadoop and HBase will be described. This warehouse is being designed to store and manipulate data into the high terabyte range. A summary will be given of the current state of data storage capabilities and

parallelization of analytics work.

2:45 Accelerated Bioinformatics - The Promises and Pitfalls
Martin Gollery, CEO and Chief Consultant, Tahoe Informatics
Server farms to feed the ever-growing need for Biocomputing processing power have become huge drains on electricity, Air Conditioning, floorspace and manpower. To reduce these problems, many labs are turning to various types of accelerators to get the power they need to get their work done faster and more efficiently than ever before. This talk will include a discussion of the various accelerators available, the companies that supply them, and specific case studies that show how each of them are used in real-world settings.

3:00 Sponsored Presentations *(Opportunities Available)*

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

Project Management and Workflow Solutions

3:45 Global Is the New Normal, How Can We Succeed in Implementing Laboratory Informatics Projects Globally
Eduard de Vries, Senior Manager, Information Technology, IDEXX Laboratories
How do you establish the right goals and guiding principles for successful implementation of laboratory informatics projects in an international multi-cultural environment and across acquisitions? This case study will describe what worked for us and change management methodologies used.

4:15 Transition of Project to Portfolio
Gurpreet Kanwar, Senior Project Manager, Information Management, Nav Canada
This presentation will help the project managers to successfully move the project to portfolio. It also provides the various techniques which can be used along portfolio managers to close the project. The speaker has been working as Project Manager for more than 10 years with experience of 18 years in IT technical project planning and implementation industry.

4:45 The Algorithm Makes the Results
Jeffrey Rosenfeld, Ph.D., Assistant Professor of Medicine, IST/ High Performance & Research Computing, New Jersey Medical School (UMDNJ)
There are currently a large number pipelines available for genome sequencing processing. Many of these pipelines rely on a number of simplifying assumptions that are not always found in the data. I will describe how the calling of complex variants and the joint annotation of nearby SNPs are critical for obtaining the correct results of sequencing. Further, I will discuss how the variability in the lengths of sequencing reads, along with the algorithms being utilized, can greatly alter the outcomes of an RNA-seq experiment.

5:15 Best of Show Awards Reception in the Exhibit Hall

6:15 Exhibit Hall Closes

THURSDAY, APRIL 11

7:00 am Breakfast Presentation Panel: Enabling Technology. Leveraging Data. Transforming Medicine. *Sponsored by* intel
Panelists:
Samuel Aronson, Executive Director, IT, Partners HealthCare Center for Personalized Genetic Medicine
Sanjay Joshi, CTO, Life Sciences, EMC Isilon
Glen Otero, Life Sciences HPC Solution Architect, Dell
Ketan Paranjape, Global Director, Healthcare & Life Sciences, Intel Corp.
Toby Bloom, Director, Informatics, Genomics Platform at Broad Institute
As we arrive at the $1000 genome, we find the fundamental problems have shifted... it is no longer about shrinking the cost of sequencing but the explosive growth of big data: the downstream analytics with rapidly evolving parameters, data sources and formats; the storage, movement and management of massive datasets and workloads; and perhaps most paradoxical of all, the challenge of articulating the results and translating the latest findings directly into improving patient outcomes. Please join Intel and our distinguished panel to discuss how collaborating with a broad range of ecosystem partners to develop innovative solutions to seemingly intractable problems emerging in healthcare and life sciences today is driving us towards the vision of personalized medicine.

» FEATURED PRESENTATION

8:00 Featured Presentation Introduction
Geoffrey Noer, Senior Director, Product Marketing, Panasas

8:10 Trends in the Trenches 2013
Chris Dagdigian, Founding Partner and Director of Technology, BioTeam, Inc.
HPC Trends in the Trenches is one of the most popular presentations of the Expo! This talk will present how common HPC problems in life science informatics have been approached by organizations of varying type and size. We will discuss observed trends in computing, workflows and data movement, along with details on particularly clever solutions observed in production environments around the world.

Managing Big Data: Genome Center Perspectives

8:45 Chairperson's Opening Remarks
Jason Wang, Co-Founder & CTO, Arpeggi, Inc.

8:50 Managing Big Data: The Genome Center Perspective
Moderator: Kevin Davies, Ph.D., Editor-in-Chief, Bio-IT World
Guy Coates, Ph.D., Informatics Systems Group, The Wellcome Trust Sanger Institute
Alexander (Sasha) Wait Zaranek, Ph.D., Director, Informatics, Personal Genome Project, Harvard Medical School; Scientific Director, Clinical Future, Inc.
Xing Xu, Ph.D., Director, Cloud Computing Product, BGI Americas Corporation
Eric Jones, Manager, Research Computing, Broad Institute
Genome centers not only have the challenge of managing petabytes of data but the implied responsibility of sharing their hard-fought solutions and best practices with the multitude of organizations lacking their IT resources. This special session draws together the IT directors of various world-class genomics institutes to discuss their technological and organizational strategies for managing big data.

9:50 Big Data: The Challenges Around the 4 Vs *Sponsored by* HITACHI Inspire the Next ©Hitachi Data Systems
Kevin Brode, Senior Director, Health & Life Sciences, Americas Hitachi Data Systems10:20 Coffee Break in the Exhibit Hall and Poster Competition Winners Announced

10:20 Coffee Break in the Exhibit Hall and Poster Competition Winners Announced

10:45 Plenary Keynote Panel Chairperson's Remarks
Kevin Davies, Ph.D., Editor-in-Chief, Bio-IT World

10:50 Plenary Keynote Panel Introduction
Yury Rozenman, Head of BT for Life Sciences, BT Global Services
Niven R. Narain, President & CTO, Berg Pharma

» **PLENARY KEYNOTE PANEL**

11:05 The Life Sciences CIO Panel
Panelists:
Remy Evard, CIO, Novartis Institutes for BioMedical Research
Martin Leach, Ph.D., Vice President, R&D IT, Biogen Idec
Andrea T. Norris, Director, Center for Information Technology (CIT) and Chief Information Officer, NIH
Gunaretnam (Guna) Rajagopal, Ph.D., VP & CIO - R&D IT, Research, Bioinformatics & External Innovation, Janssen Pharmaceuticals
Cris Ross, Chief Information Officer, Mayo Clinic
Matthew Trunnell, CIO, Broad Institute of MIT and Harvard

12:15 Luncheon in the Exhibit Hall with Poster Viewing

Panel Session:Building the IT Architecture of the New York Genome Center

2:00 Panel Session: Building the IT Architecture of the New York Genome Center
Moderator: Kevin Davies, Ph.D., Editor-in-Chief, Bio-IT World
Christopher Dwan, Acting Senior Vice President, IT, New York Genome Center
Kevin Shianna, Senior Vice President, Sequencing Operations, New York Genome Center
Sanjay Joshi, CTO, Life Sciences, EMC Isilon Storage Division
Robert B. Darnell, M.D., Ph.D., President & Scientific Director, New York Genome Center
George Gosselin, CTO, Computer Design & Integration LLC
In 2011, a consortium of 11 major academic and medical organizations in and around New York announced the creation of the New York Genome Center (NYGC). Under the direction of Nancy Kelley, the NYGC aspires to be a world-class genomics and medical research center, and is currently undergoing construction in the heart of Manhattan. NYGC management has the opportunity to design and create a state-of-the-art IT and data management infrastructure to handle, store and share the output from what will rapidly become one of the world's foremost genome sequencing facilities. This series of talks will describe the thinking that went into the design, creation and construction of the NYGC's IT infrastructure and entire data management strategy.

4:00 Conference Adjourns

Track 3
Cloud Computing
Riding the Cloud to Next-Generation Computing

Track 3 focuses on integrated data infrastructure and information management leveraging Cloud-based technologies. It will showcase simple turnkey cloud-based applications for small businesses/labs and portable healthcare, as well as collaborative efforts that integrate semantics, AI and statistics for intelligent information retrieval from big data on the fly.

TUESDAY, APRIL 9

7:00 am Workshop Registration and Morning Coffee

8:00 Pre-Conference Workshops*
Beyond the Cloud: Improving the R&D Innovation Process through Cloud Services
Cloud Computing in Hospital Data Management and Integration
**Separate Registration Required*

2:00 - 7:00 pm Main Conference Registration

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

4:05 Keynote Introduction
Kevin Brode, Senior Director, Health & Life Sciences, Americas Hitachi Data Systems

» 4:15 PLENARY KEYNOTE
Do Network Pharmacologists Need Robot Chemists?
Andrew L. Hopkins, DPhil, FRSC, FSB, Division of Biological Chemistry and Drug Design, College of Life Sciences, University of Dundee

5:00 Welcome Reception in the Exhibit Hall with Poster Viewing
*Drop off a business card at the CHI Sales booth for a chance to win 1 of 2 iPads® or 1 of 2 Kindle Fires®!**
**Apple ® and Amazon are not sponsors or participants in this program*

WEDNESDAY, APRIL 10

7:00 am Registration and Morning Coffee

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

8:05 Keynote Introduction
Sanjay Joshi, CTO, Life Sciences, EMC Isilon

» 8:15 PLENARY KEYNOTE
Atul Butte, M.D., Ph.D., Division Chief and Associate Professor, Stanford University School of Medicine; Director, Center for Pediatric Bioinformatics, Lucile Packard Children's Hospital; Co-founder, Personalis and Numedii

8:55 Benjamin Franklin Award & Laureate Presentation

9:15 Best Practices Award Program

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

Risk and Strategy for Pharma in the Cloud

10:50 Chairperson's Remarks

11:00 Pharma Disruptors: A Real-World Look Into How Cloud Computing Can Impact Your Business
Nathan McBride, Vice President, IT, AMAG Pharmaceuticals
The IT Team at AMAG Pharmaceuticals ignored the trends and created a scalable enterprise cloud model and eliminated their data center in the process. This came with a realized reduction of over 60% in costs with only five personnel in IT. Today, AMAG continues to push the boundaries of innovation with the cloud model they have constructed.

11:30 Use of Cloud Services and Application Virtualization within Roche Research and Early Development
Bryn Roberts, Ph.D., Global Head Informatics, Pharma Research and Early Development , F. Hoffmann-La Roche Ltd.
Thomas Kandl, Global Head Scientific Computing Services, Pharma Research and Early Development Informatics, F. Hoffmann-La Roche Ltd.
The use of Cloud services is growing rapidly due to a number of advantages, including lower costs, ability to scale, enabling mobility and support for external collaboration. Similarly, application virtualization has significant cost and time benefits, and provides the ability to manage large numbers of applications across diverse devices and operating systems.

12:00 pm Beyond the Cloud: How Cloud Services Can Drive Performance in Pharma R&D *Sponsored by* BT
David Brown, CTO, BT Life Sciences, BT Global Services
As so much of the debate about cloud computing has focused on technology, this presentation will look at why pharma 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.

12:30 Luncheon Presentation I: Big Data in the Cloud: A New Age of Collaboration for Life Sciences *Sponsored by* aspera
Richard Heitmann, Vice President, Marketing, Aspera
Life science researchers have a new range of cloud-enabled tools to simplify workflows and greatly enhance the transport, analysis, transformation, and sharing of big data. While the inherent advantages of cloud computing are numerous, the bottlenecks of cloud infrastructure have prevented its adoption in the life sciences field. New technologies and cloud architectures have overcome these technical challenges, enabling scale-out transfer, analysis and sharing of next-gen sequencing and large volumes of scientific data, often between far-flung collaborators. This innovation enabled genomic data to be transported at a sustained rate of almost 10 Gbps over a new link connecting prominent US and China research and education networks and is also used by cloud-based bio-informatics platform from BGI and BT Life Sciences.

1:00 The Convergence of Big Data Analytics with HPC Cloud *Sponsored by* IBM
Jeff Karmiol, Senior Product Manager, Platform Computing, HPC Cloud, IBM
Life science research continues to push the boundaries for more compute cycles and is looking to high performance computing (HPC) cloud technology for best practices in managing these

environments. We now see the rapid evolution of HPC for big data analytics and a convergence of big data analytics with HPC cloud. This presentation will talk about how cloud technology can be used to provision, flex and manage multiple multi-tenant analytics and high performance computing clusters within a shared pool of cloud resources while meeting the needs of the most demanding compute-intensive and big data workloads.

Cloud for Collaboration

1:40 Chairperson's Remarks

1:45 Next-Generation Bioinformatics Cloud Infrastructure for Global Collaboration
Theodore Omtzigt, Ph.D., CEO and Founder, Stillwater Supercomputing Inc.
With the proliferation of NGS instruments at core facilities the collected genome information will become distributed. To leverage the collective information large data sets need to be shared among a growing set of research teams and geographically dispersed organizations. We describe our automated cloud computing solution that seamlessly connects core facilities and research teams.

2:15 Genestack Platform for Bioinformatics R&D
Misha Kapushesky, Ph.D., CEO, Genestack Limited
Genestack Platform is a universal collaborative ecosystem for bioinformatics research and development. It allows users to store and share large data sets securely within and across organizations, with free access to public data from major databases. The platform includes open-source and proprietary genomics applications, working together independent of file formats. For developers an SDK, APIs and a marketplace are provided.

2:45 Utility Supercomputing: Revolutions in Computational Sciences and Genomics
Jason Stowe, CEO, Cycle Computing
Sponsored by CYCLE COMPUTING

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

NGS Analysis in the Cloud

3:45 Integrated Research Data management and Analysis in NGS using Globus Online, Galaxy and Amazon Web Services
Ravi Madduri, Fellow, Computation Institute, University of Chicago; Project Manager, Math and Computer Science Division, Argonne National Lab
In this talk we will present a robust, scale on-demand solution that provides end-to-end research data management for Next-Gen Sequencing Analysis using Galaxy, Globus Online and Amazon Web Services. The emphasis is on providing the researcher with a high degree of flexibility to inspect, customize, and configure NGS analysis tools and workflows, and share findings with collaborators.

4:15 Whole Genome Sequencing Data Analysis in the Cloud
Kurt Prenger, IT Senior High Performance Computing Analyst, Application Services Research & Development, Johnson & Johnson
By utilizing cloud resources and open source toolsets, our team was able to reduce the time taken to process 50 Whole Human Genomes from ~3 years sequentially on a local machine to ~3 days in the cloud. The coordination between processing steps was automated to limit the need for manual intervention, and basic checkpoints were created to determine if steps were completing correctly.

4:45 Kickstarting the Worldwide Genome Web
Dan Maltbie, CTO, Annai Systems Inc.
Genomics has triggered a transformative change: the world is now embracing genomics for the advancement of biological research, and more particularly for personalized medicine. Projects such as The Cancer Genome Atlas, The 1000 Genomes Project, and the International Cancer Genome Consortium are a few examples of this fundamental shift. What is needed to foster and accelerate these advancements is a system of interlinked "big data" genomics content (and other data types) that is globally accessible through a secure Internet, similar to the way the original Worldwide Web (WWW) originated and grew, from isolated prototype solutions to a global ubiquitous web. This talk will present how Annai Systems is kickstarting the Worldwide Genome Web

5:15 Best of Show Awards Reception in the Exhibit Hall

6:15 Exhibit Hall Closes

THURSDAY, APRIL 11

7:00 am Breakfast Presentation Panel: Enabling Technology. Leveraging Data. Transforming Medicine. *Sponsored by* intel
Panelists:
Samuel Aronson, Executive Director, IT, Partners HealthCare Center for Personalized Genetic Medicine
Sanjay Joshi, CTO, Life Sciences, EMC Isilon
Glen Otero, Life Sciences HPC Solution Architect, Dell
Ketan Paranjape, Global Director, Healthcare & Life Sciences, Intel Corp.
Toby Bloom, Director, Informatics, Genomics Platform at Broad Institute
As we arrive at the $1000 genome, we find the fundamental problems have shifted... it is no longer about shrinking the cost of sequencing but the explosive growth of big data: the downstream analytics with rapidly evolving parameters, data sources and formats; the storage, movement and management of massive datasets and workloads; and perhaps most paradoxical of all, the challenge of articulating the results and translating the latest findings directly into improving patient outcomes. Please join Intel and our distinguished panel to discuss how collaborating with a broad range of ecosystem partners to develop innovative solutions to seemingly intractable problems emerging in healthcare and life sciences today is driving us towards the vision of personalized medicine.

» FEATURED PRESENTATION

8:00 Featured Presentation Introduction
Geoffrey Noer, Senior Director, Product Marketing, Panasas

8:10 Trends in the Trenches 2013
Chris Dagdigian, Founding Partner, Director, Technology, BioTeam, Inc.
HPC Trends in the Trenches is one of the most popular presentations of the Expo! This talk will present how common HPC problems in life science informatics have been approached by organizations of varying type and size. We will discuss observed trends in computing, workflows and data movement, along with details on particularly clever solutions observed in production environments around the world.

Open Innovation

8:45 Chairperson's Opening Remarks

8:50 Virtual Screening of 4.5 Billion Compound-Target Pairs Using AutoDock Vina on Google Exacycle
James Swetnam, Visiting Research Scientist, Cloud Platforms, Google
The current trend in scientific computing is toward low-cost distributed systems of commodity hardware. Using Google Exacycle, we computed 4.5 billion compound-target energy scores between 538,501 compounds and 8,300 receptor conformations corresponding to 589 unique targets using AutoDock Vina. To our knowledge, this is the largest virtual screen ever performed.

9:20 Computing in the Sky: MOON Computing + Cloud Computing
Wu Feng, Ph.D., Elizabeth & James Turner Associate Professor, Computer Science, Electrical & Computer Engineering, Virginia Bioinformatics Institute, Virginia Tech
Project MOON (MapReduce On Opportunistic eNvironments) proactively harvests the unused compute cycles of volatile computing resources and combines them with a small number of dedicated computing resources to provide the illusion of a robust supercomputer. This substantially enhances the return on investment on institutional computing resources.

9:50 Challenges in the Era of Big Genomic Data and Our Practices in BGI

Sponsored by

Xing Xu, Ph.D., Director, Cloud Computing Products, BGI

While the amount of next generation sequencing (NGS) data grows exponentially, effective genomic data transferring, sharing, processing, and management encounter substantial scientific and technical challenges. In this session, we will share BGI's practice and experience how we handle these challenges in ultrafast data transfer, cloud computing, algorithm development with different HPC frameworks (Hadoop and GPU) and data management (iRODS).

10:20 Coffee Break in the Exhibit Hall and Poster Competition Winners Announced

10:45 Plenary Keynote Panel Chairperson's Remarks

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

10:50 Plenary Keynote Panel Introduction

Yury Rozenman, Head of BT for Life Sciences, BT Global Services
Niven R. Narain, President & CTO, Berg Pharma

» PLENARY KEYNOTE PANEL

11:05 The Life Sciences CIO Panel

Panelists:
Remy Evard, CIO, Novartis Institutes for BioMedical Research
Martin Leach, Ph.D., Vice President, R&D IT, Biogen Idec
Andrea T. Norris, Director, Center for Information Technology (CIT) and Chief Information Officer, NIH
Gunaretnam (Guna) Rajagopal, Ph.D., VP & CIO - R&D IT, Research, Bioinformatics & External Innovation, Janssen Pharmaceuticals
Cris Ross, Chief Information Officer, Mayo Clinic
Matthew Trunnell, CIO, Broad Institute of MIT and Harvard

12:15 pm Luncheon in the Exhibit Hall with Poster Viewing

Panel Session:Building the IT Architecture of the New York Genome Center

2:00 Panel Session: Building the IT Architecture of the New York Genome Center

Moderator: Kevin Davies, Ph.D., Editor-in-Chief, Bio-IT World
Christopher Dwan, Acting Senior Vice President, IT, New York Genome Center
Kevin Shianna, Senior Vice President, Sequencing Operations, New York Genome Center
Sanjay Joshi, CTO, Life Sciences, EMC Isilon Storage Division
Robert B. Darnell, M.D., Ph.D., President & Scientific Director, New York Genome Center
George Gosselin, CTO, Computer Design & Integration LLC

In 2011, a consortium of 11 major academic and medical organizations in and around New York announced the creation of the New York Genome Center (NYGC). Under the direction of Nancy Kelley, the NYGC aspires to be a world-class genomics and medical research center, and is currently undergoing construction in the heart of Manhattan. NYGC management has the opportunity to design and create a state-of-the-art IT and data management infrastructure to handle, store and share the output from what will rapidly become one of the world's foremost genome sequencing facilities. This series of talks will describe the thinking that went into the design, creation and construction of the NYGC's IT infrastructure and entire data management strategy.

4:00 Conference Adjourns

Track 4
Bioinformatics
Understanding Massive Quantities of –omic Information across Research Initiatives

Track 4 explores data and its application across multiple research initiatives. Topics covered will include data mining/modeling, computational tools, web portals, microarray, and clinical applications such as cancer and required tools to identify clinically actionable variants.

TUESDAY, APRIL 9

7:00 am Workshop Registration and Morning Coffee

8:00 Pre-Conference Workshops*
**Separate Registration Required*

2:00 - 7:00 pm Main Conference Registration

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

4:05 Keynote Introduction
Kevin Brode, Senior Director, Health & Life Sciences, Americas Hitachi Data Systems

» 4:15 PLENARY KEYNOTE
Do Network Pharmacologists Need Robot Chemists?
Andrew L. Hopkins, DPhil, FRSC, FSB, Division of Biological Chemistry and Drug Design, College of Life Sciences, University of Dundee

5:00 Welcome Reception in the Exhibit Hall with Poster Viewing
*Drop off a business card at the CHI Sales booth for a chance to win 1 of 2 iPads® or 1 of 2 Kindle Fires®!**
**Apple ® and Amazon are not sponsors or participants in this program*

WEDNESDAY, APRIL 10

7:00 am Registration and Morning Coffee

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

8:05 Keynote Introduction
Sanjay Joshi, CTO, Life Sciences, EMC Isilon

» 8:15 PLENARY KEYNOTE
Atul Butte, M.D., Ph.D., Division Chief and Associate Professor, Stanford University School of Medicine; Director, Center for Pediatric Bioinformatics, Lucile Packard Children's Hospital; Co-founder, Personalis and Numedii

8:55 Benjamin Franklin Award & Laureate Presentation

9:15 Best Practices Award Program

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

10:50 Chairperson's Remarks
Michael Liebman, Ph.D., Managing Director, Strategic Medicine, Inc.

» FEATURED PRESENTATION

11:00 Tools for Revolutionizing Translational Cancer Medicine
Kevin Hrusovsky, President, Life Sciences & Technology, PerkinElmer, Inc.

Sponsored by
PerkinElmer
For the Better

While breakthroughs abound in cancer research, there is a profound disconnect in translating these discoveries to clinical medicine. This talk will discuss how combining the "*in vitro*-to-*in vivo*-to human" continuum of research tools with a powerful *in silico* infrastructure has successfully bridged the chasm from lab to clinic, particularly in the field of cancer medicine and personalized health.

Bioinformatics across Multiple Research Initiatives

11:30 Biological Research through Omic-Data Integration Using the "Programmable Web"
Matt Roth, Ph.D., Assistant Professor, Human Genetics, Baylor College of Medicine
This talk presents results from a human breast cancer study that utilized "programmable web" technology via Genboree to drive "virtual data integration" by bringing together only relevant "omic" data from multiple physical locations just in time for analysis. The results presented will illustrate how virtual data integration across multiple research initiatives (large and small) can be applied to any disease.

12:00 pm CECARDIS, An International Consortium to Evaluate Comparative Effectiveness in Cardiovascular Disease Risk Assessment: Algorithms, Biomarkers and Diagnostics
Michael Liebman, Ph.D., Managing Director, Strategic Medicine, Inc.
Sabrina Molinaro, Ph.D., Institute for Clinical Physiology, National Research Council, Italy
CECARDIS is an international consortium of hospitals, ministries of health, and government agencies that compare clinical approaches, procedures/devices and guidelines in large populations exhibiting symptoms of coronary artery disease and the impact of biomarkers in diagnosis/treatment. CECARDIS is developing a platform to support ongoing evaluation of new patient records and to compare effectiveness of existing technologies for prevention, diagnosis and treatment of CVD.

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

1:40 Chairperson's Remarks
Saras Saraswathi Ph.D., Postdoctoral Research Associate, Battelle Center for Mathematical Medicine, The Research Institute at Nationwide Children's Hospital

1:45 3D Imaging and Informatics Approaches to Diagnose Genetic Conditions
Curtis Deutsch, Ph.D., Director, Psychobiology Program, Eunice Kennedy Shriver Center, University of Massachusetts Medical School
With the support of NIH, we have developed the first quantitative normative database to diagnose craniofacial abnormalities. This new informatics resource, combined with novel methods in 3D surface imaging and 3D morphometry, provides the means of defining features of medical genetic conditions. These techniques permit, for the first time, objective and reliable quantitative diagnosis on a graded continuum.

2:15 Bounded Rationality Approach to Artificial Intelligence and Its Implications for Understanding and Treatment of Autism
Simon Berkovich, Ph.D., Professor, Computer Science, The George Washington University
A "Big Data" computational model for the brain manipulates explicitly with a small portion of data on top of an implicit context of all other data. The resultant bounded rationality scheme of Artificial Intelligence relies on simple operational models enhanced with context-determined selections. This presentation discusses "Big Data" processing ideology that might be useful for understanding the mechanisms of autism.

2:45 H3 Biomedicine / Tessella Translational Informatics Platform (TIP)
Sponsored by Tessella Technology & Consulting
Stephen Kottmann, Ph.D., Consultant, Tessella Inc.
Lihua Yu, Ph.D., Director, Bioinformatics, H3 Biomedicine Inc.
Recent efforts, in both the public and private sectors, to assemble large datasets of cancer cell line pharmacogenomic profiles have proven effective at identifying biomarkers for drug sensitivity and resistance. Here we describe the theory and implementation of an informatics platform developed by H3 Biomedicine and Tessella, which provides flexible aggregation and interrogation of pharmacogenomics data from many sources.

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

Gene Mapping & Expression

3:45 DB Genomic Datasets Hub: An Efficient Starting Point for Managing and Analyzing Genomewide Studies in GenePattern, Integrative Genomics Viewer, and R/Bioconductor
David Weiss, Ph.D., CEO, InSilico Genomics
Alain Coletta, Ph.D., Co-Founder and CTO, InSilico Genomics
The InSilico DB platform is a powerful collaborative environment, with advanced capabilities for biocuration, datasets subsetting and combination, and datasets sharing. InSIlico DB solution architecture will be presented along with a live demo of the InSilico DB online platform. Learn how more than 1000 users from top academic and research institutions are using InSilico DB in their daily research.

4:15 Constructing a Comprehensive Map for Molecules Implicated in Obesity and Its Induced Disorders
Kamal Rawal, Ph.D., Faculty, Biotechnology and Bioinformatics, Jaypee Institute of Information Technology
We have constructed a comprehensive map of all the molecules (genes, proteins, and metabolites) reported to be implicated in obesity. This map paves the way to understanding the pathophysiology of obesity and identify drug targets and off-targets for existing drugs. This talk discusses the integrated approach we used in combining public resources, abstracts, and research articles to construct this map.

4:45 Quality Assurance: An Essential Step for Gene Expression Analysis Using Deep Sequencing
Sponsored by Maverix BIOMICS
Dan Kearns, Director, Software Development, Maverix Biomics, Inc.
Dave Mandelkern, CEO & Co-Founder, Maverix Biomics, Inc.
With the advancement of deep sequencing technologies, researchers expect to obtain high quality results from their studies. However, this cannot be obtained solely by successful sequencing runs. Multiple data checks and pre-processing must be performed before downstream analysis. In this case study, we will present an automated quality assurance pipeline that helps improve gene expression analysis results.

5:00 DDN LS Appliance - Simple Platform for NGS Analysis, Data Distribution and Collaboration
Sponsored by DataDirect NETWORKS Information in Motion
Jose L. Alvarez, WW Director Life Sciences, DataDirect Networks
With this unique approach the DDN LS appliance can deliver flexible data ingest options, optimized data analysis resources, a policy based data tiering/archive solution and a geo-distributed secure collaboration platform. The appliance delivers 1.46X better performance on popular LS applications like Bowtie when compared to NFS based solutions.

5:15 Best of Show Awards Reception in the Exhibit Hall

6:15 Exhibit Hall Closes

THURSDAY, APRIL 11

7:00 am Breakfast Presentation *(Sponsorship Opportunity Available)* **or Morning Coffee**

Gene Mapping & Expression

8:45 Chairperson's Opening Remarks
Mathukumalli Vidyasagar, Ph.D., Cecil & Ida Green Chair in Systems Biology Science; Head, Bioengineering Department, University of Texas at Dallas

8:50 Network Biology and Personalized Medicine in Multiple Sclerosis
Mark Chance, Ph.D., Vice Dean for Research, Proteomics, Case Western Reserve University
Almost nothing is known about biological factors underlying the remarkable disease heterogeneity observed across multiple sclerosis (MS) patients, and there are no accurate biological predictors of disease severity that can be used for guiding clinical treatment options. Learn about the network biology methods we are using to analyze blood cell gene expression and understand good and poor responders to therapy.

9:20 GeneSeer: A Flexible, Easy-to-Use Tool to Aid Drug Discovery by Exploring Evolutionary Relationships between Genes across Genomes
Philip Cheung, Bioinformatics Group Leader, Scientific Computing, Dart Neuroscience
GeneSeer is a publicly available tool that leverages public sequence data, gene metadata information, and other publicly available data to calculate and display orthologous and paralogous gene relationships for all genes from several species, including yeasts, insects, worms, vertebrates, mammals, and primates such as human. This talk describes GeneSeer's underlying methods and the user-friendly interface.

9:50 Cloud Computing For Smart People
Sponsored by Bright Computing
Dave Maples, Senior Vice President, Bright Computing
Smart people are turning to the cloud as a powerful option for pharmaceutical and life sciences computing. This presentation is about how to make the most of cloud computing without becoming IT experts or reallocating research time to manage cloud resources. Two scenarios will be offered: creating cloud-based servers on the fly, and extending on-premise servers into Amazon EC2.

10:20 Coffee Break in the Exhibit Hall and Poster Competition Winners Announced

10:45 Plenary Keynote Panel Chairperson's Remarks
Kevin Davies, Ph.D., Editor-in-Chief, Bio-IT World

10:50 Plenary Keynote Panel Introduction
Yury Rozenman, Head of BT for Life Sciences, BT Global Services
Niven R. Narain, President & CTO, Berg Pharma

» PLENARY KEYNOTE PANEL

11:05 The Life Sciences CIO Panel
Panelists:
Remy Evard, CIO, Novartis Institutes for BioMedical Research
Martin Leach, Ph.D., Vice President, R&D IT, Biogen Idec
Andrea T. Norris, Director, Center for Information Technology (CIT) and Chief Information Officer, NIH
Gunaretnam (Guna) Rajagopal, Ph.D., VP & CIO - R&D IT, Research, Bioinformatics & External Innovation, Janssen Pharmaceuticals
Cris Ross, Chief Information Officer, Mayo Clinic
Matthew Trunnell, CIO, Broad Institute of MIT and Harvard

12:15 Luncheon in the Exhibit Hall with Poster Viewing

Panel Session: Building the IT Archetecture of the New York Genome Center

2:00 Panel Session: Building the IT Architecture of the New York Genome Center
Moderator: Kevin Davies, Ph.D., Editor-in-Chief, Bio-IT World
Christopher Dwan, Acting Senior Vice President, IT, New York Genome Center
Kevin Shianna, Senior Vice President, Sequencing Operations, New York Genome Center
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Robert B. Darnell, M.D., Ph.D., President & Scientific Director, New York Genome Center
George Gosselin, CTO, Computer Design & Integration LLC

In 2011, a consortium of 11 major academic and medical organizations in and around New York announced the creation of the New York Genome Center (NYGC). Under the direction of Nancy Kelley, the NYGC aspires to be a world-class genomics and medical research center, and is currently undergoing construction in the heart of Manhattan. NYGC management has the opportunity to design and create a state-of-the-art IT and data management infrastructure to handle, store and share the output from what will rapidly become one of the world's foremost genome sequencing facilities. This series of talks will describe the thinking that went into the design, creation and construction of the NYGC's IT infrastructure and entire data management strategy.

4:00 Conference Adjourns

Track 5
Next-Gen Sequencing Informatics
NGS, Genome-Scale Screening, and HTP Proteomics

Track 5 is dedicated to advances in analysis and intepretation of next-gen data. Topics to be covered include analysis of sequence variants related to cancer research from NGS data, instruments facilitate a cloud approach for NGS, analysis tools and workflows, and network biology/network medicine.

TUESDAY, APRIL 9

7:00 am Workshop Registration and Morning Coffee

8:00 Pre-Conference Workshops*
**Separate Registration Required*

2:00 - 7:00 pm Main Conference Registration

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

4:05 Keynote Introduction
Kevin Brode, Senior Director, Health & Life Sciences, Americas Hitachi Data Systems

» 4:15 PLENARY KEYNOTE
Do Network Pharmacologists Need Robot Chemists?
Andrew L. Hopkins, DPhil, FRSC, FSB, Division of Biological Chemistry and Drug Design, College of Life Sciences, University of Dundee

5:00 Welcome Reception in the Exhibit Hall with Poster Viewing
*Drop off a business card at the CHI Sales booth for a chance to win 1 of 2 iPads® or 1 of 2 Kindle Fires®!**
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WEDNESDAY, APRIL 10

7:00 am Registration and Morning Coffee

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

8:05 Keynote Introduction
Sanjay Joshi, CTO, Life Sciences, EMC Isilon

» 8:15 PLENARY KEYNOTE
Atul Butte, M.D., Ph.D., Division Chief and Associate Professor, Stanford University School of Medicine; Director, Center for Pediatric Bioinformatics, Lucile Packard Children's Hospital; Co-founder, Personalis and Numedii

8:55 Benjamin Franklin Award & Laureate Presentation

9:15 Best Practices Award Program

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

Best Practices for Genomic Data Interpretation & Analysis

10:50 Chairperson's Remarks
Steve Dickman, Founder & CEO, CBT Advisors, Inc.

11:00 CLARITY Challenge
Shamil Sunyaev, Ph.D., Associate Professor, Division of Genetics, Department of Medicine, Brigham and Women's Hospital/Harvard Medical School

11:30 HLA and KIR Typing from NGS Reads with Omixon Target
Sponsored by OMIXON BIOCOMPUTING SOLUTIONS
Attila Berces, Ph.D., CEO, Omixon
HLA is the most polymorphic region of the human genome with several segmental duplications and its analysis is a computational challenge. In this presentation I will show examples including validation studies of HLA typing from various sources of genomic data: whole genome, whole exome, targeted amplicon sequencing with Illumina, Ion Torrent and Roche sequencer.

11:45 Comparison of Genome Analysis Tools
Sponsored by arpeggi
Jason Wang, Co-founder & CTO, Arpeggi, Inc.
A major impediment to clinical sequencing is the paucity of analysis standards and comparison metrics. We present our progress towards developing analysis standards, as well an open-access collaborative tool that enables anyone to define comparison metrics and compare tool performance. We hope that in making available this resource we can help fuel a community-driven solution for standardizing genome analysis pipelines.

12:00 Case Study: Sequencing Informatics System to Profile Genetic Changes in Tumors
Long Phi Le, M.D., Ph.D., Department of Pathology, Massachusetts General Hospital
This presentation will discuss the development of a sequencing informatics system to profile genetic changes in tumors that is in collaboration between PerkinElmer with Massachusetts General Hospital. This system, based on PerkinElmer's Geospiza platforms, will allow genotype analysis to define key targets.

12:30 Ion Torrent Informatics Enables Semiconductor Sequencing
Sponsored by life technologies™
Darryl León , Ph.D., Associate Director, Product Management, Ion Torrent, Life Technologies
Data generated by the Ion Torrent Personal Genome Machine Sequencer or the Ion Torrent Proton Sequencer are analyzed by Torrent Suite Software. An overview of the data analysis steps will be provided. Torrent Suite offers a flexible plug-in system allowing software developers the ability to deliver custom analysis solutions using the compute resources associated with the local Torrent Server. For researchers with need for either rich annotations or controlled data analysis, the Ion Reporter Software offers a streamlined data analysis and decision engine for use with amplicons, exomes, or genomes.

1:40 Chairperson's Remarks
Jeffrey Rosenfeld, Ph.D., IST/High Performance & Research Computing, University of Medicine & Dentistry of New Jersey (UMDNJ)

1:45 Data Intensive Academic Grid (DIAG): A Free Computational Cloud Infrastructure Designed for Bioinformatics Analysis
Anup Mahurkar, Executive Director, Software Engineering and IT, Institute for Genome Sciences, University of Maryland School of Medicine
We have deployed the NSF funded Data Intensive Academic Grid (DIAG), a free computational cloud designed to meet the analytical needs of the bioinformatics community. DIAG has 200+ registered users from 130 institutions worldwide who conduct large-scale genomics, transcriptomics, and metagenomics data analysis. Learn about the grid's architecture, how to access this free resource, and success stories.

2:15 Performance Comparison of Variant Detection Tools for Next Generation Sequencing (NGS) Data: An Assessment Using a Pedigree-Based NGS Dataset and SNP Array
Ming Yi, Ph.D. IT Manager, Functional Genomic Group, Advanced Biomedical Computing Center, SAIC-Frederick at Frederick National Laboratory for Cancer Research (formerly National Cancer Institute)
There is an urgent need for the NGS community to be able to make the right choice out of a large collection of available SNP detection tools. Our methodology offers a great example of comparing SNP discovery tools and paving a way to expand such methods in more global scope for comparison.

2:45 Informatics in the Cloud *Sponsored by* amazon web services
Karan Bhatia, Ph.D., Solutions Architect, Amazon Web Services
Learn about how to easily create sophisticated, scalable, secure pipelines to accelerate life science research with Amazon Web Services. In this presentation, you will learn how to drive scale out, tightly coupled and Hadoop based workflows on Amazon EC2, a utility computing platform that provides a perfect fit for data management and collaboration.

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

Gene Mapping & Expression

3:45 InSilico DB Genomic Datasets Hub: An Efficient Starting Point for Managing and Analyzing Genomewide Studies in GenePattern, Integrative Genomics Viewer, and R/Bioconductor
David Weiss, Ph.D., CEO, InSilico Genomics
Alain Coletta, Ph.D., Co-Founder and CTO, InSilico Genomics
The InSilico DB platform is a powerful collaborative environment, with advanced capabilities for biocuration, datasets subsetting and combination, and datasets sharing. InSIlico DB solution architecture will be presented along with a live demo of the InSilico DB online platform. Learn how more than 1000 users from top academic and research institutions are using InSilico DB in their daily research.

4:15 Constructing a Comprehensive Map for Molecules Implicated in Obesity and Its Induced Disorders
Kamal Rawal, Ph.D., Faculty, Biotechnology and Bioinformatics, Jaypee Institute of Information Technology
We have constructed a comprehensive map of all the molecules (genes, proteins, and metabolites) reported to be implicated in obesity. This map paves the way to understanding the pathophysiology of obesity and identify drug targets and off-targets for existing drugs. This talk discusses the integrated approach we used in combining public resources, abstracts, and research articles to construct this map.

4:45 Quality Assurance: An Essential Step for Gene Expression Analysis Using Deep Sequencing *Sponsored by* Maverix BIOMICS
Dan Kearns, Director, Software Development, Maverix Biomics, Inc.
Dave Mandelkern, CEO & Co-Founder, Maverix Biomics, Inc.
With the advancement of deep sequencing technologies, researchers expect to obtain high quality results from their studies. However, this cannot be obtained solely by successful sequencing runs. Multiple data checks and pre-processing must be performed before downstream analysis. In this case study, we will present an automated quality assurance pipeline that helps improve gene expression analysis results.

5:00 DDN LS Appliance - Simple Platform for NGS Analysis, Data Distribution and Collaboration *Sponsored by* DataDirect NETWORKS Information in Motion
Jose L. Alvarez, WW Director Life Sciences, DataDirect Networks
With this unique approach the DDN LS appliance can deliver flexible data ingest options, optimized data analysis resources, a policy based data tiering/archive solution and a geo-distributed secure collaboration platform. The appliance delivers 1.46X better performance on popular LS applications like Bowtie when compared to NFS based solutions.

5:15 Best of Show Awards Reception in the Exhibit Hall

6:15 Exhibit Hall Closes

THURSDAY, APRIL 11

7:00 am Breakfast Presentation *(Sponsorship Opportunity Available)* **or Morning Coffee**

Gene Mapping & Expression

8:45 Chairperson's Opening Remarks

8:50 Network Biology and Personalized Medicine in Multiple Sclerosis
Mark Chance, Ph.D., Vice Dean for Research, Proteomics, Case Western Reserve University
Almost nothing is known about biological factors underlying the remarkable disease heterogeneity observed across multiple sclerosis (MS) patients, and there are no accurate biological predictors of disease severity that can be used for guiding clinical treatment options. Learn about the network biology methods we are using to analyze blood cell gene expression and understand good and poor responders to therapy.

9:20 GeneSeer: A Flexible, Easy-to-Use Tool to Aid Drug Discovery by Exploring Evolutionary Relationships between Genes across Genomes
Philip Cheung, Bioinformatics Group Leader, Scientific Computing, Dart Neuroscience
GeneSeer is a publicly available tool that leverages public sequence data, gene metadata information, and other publicly available data to calculate and display orthologous and paralogous gene relationships for all genes from several species, including yeasts, insects, worms, vertebrates, mammals, and primates such as human. This talk describes GeneSeer's underlying methods and the user-friendly interface.

9:50 Sponsored Presentations *(Opportunities Available)*

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4:00 Conference Adjourns

Track 6
Systems Pharmacology
Pathways to Patient Response

Track 6 focuses on how compounds (drugs) work in the body. How are they influenced by various 'omics'? How do they vary by tissue? The practical implications of such a compound-centric approach are exciting: new targets, new screens, new markers, new understanding of drug failure mechanisms. The systems computational tool sets including multi-scale modeling, simulation, web-based platforms, etc. will be emphasized.

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**Separate Registration Required*

2:00 - 7:00 pm Main Conference Registration

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8:05 Keynote Introduction
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9:15 Best Practices Award Program

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

Pharmacodynamic Models

11:00 Chairperson's Remarks
Eugene Myshkin, Senior Research Scientist, Thomson Reuters

» **FEATURED SPEAKER**

11:10 Systems Pharmacology in a Post-Genomic Era
Peter Sorger, Ph.D., Professor, Systems Biology, Harvard Medical School; Co-Chair, Harvard Initiative in Systems Pharmacology
I will describe the emergence of "systems pharmacology" as a means to guide the creation of new molecular matter, study cellular networks and their perturbation by drugs, understand pharmaco-kinetics and pharmaco-dynamics in mouse and man and design and analyze clinical trial data. The approach combines mathematical modeling with empirical measurement as a means to tackle basic and clinical problems in pharmacology.

12:00 pm Systems Pharmacology Approaches to Drug Repositioning
Sponsored by THOMSON REUTERS
Eugene Myshkin, Senior Research Scientist, Thomson Reuters
Drug repositioning requires advanced computational approaches and comprehensive knowledgebase information to reach success. Thomson Reuters will present on recent advances in drug repositioning approaches, their validation and performance, best practices in using systems biology content, and successful case studies.

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

High Content Analysis: Cancer Cell Lines

1:40 Chairperson's Remarks
William Reinhold, Manager, Genomics and Bioinformatics Group, Laboratory of Molecular Pharmacology (LMP), National Cancer Institute (NCI)

1:45 Systems Pharmacology Using CellMiner and the NCI-60 Cancerous Cell Lines
William Reinhold, Manager, Genomics and Bioinformatics Group, Laboratory of Molecular Pharmacology (LMP), National Cancer Institute (NCI)
CellMiner is a web-based application that allows rapid access to and comparison between 20,503 compound activities and the expression levels of 26,065 genes and 360 microRNAs. Included are 102 FDA-approved drugs as well as 53 in clinical trials. The tool is designed for the non-informatisist, and allows the user wide latitude in defining the question of interest.

2:15 Oncology Drug Combinations at Novartis
Joseph Lehár, Ph.D., Director of Bioinformatics OTR, Oncology Translational Medicine, Novartis Institutes for Biomedical Research
In collaboration with academic and industrial partners, we have generated mutation status, gene copy number, and gene expression data for a library of 1,000 cancer cell lines, representing most cancer lineages and common genetic backgrounds. We expect this large-scale campaign to enable efficient patient selection for clinical trials on existing cancer drugs, reveal many therapeutically promising drug synergies or anti-resistance combinations, and provide unprecedented detail on functional interactions between cancer signaling pathways.

2:45 Selected Oral Poster Presentation: Genotype-Based Analysis for Cancer Therapy Using Large-Scale Data Modeling
Nayoung Kim, Ph.D. Candidate, Biological Sciences, Sookmyung

Women's University
An integrative approach of large-scale omics and drug response data on various cell lines enables us to identify the cellular signaling and drug sensitivity in cancer. Signatures in different levels of biological process such as gene expression, protein expression and protein activation have applications in finding novel diagnostic or prognostic biomarkers. They are also key components in accelerating mechanism-based drug discovery or genotype-specific repositioning. Here we present a system-level analysis of cell line data for predicting the sensitivity and mechanisms of targeted drug response based on major genotypes of cancers. Association study with the genotypic classification was performed on drug data and omics data such as transcriptome, proteome and phosphateome on human cancer cell lines. This approach reproduced the known patterns of mechanism-based drug response in cancers. Also, gene and protein signatures significantly associated with genotype were identified and integrated into a drug-oriented network. Furthermore, we process the optimization of public gene sets to draw an advanced pathway-based interpretation using omics data and develop RNAi screening systems for analysis of cancer-regulation markers and anticancer effects perturbed by mutation. This study provides an integrated approach for omics, drug response data and cancer mutation types in cancers.

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

Pharmacodynamic Models for Oncology

3:45 Systems Biology in Cancer Immunotherapy: Applications in the Understanding of Mechanism of Action and Therapeutic Response
Debraj GuhaThakurta, Ph.D., Associate Director, Systems Biology, Dendreon Corporation
We are using high-content platforms (DNA and protein microarrays, RNA-seq) in various stages of the development of cellular immunotherapies for cancer. We will provide examples of genomic applications that can aid in the mechanistic understanding and the discovery of molecular markers associated with the efficacy of a cancer immunotherapy.

4:15 Use of Systems Pharmacology to Aid Cancer Clinical Development
Anna Georgieva Kondic, Ph.D., MBA, Senior Principal Scientist, Modeling and Simulation, Merck Research Labs
The last few years have seen an increased use of physiologically-based pharmacokinetics and pharmacodynamics models in Oncology drug development. This is partially due to an improved mechanistic understanding of disease drivers and the collection of better patient-level quantitative data that lends itself to modeling. In this talk, a suite of studies where systems modeling was successfully used to inform either preclinical to clinical transition or clinical study design will be presented. The talk will complete with a potential systems pharmacology framework that can be used systematically in drug development.

4:45 Two-Edged Swords in Epigenetic Modifications: The Vertebrate DNA Methyltransferases
C.-K. James Shen, Ph.D., Distinguished Research Fellow, Institute of Molecular Biology, Academia Sinica
Methylation at the 5-position of cytosine (C) to generate 5-methylcytosine (5-mC) on the vertebrate genomes is an essential epigenetic modification that regulates different biological processes including carcinogenesis. This modification has been known to be accomplished by the combined catalytic actions of three DNA methyltransferases (DNMTs), the *de novo* enzymes DNMT3A/ DNMT3B and the maintenance enzyme DNMT1. This property of DNMTs and the imbalance of CpG methylation in cancer cells have led to the development of cancer therapeutic drugs/ chemicals targeting the DNA methylation activities of DNMTs. However, we have recently discovered that the mammalian DNMTs could also act as active DNA 5-mC demethylases in a Ca++ion-and redox state-dependent manner. This suggests new directions for re-investigation of the structures of DNMTs and their functions in the genome wide and/or local DNA methylation in the mammalian cells. In particular, the concept and strategies for drug therapy targeting the DNMTs may need to be re-evaluated.

5:15 Best of Show Awards Reception in the Exhibit Hall

6:15 Exhibit Hall Closes

THURSDAY, APRIL 11

7:00 am Breakfast Presentation *(Sponsorship Opportunity Available)* **or Morning Coffee**

Modeling and Mining Targets

8:45 Chairperson's Opening Remarks
I-Ming Wang, Ph.D., Associate Scientific Director, Research Solutions and Bioinformatics, Informatics and Analysis, Merck Research Laboratory

8:50 Systems Biology Approach for Identification of New Targets and Biomarkers
I-Ming Wang, Ph.D., Associate Scientific Director, Research Solutions and Bioinformatics, Informatics and Analysis, Merck Research Laboratory
A representative gene signature was identified by an integrated analysis of expression data in twelve rodent inflammatory models/tissues. This "inflammatome" signature is highly enriched in known drug target genes and is significantly overlapped with macrophage-enriched metabolic networks (MEMN). The identification of this "inflammatome" gene signature extends the coverage of MEMN beyond adipose and liver in the metabolic disease to multiple diseases.

9:20 Optimizing Therapeutic Index (TI) by Exploring Co-Dependencies of Target and Therapeutic Properties
Madhu Natarajan, Ph.D., Associate Director, Computational Biology, Discovery Research, Shire HGT
Conventional drug-discovery informatics workflows employ combinations of mechanistic/probabilistic in-silico methods to rank lists of targets; therapeutics are then developed for "optimal" targets. I describe a systems pharmacology approach that instead integrates systematic in-silico therapeutic perturbation with models of target/disease biology to identify conditions for optimal TI; non-intuitively optimal TI is sometimes achieved by pairing sub-optimal targets with therapeutics having appropriate properties.

9:50 Leveraging Mathematical Models to Understand Population Variability in Response to Cardiac Drugs
Eric Sobie, Ph.D., Associate Professor, Pharmacology & Systems

Therapeutics, Icahn School of Medicine, Mount Sinai School of Medicine
Mathematical models of heart cells and tissues are sufficiently advanced that the models can predict mechanisms underlying pro-arrhythmic or anti-arrhythmic effects of drugs. At present, however, these models are not adequate for understanding variability across a population, i.e., why a drug may be effective in one patient but ineffective in another patient. I will describe novel computational approaches my laboratory has developed to quantify and predict differences between individuals in response to cardiac drugs.

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12:15 pm Luncheon in the Exhibit Hall with Poster Viewing

Modeling Molecular and Pathophysiological Data

1:55 Chairperson's Remarks
Jake Chen, Ph.D., Associate Professor, Indiana University School of Informatics & Purdue University Department of Computer Science; Director, Indiana Center for Systems Biology and Personalized Medicine

2:00 Predicting Adverse Side Effects of Drugs Using Systems Pharmacology
Jake Chen, Ph.D., Associate Professor, Indiana University School of Informatics & Purdue University Department of Computer Science; Director, Indiana Center for Systems Biology and Personalized Medicine
An new way of studying drug toxicity is to incorporate biomolecular annotation and network data with clinical observations of drug targets upon drug perturbations. I will describe the development of a novel computational modeling framework, with which we demonstrated the highest drug toxicity prediction accuracies ever reported by far. Adoption of this framework may have profound practical drug discovery implications.

2:30 Holistic Integration of Molecular and Physiological Data and Its Application in Personalized Healthcare
David de Graaf, Ph.D. President and CEO, Selventa
There are multiple industry-wide challenges in aggregating molecular and pathophysiological data for systems pharmacology to transform the process of drug discovery and development. One way to address this challenge is to utilize a common computable biological expression language (BEL). An application of BEL and its use in identifying clinically relevant predictive biomarkers for patient stratification will be presented.

3:00 The Role of Informatics in ADME Pharmacogenetics
Boyd Steere, Ph.D., Senior Research Scientist, Lilly Research Laboraories, IT Research Informatics, Eli Lilly
The leveraging of pharmacogenetics to support decisions in early-phase clinical trial design requires informatics methods to integrate, visualize, and analyze heterogeneous data sets from many different discovery platforms. This presentation describes challenges and solutions in making sense of diverse sets of genetic, protein, and metabolic data in support of ADME pharmacology projects.

3:30 A Systems Pharmacology Approach to Understand and Optimize Functional Selectivity for Non-Selective Drugs
Joshua Apgar, Principal Scientist, Systems Biology, Dept. of Immunology & Inflammation, Boehringer Ingelheim Pharmaceuticals, Inc.
In vivo functional selectivity is complicated and is affected by multiple feedback processes within and between the various on- and off-target pathways. These systems level processes are often impossible to reconstruct *in vitro*. We were able to identify, *in silico*, molecular properties that are critical to driving functional selectivity. The models capture the key systems pharmacology needed to understand the on- an off- target effects.

4:00 Conference Adjourns

Track 7
eClinical Trials Solutions
Innovative Management in Clinical Trials

Track 7 explores views, insights, and informatics challenges related to innovative clinical research management. Themes covered include innovations in development planning and protocol design; new approaches to sponsor-CRO and sponsor-site relationships; novel patient recruitment and retention strategies and practices; clinical ops and project management; clinical trial technologies and data integration; and utilization of EHRs to optimize trial design and management.

TUESDAY, APRIL 9

7:00 am Workshop Registration and Morning Coffee

8:00 Pre-Conference Workshops*
Advancing the Use of EHR/EMR for Clinical Research and Drug Development: Breaking Down Barriers & Building Up Bridges
Cloud Computing in Hospital Data Management and Integration

**Separate Registration Required*

2:00 - 7:00 pm Main Conference Registration

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Cindy Crowninshield, RD, LDN, Conference Director, Cambridge Healthtech Institute

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» 4:15 PLENARY KEYNOTE
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Andrew L. Hopkins, DPhil, FRSC, FSB, Division of Biological Chemistry and Drug Design, College of Life Sciences, University of Dundee

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Leveraging Data and Technology for Protocol Feasibility and Patient Recruitment

10:50 Chairperson's Remarks
Jennifer Wulff, Director, Clinical Innovation, Pfizer World Wide Research & Development

11:00 Impact of the Electronic Health Record on Research
Doug Berman, Deputy Director, Academic Research Systems, University of California San Francisco
Medical centers nationwide have been adopting Electronic Health Record systems rapidly. These systems have the potential to make large and meaningful contributions to clinical trials and other research activities. This talk will review the experience, challenges and achievements of an academic medical center.

11:30 Using Real World Data to Facilitate Protocol Feasibility Assessment and Patient Recruitment
Sergio Eslava, M.D., Principal Biomedical Informatics Scientist, Biomedical Informatics, Real World Evidence, AstraZeneca
This presentation focuses on how real world data sources such as electronic health records, personal health records and patient centric communities can facilitate clinical protocol design and feasibility assessment as well as patient recruitment for clinical trials. The use of these data sources can result in cost reduction and increased efficiency in designing and executing clinical studies.

12:00 pm Real-World Data: Mining Electronic Health Records for Clinical Trial Recruitment and Personalized Medicine
Sponsored by CliniWorks
Abigail Bracha, Ph.D., Vice President, Clinical Research & Informatics, CliniWorks, Inc.
CliniWorks is working across the product lifecycle from clinical trial recruitment though post-approval outcomes analyses and pharmacovigilance. CliniWorks will speak about mining real-world patient data to determine patient eligibility for clinical trial inclusion. The use of disease biomarkers and genetic profiling, which are an increasingly critical component of drug development and personalized medicine, will also be addressed.

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

Optimizing Trial Management with Technology

1:40 Chairperson's Remarks
Suresh Kannan, Vice President, Product Development, Clinical Trial Optimization Solutions, IMS Health

1:45 Considerations for Planning and Assigning Trial Optimization Resources
Daniel Chain, Informatics Analyst, Global Trial Optimization, Merck
Successfully developing a drug and bringing it to market is expensive. Pharmaceutical development resources must therefore be optimally

allocated to avoid adding to the expense. This session will cover techniques that can be used to predict trial optimization resource demands.

2:15 Rethinking Clinical Research Challenges in a Data-Rich World
Jennifer Wulff, Director, Clinical Innovation, Pfizer World Wide Research & Development
All too familiar are the many challenges faced across the drug development process, including target validation, patient recruitment, site selection and data reporting. How can, and do we think differently about tackling those challenges using the growing availability of real world data? How can we innovate parts of the clinical research process using a combination of new technology and electronic data?

2:45 Electronic Source Documentation in Clinical Trials - Integration with EDC/CTMS: A Case Study *Sponsored by* PRIMESOFT
Thomas E. Serena, M.D., Founder, Serena Group
Conducting studies using an iPad/tablet based eSource Document System makes it efficient to capture reliable, quality, traceable and validated source data directly on eSource documents, improves the productivity of investigative sites and making the Source Documents/CRF's availability for monitoring immediately; reducing monitoring time and costs and expediting the entire process of Clinical Trials. Through a case study example, attendees will gain good understanding of eSource Documents.

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

3:45 A Common Tool for Investigator Site eSource-Readiness Assessment across Companies and across US & EU
Catherine Celingant, Senior Director, Medical Business Operations, Medical Strategy & Operations, Millennium: The Takeda Oncology Company
The eClinical Forum developed an assessment tool that sponsors, EHR system vendors, CROs, and clinical investigators can successfully use to evaluate EHR systems that will be the source of pertinent clinical research data. The assessment tool is currently being piloted at many investigator sites in both the US and Europe using several different research sponsors and EHR vendors.

4:15 Co-Presentation: POC Today/Practical Application Tomorrow: An Inside Look at How Several Companies Are Exploring Identity Management in the eClinical Trial Space
Mollie Shields-Uehling, MA, President and CEO, SAFE-BioPharma Association
Kerri Weingard, COO, Verified Clinical Trials
The presentation discusses the way several global companies are utilizing universal identity management to maximize use of mobile devices in clinical trials. The information will be based on the results of numerous proofs of concept currently underway, including use of tablets to collect patient data, signing ePrescriptions, managing access to clinical portals.

4:45 Co-Presentation: Best Practices for Risk-Based Approaches to the Monitoring of Clinical Trials *Sponsored by* perceptive INFORMATICS
Paula McHale, Senior Director, Product Management, DataLabs EDC
Deborah Lucas, Principal ePRO Analyst, Biogen Idec
With the adoption of risk-based monitoring those engaged in clinical trial conduct must refocus energies on aspects of the clinical trial that matter most, such as protocol compliance, subject safety, data timeliness, and data integrity. Through the use of more up-to-date methodologies and technologies, companies can effectively address these concerns while saving both time and money. In light of the current buzz around risk based approaches to monitoring of clinical trials, the eClinical Forum created a task force to prepare a Best Practices Guideline to Monitoring of Clinical Trials. A more holistic approach to risk identification and mitigation is discussed and promoted.

5:15 Best of Show Awards Reception in the Exhibit Hall

6:15 Exhibit Hall Closes

THURSDAY, APRIL 11

7:00 am Breakfast Presentation *(Sponsorship Opportunity Available)* **or Morning Coffee**

Data Collection and Integration

8:45 Chairperson's Opening Remarks
Laurie Milligan, Director, IT Strategy, R&D IT, Medicines Development Capabilities, GlaxoSmithKline

8:50 Clinical Trial Data Quality in the Cloud
Julia Zhang, Ph.D., Director, Strategy, Standard and Architect, Genzyme
This presentation discusses how to improve data quality by implementing standards, efficiently using metadata repository, and applying cloud technology to enhance process efficiency and effectiveness. The discussion discusses how to develop data governance, design data with the enterprise vision in mind, set strategy for data collection, processing and reporting through implemented standards and cloud technology.

9:20 Empowering the Cardiovascular Translational Exploration through a Unified Pre-Clinical and Clinical Data Environment
Xia Wang, Ph.D., Principal Biomedical Informatics Scientist, Global Medicines Development, R&D, AstraZeneca LPs
The presentation provides a case study to develop a clinical/pre-clinical cardiovascular (CV) data exploration environment that enables end users to search, query, visualize, analyze and export CV data rapidly, across *in vitro* assays, *in vivo* animal studies, and clinical trials. This will lay the foundations to integrate and analyze other domains of clinical/pre-clinical data.

9:50 Using Collaborative Analytics to Transform Global Site Allocation
Fabio Thiers, M.D., Ph.D., CEO, ViS Research Institute
Global site allocation is cost-inefficient and needs to be revamped. The problem is that analytics about sites and locations where they operate is disaggregated, outdated, highly complex or simply non-existent. Issues with the current evaluation systems lead to heavy reliance on one-off requests for information (feasibility questionnaires), which rarely lead to long standing relationships between sites/investigators and sponsors. The solution is an open access analytics platform where multidimensional disease-specific feasibility analytics can be securely shared, kept up-to-date, and be easily understood. The benefits are faster/better site selection at substantially lower costs.

10:20 Coffee Break in the Exhibit Hall and Poster Competition Winners Announced

10:45 Plenary Keynote Panel Chairperson's Remarks
Kevin Davies, Ph.D., Editor-in-Chief, Bio-IT World

10:50 Plenary Keynote Panel Introduction
Yury Rozenman, Head of BT for Life Sciences, BT Global Services
Niven R. Narain, President & CTO, Berg Pharma

» PLENARY KEYNOTE PANEL

11:05 The Life Sciences CIO Panel
Panelists:
Remy Evard, CIO, Novartis Institutes for BioMedical Research
Martin Leach, Ph.D., Vice President, R&D IT, Biogen Idec
Andrea T. Norris, Director, Center for Information Technology (CIT) and Chief Information Officer, NIH
Gunaretnam (Guna) Rajagopal, Ph.D., VP & CIO - R&D IT, Research, Bioinformatics & External Innovation, Janssen Pharmaceuticals
Cris Ross, Chief Information Officer, Mayo Clinic
Matthew Trunnell, CIO, Broad Institute of MIT and Harvard

12:15 Luncheon in the Exhibit Hall with Poster Viewing

Collaborations in Clinical Trials

1:55 Chairperson's Remarks
Mollie Shields-Uehling, MA, President and CEO, SAFE-BioPharma Association

2:00 Collaboration within the Pharma Industry to Improve the Quality of Clinical Studies and Bring New Medicines to Patients Faster
Laurie Milligan, Director, IT Strategy, R&D IT, Medicines Development Capabilities, GlaxoSmithKline
The Pharma industry continues to simplify aspects of clinical development by focusing on people, process, standards, and technology. This is a fundamental transformation in the ways we work and the ways we use technology. To achieve this, we should consider our internal organizations as well as collaboration across the industry.

2:30 The Pooled Resource Open-Access ALS Clinical Trials (PRO-ACT) Platform as a Unique Industry, Academic, and Foundation Collaboration to Generate a Novel Research Resource
Alexander Sherman, Director, Systems, Neurological Clinical Research Institute, Massachusetts General Hospital
A Pooled Resource Open-access ALS Clinical Trials (PRO-ACT) platform allows merging of data from existing public and private sources of completed Phase II and III trials. Data mining of PRO-ACT is expected to lead to the identification of disease biomarkers, provide insight into the natural history of disease, as well as insights into the design and interpretation of clinical trials.

3:00 Advancing Translational Research through Web-Portal Access to Clinical Trials Data, Analyses and Bio-Repository Information
Adam Asare, Ph.D., Senior Director, Data Analysis & Data Management, Biomarker & Discovery Research, Immune Tolerance Network
The Immune Tolerance Network has developed ITN TrialShare, a web portal application providing research collaborators access to clinical, research assay and specimen data along with tools for data visualization and collaborations. Hear lessons learned from committing to an open source software framework and ongoing challenges with clinical trials and research assay data management.

3:30 The Image Collaborative Portal: A Distributed Solution Driving Substantial Cost Savings in Managing Imaging Clinical Trials
Jay Bergeron, Senior Manager, Translational and Bioinformatics, Pfizer, Inc.
Collecting medical images from multi-site clinical trials requires coordination across acquisition sites, safety monitors, and sponsors. The Image Collaborative Portal substantially contains costs by alleviating the need for a CRO image custodian. Learn how this distributed approach to image study management via cloud services, presents a new scalable, extensible and cost effective model for study conduct.

4:00 Conference Adjourns

Track 8
Data Visualization and Exploration Tools
From Discovery to the Clinic

Data visualization goes far beyond the generation of (interactive) images based on some large data sets. There is a growing body of knowledge about how to design, implement and evaluate visualization techniques and tools that offer real value to the user. Track 8 presents carefully chosen talks that showcase novel visualization approaches that address important challenges in genomic data, networks, microscopy, imaging and the support of discovery, clinical and translational research.

TUESDAY, APRIL 9

7:00 am Workshop Registration and Morning Coffee

8:00 Pre-Conference Workshops*
**Separate Registration Required*

2:00 - 7:00 pm Main Conference Registration

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

4:05 Keynote Introduction
Kevin Brode, Senior Director, Health & Life Sciences, Americas Hitachi Data Systems

» 4:15 PLENARY KEYNOTE
Do Network Pharmacologists Need Robot Chemists?
Andrew L. Hopkins, DPhil, FRSC, FSB, Division of Biological Chemistry and Drug Design, College of Life Sciences, University of Dundee

5:00 Welcome Reception in the Exhibit Hall with Poster Viewing
*Drop off a business card at the CHI Sales booth for a chance to win 1 of 2 iPads® or 1 of 2 Kindle Fires®!**
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WEDNESDAY, APRIL 10

7:00 am Registration and Morning Coffee

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

8:05 Keynote Introduction
Sanjay Joshi, CTO, Life Sciences, EMC Isilon

» 8:15 PLENARY KEYNOTE
Atul Butte, M.D., Ph.D., Division Chief and Associate Professor, Stanford University School of Medicine; Director, Center for Pediatric Bioinformatics, Lucile Packard Children's Hospital; Co-founder, Personalis and Numedii

8:55 Benjamin Franklin Award & Laureate Presentation

9:15 Best Practices Award Program

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

Visualization Tools in Development to Support Discovery and Translational Research

Chairperson's Remarks
Nils Gehlenborg, Ph.D., Research Associate, Center for Biomedical Informatics, Harvard Medical School

10:50 Understanding Biomedical Complexity through Visualization
Lawrence Hunter, Ph.D., Director, Center for Computational Pharmacology, Professor, Computer Science, University of Colorado
The profusion of high-throughput instruments and the explosion of new results in the scientific literature, particularly in molecular biomedicine, is both a blessing and a curse to the bench researcher. Even knowledgeable and experienced scientists can benefit from computational tools that help navigate this vast and rapidly evolving terrain; however, effective design and implementation of computational tools that genuinely facilitate the generation of novel and significant scientific insights remains poorly understood. In this talk, I will discuss visual approaches to knowledge-based analysis of biomedical data, and present some new ideas about Degree of Interest functions that might be used to guide visual explorations.

11:10 Seeing the Forest through the Trees: Integrating *in silico*, *in vitro* and *in vivo* Data for Small Molecule Knowledge Discovery
Jeffrey Sutherland, Prinicipal Research Scientist and Group Leader, IT Informatics, Eli Lilly and Co.
In silico, *in vitro* and *in vivo* data are distributed across many internal databases and effectively querying and visualizing the data requires an integration framework coupled with an advanced visualization platform. This presentation will demonstrate data integration and visualization platforms used within discovery research at Lilly, including applications for target identification, compound design and lead optimization.

11:35 Data Visualization in Discovery and Clinical Research: Art, Science, and Intuition
Dimitris K. Agrafiotis, Vice President, Informatics & Enterprise Architecture, Covance

12:00 pm Whence the Data? The Importance of Feeding the Right Data to Your Visualizations
Sponsored by CAMBRIDGE SEMANTICS
Lee Feigenbaum, Vice President, Marketing & Technology, Cambridge Semantics
Visualizations are only as good as the data that drives them. And frequently, the right data comes from many & diverse sources. This talk presents the case for Unified Information Access, a paradigm that lets you easily combine structured and unstructured data from inside and outside your organization in support of ever-evolving data exploration & visualization. We'll look at examples from competitive intelligence, safety, & assay data management.

12:30 Visual Analytics in Healthcare
Sponsored by IBM
David Gotz, Ph.D., Research Staff Member, Healthcare Analytics Research Group, IBM T.J. Watson Research Center
As the adoption rates grow for electronic medical systems, clinical institutions are amassing ever-larger collections of patient-centered data. Visual analysis techniques, designed to mine and interactively visualize this data in the context of individual patients, are enabling new opportunities for personalized data-driven clinical insights. This talk will provide an overview of our emerging work in this area and include demonstrations of some prototype visualizations.

1:40 Chairperson's Remarks

Jeffrey Sutherland, Prinicipal Research Scientist and Group Leader, IT Informatics, Eli Lilly and Co.

1:45 Visualizing and Interpreting Pathway Analysis Results to Aid Drug Repurposing
Gary Bader, Ph.D., Associate Professor, The Donnelly Centre, University of Toronto
Enrichment maps organize the results of gene set enrichment analysis as a network to provide a quick visual summary of gene function enrichment. Users can explore the map to zoom in to functions of interest for deeper exploration. I will also briefly present the application of pathway analysis for drug repurposing in cancer.

2:15 Visual Analytics Case Study: Making Data Translatable
Luiz Miguel Camargo, Associate Principle Scientist, Translational & Health Informatics, Informatics IT, Merck & Co.
Deriving and prioritizing actionable hypotheses to guide drug discovery requires transformation of multidimensional data and 'known' biology into frameworks for intuitive exploration and interpretation. Combining aggregated phenotypic/pathway information with visual analytics generates comprehensive, interactive biological landscapes toward this end.

2:45 The Shape of Data Can Impact Cancer Outcomes *Sponsored by* AYASDI
Pek Lum, Ph.D., Vice President, Solutions, Ayasdi
Using the entire Cancer Genome Atlas (TCGA) dataset, Dr. Lum will present how a new approach called Topological Data Analysis (TDA) reveals novel DNA variations of tumors, discovers new cancer sub-populations and provides evidence on how cancer diseases are similar across different genetic populations automatically without asking any questions.

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

3:45 Organizing and Mining Data for Biologics Research
Hugo O. Villar, Ph.D., President, Altoris, Inc.
Therapeutics research is undergoing a transformation with the more extensive use of biologics. The amount of information being generated by researchers in the field has exposed some limitations in the informatics tools available. Particularly lacking are tools to analyze the experimental results generated for hundreds of biopolymers, including peptides and other biotherapeutics. SARvision|Biologics is a desktop application to fill in the gap that exists in research informatics to deal with data on biologics. The software can be used to mine and visualize trends in data generated for biologics. At the same time, it illustrates how some concepts from small molecule SAR can be effectively be adapted to guide biologics research.

4:05 Data Visualization Case Study: Integration of a Spotfire Web Player Mashup into a Discovery Search Application
Jason Gratt, Ph.D., Lead Software Engineer, Research and Development Systems, Information Technology Group, Millennium Pharmaceuticals
An overview of Millennium's Discovery Data Viewer (a custom search tool used by ~100 Medicinal Chemists), and how the Spotfire Web Player was integrated into it to provide users with advanced, interactive visualization features for hypothesis generation and confirmation.

4:25 Caleydo enRoute: Visualizing Large Quantities of Experimental Data in the Context of Pathways
Alexander Lex, Ph.D., Research Scientist, Visual Computing Group, Harvard School of Engineering and Applied Sciences
Caleydo enRoute takes a new approach to visualizing experimental data in the context of pathways. By dynamically extracting paths out of well known pathway maps enRoute can show hundreds of experimental values for every node. Consequently enRoute is the ideal tool to analyze the effects of experimental data for both individual samples or groups of samples on pathways, enabling analysts to work with large datasets as, for example, generated by The Cancer Genome Atlas (TCGA).

4:45 Sponsored Presentations *(Opportunities Available)*

5:15 Best of Show Awards Reception in the Exhibit Hall

6:15 Exhibit Hall Closes

THURSDAY, APRIL 11

7:00 am Breakfast Presentation *(Sponsorship Opportunity Available)* **or Morning Coffee**

8:00 Technology Demo
Presenters from the Data Visualization track will be demoing their visualization and exploration tools in an informal setting just prior to the session continuing for the day. If you want to see the tools in action or learn more about a specific tool, come along and enjoy morning coffee with us!

Visualization of Genomic Data

8:45 Chairperson's Opening Remarks
Jill P. Mesirov, Ph.D., Associate Director and Chief Informatics Officer, Director, Computational Biology and Bioinformatics, Broad Institute of MIT and Harvard

8:50 Visualizing and Analyzing Chromatin Accessibility from Clinical Samples of Renal Cell Carcinoma
Michael J. Buck, Ph.D., Assistant Professor, Biochemistry, SUNY Buffalo; NY State Center of Excellence in Bioinformatics and Life Sciences , Cancer Genetics Roswell Park Cancer Institute; Co-Director, Next-Gen Sequencing and Expression Analysis Core; Director WNYSTEM Stem Cell Sequencing/Epigenomics Facility
Using Formaldehyde-Assisted Isolation of Regulatory Elements (FAIRE) combined with Next-generation sequencing (FAIRE-seq) we identify changes in chromatin accessibility in human solid tumors. To examine this and other chromatin datasets we have developed a suite of chromatin architecture tools (ArchAligh, ArchTex, and ArchBlast) and will present exciting findings from these tool when applied to renal cell carcinoma.

9:20 The Integrative Genomics Viewer (IGV)
James T. Robinson, Ph.D., Principle Software Engineer, Cancer Informatics, The Broad Institute of MIT and Harvard
We describe the Integrative Genomics Viewer (IGV), a flexible, high-performance viewer that enables intuitive real-time exploration of genomic datasets. This ability to dynamically and flexibly integrate multiple different datasets and view them at any scale allows investigators to elucidate complex biological relationships that are otherwise not readily apparent.

9:50 Disease Maps & Evaluating New Opportunities: How The Children's Tumor Foundation and Thomson Reuters Are Collaborating for a Better Future *Sponsored by* THOMSON REUTERS
Annette Bakker, Ph.D., CSO, Children's Tumor Foundation
Elona Hart, Research Scientist, Biologist, Thomson Reuters
The Children's Tumor Foundation is the leading nonprofit funding source of Neurofibromatosis (NF) research in the world aimed at accelerating the transition from bench to bedside. Learn how their collaboration with Thomson Reuters is helping to develop new approaches to investing and show future research opportunities.

10:20 Coffee Break in the Exhibit Hall and Poster Competition Winners Announced

10:45 Plenary Keynote Panel Chairperson's Remarks
Kevin Davies, Ph.D., Editor-in-Chief, Bio-IT World

10:50 Plenary Keynote Panel Introduction
Yury Rozenman, Head of BT for Life Sciences, BT Global Services
Niven R. Narain, President & CTO, Berg Pharma

» PLENARY KEYNOTE PANEL

11:05 The Life Sciences CIO Panel
Panelists:
Remy Evard, CIO, Novartis Institutes for BioMedical Research
Martin Leach, Ph.D., Vice President, R&D IT, Biogen Idec
Andrea T. Norris, Director, Center for Information Technology (CIT) and Chief Information Officer, NIH
Gunaretnam (Guna) Rajagopal, Ph.D., VP & CIO - R&D IT, Research, Bioinformatics & External Innovation, Janssen Pharmaceuticals
Cris Ross, Chief Information Officer, Mayo Clinic
Matthew Trunnell, CIO, Broad Institute of MIT and Harvard

12:15 pm Luncheon in the Exhibit Hall with Poster Viewing

1:55 Chairperson's Remarks
Anne E. Carpenter, Ph.D., Director, Imaging Platform, Broad Institute of Harvard and MIT

2:00 New Insights from Dynamic Exploration of Genomics Data
Carl Meinhof, Ph.D., Manager, Research Informatics, Ceres, Inc.
Exploration of large genomic data sets requires the ability to navigate through the genome and dynamically zoom in and out of regions of interest without delay. The ability to visualize genomic data in real-time yields new insights and also brings to light new questions. The Persephone genome explorer application enables dynamic exploration of large, diverse genomic data sets.

2:20 Visual Exploration of Cancer Genomics Data for Identification and Characterization of Tumor Subtypes
Nils Gehlenborg, Ph.D., Research Associate, Center for Biomedical Informatics, Harvard Medical School
Caleydo StratomeX is a visual exploration system developed to support the identification and characterization of tumor subtypes in large patient populations. The system integrates multiple genomic data types with clinical data, enabling analysts to efficiently generate and confirm hypotheses about tumor subtypes and to evaluate their functional properties and clinical effects.

2:40 JBrowse: A Next-Generation Genome Browser
Robert Buels, JBrowse Lead Developer, University of California Berkeley
JBrowse is a next-generation web-based genome browser built from the ground up with JavaScript and HTML5. JBrowse offers advanced integration, fluid interactivity, and native support for very large datasets (such as deep-coverage resequencing alignments) that were once possible only for desktop-based genome viewers, while at the same time enabling the reproducible deployments and seamless data interchange that are possible in a cloud-based application.

Microscopy/Imaging

3:00 Visualizing High-Throughput Microscopy Imaging Data
Anne E. Carpenter, Ph.D., Director, Imaging Platform, Broad Institute of Harvard and MIT
High-throughput screening using fluorescence microscopy generates hundreds of thousands of images, showing the response of trillions of cells to chemical or genetic perturbations being tested. Assistive computational tools are needed to identify samples of interest and patterns in this data.

3:30 Integrating High Content Imaging of 3D Organotypic Tumor Cultures Into Basic and Preclinical Cancer Research
Andrew J. Ewald, Ph.D., Assistant Professor, Departments of Cell Biology and Oncology, Johns Hopkins Medical Institutions
We developed innovative primary tumor isolation, 3D culture, and high-content imaging strategies to analyze the relative contributions of tumor cell populations to invasion, dissemination, and therapeutic resistance in real-time. We will discuss medium throughput imaging and analysis techniques to integrate these results into preclinical research.

4:00 Conference Adjourns

Track 9
Drug Discovery Informatics
Thinking of Drugs Outside of the Box

Track 9 will showcase collaborations that address the challenge of information integration and standardization for drug discovery, recent researches on pharmacogenomics through the integration of clinical genomics information system with electronic medical records, in order to advance human health through genomics research. Novel informatics approaches in drug discovery, in areas such as tissue-specific mutations and epigenetics will also be examined.

TUESDAY, APRIL 9

7:00 am Workshop Registration and Morning Coffee

8:00 Pre-Conference Workshops*
Quality Practices for R&D Informatics Platform Selection and Solution Development
Advancing the Use of EHR/EMR for Clinical Research and Drug Development: Breaking Down Barriers & Building Up Bridges

**Separate Registration Required*

2:00 - 7:00 pm Main Conference Registration

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

4:05 Keynote Introduction
Kevin Brode, Senior Director, Health & Life Sciences, Americas Hitachi Data Systems

» 4:15 PLENARY KEYNOTE
Do Network Pharmacologists Need Robot Chemists?
Andrew L. Hopkins, DPhil, FRSC, FSB, Division of Biological Chemistry and Drug Design, College of Life Sciences, University of Dundee

5:00 Welcome Reception in the Exhibit Hall with Poster Viewing
*Drop off a business card at the CHI Sales booth for a chance to win 1 of 2 iPads® or 1 of 2 Kindle Fires®!**
**Apple ® and Amazon are not sponsors or participants in this program*

WEDNESDAY, APRIL 10

7:00 am Registration and Morning Coffee

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

8:05 Keynote Introduction
Sanjay Joshi, CTO, Life Sciences, EMC Isilon

» 8:15 PLENARY KEYNOTE
Atul Butte, M.D., Ph.D., Division Chief and Associate Professor, Stanford University School of Medicine; Director, Center for Pediatric Bioinformatics, Lucile Packard Children's Hospital; Co-founder, Personalis and Numedii

8:55 Benjamin Franklin Award & Laureate Presentation

9:15 Best Practices Award Program

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

Information Management And Collaborative Drug Discovery

10:50 Chairperson's Remarks
Yuriy Gankin, Ph.D., CSO, Knowledge Management, GGA Software Services LLC

11:00 Scientific Information as a Business Asset – Driving Productivity at Merck Research Labs Through Novel Approaches to Scientific Information Management
John Koch, Director, Scientific Information Architecture, MRL Informatics, Merck
Biopharma companies often struggle to manage scientific information – study results, analyses and historical record are lost due to poor information management practices and failure to produce information in a way that can be leveraged for future purposes. We will share examples of our strategy for improving information management through a set of capabilities focused on Information Search, Access and Architecture.

11:30 OMOP - A Public Private Partnership between Pharma and the FDA to Study Methods for Observational Studies
Christian Reich, Ph.D., Head of Discovery Informatics, AstraZeneca Pharmaceuticals, Inc.

12:00 pm Where Innovation Sparks – Enabling Scientific Collaboration in Fast-Growing, International R&D Companies *Sponsored by* idbs
Paul Denny-Gouldson, Ph.D., Vice President, Translational Medicine, IDBS
Scientists are social creatures and most innovation sparks when people come together. Too often a lack of transparency and 'right-time' access to real experimental data remains a major barrier to effective internal, external and multinational collaboration. Using scientifically aware, scalable data management systems enables virtual lab meetings to unlock every company's biggest asset: the innovation power of their own scientists.

12:15 Solving the Informatics Challenges in Collaborative Network Research *Sponsored by* accelrys®
Rob Brown, Ph.D., Senior Director, Life Sciences Research, Accelrys Inc
As discovery organizations move rapidly towards a collaborative network model for research, research IT organizations are presented with significant challenges in supporting their scientists and the external partners. We will present software solutions that can help solve the problems of tech transfer and collaborative data exchange and present case studies on the use of these solutions from both the pharma/biotech and CRO point of view.

12:30 Luncheon Presentation: Tools for Toolmakers, 10 Years of Open Innovation at OpenEye *Sponsored by* OpenEye Scientific Software
Robert Tolbert, Ph.D., Senior Vice President, Development, OpenEye Scientific Software

1:40 Chairperson's Remarks
Yuriy Gankin, Ph.D., CSO, Knowledge Management, GGA Software Services LLC

1:45 Collaborative Discovery: The eTRIKS Approach
Ian Dix, Ph.D., Director Analytics, Information and Knowledge Engineering, R&D Information, AstraZeneca
Yike Guo, Professor, Computing, Imperial College London

Novel Approaches To Drug Discovery

2:15 Deuterium Modification as a New Branch of Medicinal Chemistry to Develop Novel, Highly Differentiated Drugs
Julie Fields Liu, Ph.D., Director, Research Management, Concert Pharmaceuticals, Inc.

2:45 Making the Molecules that Matter: The Integrated Approach to Discovery *Sponsored by* SCHRÖDINGER.
John Conway, Vice President, Scientific Informatics & Services, Schrodinger
Matt Wessel, Senior Principal Scientist, Schrodinger
The key elements that drive success in drug discovery are improved science, knowledge acquisition, coherent goals leading to rapid decision making, and the ability to collaborate across sites and organizations. At Schrodinger, we are building a platform that — for the first time — truly enables these elements, and more. Here, we will outline our vision, describe a success story which exemplifies the vision, and detail how Schrodinger will deliver this platform.

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

3:45 Cataloging Gene Clusters of Bacterial Secondary Metabolism to Enable Drug Discovery
Daniel Udwary, Ph.D., Assistant Professor, Biomedical and Pharmaceutical Sciences, University of Rhode Island
Natural products produced by microbes have been a plentiful source of medicinal compounds for decades, though few have made it to the clinic in recent years. To attempt to identify new sources, we have completed construction of a database that catalogs natural product biosynthetic pathways from all available completed bacterial genome sequences. We are now using this data to identify potentially useful pathways and chemistry, and to explore overlooked organisms with strong biosynthetic potential." to the end.

4:15 Knowledge Mining in Genome-Scale Protein-Interaction Networks to Understand Drug Resistance
Nagasuma Chandra, Ph.D., Associate Professor, Biochemistry, Indian Institute of Science Department of Biochemistry, Indian Institute of Science
Drug resistance is posing to be a major problem for anti-infective therapy. Using large-scale informatics, an integrated network model that considers known functional, structural and expression information in drug-exposed mycobacterial cells (that cause tuberculosis) has been used to identify potential molecular pathways which the bacterium could be using to trigger resistance to drugs.

4:45 Data and Knowledge Management in the Pharma Environment
Vishal Rosha, Senior Scientist, BioProcess Research & Development, Novartis Pharma AG
As the technology is growing day by day and a more scientific approach is required. "Sound Science," as required by the US FDA, suggests gaining more knowledge about the process, which requires more information and leads to more data needed, there is strong belief that the impact of data management concepts and the effort of translation data into information and knowledge are underestimated. The huge amount of data which is generated during the process has to be translated into information and knowledge. In this presentation we identify the gaps of current data/ knowledge management concepts. An assessment was performed to demonstrate from which source the related unit operation receives data and to which unit operation it feeds back. In addition, an evaluation was performed to identify the gaps of established concepts and methods which support the translation of data into information and knowledge.

5:15 Best of Show Awards Reception in the Exhibit Hall

6:15 Exhibit Hall Closes

THURSDAY, APRIL 11

7:00 am Breakfast Presentation *(Sponsorship Opportunity Available)* **or Morning Coffee**

Integrating Clinical Information into Drug Discovery

8:45 Chairperson's Opening Remarks
Mathukumalli Vidyasagar, Ph.D., Cecil & Ida Green Chair in Systems Biology Science; Head, Bioengineering Department, University of Texas at Dallas

8:50 The Challenges in Integrating Information During the Discovery of Biomarkers in Cancer Patients Treated with Chemotherapy: A Pharmacology and Oncology Perspective
Federico Innocenti, M.D., Ph.D., Associate Professor, University of North Carolina at Chapel Hill; Associate Director , Institute for Pharmacogenomics and Individualized Therapy
Genomic studies for discovering biomarkers of outcome of patients treated with chemotherapy are quite advanced. However, we face the interpretative difficulty in connecting the dots among clinical data, genomic information (both of the host and the tumor), and functional annotation of genomic regions. This presentation will provide an oncology and pharmacology perspective of the contemporary challenges of integrative analyses that could (and should) aid the discovery of clinically useful markers for enrichment of responsive populations during drug development, as well as for improving patient management at the bed side.

9:20 Integrating Molecular and Clinical Data to Expedite Translation in Computational Drug Repurposing
Joel Dudley, Ph.D., Director, Biomedical Informatics; Assistant Professor, Genetics and Genomic Sciences, Institute for Genomics and Multiscale Biology, Mount Sinai School of Medicine
Konrad J. Karczewski, Ph.D. Candidate, Biomedical Informatics, Stanford University
Although drug repurposing approaches that leverage approved therapies can potentially expedite the drug development process by leveraging existing drug safety data, establishing efficacy for alternative indications can remain just as challenging as in novel drug development. Because many patients are prescribed approved therapies for their primary indications, there is a wealth of clinical data captured in electronic medical record (EMR) systems that could potentially inform on the system-wide physiological and pathophysiological effects of the approved therapies in humans. In this talk I will discuss efforts to integrate public gene expression data with clinical data captured from EMR systems to expedite translation in computational drug repurposing.

9:50 Managing Information Challenges with Elsevier Life Science Solutions *Sponsored by* ELSEVIER
Shuhag Ghosh, Vice President, Global Marketing, Elsevier Life Science Solutions
From increasing discoverability to making sense of ever-growing data sets to leveraging new data sources, Life Sciences organizations face challenges in making more informed and effective decisions based on a changing landscape. Elsevier Life Science Solutions is a suite of interoperable domain-specific decision support tools built from our understanding of and commitment to Life Sciences. This suite is designed to enhance how organizations make decisions and to power information flows across discovery, pre-clinical, clinical and post-market domains, for end-to-end success. The potential to leverage customized taxonomies, newly mined content sources and internal data in the suite changes how organizations interact with information to conduct R&D.

10:20 Coffee Break in the Exhibit Hall and Poster Competition Winners Announced

10:45 Plenary Keynote Panel Chairperson's Remarks
Kevin Davies, Ph.D., Editor-in-Chief, Bio-IT World

10:50 Plenary Keynote Panel Introduction
Yury Rozenman, Head of BT for Life Sciences, BT Global Services
Niven R. Narain, President & CTO, Berg Pharma

» PLENARY KEYNOTE PANEL

11:05 The Life Sciences CIO Panel
Panelists:
Remy Evard, CIO, Novartis Institutes for BioMedical Research
Martin Leach, Ph.D., Vice President, R&D IT, Biogen Idec
Andrea T. Norris, Director, Center for Information Technology (CIT) and Chief Information Officer, NIH
Gunaretnam (Guna) Rajagopal, Ph.D., VP & CIO - R&D IT, Research, Bioinformatics & External Innovation, Janssen Pharmaceuticals
Cris Ross, Chief Information Officer, Mayo Clinic
Matthew Trunnell, CIO, Broad Institute of MIT and Harvard

12:15 Luncheon in the Exhibit Hall with Poster Viewing

Pharmacogenomics and Personalized Medicine

1:55 Chairperson's Remarks
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

2:00 The MicroRNA-Drug Resistance Connection: A New Era of Personalized Medicine Using Non-coding RNA Begins
Prasun J. Mishra, Ph.D., Earl Stadtman Investigator Candidate, Center for Cancer Research, National Cancer Institute, National Institutes of Health
Cumulative evidence now suggests that specific miRNAs and genetic variations interfering with miRNA function (miRNA polymorphisms) are involved in the prognosis and progression of a variety of diseases and can serve as biomarkers to predict drug response. Detection of prognostic-miRNAs and miRNA polymorphisms can potentially improve diagnosis, treatment and prognosis in patients and has profound implications in the fields of pharmacogenomics and personalized medicine.

2:30 Discovery of Candidate Biomarkers of Anti-Cancer Drug Sensitivity by High-Throughput Screening of 1,000 Cell Lines
Cyril H. Benes, Ph.D., Director, Center for Molecular Therapeutics, Massachusetts General Hospital Cancer Center
In order to translate into cancer care the genomic characterization of cancers, there is a need to understand how variations in genome influence therapeutic responses and which genome variants might constitute good targets. We use a collection of 1,000 genetically characterized tumor cell lines to define molecular determinant of drug sensitivity *in vitro*. Strikingly, this approach captures essentially all genotype-drug sensitivity associations leveraged in the clinic to date and identifies a large number of novel correlates as candidate biomarkers for the development and application of cancer therapeutics.

3:00 Beyond ENCODE: Placing Long Non-Coding RNA Genes into Regulatory Networks for Therapeutics
Leonard Lipovich, Ph.D., Assistant Professor, Center for Molecular Medicine and Genetics, Wayne State University
In 2012, the ENCODE (Encyclopedia of DNA Elements) Consortium revealed an abundance of long non-coding RNA (lncRNA) genes in the human genome. We analyzed the transcriptome of three human systems - two cancers (breast cancer and melanoma) and the in-vivo human epileptic brain - and validated lncRNA functions by reverse genetic tools. Our results demonstrate that certain primate-specific lncRNAs, antisense to protein-coding genes, directly and specifically regulate those genes. We present a computational model which places these non-conserved lncRNAs into therapeutically targetable disease networks.

3:30 Interactive Medical Decision Trees: Using Up-To-Date Genomics and Information Echnology to Bring Personalized Care to Regional Populations
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

4:00 Conference Adjourns

Track 10
Clinical Omics
Tools for Bridging Research Data and the Clinic

Track 10 explores the shift from discovery research into clinical implementation. The ability to integrate and interrogate multiple 'omic data sets is critical for the understanding of disease and will only be accomplished through stringent data management, analysis, interpretation, and quantification. Ultimately, placing verified analytical tools in the hands of biomedical experts, and translating insights found between diverse datasets, will ensure that patients receive the correct diagnosis and individualized treatment.

TUESDAY, APRIL 9

7:00 am Workshop Registration and Morning Coffee

8:00 Pre-Conference Workshops*
Software for Clinical Genomics

**Separate Registration Required*

2:00 - 7:00 pm Main Conference Registration

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

4:05 Keynote Introduction
Kevin Brode, Senior Director, Health & Life Sciences, Americas Hitachi Data Systems

» 4:15 PLENARY KEYNOTE
Do Network Pharmacologists Need Robot Chemists?
Andrew L. Hopkins, DPhil, FRSC, FSB, Division of Biological Chemistry and Drug Design, College of Life Sciences, University of Dundee

5:00 Welcome Reception in the Exhibit Hall with Poster Viewing
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WEDNESDAY, APRIL 10

7:00 am Registration and Morning Coffee

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

8:05 Keynote Introduction
Sanjay Joshi, CTO, Life Sciences, EMC Isilon

» 8:15 PLENARY KEYNOTE
Atul Butte, M.D., Ph.D., Division Chief and Associate Professor, Stanford University School of Medicine; Director, Center for Pediatric Bioinformatics, Lucile Packard Children's Hospital; Co-founder, Personalis and Numedii

8:55 Benjamin Franklin Award & Laureate Presentation

9:15 Best Practices Award Program

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

Positioning IT to Support Clinical Laboratories

10:50 Chairperson's Remarks
Malcolm Tutor, Bio Specimen Tracking (itBioPath) Project Manager, Data Specialist, Research Informatics, Huntsman Cancer Institute, University of Utah

» FEATURED PRESENTATION

11:00 Preparing Laboratories for the Tidal Wave - Prepositioning Information Technology Needed to Support Deeper Use of Genetics in the Clinical Laboratory
Sandy Aronson, Executive Director, IT, Partners HealthCare Center for Personalized Genetic Medicine (PCPGM)
Clinical genetic tests covering large numbers of genes are becoming increasingly common. These tests create new and growing challenges for laboratories who need to interpret rapidly increasing numbers of variants identified in each test. This talk will describe and provide an example of an infrastructure for managing the process of interpreting complex genetic tests and reporting results to deliver maximum clinical value.

11:30 Dealing with the Data Deluge: IT and Informatics Infrastructure Supporting WGS Based Molecular Diagnostics
Elizabeth Worthey, Ph.D., Assistant Professor, Pediatrics & Bioinformatics Program, Human & Molecular Genetics Center, Medical College of Wisconsin
At MCW/CHW whole genome sequencing is already being used for clinical diagnostic purposes as part of a Genomic Medicine clinic. Supporting this endeavor and planning for the wider expansion of these technologies across clinical departments has required significant investment in IT. This talk will highlight the current structure at our midsized regional medical center and discuss IT challenges faced during development of our WGS based MDx program.

Sponsored by ORACLE HEALTH SCIENCES

12:00 pm Integrating Cross-platform 'Omics' and Clinical Data to Accelerate Personalized Medicine
Jonathan Sheldon, Ph.D., Global Senior Director, Translational Medicine, Oracle Health Sciences
This presentation will focus on our work to provide a scalable, secure platform for personalized medicine that accelerates biomarker discovery, validation and delivery to the point of care. We will discuss our methodology to integrate cross platform 'omics' data with high quality clinical data in a manner that is agnostic to the scientific approach. This approach provides an integrated view across genotype and phenotype whilst ensuring scalability at hundreds of thousands of whole genome

Sponsored by BioFortis

12:30 Luncheon Presentation: Is Your Informatics Infrastructure Limiting Your Biomarker-Based Research?
Matt Clark, Ph.D., Director, Professional Services, BioFortis, Inc
From biobanking, through clinical studies to translational research, biomarker-based discovery is challenging traditional informatics.We will present softwaresolutions for bridging the information gap between research and the clinic to provide a unified holistic view of data, which can then be explored by researchers using deep collaboration tools to generate

scientific insights.

Software Spotlights

1:40 Chairperson's Remarks
Dana L. Abramovitz, Ph.D., Senior Director, Scientific & Corporate Strategy, Strand Life Sciences

1:45 *"Software Spotlight"* *(Sponsorship Opportunity Available)*
Obtaining clinical 'omic data is relatively easy; it's the making sense and interpreting the data that's hard. While there are many commercial software solutions and pipelines for managing raw genome sequence data, providing the medical interpretation and delivering a clinical diagnosis will be the critical step in making good on the promise of genomic medicine. This session will showcase how genomic data analysis companies are streamlining the genomic diagnostic process through:

- Transferring raw sequencing data
- Interpreting genetic variations
- Building new software and cloud-based analysis pipelines
- Investigating the 'omic basis of disease
- Integrating with other clinical data systems
- Creating new medical-grade databases
- Reporting relevant clinical information in a physician-friendly manner
- Creating a continuous learning feedback

1:45 NextBio Clinical - A Patient-Centered Platform for Biomarker Discovery, Patient Selection and Target Epidemiology *Sponsored by* NEXTBIO
Ilya Kupershmidt, Cofounder, Vice President, Products, NextBio

2:00 Rapid Identification of Disease Causative Mutations *Sponsored by* Cypher Genomics
Ali Torkamani, Ph.D., Co-Founder & CSO, Cypher Genomics

2:15 Comprehensive Web-Based Platform, Integrating Genomics in Primary Care to Prevent Chronic Disease *Sponsored by* genophen
Hossein Fakhrai-Rad, Ph.D., CEO, President, and Co-founder, Genophen
Complex chronic diseases are caused by the interactions of genetic, medical, environmental & behavioral factors, but there is no single source today looking at the problem comprehensively. Genophen has developed a healthcare software platform that assesses an individual's disease risks comprehensively and provides a personalized and actionable set of recommendations to keep individuals healthy, for longer.

2:30 Clinical Research: An Integrated Data Approach

Malcolm Tutor, Bio Specimen Tracking (itBioPath) Project Manager, Data Specialist, Research Informatics, Huntsman Cancer Institute, University of Utah
Finding a cure for cancer is a monumental undertaking and the researchers at Huntsman Cancer Institute at the University of Utah have embraced the concept that data collaboration is one of the key elements in solving this puzzle. By bringing together disparate data sources (bio-specimen data, genomic data, familial history data, clinical data and pathology data), the researchers at HCI are able to find new ways to cure, predict and prevent cancer.

3:00 *(Sponsorship Opportunity Available)*

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

Clinical Data Storage and Management

3:45 Sequencing in the Private Cloud *Sponsored by* EMC® ISILON
Sanjay Joshi, CTO, Life Sciences, EMC Isilon Storage Division
With the ENCODE project spotlighting the complexity of the human genome, the case for whole genome sequencing has been made. As the regulatory industry readies the implementation guidelines, the four tenets of Big Data are becoming obvious: Volume, Variability and Veracity. We will showcase the components of a Private Cloud infrastructure for the genomics pipeline.

4:15 A Comprehensive Map of Microsatellite Repeat Variation in Human Genomes
David Mittelman, Ph.D., Associate Professor, Virginia Bioinformatics Institute, Virginia Tech; Associate Professor, Department of Basic Science, Virginia Tech Carilion School of Medicine
The utility of accurately and globally measuring tandem repeats spans medicine, genetics and biotechnology; repeats influence clinical and subclinical phenotypes, and are signatures for genomic instability and cancer. We present an integrated germline and somatic variant caller for microsatellite repeats that can be applied to whole genome and exome datasets. Further we present a public database resource in which we have cataloged repeat variation across worldwide human populations.

4:45 DMuDB, A Database of Clinical Quality Genetic Variants
Andrew Devereau, Director, National Genetics Reference Laboratory Manchester, Genetic Medicine, Central Manchester University Hospitals NHS Foundation Trust
The Diagnostic Mutation Database project (DMuDB) was funded by the UK Government to provide confidential sharing of clinical-quality variant data between National Health Service diagnostic genetic laboratories. It has now grown to contain nearly 44,000 variants in 73 genes, and is available to diagnostic laboratories worldwide as a subscription service. I will describe the challenges of the project, the future of the service, and the role of data sharing for clinical use.

5:15 Best of Show Awards Reception in the Exhibit Hall

6:15 Exhibit Hall Closes

THURSDAY, APRIL 11

7:00 am Breakfast Presentation *(Sponsorship Opportunity Available)* **or Morning Coffee**

Delivering 'Omic Diagnosis to Patients and Physicians

8:45 Chairperson's Opening Remarks

» **FEATURED PRESENTATION**

8:50 Delivering Genomic Medicine to Patients
Heidi L. Rehm, Ph.D., FACMG, Director, Laboratory for Molecular Medicine, Partners HealthCare Center for Personalized Medicine and Assistant Professor of Pathology, Harvard Medical School
Laboratories and clinicians must become experts in all genes and diseases as genome analyses returns many unsuspected and unfamiliar results. This talk will address solutions for these challenges through software tools, data sharing efforts in variant interpretation and studying the return of genome results though the MedSeq study, a pilot clinical trial for returning whole genome sequencing results or ordinary physicians and their patients.

9:20 Improved Gene Test Reporting in the Modern 'Omics Era
David K. Crockett, Ph.D., Director, Research Informatics, ARUP Laboratories
Structured results annotation and detailed laboratory interpretation are critical elements to improve gene test reporting in this era of high throughput sequencing. Clinical offerings of gene panels, exome or genome testing will necessitate parallel strategic advancements in test reporting. This effort includes structured data capture, summarizing supporting evidence, building target audience templates and objective framework for evaluation of variants of uncertain significance.

9:50 Syapse and InVitae Use Case: How to Implement a Next Generation IT and Informatics Infrastructure for Omics Diagnostics and Clinical Reporting *Sponsored by* Syapse

Jonathan Hirsch, M.Sc., Neuroscience, Founder & President, Syapse
John Major, M.Sc., Bioinformatics, InVitae
Implementing a clinical omics test requires a sophisticated, robust IT and informatics infrastructure. Historically, laboratories have been faced with the choice of rigid off-the-shelf software that does not fully solve their needs or building a custom system, both requiring large time and monetary investments. We will describe the implementation of Syapse's software solution at InVitae, illustrating how Syapse's configurable data models and programmatic interfaces enable rapid, cost-effective adoption. Syapse will announce a breakthrough solution for storing and working with omics data and reporting results to the clinic.

10:05 Sponsored Presentation *(Opportunity Available)*

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12:15 pm Luncheon in the Exhibit Hall with Poster Viewing

Clinical Implementation

1:55 Chairperson's Remarks
Tim Lautenschlaeger, M.D., Assistant Professor, Radiation Oncology, The Ohio State University

2:00 Integrated Genome-Phenome Analysis
Michael Segal, M.D., Ph.D., Founder and Chief Scientist, SimulConsult
State-of-the-art diagnostic decision support includes analysis of a patient's pertinent positive and negative clinical findings, and compares this to detailed phenotypes for thousands of diseases. When "phenome analysis" is analyzed together with an annotated genome variant table, the data combines to give an integrated genome-phenome analysis. The power of this approach is further enhanced by the ability of such software to advise not only about likely diagnoses, but about which genetic variants are most pertinent.

2:30 Clinical Research in the Age of Integrated Personalized Omics Profiles (iPOP's)
Robin Haring, Ph.D., Epidemiologist, Institute of Clinical Chemistry and Laboratory Medicine, University Medicine Greifswald, Ferdinand-Sauerbruch-Strasse
Recent advances of diverse high-throughput technologies enabled the application of 'Omics' (genomics, metabolomics, transcriptomics) to epidemiological and clinical research. Integrating multi-omic molecular biomarker promises to not only improve the diagnosis, treatment, and monitoring of specific clinical endpoints, but also to unravel insights into the complexities of human pathophysiology at a population-level.

3:00 Methods for the Interpretation of Next-Generation Sequencing Data for Clinical Phenotypes
Benjamin M. Neale, Ph.D, Medical and Population Genetics, Broad Institute of MIT and Harvard

3:30 Clinical 'Omics in Radiation Oncology
Tim Lautenschlaeger, M.D., Assistant Professor, Radiation Oncology, The Ohio State University
We will present examples of how the integration of omics research with traditional radiation therapy details could improve the ability to predict treatment side effects. Further we will discuss some of the technical difficulties that remain to be overcome to optimize and automate maintenance and update of a clinical radiation oncology omics data resource.

4:00 Conference Adjourns

Track 11

Collaborations and Open Access Innovations

Collaborative and Open Access Models for Advancing Research, Discovery and Personalized Medicine

Track 11 explores open source solutions in the life sciences software development vs. licensing, collaborative research models, data security and regulations, patents and IP on key technologies and research tools, data integration that provide exchange support for a wide variety of basic, clinical and translational research efforts.

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9:15 Best Practices Award Program

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

10:50 Chairperson's Remarks

11:00 The Pistoia Alliance: Pre-competitive Collaboration, Translational Research, and the Appification of Science
Ramesh Durvasula, Ph.D., Director, Research Informatics, Bristol-Myers Squibb; Board Member, Pistoia Alliance

For several years, the Pistoia Alliance has pushed the envelope in pre-competitive collaborations in research informatics. In this talk, we will share our strategy of two key priorities: enabling Translational Research collaborations, and the highly potential energy of "apps" in our industry. Both of these subjects require strong cross-industry collaboration, and we will discuss how Pistoia is lowering the barriers to innovation in the life sciences.

Data Management

11:30 Creating an Intelligent and Automated Analytical Laboratory
Dana Vanderwall, Associate Director, Research Informatics and Automation, Bristol Myers Squibb
Imagine an intelligent analytical laboratory where one-click reports can be generated from any analytical instrument platform. An automated laboratory where data, methods, hardware components are seamlessly shared between disparate platforms. This presentation will introduce the current effort of the Allotrope Foundation, a consortium of pharmaceutical companies, in developing an open-source Framework for managing analytical data generated by different analytical platforms.

12:00 pm GGA Software Services' Indigo ELN: The Open-Source Version of Pfizer's Chemistry ELN
Steven Trudel, Business Partner, Chemistry and Pharmacology, Pfizer, Inc.
Yuriy Gankin, Ph.D., Chief Scientific Officer, GGA Software Services LLC
GGA Software Services has partnered with Pfizer to develop and offer Indigo ELN, an open-source version of Pfizer's Chemistry Electronic Lab Notebook. Indigo ELN can be deployed internally at pharmaceutical companies or externally at partners and vendors. It offers pharmaceutical companies a cost-effective way for their partner ecosystem to collect and share data in a standardized format. This talk will describe the history and benefits of Indigo ELN; its uses for preparing, planning, and analyzing experiments; and its capability to integrate with commercial products and other open-source applications.

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

Data Sharing

1:40 Chairperson's Remarks
Scott Wilkins, Informatics Director, R&D Information, AstraZeneca

1:45 The Lilly Open Innovation Drug Discovery Program (OIDD)
Daniel Robertson, Ph.D., Senior Director, LRL IT Research, Eli Lilly & Co.
Through OIDD, Lilly has established a network of top global research talent at academic and biotech institutions to provide them access to proprietary, *in vitro* phenotypic and target-based assays (PD2 and TargetD2). This partnership is supported by the program's website portal and application, which lowers the barrier for collaborations between investigators working inside and outside the Lilly walls.

2:15 Can Data Fly? Multiple Stakeholders Advance Data Liquidity for Cancer Research and Care

Marcia Kean, Chairman, Strategic Initiatives, Feinstein Kean Healthcare
Kris Joshi, Vice President, Global Health Sciences, Oracle
Following the 2012 Institute of Medicine workshop on Cancer Informatics, concerned stakeholders from every segment of the biomedical ecosystem got together to address the huge technical and cultural obstacles. The Data Liquidity Coalition is now up and running, designing practical projects and advocating for policy change to drive standards-based capabilities for seamless data exchange.

2:45 Developing a Global Innovation Capability to Accelerate R&D Productivity
Scott Wilkins, Informatics Director, R&D Information, AstraZeneca
Producing new medicines that are safe and efficacious creates numerous challenges along the way during the years they take to research and develop. At AstraZeneca, we have approximately 10,000 R&D colleagues with scientific and medical expertise around the world. This is a great asset but our colleagues are spread across multiple locations, tend to be focused on specific tasks, and interact with a limited number of people. Consequently, there's a significant opportunity to better enable our experts to solve important scientific challenges regardless of location, or therapeutic area. To enable this, we've launched global cultural and technical initiatives to increase collaborative behaviors and deliver a new innovation platform to connect scientists around the world to solve our most challenging scientific problems. Today, we've connected over 7,000 scientists to solve multiple R&D Challenges thus increasing our productivity as an organization to bring the best medicines to patients as soon as possible. Our next steps are to build on the success within our R&D organisation to bridge across other corporate functions, and create an integrated innovation ecosystem to connect external partners as well.

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

3:45 The Multiple Myeloma Research Portal: Integration of Analytic Tools and Data Mining of Clinical and Molecular Data to Fuel Research and Drug Discovery
Carolyn Hoban, Sc.D., MMRF, Director, Translational Research, Multiple Myeloma Research Foundation
We will present the design of the research and community portal that opens new models for collaborative research, data sharing and hypothesis generation. The longitudinal study, CoMMpass, tracking genome wide changes associated with the natural history of myeloma from diagnosis through treatment serves as the data foundation for creating a world class knowledge base in the 'omics of myeloma.

4:15 Open Source, Open Medicine, Open Mind
Andreas Kogelnik, MD, Ph.D., Founder, Open Medicine Institute
The Open Medicine Institute was founded on the principle of open source code, to promote healthcare innovation via collaboration and focus on tackling diseases such as Autism, Chronic Fatigue, Multiple Sclerosis. Details of the OpenMedNet system and examples of collaborative interaction leading to improved medical outcomes will be discussed.

4:45 Productivity and Quality Benefits from a Platform Enabled Authoring Environment *Sponsored by* accelrys®
Dennis Curran, Director, Product Management, Accelrys
Research is no longer an isolated researcher running a series of related experiments following a single key hypothesis. Many of today's researchers have a wide array of real time dependencies on both internal and external associates in order to complete an experimental program. The documentation and authoring tools must advance to enable the planning, data capture, and analysis to be performed without constant switching between applications, emails, file servers, and paper printouts. The Accelrys Electronic Lab Notebook offers an advanced platform for aggregating data from multiple sources when creating the experimental records necessary for IP and Regulatory obligations. The Accelrys Enterprise Platform helps eliminate manual data transformations and cut and paste operations by integrating into your laboratory tools and providing quality and timely data operations.

5:15 Best of Show Awards Reception in the Exhibit Hall

6:15 Exhibit Hall Closes

THURSDAY, APRIL 11

7:00 am Breakfast Presentation *(Sponsorship Opportunity Available)* **or Morning Coffee**

Data Sharing

8:45 Chairperson's Opening Remarks
Xue-wen Chen, Ph.D., Department Chair & Professor, Computer Science, Wayne State University

8:50 tranSMART: A Year of Innovation and Growth of an Open Source Community
Dan Housman, Community Manager and Member, Project Management/ Oversight Team, tranSMART Project; Chief Technology Officer, Recombinant Data Corp.
Eight of the top twelve biopharmaceutical companies have adopted tranSMART, the knowledge management platform originally developed to share drug research and development data within Johnson & Johnson. Since its release into open source in April 2012, a community of industry and academic leaders has formed, all of whom seek to innovate and collaborate toward a shared vision.

9:20 Reproducible Research: Using Open Source Tools and Public Data to Build Machine Learning Models in Support of Antimalarial Drug Discovery
Paul Kowalczyk, Ph.D., Senior Computational Chemist, Integrated Parasitology, SCYNEXIS
We present our efforts at developing machine learning models in support of antimalarial drug discovery. The data is in the public domain, and the tools are open-source. The resulting models are meant to be freely shared among collaborators. The models are made available with all elements required to reproduce, expand and update. The models represent an instantiation of reproducible research.

9:50 Open, Collaborative, and Transformative: Exploring and Connecting Bioactive Chemistry Across Biomedical Documents and Databases with Public Tools
Christopher Southan, Ph.D., Principal Consultant, TW2Informatics
Although there are ~ 50 million chemical structure in public databases, many millions of bioactive compounds are still entoombed in documents. In addition linking chemistry between patents, papers, abstracts and databases has been patchy. However, new tools such as chemicalize.org, OPSIN, OSCA, Venny, CheS-Mapper and InChIKey indexing by Google, have transformed the extraction, analysis and connectivity of structures from text. Extractions can also be triaged against PubChem that now contains 14.5 million patent-extracted compounds from SureChemOpen, SCRIPDB, Thomson and IBM as well as 1 million from journals via ChEMBL and PubMed. These advances present new collaborative options such as sharing extracted neglected disease patents with SAR annotations on Figshare.

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Matthew Trunnell, CIO, Broad Institute of MIT and Harvard

12:15 Luncheon in the Exhibit Hall with Poster Viewing

Collaborations in Clinical Trials

1:55 Chairperson's Remarks
Mollie Shields-Uehling, MA, President and CEO, SAFE-BioPharma Association

2:00 Collaboration within the Pharma Industry to Improve the Quality of Clinical Studies and Bring New Medicines to Patients Faster
Laurie Milligan, Director, IT Strategy, R&D IT, Medicines Development Capabilities, GlaxoSmithKline
The Pharma industry continues to simplify aspects of clinical development by focusing on people, process, standards, and technology. This is a fundamental transformation in the ways we work and the ways we use technology. To achieve this, we should consider our internal organizations as well as collaboration across the industry.

2:30 The Pooled Resource Open-Access ALS Clinical Trials (PRO-ACT) Platform as a Unique Industry, Academic, and Foundation Collaboration to Generate a Novel Research Resource
Alexander Sherman, Director, Systems, Neurological Clinical Research Institute, Massachusetts General Hospital
A Pooled Resource Open-access ALS Clinical Trials (PRO-ACT) platform allows merging of data from existing public and private sources of completed Phase II and III trials. Data mining of PRO-ACT is expected to lead to the identification of disease biomarkers, provide insight into the natural history of disease, as well as insights into the design and interpretation of clinical trials.

3:00 Advancing Translational Research through Web-Portal Access to Clinical Trials Data, Analyses and Bio-Repository Information
Adam Asare, Ph.D., Senior Director, Data Analysis & Data Management, Biomarker & Discovery Research, Immune Tolerance Network (ITN)
The Immune Tolerance Network has developed ITN TrialShare, a web portal application providing research collaborators access to clinical, research assay and specimen data along with tools for data visualization and collaborations. Hear lessons learned from committing to an open source software framework, ongoing challenges with clinical trials and research assay data management, latest projects, and issues with HIPAA compliance.

3:30 The Image Collaborative Portal: A Distributed Solution Driving Substantial Cost Savings in Managing Imaging Clinical Trials
Jay Bergeron, Senior Manager, Translational and Bioinformatics, Pfizer, Inc.
Collecting medical images from multi-site clinical trials requires substantial coordination across acquisition sites, safety monitors, and sponsors. The Image Collaborative Portal (ICP) is used to substantially contain costs by alleviating the need for a CRO image custodian. Learn how this distributed approach to image study management via cloud services, presents a new scalable, extensible and cost effective model for study conduct.

4:00 Conference Adjourns

Track 12
Cancer Informatics
Applying Computational Biology to Cancer Research & Care

Track 12 explores the trends and challenges in cancer research/care. Topics will cover data access, analysis, integration, management, and application for biological interpretation to aid in research at the benchside or care at the bedside.

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**Apple ® and Amazon are not sponsors or participants in this program*

WEDNESDAY, APRIL 10

7:00 am Registration and Morning Coffee

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

8:05 Keynote Introduction
Sanjay Joshi, CTO, Life Sciences, EMC Isilon

» 8:15 PLENARY KEYNOTE
Atul Butte, M.D., Ph.D., Division Chief and Associate Professor, Stanford University School of Medicine; Director, Center for Pediatric Bioinformatics, Lucile Packard Children's Hospital; Co-founder, Personalis and Numedii

8:55 Benjamin Franklin Award & Laureate Presentation

9:15 Best Practices Award Program

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

10:50 Chairperson's Remarks
Michael Liebman, Ph.D., Managing Director, Strategic Medicine, Inc.

» FEATURED PRESENTATION

11:00 Tools for Revolutionizing Translational Cancer Medicine
Sponsored by PerkinElmer For the Better
Kevin Hrusovsky, President, Life Sciences & Technology, PerkinElmer, Inc.
While breakthroughs abound in cancer research, there is a profound disconnect in translating these discoveries to clinical medicine. This talk will discuss how combining the "*in vitro*-to-*in vivo*-to human" continuum of research tools with a powerful *in silico* infrastructure has successfully bridged the chasm from lab to clinic, particularly in the field of cancer medicine and personalized health.

Bioinformatics across Multiple Research Initiatives

11:30 Biological Research through Omic-Data Integration Using the "Programmable Web"
Matt Roth, Ph.D., Assistant Professor, Human Genetics, Baylor College of Medicine
This talk presents results from a human breast cancer study that utilized "programmable web" technology via Genboree to drive "virtual data integration" by bringing together only relevant "omic" data from multiple physical locations just in time for analysis. The results presented will illustrate how virtual data integration across multiple research initiatives (large and small) can be applied to any disease.

12:00 pm CECARDIS, An International Consortium to Evaluate Comparative Effectiveness in Cardiovascular Disease Risk Assessment: Algorithms, Biomarkers and Diagnostics
Michael Liebman, Ph.D., Managing Director, Strategic Medicine, Inc.
Sabrina Molinaro, Ph.D., Institute for Clinical Physiology, National Research Council, Italy
CECARDIS is an international consortium of hospitals, ministries of health, and government agencies that compare clinical approaches, procedures/devices and guidelines in large populations exhibiting symptoms of coronary artery disease and the impact of biomarkers in diagnosis/treatment. CECARDIS is developing a platform to support ongoing evaluation of new patient records and to compare effectiveness of existing technologies for prevention, diagnosis and treatment of CVD.

12:30 Luncheon Presentation: Is Your Informatics Infrastructure Limiting Your Biomarker-Based Research?
Sponsored by BioFortis
Matt Clark, Ph.D., Director, Professional Services, BioFortis, Inc
From biobanking, to clinical studies and translational research, biomarker-based discovery is being limited by traditional informatics. The BioFortis Next Generation Biobanking software platform empowers investigative biomarker research by harmonizing data from the distributed research ecosystem of vendors, partners and collaborators, while offering deep collaboration tools to better generate scientific insights. Case studies will be presented.

High Content Analysis: Cancer Cell Lines

1:40 Chairperson's Remarks

1:45 Systems Pharmacology Using CellMiner and the NCI-60 Cancerous Cell Lines
William Reinhold, Manager, Genomics and Bioinformatics Group, Laboratory of Molecular Pharmacology (LMP), National Cancer Institute (NCI)
CellMiner is a web-based application that allows rapid access to and comparison between 20,503 compound activities and the expression levels

of 26,065 genes and 360 microRNAs. Included are 102 FDA-approved drugs as well as 53 in clinical trials. The tool is designed for the non-informatisist, and allows the user wide latitude in defining the question of interest.

2:15 Oncology Drug Combinations at Novartis
Joseph Lehár, Ph.D., Director of Bioinformatics OTR, Oncology Translational Medicine, Novartis Institutes for Biomedical Research
In collaboration with academic and industrial partners, we have generated mutation status, gene copy number, and gene expression data for a library of 1,000 cancer cell lines, representing most cancer lineages and common genetic backgrounds. We expect this large-scale campaign to enable efficient patient selection for clinical trials on existing cancer drugs, reveal many therapeutically promising drug synergies or anti-resistance combinations, and provide unprecedented detail on functional interactions between cancer signaling pathways.

2:45 Selected Oral Poster Presentation: Genotype-Based Analysis for Cancer Therapy Using Large-Scale Data Modeling
Nayoung Kim, Ph.D. Candidate, Biological Sciences, Sookmyung Women's University
An integrative approach of large-scale omics and drug response data on various cell lines enables us to identify the cellular signaling and drug sensitivity in cancer. Signatures in different levels of biological process such as gene expression, protein expression and protein activation have applications in finding novel diagnostic or prognostic biomarkers. They are also key components in accelerating mechanism-based drug discovery or genotype-specific repositioning. Here we present a system-level analysis of cell line data for predicting the sensitivity and mechanisms of targeted drug response based on major genotypes of cancers. Association study with the genotypic classification was performed on drug data and omics data such as transcriptome, proteome and phosphateome on human cancer cell lines. This approach reproduced the known patterns of mechanism-based drug response in cancers. Also, gene and protein signatures significantly associated with genotype were identified and integrated into a drug-oriented network. Furthermore, we process the optimization of public gene sets to draw an advanced pathway-based interpretation using omics data and develop RNAi screening systems for analysis of cancer-regulation markers and anticancer effects perturbed by mutation. This study provides an integrated approach for omics, drug response data and cancer mutation types in cancers.

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

Pharmacodynamic Models for Oncology

3:45 Systems Biology in Cancer Immunotherapy: Applications in the Understanding of Mechanism of Action and Therapeutic Response
Debraj GuhaThakurta, Ph.D., Associate Director, Systems Biology, Dendreon Corporation
We are using high-content platforms (DNA and protein microarrays, RNA-seq) in various stages of the development of cellular immunotherapies for cancer. We will provide examples of genomic applications that can aid in the mechanistic understanding and the discovery of molecular markers associated with the efficacy of a cancer immunotherapy.

4:15 Talk Title to be Announced
Anna Georgieva Kondic, Ph.D., Senior Principal Scientist, Modeling and Simulation, Merck Research Labs

4:45 Two-Edged Swords in Epigenetic Modifications: The Vertebrate DNA Methyltransferases
C.-K. James Shen, Ph.D., Distinguished Research Fellow, Institute of Molecular Biology, Academia Sinica
Methylation at the 5-position of cytosine (C) to generate 5-methylcytosine (5-mC) on the vertebrate genomes is an essential epigenetic modification that regulates different biological processes including carcinogenesis. This modification has been known to be accomplished by the combined catalytic actions of three DNA methyltransferases (DNMTs), the *de novo* enzymes DNMT3A/ DNMT3B and the maintenance enzyme DNMT1. This property of DNMTs and the imbalance of CpG methylation in cancer cells have led to the development of cancer therapeutic drugs/ chemicals targeting the DNA methylation activities of DNMTs. However, we have recently discovered that the mammalian DNMTs could also act as active DNA 5-mC demethylases in a Ca++ion-and redox state-dependent manner. This suggests new directions for re-investigation of the structures of DNMTs and their functions in the genome wide and/or local DNA methylation in the mammalian cells. In particular, the concept and strategies for drug therapy targeting the DNMTs may need to be re-evaluated.

5:15 Best of Show Awards Reception in the Exhibit Hall

6:15 Exhibit Hall Closes

THURSDAY, APRIL 11

7:00 am Breakfast Presentation *(Sponsorship Opportunity Available)* **or Morning Coffee**

Integrating Clinical Information into Drug Discovery

8:45 Chairperson's Opening Remarks

8:50 The Challenges in Integrating Information During the Discovery Of Biomarkers in Cancer Patients Treated with Chemotherapy: A Pharmacology and Oncology Perspective
Federico Innocenti, M.D., Ph.D., Associate Professor, University of North Carolina at Chapel Hill; Associate Director , Institute for Pharmacogenomics and Individualized Therapy
Genomic studies for discovering biomarkers of outcome of patients treated with chemotherapy are quite advanced. However, we face the interpretative difficulty in connecting the dots among clinical data, genomic information (both of the host and the tumor), and functional annotation of genomic regions. This presentation will provide an oncology and pharmacology perspective of the contemporary challenges of integrative analyses that could (and should) aid the discovery of clinically useful markers for enrichment of responsive populations during drug development, as well as for improving patient management at the bed side.

9:20 "Integrating Molecular and Clinical Data to Expedite Translation in Computational Drug Repurposing
Joel Dudley, Ph.D., Director of Biomedical Informatics, Mount Sinai School of Medicine
Although drug repurposing approaches that leverage approved therapies can potentially expedite the drug development process by leveraging existing drug safety data, establishing efficacy for alternative indications can remain just as challenging as in novel drug development. Because many patients are prescribed approved therapies for their primary indications, there is a wealth of clinical data captured in electronic medical record (EMR) systems that could potentially inform on the system-wide physiological and pathophysiological effects of the approved therapies in humans. In this talk I will discuss efforts to integrate public gene expression data with clinical data captured from EMR systems to expedite translation in computational drug repurposing.

9:50 Managing Information Challenges with Elsevier Life Science Solutions
Shuhag Ghosh, Vice President, Global Marketing, Elsevier Life Science Solutions
From increasing discoverability to making sense of ever-growing data sets to leveraging new data sources, Life Sciences organizations face challenges in making more informed and effective decisions based on a changing landscape. Elsevier Life Science Solutions is a suite of interoperable domain-specific decision support tools built from our understanding of and commitment to Life Sciences. This suite is designed to enhance how organizations make decisions and to power information flows across discovery, pre-clinical, clinical and post-market domains, for

end-to-end success. The potential to leverage customized taxonomies, newly mined content sources and internal data in the suite changes how organizations interact with information to conduct R&D.

10:20 Coffee Break in the Exhibit Hall and Poster Competition Winners Announced

10:45 Plenary Keynote Panel Chairperson's Remarks
Kevin Davies, Ph.D., Editor-in-Chief, Bio-IT World

10:50 Plenary Keynote Panel Introduction
Yury Rozenman, Head of BT for Life Sciences, BT Global Services
Niven R. Narain, President & CTO, Berg Pharma

» PLENARY KEYNOTE PANEL

11:05 The Life Sciences CIO Panel
Panelists:
Remy Evard, CIO, Novartis Institutes for BioMedical Research
Martin Leach, Ph.D., Vice President, R&D IT, Biogen Idec
Andrea T. Norris, Director, Center for Information Technology (CIT) and Chief Information Officer, NIH
Gunaretnam (Guna) Rajagopal, Ph.D., VP & CIO - R&D IT, Research, Bioinformatics & External Innovation, Janssen Pharmaceuticals
Cris Ross, Chief Information Officer, Mayo Clinic
Matthew Trunnell, CIO, Broad Institute of MIT and Harvard

12:15 Luncheon in the Exhibit Hall with Poster Viewing

Panel Session: Building the IT Architecture of the New York Genome Center

2:00 Panel Session: Building the IT Architecture of the New York Genome Center
Moderator: Kevin Davies, Ph.D., Editor-in-Chief, Bio-IT World
Christopher Dwan, Acting Senior Vice President, IT, New York Genome Center
Kevin Shianna, Senior Vice President, Sequencing Operations, New York Genome Center
Robert B. Darnell, M.D., Ph.D., President & Scientific Director, New York Genome Center
George Gosselin, CTO, Computer Design & Integration LLC
In 2011, a consortium of 11 major academic and medical organizations in and around New York announced the creation of the New York Genome Center (NYGC). Under the direction of Nancy Kelley, the NYGC aspires to be a world-class genomics and medical research center, and is currently undergoing construction in the heart of Manhattan. NYGC management has the opportunity to design and create a state-of-the-art IT and data management infrastructure to handle, store and share the output from what will rapidly become one of the world's foremost genome sequencing facilities. This series of talks will describe the thinking that went into the design, creation and construction of the NYGC's IT infrastructure and entire data management strategy.

4:00 Conference Adjourns

SPONSORSHIP, EXHIBIT, AND LEAD GENERATION OPPORTUNITIES

Bio-IT World is the premier event in North America attracting 2,500+ IT professionals, senior level scientists, and executives from organizations including pharmaceutical, biotechnology, health systems, academia, government and national laboratories.

Cambridge Healthtech Institute (CHI) has customized sponsorship packages designed to help your company fulfill its marketing and lead generation objectives. This year, over 50% of our clients re-signed on-site for exhibit space in 2013, demonstrating a strong ROI. This does not take into account the multiple companies who were not able to re-sign a year in advance, but provided very positive feedback about participating in the coming year.

Agenda Presentations
Showcase your solutions to a guaranteed, highly-targeted audience. Package includes a 15 or 30-minute podium presentation within the scientific agenda, exhibit space, on-site branding and access to cooperative marketing efforts by CHI.

Breakfast & Luncheon Presentations
Opportunity includes a 30-minute podium presentation. Boxed lunches are delivered into the main session room, which guarantees audience attendance and participation. A limited number of presentations are available for sponsorship and they will sell out quickly. Sign on early to secure your talk!

Invitation-Only VIP Dinner/Hospitality Suite
Sponsors will select their top prospects from the conference pre-registration list for an evening of networking at the hotel or at a choice local venue. CHI will extend invitations and deliver prospects. Evening will be customized according to sponsor's objectives i.e.:

- Purely social
- Focus group
- Reception style
- Plated dinner with specific conversation focus

Exhibit
Exhibitors will enjoy facilitated networking opportunities with high-level conference delegates. Speak face-to-face with prospective clients and showcase your latest product, service, or solution.

Inquire about additional branding opportunities!

Looking for additional ways to drive leads to your sales team? CHI can help!

We offer clients numerous options for custom lead generation programs to address their marketing and sales needs, including:

- Live Webinars
- White Papers
- Market Surveys
- Podcasts and More!

Benefits of working with CHI for your lead generation needs:

- Your campaign will receive targeted promotion to CHI's unparalleled database of over 800,000 individuals, all of which are involved in all sectors of the life sciences – lists can be segmented based on geography, research area, title and industry.
- All custom lead generation programs are promoted through our experienced marketing team that will develop and drive targeted campaigns to drive awareness and leads to your lead generation program.
- For our webinar programs, we offer assistance in procuring speakers for your web symposia through our extensive roster of industry recognized speakers across multiple disciplines within life sciences, as well as provide an experienced moderator and dedicated operations team to coordinate all efforts.
- If choosing a white paper program, we can offer editorial experience and provide an industry recognized author to write your white paper.

New Product Showcase

NEW PRODUCT SHOWCASE
Bio-IT World Conference & Expo 2013

CHI is committed to ensure that all delegates visit the exhibit hall by holding welcoming receptions, refreshment breaks, and raffles! As an exhibitor, you have the opportunity to display your new product literature within the showcase area at NO ADDITIONAL COST!

How Will CHI Help Promote Your New Product?

- Email Campaigns
- Conference Website
- Press Releases
- On-Site Signage
- Program Guide
- On-Site Kiosk for Literature Display

Ask us about an upgrade!

Best of Show

Bio-IT World CONFERENCE & EXPO '13 BEST of SHOW

The Best of Show Awards offers exhibitors of the Bio-IT World Conference and Expo an exclusive opportunity to distinguish and highlight their esteemed products ranging from an innovative application, technology, tool, or solution from the competition. Judged by a team of leading industry experts and Bio-IT World editors, this awards program identifies exceptional innovation in technologies used by life science professionals today.

Products considered are new products, or significant product upgrades, introduced between April 2012 and April 2013. Winners are judged based on the products' technical merit, functionality, innovation, and in-person presentations to the judges at the show.

**Please Note: Selection is not based upon level of sponsorship or exhibit participation*

To learn more about this program, and submission deadlines, please contact:
Julie DiGiovine – Marketing Manager
781-972-5445 | jdigiovine@healthtech.com

For sponsorship and exhibit information, please contact:

Companies A-K:
Katelin Fitzgerald
Business Development Manager
781-972-5458 | kfitzgerald@healthtech.com

Companies L-Z:
Tim McLucas
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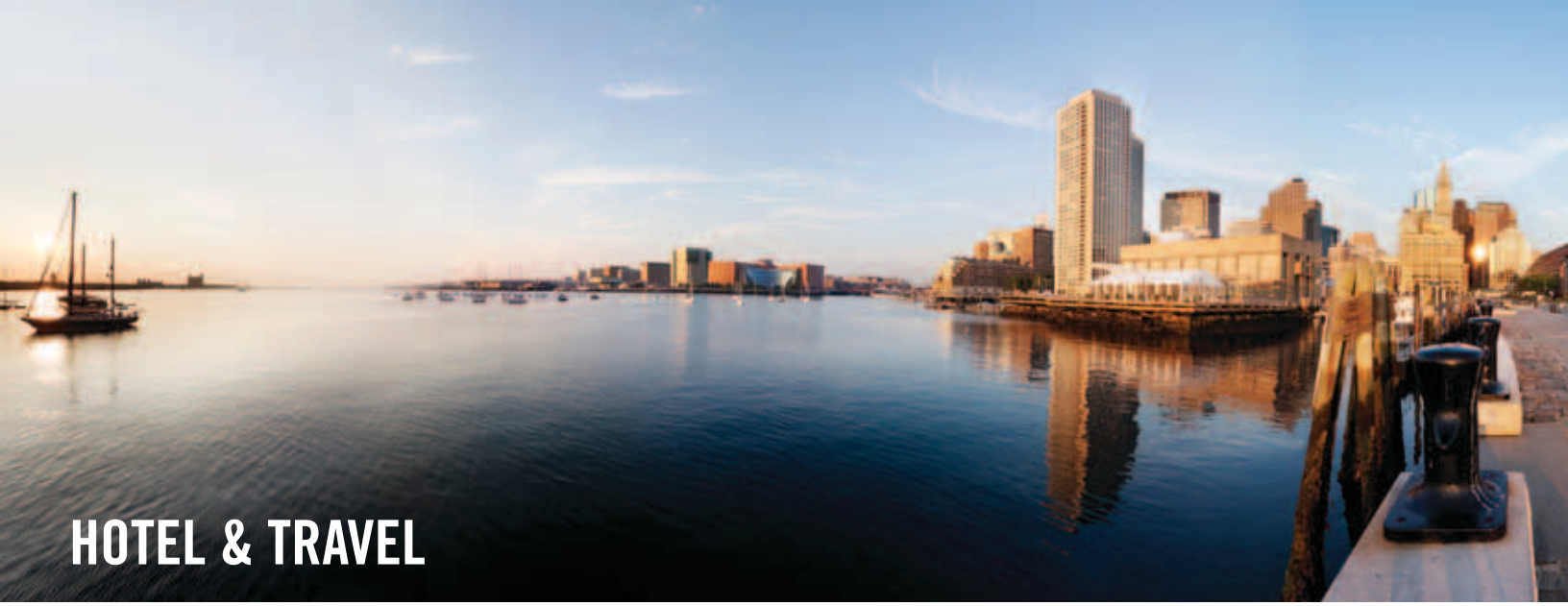

HOTEL & TRAVEL

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: 617-385-4514
Reservations: **Bio-ITWorldExpo.com**

Discounted Room Rate: $244 s/d
Discounted Room Rate Cut-off Date: March 1, 2013

Please visit Bio-ITWorldExpo.com 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, airport transportation, and visiting Boston and New England, visit the Hotel & Travel page at Bio-ITWorldExpo.com.

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Pricing and Registration Information

PRE-CONFERENCE WORKSHOPS

	Commercial	Academic, Government, Hospital-affiliated	Student*
One Half-Day Workshop	$595	$295	$145
Two Half-Day Workshops	$895	$495	$245

Please refer to Workshop list on page 3-4

CONFERENCE PRICING (excludes workshops)

Registrations after March 8, 2013, and on-site	$1995	$950	$325

Conference Tracks	
Track 1: IT Infrastructure - Hardware	Track 7: eClinical Trials Solutions
Track 2: Software Development	Track 8: Data Visualization
Track 3: Cloud Computing	Track 9: Drug Discovery Informatics
Track 4: Bioinformatics	Track 10: Clinical Omics
Track 5: Next-Gen Sequencing Informatics	Track 11: Collaborations and Open Access Innovations
Track 6: Systems Pharmacology	Track 12: Cancer Informatics

**Student rate cannot be combined with any other discount offers, except poster discount. Full time graduate students and PhD Candidates qualify for the student rate. Students must present a valid/current student ID to qualify for the student rate. Limited to the first 100 students that apply.*

CONFERENCE DISCOUNTS

Exclusive Offer to Attend Medical Informatics World Conference**

Paid attendees of Bio-IT World Conference & Expo can attend the co-located Medical Informatics World Conference (April 8-9) for a special discounted rate (20% discount off the registration fee for the main conference). Medical Informatics World and Bio-IT World Expo are being held back-to-back to complete the week of scientific content by bridging the healthcare and life science worlds.

To receive this exclusive 20% discount, mention keycode **1320BITXP** when registering for Medical Informatics World Conference. Please note: Our records must indicate you are a paid attendee of Bio-IT World Conference & Expo 2013 to qualify.

***Discount applies to paid attendees of Bio-IT World Conference & Expo 2013 only. Applies to new registrations only and cannot be combined with other discount offers, except poster discount. Discount does not apply to pre-conference workshops.*

Poster Submission-Discount ($50 Off)
Poster abstracts are due by March 1, 2013. Once your registration has been fully processed, we will send an email containing a unique link allowing you to submit your poster abstract. If you do not receive your link within 5 business days, please contact jring@healthtech.com. *CHI reserves the right to publish your poster title and abstract in various marketing materials and products.

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REGISTER 3 - 4th IS FREE: Individuals must register for the same conference or conference combination and submit completed registration form together for discount to apply.

Additional discounts are available for multiple attendees from the same organization. For more information on group rates contact David Cunningham at +1-781-972-5472

If you are unable to attend but would like to purchase the Bio-IT World Conference & Expo 2013 conference CD for $750 (plus shipping), please visit Bio-ITWorldExpo.com. Massachusetts delivery will include sales tax.

Please refer to the Registration Code below:

ADDITIONAL REGISTRATION DETAILS

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

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.

To view our Substitutions/Cancellations Policy, go to http://www.healthtech.com/regdetails

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

How to Register: **Bio-ITWorldExpo.com**

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Please use keycode **1320F** when registering!