Final Agenda

10th ANNIVERSARY 2002-2012

Cambridge Healthtech Institute's Eleventh Annual

Bio·IT World CONFERENCE & EXPO '12

April 24 – 26, 2012 • World Trade Center • Boston, MA

Enabling Technology. Leveraging Data. Transforming Medicine.

CONCURRENT TRACKS:

1. IT Infrastructure – Hardware
2. IT Infrastructure – Software
3. Cloud Computing
4. Bioinformatics
5. Next-Generation Sequencing Informatics
6. Systems and Multiscale Biology
7. eClinical Solutions
8. eHealth and HIT Solutions for Personalized Medicine
9. Drug Discovery Informatics
10. Molecular Diagnostics Informatics NEW!
11. Open Source Solutions NEW!
12. Cancer Informatics NEW!

EVENT FEATURES:

- Access All 12 Tracks for One Price
- Network with 2,000+ Global Attendees
- Hear 125+ Technology and Scientific Presentations
- Connect with Attendees Using CHI's Intro-Net
- Choose from 16 Pre-Conference Workshops
- See the Winners of the following 2012 Awards: Benjamin Franklin, Best of Show, and Best Practices
- View Novel Technologies and Solutions in the Expansive Exhibit Hall
- And Much More!

KEYNOTE PRESENTATIONS BY:

Eric D. Perakslis, Ph.D.,
CIO and Chief Scientist of Informatics, U.S. Food and Drug Administration

Martin Leach, Ph.D.,
CIO, Broad Institute of MIT and Harvard

Jill P. Mesirov, Ph.D.,
Associate Director and Chief Informatics Officer; Director, Computational Biology and Bioinformatics, Broad Institute of MIT and Harvard

KEYNOTE PANEL:

A special plenary session featuring trends and challenges in cancer research:

Julian Adams, Ph.D., President, Research and Development, Infinity Pharmaceuticals, Inc.

Jose Baselga, M.D., Ph.D., Chief and Bruce A. Chabner Chair, Division of Hematology/Oncology, Massachusetts General Hospital; Associate Director, Massachusetts General Hospital Cancer Center; Professor of Medicine, Harvard Medical School

Sir John Burn, MD, FMedSci, Professor of Clinical Genetics, Institute of Genetic Medicine, Newcastle University, UK; Genetics Lead, National Institute of Health Research, UK; Medical Director, QuantuMDx Ltd

John Quackenbush, Ph.D., Professor, Biostatistics and Computational Biology, Cancer Biology Center for Cancer Computational Biology, Dana-Farber Cancer Institute

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Bio-ITWorldExpo.com

SCHEDULE-AT-A-GLANCE

Tuesday, April 24, 2012	
8:00am – 4:00pm	Pre-Conference Workshops
4:00 – 5:00pm	Plenary Keynotes
5:00 – 7:00pm	Exhibit Hall Open
5:00 – 7:00pm	Welcome Reception in the Exhibit Hall with Poster Viewing
Wednesday, April 25, 2012	
7:55 – 9:45am	Plenary Keynote, Benjamin Franklin Awards Presentation, and Best Practices Awards Program
9:45am – 6:15pm	Exhibit Hall Open with Poster Viewing
9:45 – 10:50am	Coffee Break in the Exhibit Hall
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 26, 2012	
8:00am - 8:40am	Featured Speaker (Tracks 1-3)
8:40am - 10:15am	Tracks 1-12
10:15am – 1:55pm	Exhibit Hall Open
10:15 – 10:45am	Coffee Break in the Exhibit Hall with Poster Competition
10:45am – 12:15pm	Plenary Keynote
12:15 – 1:55pm	Lunch in the Exhibit Hall with Poster Viewing
1:55 – 4:00pm	Tracks 1-12

KEYNOTE PRESENTATIONS BY:

Eric D. Perakslis, Ph.D., CIO and Chief Scientist of Informatics, U.S. Food and Drug Administration

Eric is currently Chief Information Officer and Chief Scientist (Informatics) at the U.S. Food and Drug Administration. In this new role, Eric is responsible for modernizing and enhancing the IT capabilities as well as the *in silico* scientific capabilities at FDA. Prior to FDA, Eric was Senior Vice President of R&D Information Technology at Johnson & Johnson Pharmaceuticals R&D and was a member of the Corporate Office of Science and Technology. Before joining J&J, Eric was the Group leader of Scientific Computing at ArQule, Inc. and he began his professional career with the Army Corps of Engineers. Eric has a Ph.D. in chemical and biochemical engineering from Drexel University and also holds B.S.Che and M.S. degrees in chemical engineering.

Martin Leach, Ph.D., CIO, Broad Institute of MIT and Harvard

Martin Leach is Chief Information Officer at the Broad Institute. In this role, he oversees and helps integrate the institute's multi-faceted computing and information technology-related endeavors. Martin comes to the Broad from Merck & Co., where he led IT for Discovery and Pre-Clinical Sciences across all the North American research sites. Over his career he has provided support and strategic vision for IT, informatics, and data-mining activities at a range of life sciences organizations, from basic research laboratories to large pharmaceutical companies. Martin received his B.Sc. in cell and molecular sciences from Anglia Polytechnic University and his Ph.D. in pharmacology from Boston University School of Medicine.

Jill P. Mesirov, Ph.D., Associate Director and Chief Informatics Officer; Director, Computational Biology and Bioinformatics, Broad Institute of MIT and Harvard

Jill Mesirov is Associate Director and Chief Informatics Officer at the Broad Institute of MIT and Harvard, where she directs Computational Biology and Bioinformatics. Mesirov is also a member of the David H. Koch Institute for Integrative Cancer Research at MIT and adjunct professor of bioinformatics at Boston University. In 1997, Jill came to the Whitehead Institute/MIT Center for Genome Research, now part of the Broad Institute, from IBM, where she was manager of computational biology and bioinformatics in the Healthcare/Pharmaceutical Solutions Organization. Before joining IBM in 1995, she was director of research at Thinking Machines Corporation for 10 years. She has also held positions in the mathematics department at the University of California at Berkeley and has served as associate executive director of the American Mathematical Society. Jill is a fellow of the American Association for the Advancement of Science, director of the International Society for Computational Biology, and former president of the Association for Women in Mathematics. She serves on numerous academic and corporate scientific advisory and journal editorial boards. Jill received her B.A. in mathematics from the University of Pennsylvania. She earned her Ph.D., and M.A. in mathematics from Brandeis University.

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Morning Workshops 8:00–11:30 am

(W1) **Beyond the Cloud: Improving the R&D Innovation Process through Cloud Services**

Sponsored by BT

Neil Lock, IT Services Program Director, BT Global Services
Adam Kraut, Principal Investigator, BioTeam
Frank Brown, CSO, Accelrys

(W2) **Leveraging SaaS for Next-Gen Sequencing: Case Study with the Galaxy Community**

Ravi Madduri, Fellow, Computation Institute, University of Chicago and Argonne National Lab
Elizabeth Bartom, Ph.D., Research Professional, Sequence Analysis Resource, U Chicago Comprehensive Cancer Center, University of Chicago

(W3) **Utilization of EHRs/EMRs for Protocol Design, Site Identification, Patient Recruitment and Pharmacovigilance**

Michael Celeste, Associate Director, Pharmacovigilance Information Management, Pfizer
Jason Colquitt, Executive Director, Research Services, Greenway Medical Technologies
Aaron Kamauu, M.D., CEO, Healthcare Data Analytics, Anolinx LLC; former Head, Healthcare Data Strategy, Roche and Genentech
Gary Lubin, CEO, Centerphase Solutions, Inc.
Jim Rogers, President & CEO, Information Technology, Nextrials

(W4) **Building and Using an Ontological Framework for Drug Discovery to Clinical Data**

Elgar Pichler, Ph.D., Independent Consultant, Boston

(W5) **Clinical Genomics**

Ronald Ranauro, Ph.D., Director, Health IT Strategy, College of American Pathologists; Managing Partner, Next Gen Informatics, Inc.
John F. Madden, M.D., Ph.D., Associate Professor, Department of Pathology, Duke University Medical Center
Mary Kennedy, CT (ASCP), MPH, Manager, Strategic Health IT Initiatives, College of American Pathologists
Gerald Beuchelt, Principal Engineer, System Software, Information Assurance, MITRE Corporation
Mark A. Kramer, Ph.D., Information Architect and Manager, Healthcare Systems, MITRE
Lynn Bry, Ph.D., Assistant Professor, Department of Pathology, Brigham and Women's Hospital

(W6) **Planning and Structuring Collaborative Innovation and Open Source Deals: Techniques and Lessons from the Leaders**

Gene Slowinski, Ph.D., Director, Strategic Alliance and Open Innovation Research, Graduate School of Management, Rutgers University

(W8) **Best of Breed Informatics**

Richard Lysakowski, Ph.D., Director of R&D and Advisor, The Collaborative Electronic Notebook Systems Association (CENSA)

For more details on the workshops, please visit www.Bio-ITWorldExpo.com

**Separate Registration Required*

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 25, during the Plenary Keynote and Awards Program.

CONNECT WITH US #BioIT12

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. The Best Practices Awards identify and showcase outstanding examples of innovative partnerships, technologies and strategies impacting research and drug development. Winners will be selected by a peer review expert panel in early 2012. Bio-IT World will present the Awards in the Amphitheater at 9:10am on Wednesday, April 25 during the Plenary Keynote and Awards Program. Deadline for entry is January 13, 2012. Full details including previous winners and entry forms are available at Bio-ITWorldExpo.com.

2012 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 25, 2012.

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!

Afternoon Workshops 12:30–4:00 pm

(W9) **Data Visualization in Biology: From the Basics to Big Data**
Nils Gehlenborg, Ph.D., Research Associate, Center for Biomedical Informatics, Harvard Medical School

(W10) **Microscopy Imaging Analysis Using CellProfiler – Quantitative Analysis of Large-Scale Biological Image Data**
Mark-Anthony Bray, Ph.D., Computational Biologist, Imaging Platform, Broad Institute

(W11) **Your Cloud, Your Way: How to Choose the Approach That's Best for You** *Sponsored by* SAVVIS
Reed Smith, Director, Cloud Product Management, Savvis
Selecting or refining your cloud approach can be a harrowing experience. Should you build one yourself? Should you go with a cloud service provider? Do you want a private or public cloud? What about Hybrid? Do you want to use a cloud broker? How do you project cost of cloud? This discussion will explore these topics and more helping new cloud users and experienced cloud veterans get the most out of the cloud.

(W12) **Enhancing R&D Effectiveness through Global ELN Deployment**
Michael H. Elliott, CEO, Atrium Research & Consulting LLC
Michael Kopach, Ph.D., Principal Research Scientist, Chemical Product Research & Development, Eli Lilly & Co.
Ralph Haffner, Head, Biologics Research Informatics, F. Hoffmann-La Roche AG
Arturo Morales, Ph.D., Global Leader, NIBR Informatics & Technology Novartis Institutes for BioMedical Research, Inc.
Ryan Bass, Senior Systems Engineer, Strategic Operations, Janssen Research & Development, Pharmaceutical Development & Manufacturing Sciences, Johnson & Johnson

(W13) **Information Management and Healthcare Delivery at Point-of-Care: Finding eHealth Savings by Coordinating Technologies and Streamlining Operations**
Sharon Marsh, Ph.D., Assistant Professor, Pharmacy and Pharmaceutical Sciences, University of Alberta
Tibor van Rooij, Ph.D. Candidate, Pharmacy and Pharmaceutical Sciences, University of Alberta; former Director of Bioinformatics, Génome Québec and Montreal Heart Institute Pharmacogenomics Centre

(W14) **Desperately Seeking Precise Knowledge: The Challenges of Resolving Drug Names against the Data Landscape**
Christopher Southan, Ph.D., Consultant, Knowledge Engineering, ChrisDS Consulting
David Wishart, Ph.D., Professor, Computing Science, University of Alberta
Louisa Bellis, Ph.D., MRSC, Chemical Content Curator, Chemogenomics and ChEMBL Databases, European Bioinformatics Institute
Larry Callahan, Ph.D., Chemist, Substance Registration System, Office of Critical Path Programs, Food and Drug Administration
Craig Knox, Bioinformatician and Programmer Analyst, University of Alberta
Chris Southan, Ph.D., B.Sc.Hons, M.Sc., Consultant, Knowledge Engineering, ChrisDS Consulting

(W15) **Harnessing Social Media for Health Informatics: Mining Social Media Data for Understanding & Improving Health-Related Behavior**
Christopher C. Yang, Associate Professor, College of Information Science and Technology, Drexel University
John Yen, Professor of Information Sciences and Technology, Penn State University

For more details on the workshops, please visit www.Bio-ITWorldExpo.com

**Separate Registration Required*

Track 1 IT Infrastructure – Hardware

TUESDAY, APRIL 24

7:00 am Workshop Registration and Morning Coffee

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

- Planning and Structuring Collaborative Innovation and Open Source Deals: Techniques and Lessons from the Leaders
- Data Visualization in Biology: From the Basics to Big Data

**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
Sanjay Joshi, Solutions Architect, Life Sciences, EMC Isilon Storage Division

4:15 PLENARY KEYNOTES

Martin Leach, Ph.D., CIO, Broad Institute of MIT and Harvard

Jill P. Mesirov, Ph.D., Associate Director and Chief Informatics Officer; Director, Computational Biology and Bioinformatics, Broad Institute of MIT and Harvard

5:00 - 7:00 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 iPod touches® or 1 of 2 Xbox 360s®*!

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WEDNESDAY, APRIL 25

7:00 am Registration and Morning Coffee

7:55 Chairperson's Opening Remarks
Phillips Kuhl, Co-Founder and President, Cambridge Healthtech Institute

8:00 Keynote Introduction
Bas Burger, President, Global Commerce, BT Global Services

8:15 PLENARY KEYNOTE

Eric D. Perakslis, Ph.D., CIO and Chief Scientist of Informatics, U.S. Food and Drug Administration

8:45 Benjamin Franklin Award & Laureate Presentation

9:10 Best Practices Award Program

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

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TECHNOLOGIES AND INFRASTRUCTURE FOR ACQUIRING, STORING, AND SHARING DATA

10:50 Chairperson's Remarks
Kevin Brode, Head, Health Sales, Hitachi Data Systems

11:00 A Nation-Wide Area Networked File System for Very Large Scientific Data
William K. Barnett, Ph.D., Director, Science Community Tools, Research Technologies, Indiana University
The National Center of Genome Analysis Support (NCGAS) at Indiana University is developing advanced cyberinfrastructures to address the challenge of exploding amounts of sequence data. This presentation will describe a nationally accessible high performance national infrastructure for sequence assembly and other genomics analyses. This architecture can help address the needs to accelerate research with large scientific data sets.

11:30 IT at Yale's Center for Genome Analysis: Two Years in the Trenches at a High-throughput Sequencing Center
Robert Bjornson, Ph.D., Research Scientist, Yale University

12:00 pm Be Prepared for the Unexpected - Architect Your Storage Infrastructure to Enable New Science
Jeff Kenkel, Specialist, Solution Consultant, Health & Life Sciences, Hitachi Data Systems

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Genomic sequencing and imaging instruments continue to generate vast amounts of data to be analyzed by multiple applications and used in collaborative research. Data needs to be stored, managed and shared. Storage infrastructures need to be designed from the start to handle rapidly changing workflows. BlueArc is a leader in file storage solutions at scale for mixed and unpredictable workflows.

12:30 Let's be Sensible: Maximizing Productivity and Research through Scientific Computing
John M. Cho, Deputy Program Manager, FDA, HP Enterprise Services

Sponsored by hp

Sustainable growth of any health & life sciences organization depends on continual refinement and innovation of existing processes and technology. That ability to innovate is directly tied to enabling collaboration between key stakeholders while providing them the ability to aggregate and analyze vast amounts of structured and unstructured scientific data. Furthermore, misalignment of critical IT infrastructure often leads to resource contention, silos of compute-intensive applications and fragmented data sources that sometimes results in duplication of effort, cost overruns and inefficient execution. In this presentation, HP will provide some high-level guidance in applying IT services, resources and technology to address complex problems, whether it be driving scientific research, reducing IT infrastructure costs within scientific computing, or enabling secure and efficient discovery of new therapies from bench to bedside.

1:40 Chairperson's Remarks
Zheng Yang, Ph.D., Associate Director, IS Business Partnering Research, Boehringer Ingelheim Pharmaceuticals, Inc.

1:45 Conquering Computational Complexities in Cancer Research Large Shared Memory and Big Dynamic Range Computing - Essential Drivers in Global Modeling of Cancer Cells
Rune Linding, Ph.D., Professor, Cellular Signal Integration Group (C-SIG), Center for Biological Sequence Analysis (CBS), Department of Systems Biology, Technical University of Denmark (DTU)

Sponsored by sgi

The size and complexity of cell-imaging, mass-spectrometry and deep-sequencing systems biology data is exploding. We perform global, non-linear algorithmic integration of these to model cancer progression. While in scale corresponding to models of climate/weather systems the underlying data is vastly more complex creating formidable computational challenges. I will discuss how computational dynamic range and large-shared memory are two critical technologies in systems biology, translational cancer research and personalized medicine.

2:15 BIO-IT: Reigning in Research Data: Adding Intelligence to Conventional File Systems

Sponsored by

Jacob Farmer, CTO, Cambridge Computer

Cambridge Computer has embarked on a project to define the best practices for content classification of research data. We are collaborating with a number of leading institutions and have completed development of a working prototype. The purpose of this talk is to share the highlights of our work, stimulate discussion, and make contact with potential collaborators.

2:45 What On Earth Are They Storing: A Deep Analysis of User Storage Behavior

Christopher Botka, Director of Research Computing, Research Information Technology Group, Harvard Medical School

Harvard Medical School has been exploring novel ways of overlaying metadata onto conventional file systems to solve a variety of problems-how various users consume storage, visualization capacity consumption trends, data retention requirements, and identify data that can be deleted or moved to a lower cost tier. This talk outlines our experiences and observations thus far and describes the next phase of the project for the coming months.

3:00 Building a Scalable IT Architecture for Next Generation Sequencing and Genomic Analysis - A Comprehensive Approach

Sponsored by

Janis E. Landry-Lane, Program Director, World Wide Deep Computing, Life Sciences/Higher Education Segments, IBM

Institutions are taking on the task of designing IT systems for NGS. Solutions that are scalable, both in terms of processing and storage, will better serve the institution long-term. There is a life-cycle management of data, and making it usable for downstream analyses and applications is an important aspect in system design. We will also discuss techniques for application acceleration without additional hardware.

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

TECHNOLOGIES AND INFRASTRUCTURE FOR ACQUIRING, STORING, AND SHARING DATA (CONT'D)

3:45 Emergency Medical Services and the Bio-IT World

Joe Acciavatti, Director, Operations and Communications, MONOC

Tim Harren, IT Director, Pro EMS

This presentation will describe the data and technology challenges that New Jersey's largest provider of EMS services face. The world of EMS and IT work hand in hand on a daily basis with the acquisition of electronic patient care reports, cardiac electrocardiograms, physician-to-field consultations, medication monitoring, and big data management. Learn about the software and technical aspects utilized to address these challenges.

4:15 The Department of Veterans Affairs Million Veteran Program and the Information Infrastructure Making it Possible

Leonard D'Avolio, Ph.D., Associate Center Director, Biomedical Informatics, Massachusetts Veterans Epidemiology Research and Information Center (MAVERIC)

Saiju Pyarajan, IT Manager, Massachusetts Veterans Epidemiology Research and Information Center (MAVERIC)

The Department of Veterans Affairs launched an initiative to recruit and enroll 1 million Veteran volunteers to contribute blood, survey data, and access to their EMRs to discover relationships between biology and health. Learn about the information infrastructure that was designed to manage the logistics of recruiting and enrolling Veterans as well as to facilitate analysis of combined phenotype and genotype data.

4:45 Parallel Storage: Addressing the Bio and Life Sciences Big Data Challenge

Sponsored by

Geoffrey Noer, Senior Director, Product Marketing, Panasas

The exponentially growing volumes of data generated by Bio IT applications (especially next-gen sequencing) compound the challenge of selecting a storage infrastructure capable of linearly scaling capacity and performance. Panasas will discuss how to address this big data storage challenge with high-performance parallel storage and how the emerging open standard parallel NFS (pNFS) protocol will further enable performance at scale.

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

6:15 Exhibit Hall Closes

THURSDAY, APRIL 26

7:00 am Breakfast Presentation

The Growth of Personalized Medicine: Big Data in the Era of the Impossibly Small

Sponsored by

Kristina M. Kermanshahche, Chief Architect of Healthcare, Intel Corporation

Alan Louie, Ph.D., Research Analyst, IDC Health Insights

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. Indeed, as we approach the scale of "impossibly small" for both technology and disease management, the complexity of problems grows by orders of magnitude. IDC will present "Trends and Challenges in Genomics Research and Personalized Medicine", followed by Intel presentation on how they collaborate with researchers and the technology ecosystem to develop innovative solutions to seemingly intractable problems emerging in life sciences today. We look forward to learning about the specific challenges

you face and optimizing our technologies to help you to accelerate discoveries.

8:00 Featured Speaker Introduction *Sponsored by*
David A. Medina, Director, Product Management, Healthcare Analytics & Life Sciences, Business Solutions, Hewlett-Packard

8:10 Featured Speaker: HPC Trends from the Trenches
Chris Dagdigian, Founding Partner and Director of Technology, BioTeam, Inc.
HPC Trends from 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.

8:40 Chairperson's Opening Remarks
Mollie Shields Uehling, CEO, SAFE-BioPharma Association

SECURITY INFORMATICS & CLOUD COMPUTING

8:45 The Role of a Standard-Based Interoperable Digital Identity in Unlocking the Cloud
Mollie Shields Uehling, CEO, SAFE-BioPharma Association

9:15 Security and Compliance for Pharma Cloud Computing
Zheng Yang, Ph.D., Associate Director, IS Business Partnering Research, Boehringer Ingelheim Pharmaceuticals, Inc.
Co-Author: Erhard Wais, Architect, IS Business Partnering Research, Boehringer Ingelheim Regional Center Vienna GmbH & Co KG.

9:45 Implementing Sequencing Services in the Cloud *Sponsored by* EMC® ISILON
Sanjay Joshi, Solutions Architect, Life Sciences, EMC Isilon Storage Division
As genome sequencing services on the cloud mature, the implementation technologies need to move from 'research-ready' to 'clinic-ready'. This means working within a standards, performance and monitoring sandbox and their interaction with high performance computing (HPC) and data life-cycle management. We will present a Cloud Standards and Trust Framework for public and private clouds and its various hybrid models.

10:15 Coffee Break in the Exhibit Hall and Poster Competition

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

10:50 Plenary Keynote Panel Introduction
Geoffrey Noer, Senior Director, Product Marketing, Panasas

11:00 Plenary Keynote Panel:
A special plenary session featuring trends and challenges in cancer research:
Julian Adams, Ph.D., President, Research and Development, Infinity Pharmaceuticals, Inc.
Jose Baselga, M.D., Ph.D., Chief and Bruce A. Chabner Chair, Division of Hematology/Oncology, Massachusetts General Hospital; Associate Director, Massachusetts General Hospital Cancer Center; Professor of Medicine, Harvard Medical School
Sir John Burn, MD, FMedSci, Professor of Clinical Genetics, Institute of Genetic Medicine, Newcastle University, UK; Genetics Lead, National Institute of Health Research, UK; Medical Director, QuantuMDx Ltd
John Quackenbush, Ph.D., Professor, Biostatistics and Computational Biology, Cancer Biology Center for Cancer Computational Biology, Dana-Farber Cancer Institute

12:15 Luncheon in the Exhibit Hall with Poster Viewing

HPC ON THE CLOUD – IMPLEMENTATION ISSUES AND HARDWARE

1:55 Chairperson's Remarks

2:00 Scaling Biosciences Research with Petabytes of Data and Ultra Fast Computing *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. Research needs have grown, R&D budgets have shrunk. Can your network keep up with increased CPU density bursts to 10Gbps, or can Latency sensitive data movement? 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.

2:30 NGS Data Storage and Management – From Data Ingestion to Archive Simplified *Sponsored by* DataDirect NETWORKS Information in Motion
Jose L. Alvarez, WW Director, Life Sciences, DataDirect Networks, Inc.
DDN is partnering with NGS industry leaders to deliver an array of flexible; highly scalable and easy to manage unified data storage solutions that are helping research groups around the world accelerate their time to discovery. Instruments data ingestion, sequencing pipeline performance, intelligent archive and sharing of research data in a geo-distributed modelwill be discussed.

3:00 Biopharma Case Study
Speaker to be Announced

3:30 Closing Featured Speaker:
Platform for Clinical Research Networks: Novel Approach towards Discoveries in Rare Diseases
Alex Sherman, Director, Systems, Department of Neurology,Massachusetts General Hospital

4:00 Conference Adjourns

Track 2 IT Infrastructure – Software

TUESDAY, APRIL 24

7:00 am Workshop Registration and Morning Coffee

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

- Planning and Structuring Collaborative Innovation and Open Source Deals: Techniques and Lessons from the Leaders
- Data Visualization in Biology: From the Basics to Big Data

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5:00 - 7:00 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 iPod touches® or 1 of 2 Xbox 360s®*!

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8:45 Benjamin Franklin Award & Laureate Presentation

9:10 Best Practices Award Program

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

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TECHNOLOGIES AND APPLICATIONS FOR ACQUIRING, MANAGING, SHARING, AND PRESENTING DATA

10:50 Chairperson's Remarks
Irene Polikoff, CEO, TopQuadrant

11:00 Radical Quality and ROI Gains Using Model Driven and DSL (Domain Specific Language) Software Development
Anthony Leotta, Bioinformatics Manager, Cold Spring Harbor Laboratory
This presentation describes a software engineering process that features model driven design. We created a framework to support the process along with implementing a Laboratory Information Management System for the CSHL Core Next Gen Sequencing facility using it. Learn how we build software with less implementation and maintenance time, allowing us to focus more on end-user needs.

11:30 Data-Rich SharePoint for Drug Discovery
James Ewen, Business Analyst, Research Informatics & Automation, Bristol-Myers Squibb Company
Jared Shockcor, Domain Architect, Research Informatics & Automation, Bristol-Myers Squibb Company
We describe a novel technology for managing Discovery operations, tracking team decisions, and communicating and sharing data. By leveraging RESTful Services, existing databases, and un-altered SharePoint, we created a Data-Rich SharePoint experience for our scientists. Learn the nature of the challenges our scientists faced and how we addressed them and the creation and implementation of the technical foundations of the technology project.

12:00 pm Maximizing the Return on your Data Assets
Sponsored by
Tessella
Technology & Consulting
Mark Evans, Digital Archiving Practice Manager, Tessella
Even as the Era of "Big Data" engulfs life sciences and researchers rush to wring immediate value from the data deluge, the long-term archiving of this valuable asset is unfortunately, widely neglected. Few industries face a more daunting data management challenge. The size of datasets is numbing, the diversity of data types is bewildering, and technologies used to produce and analyze the data are advancing at an ever increasing rate. Coping with obsolescence is becoming a real challenge.

12:15 A Shared Services Platform for Bio-informatics and Hadoop Applications
Sponsored by
Platform Computing
an IBM Company
Jeremy Chambers, Solution Architect, Platform Computing, an IBM Company
This session looks at the benefits of adopting a multi-tenant big data cluster platform for bio-informatics applications. In this session, we introduce a shared services platform capable of running multiple bio-informatics applications including MapReduce applications on the same shared grid, while delivering guaranteed SLAs to different lines of business. With such a shared services platform, IT organizations can achieve higher resource utilization and cost savings as well as improved application performance.

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

1:40 Chairperson's Remarks
Paul Lappas, Director, Products, Piston Cloud Computing

1:45 Insilico DB: An Efficient Web-Based Collaborative Platform for Managing and Sharing Genomic Datasets that Are Tightly Integrated with Analysis Platforms Genepattern and R/Bioconductor
David Y. Weiss Solís, Ph.D., Project Lead, InSilico Project, U.L.B. -

Université Libre de Bruxelles
Alain Coletta, Ph.D., Development Leader, InSilico Project, U.L.B. - Université Libre de Bruxelles
InSilico DB (http://insilico.ulb.ac) allows to manage and share large collections of genomic data. Advanced search, meta-data editing, and data normalization capabilities allow for efficient use of stored data. Proprietary, as well as 99,349 expert-verified, re-normalized assays pre-installed can be immediately analysed in GenePattern (GUI) and R/Bioconductor (Command-line). Ongoing integration with GenomeSpace will further enhance the analysis options available through InSilico DB.

2:15 Having a Mobile App Presence: Necessary or Nice to Have?
Steven Muskal, Ph.D., Chief Executive Officer, Eidogen-Sertanty, Inc.

2:45 Semantic Web for Flexible Competitive Intelligence
Sponsored by CAMBRIDGE SEMANTICS
Rob Gonzalez, Senior Product Manager, Cambridge Semantics & Editor-in-Chief, Semantic University
Semantic Web technologies are the only technologies that are powerful, flexible, and mature enough to handle the diverse and ever-changing information needs of the pharmaceutical industry. Come learn how 5 of the top 10 pharma companies are using Cambridge Semantics' Anzo platform to deliver key competitive intelligence insights to stakeholders in R&D, business development, sourcing, and marketing.

3:00 Using Ontologies to Enhance Analytic Capabilities
Sponsored by revelytix emergent analytics® spry agile analytics
Todd Jones, Senior Information Architect, Spry, Inc.
Paul Bradley, Senior Vice President, Account Management, Revelytix
Ontologies allow many different artifacts to be described using a common, executable language. Through these precise descriptions, information can be federated from different sources at run time, providing a single, holistic, traceable view. Using ontologies and semantic technologies as the underlying information management environment can greatly enhance the quality and accuracy of analytic capabilities.

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

TECHNOLOGIES AND APPLICATIONS FOR ACQUIRING, MANAGING, SHARING, AND PRESENTING DATA

3:45 Emergency Medical Services and the Bio-IT World
Joe Acciavatti, Director, Operations and Communications, MONOC
Tim Harren, IT Director, Pro EMS
This presentation will describe the data and technology challenges that New Jersey's largest provider of EMS services face. The world of EMS and IT work hand in hand on a daily basis with the acquisition of electronic patient care reports, cardiac electrocardiograms, physician-to-field consultations, medication monitoring, and big data management. Learn about the software and technical aspects utilized to address these challenges.

4:15 The Department of Veterans Affairs Million Veteran Program and the Information Infrastructure Making it Possible
Leonard D'Avolio, Ph.D., Associate Center Director, Biomedical Informatics, Massachusetts Veterans Epidemiology Research and Information Center (MAVERIC)
Saiju Pyarajan, IT Manager, Massachusetts Veterans Epidemiology Research and Information Center (MAVERIC)
The Department of Veterans Affairs launched an initiative to recruit and enroll 1 million Veteran volunteers to contribute blood, survey data, and access to their EMRs to discover relationships between biology and health. Learn about the information infrastructure that was designed to manage the logistics of recruiting and enrolling Veterans as well as to facilitate analysis of combined phenotype and genotype data.

4:45 Parallel Storage: Addressing the Bio and Life Sciences Big Data Challenge
Sponsored by panasas
Geoffrey Noer, Senior Director, Product Marketing, Panasas
The exponentially growing volumes of data generated by next-generation sequencers and other BioIT applications tends to compound storage consolidation and scalability challenges. In this presentation, Panasas will discuss how building a private cloud backed by scalable, high-performance parallel storage is the best solution for the unique challenges presented by bio and life sciences applications.

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

6:15 Exhibit Hall Closes

THURSDAY, APRIL 26

8:00 am Featured Speaker Introduction
Sponsored by hp
David A. Medina, Director, Product Management, Healthcare Analytics & Life Sciences, Business Solutions, Hewlett-Packard

8:10 Featured Speaker: HPC Trends from the Trenches
Chris Dagdigian, Founding Partner and Director of Technology, BioTeam, Inc.
HPC Trends from 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.

8:40 Chairperson's Opening Remarks
David A. Medina, Director, Product Management, Healthcare Analytics & Life Sciences, Business Solutions, Hewlett-Packard

8:45 Neuroimaging Informatics: From Cancer to Connectomes
Daniel Marcus, Ph.D., Director, Neuroinformatics Research Group, Washington University School of Medicine; President, Radiologics, Inc.
Diseases and disorders of the brain remain among the most intractable in medicine. For reasons both known (traumatic brain injury, Alzheimer's disease) and unknown (autism), their prevalence continues to increase. Neuroimaging, with its ability to portray the architecture and function of the brain in both health

and disease, promises to play a major role in developing a better understanding of and better treatments for these conditions.

9:15 Pathway to Global Product Safety and Quality, Mobility and Big Data
Michael Coene, Chief Technology Officer, FDA

9:45 High-Speed Data Movement for Effective Global Collaboration in Genomic Research

Sponsored by aspera

Michelle Munson, President & Co-founder, Aspera, Inc.
To collaborate effectively, scientific organizations need to implement large-scale computing and networking infrastructure, select storage systems and integrate high-speed transport technologies to power the collection and distribution of terabytes of sequencing data to researchers globally. Learn about best practices, requirements and challenges of IT infrastructure designs and how Aspera powers data movement in support of global research.

10:15 Coffee Break in the Exhibit Hall and Poster Competition

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

10:50 Plenary Keynote Panel Introduction
Geoffrey Noer, Senior Director, Product Marketing, Panasas

11:00 Plenary Keynote Panel: A special plenary session featuring trends and challenges in cancer research:

Julian Adams, Ph.D., President, Research and Development, Infinity Pharmaceuticals, Inc.

Jose Baselga, M.D., Ph.D., Chief and Bruce A. Chabner Chair, Division of Hematology/Oncology, Massachusetts General Hospital; Associate Director, Massachusetts General Hospital Cancer Center; Professor of Medicine, Harvard Medical School

Sir John Burn, MD, FMedSci, Professor of Clinical Genetics, Institute of Genetic Medicine, Newcastle University, UK; Genetics Lead, National Institute of Health Research, UK; Medical Director, QuantuMDx Ltd

John Quackenbush, Ph.D., Professor, Biostatistics and Computational Biology, Cancer Biology Center for Cancer Computational Biology, Dana-Farber Cancer Institute

12:15 Luncheon in the Exhibit Hall with Poster Viewing

OPEN SOURCE PLATFORMS AND COLLABORATIVE TECHNOLOGIES

1:55 Chairperson's Remarks

2:00 User Gateway: A System to Accelerate Molecular Epidemiology
Christopher Farah, Ph.D., Bioinformatics and GIS Specialist, Maine Institute for Human Genetics and Health, Eastern Maine Healthcare Systems
Co-authored with Janet Hock, B.D.S., Ph.D., Senior Investigator, Maine Institute for Human Genetics and Health, Eastern Maine Healthcare Systems
User Gateway is web-based, open source software developed to bridge cancer diagnosis, annotations from banked specimens, and clinical data to outcomes and environmental history. By incorporating GIS technology, existing biobanking functionality is extended through two key functions: advanced specimen requisition and spatiotemporal analysis of patient data. Learn about the core functionality of the software, followed by a software demonstration. Novel use cases will be highlighted.

2:30 A Scientific Spreadsheet for Big Data Analysis, Reporting, and Real-time Collaboration
Mario Morales, Statistician, Simulmedia, Inc.; Programmer, Stanford University School of Medicine
We will present new tools and services that have been designed in collaboration with BD to improve the productivity of biostatisticians, to allow them to work with large volumes of data on a private cloud and on EC2 and to collaborate easily.

3:00 Development and Implementation of Distributed Health Data Networks: Lessons from Medical Product Safety, Public Heath Surveillance, and Comparative Effectiveness Research
Jeffrey Brown, Ph.D., Assistant Professor, Population Medicine, Harvard Pilgrim Health Care Institute, Harvard Medical School
This presentation describes the development, implementation and selected uses of an open-source software platform (PopMedNetTM) for the creation of distributed health data networks. A distributed health data network advances the secondary use of electronic health information by creating standardized and re-usable data sources in multiple sites, as well as tools to use it. Understand the barriers in creating a distributed health network and approaches for overcoming them.

3:30 Closing Featured Speaker
Platform for Clinical Research Networks: Novel Approach towards Discoveries in Rare Diseases
Alex Sherman, Director, Systems, Department of Neurology, Massachusetts General Hospital
This presentation describes a TREAT ALS™ software platform that is currently deployed to support a clinical research network in Lou Gehrig's disease and allows investigators from 100+ academic institutions around the world to collaborate, share data, and biological specimen. This is a unique solution and approach in managing disease-specific research networks and may serve as a model for academic and industry collaboration in finding cures for rare diseases.

4:00 Conference Adjourns

Track 3 Cloud Computing

TUESDAY, APRIL 24

7:00 am Workshop Registration and Morning Coffee

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

- Beyond the Cloud: Improving the R&D Innovation Process through Cloud Services
- Cloud Computing

**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
Sanjay Joshi, Solutions Architect, Life Sciences, EMC Isilon Storage Division

4:15 PLENARY KEYNOTES

Martin Leach, Ph.D., CIO, Broad Institute of MIT and Harvard

Jill P. Mesirov, Ph.D., Associate Director and Chief Informatics Officer; Director, Computational Biology and Bioinformatics, Broad Institute of MIT and Harvard

5:00 - 7:00 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 iPod touches® or 1 of 2 Xbox 360s®*!

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WEDNESDAY, APRIL 25

7:00 am Registration and Morning Coffee

7:55 Chairperson's Opening Remarks
Phillips Kuhl, Co-Founder and President, Cambridge Healthtech Institute

8:00 Keynote Introduction
Bas Burger, President, Global Commerce, BT Global Services

8:15 PLENARY KEYNOTE

Eric D. Perakslis, Ph.D., CIO and Chief Scientist of Informatics, U.S. Food and Drug Administration

8:45 Benjamin Franklin Award & Laureate Presentation

9:10 Best Practices Award Program

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

Sponsored by
CYCLE COMPUTING

IT INFRASTRUCTURE ON THE CLOUD

10:50 Chairperson's Remarks
Christopher Brown, CTO, Opscode

11:00 Building a Scalable Pharmacometrics Platform in the Cloud
Jeffrey Hane, Ph.D., COO and CIO, Metrum Research Group
Adam Kraut, Senior Scientific Consultant, Services, BioTeam

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BIOTEAM
Enabling Science

Moving single applications to the cloud is yesterday's news. Today we build agile infrastructures for leading edge research providers. From elastic HPC clusters to collaborative decision support systems, we will reveal the challenges and introduce best practices in modern research computing in the cloud.

11:30 CVRG: Making Cardiovascular Collaborations Easier in the Cloud
Stephen Granite, Director of Database and Software Development, Center for Cardiovascular Bioinformatics and Modeling, Institute for Computational Medicine, The Johns Hopkins University

The cardiovascular (CV) community needs software tools for managing diverse types of CV data. The CV Research Grid (CVRG) serves the needs of basic and clinical researchers by providing seamless, secure access to study datasets and analysis tools. The CVRG has moved towards the Software as a Service approach, delivering powerful data management and analysis tools to our users that are accessed through the web browser.

12:00 pm HVC -High Volume Computing - Going Where No Research Has Gone Before
Jason Stowe, CEO Cycle Computing

Sponsored by
CYCLE COMPUTING

There was a time when it wouldn't even have been considered - too few computing resources, too much time to complete. But now taking a 10, 20, 100 or 1000 year compute problem and solving it by deploying a very large scale (10s of thousands of cores) compute cluster in the cloud is real. Cycle Computing has taken cloud HPC to new heights of scale and agility. The unthinkable research is now doable. Securely.

12:30 Federation of the Cloud – A World of Options
Michael Cardy, M.Sc., Global Chief Technology Officer, OnX Enterprise Solutions

Sponsored by
OnX Enterprise Solutions

The Cloud continues to rapidly evolve — the latest phase being the Federated Cloud. As organizations look to leverage existing investments in cloud infrastructure residing in their data centers and seamlessly integrate with an external provider's cloud, they realize both elements must work together in federation. Join OnX Enterprise Solutions as we explore the impact and opportunities of federated cloud services.

CLOUD AS A STRATEGIC RESOURCE

1:40 Chairperson's Remarks
Peter J. Boler, Vice President, Life Sciences & Healthcare, Persistent Systems

1:45 Hybrid Strategies for Biomedical Research Data Management
Vas Vasiliadis, Director, Products, Computation Institute, University of Chicago

While some early adopters have realized benefits by incorporating clouds into their analysis pipelines, many challenges remain. In this presentation we will highlight the critical issues associated

with research data management, and describe alternative approaches for addressing these challenges by optimizing the use of local, distributed and cloud-hosted resources.

2:15 Building a Collaborative Informatics Platform for Translational Research: An IMI Project Experience
Yike Guo, Ph.D., Professor, Computing Science, Computing, Imperial College London
In this presentation, we present the design and development of a collaborative research platform for cross-institutional collaborative clinical/ preclinical research and biomarker discovery. Such a platform contains a rich set of advanced methods and systems for large-scale omics data analysis and supports KM tasks for European IMI projects in large scale.

2:45 Next Generation Bioinformatical Analysis on the Cloud *Sponsored by* 华大基因 BGI
Sifei He, Director, BGI Cloud, BGI; Xing Xu, Senior Product Manager, Bioinformatics Center, BGI; Lin Fang, Director, Bioinformatics Center, BGI
While the $1000 genome continues to be a thrilling race, effective genome data mining, interpretation and management presents substantial scientific and technology challenges. This session will share BGI's vision and strategy followed by a LIVE DEMO on BGI Cloud, a key enabling platform that provides efficient and undisruptive way to consume streamlined bioinformatical analysis services for future genomics research and monetization.

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

3:45 Balancing and Augmenting Local Resources with Remote Clouds
Angel Pizarro, Director, ITMAT Bioinformatics Facility, Institute for Translational Medicine and Therapeutics, University of Pennsylvania
Data production advances in next-generation sequencing caused a shortage of compute and data center resources for the Penn Genome Frontiers Institute. Local resources could not be procured fast enough to meet demand. PGFI turned to The Cloud to expand its computational capacity. This talk will consist of a deep-dive technical discussion about enabling technologies that were used to augment local high-performance compute clusters with external cloud resources.

4:15 Virtual Screening On Demand in the Amazon Cloud
Donovan Chin, Ph.D., Senior Investigator I, Novartis Institute for Biomedical Reseach
Virtual Screening is a tool for drug discovery that uses computational power and computer models of drug interaction to filter very large collections of chemical compounds down to a manageable number that may tested for bioactivity. We will discuss our efforts to expand this tool onto the Amazon cloud in way that is able to meet the immediate needs of drug discovery, while at the same time leveraging our internal cloud computing environment in an efficient and cost effective way.

4:45 HP Sequence Services - Building an Open Commercial NGS Platform *Sponsored by* hp
Etzard Stolte, Ph.D., CTO, Life Sciences, Hewlett-Packard EMEA
Offering a secure, easy-to-use, pay-as-you-go Cloud service for next-generation-sequence analysis and storage is challenging. With real-world requirements like proper application life-cycle-management, regional data constraints, and analysis quality control, building an open commercial NGS platform becomes a hard IT problem. This presentation will introduce key successes and compromises made during implementation of HP Sequence Services.

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

6:15 Exhibit Hall Closes

THURSDAY, APRIL 26

8:00 am Featured Speaker Introduction *Sponsored by* hp
David A. Medina, Director, Product Management, Healthcare Analytics & Life Sciences, Business Solutions, Hewlett-Packard

8:10 Featured Speaker: HPC Trends from the Trenches
Chris Dagdigian, Founding Partner and Director of Technology, BioTeam, Inc.
HPC Trends from 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.

HPC AND PHARMA IN THE CLOUD

8:40 Chairperson's Opening Remarks
Michael A. Schulman, M.Sc., Director, Marketing, ScaleMP, Inc.

8:45 Enabling Research in the Cloud *Sponsored by* amazon web services
Matt Wood, Ph.D., Product Manager for HPC and Big Data, Amazon Web Services

Panel Discussion: HPC/Life Science in the Cloud
Moderator: Deepak Singh, Ph.D., Principal Product Manager, Amazon EC2, Amazon Web Services
Panelists:
Anushka Brownley, Product Manager, Cloud Project, Complete Genomics
Angel Pizarro, Director, Institute for Translational Medicine & Therapeutics, University of Pennsylvania
Stephen Litster, Ph.D., Global Lead, Scientific Computing, Novartis Institute for Biomedical Research

9:45 Beyond the Cloud: How Cloud Services Can Drive Performance in Pharma R&D *Sponsored by* BT
John Gillam, IT Services Programme Director, 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 organizations need to do to make cloud solutions work for them along with the how and why.

10:15 Coffee Break in the Exhibit Hall and Poster Competition

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

10:50 Plenary Keynote Panel Introduction
Geoffrey Noer, Senior Director, Product Marketing, Panasas

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A special plenary session featuring trends and challenges in cancer research:
Julian Adams, Ph.D., President, Research and Development, Infinity Pharmaceuticals, Inc.

Jose Baselga, M.D., Ph.D., Chief and Bruce A. Chabner Chair, Division of Hematology/Oncology, Massachusetts General Hospital; Associate Director, Massachusetts General Hospital Cancer Center; Professor of Medicine, Harvard Medical School

Sir John Burn, MD, FMedSci, Professor of Clinical Genetics, Institute of Genetic Medicine, Newcastle University, UK; Genetics Lead, National Institute of Health Research, UK; Medical Director, QuantuMDx Ltd

John Quackenbush, Ph.D., Professor, Biostatistics and Computational Biology, Cancer Biology Center for Cancer Computational Biology, Dana-Farber Cancer Institute

12:15 Luncheon in the Exhibit Hall with Poster Viewing

SECURITY AND CONTROL IN THE CLOUD

1:55 Chairperson's Remarks

2:00 An Expert's Guide through the Identity Landscape
Rich Furr, Head, Global Regulatory Affairs and Chief Compliance Officer, Staff, SAFE-BioPharma Association
The presentation will provide an overview of US and EU government and industry-driven identity management initiatives to develop a trusted internet identity capability community. It will cover topics like identity credentials, identity trust infrastructures, applicable standards, governance models and approaches to cloud based identity management.

2:30 Solution-as-a-Service: Pharmacovigilance Systems on the Multi-Tenanted Platform
Ramin Daron, IT Director, Information Technology, Johnson & Johnson
This presentation is intended to engage industry in discussion about the viability and the challenges to be cleared in order for the multi-tenanted PV Platform to be operationalized at scale and to acheive its value proposition. Concepts of data ownership and security, performance metrics, architectural decisions and changing perceptions to be offered for consideration.

3:00 Clinical Trial Simulations Using Cloud Computing
Russell Towell, Senior Informatics Engineer, Scientific Computing Services, Bristol-Myers Squibb
Tarek Leil, Director, Cardiovascular and Metabolics Pharmacometrics, Bristol-Myers Squibb
Clinical trial simulations are an integral part of the drug development process and require CPU intensive compute resources. Leveraging cloud computing to provision CPU clusters can dramatically reduce the cycle time of trial simulations enhancing its application across drug development portfolios.

3:30 Closing Featured Speaker Introduction
Jonathan Sheldon, Ph.D., Global Senior Director, Translational Medicine, Oracle Health Sciences

3:40 Closing Featured Speaker:
GeneStack — Universal Platform for Genomics Application Development
Misha Kapushesky, CEO GeneStack Ltd.

4:00 Conference Adjourns

TUESDAY, APRIL 24

7:00 am Workshop Registration and Morning Coffee

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

- Leveraging Saas for Next-Gen Sequencing: Case Study with the Galaxy Community
- Data Visualization in Biology: From the Basics to Big Data

**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
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4:15 PLENARY KEYNOTES

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Jill P. Mesirov, Ph.D., Associate Director and Chief Informatics Officer; Director, Computational Biology and Bioinformatics, Broad Institute of MIT and Harvard

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WEDNESDAY, APRIL 25

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8:00 Keynote Introduction
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8:15 PLENARY KEYNOTE

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8:45 Benjamin Franklin Award & Laureate Presentation

9:10 Best Practices Award Program

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

Sponsored by
CYCLE COMPUTING

DATA MODELING AND COMPUTATIONAL INTEGRATIVE TOOLS

10:50 Chairperson's Remarks
William O'Neill, Ph.D., Professor, Bioengineering, University of Illinois at Chicago

11:00 Translational Integrity and Continuity: Individualized Biomedical Data Integration
Xiaoming Wang, Ph.D. Fellow, Computation Institute, University of Chicago and Argonne National Laboratory
This presentation describes an established warehousing system, translational data marts (TraM), to describe the impact of conceptual modeling on the system flexibility, sustainability, and scalability; data integration workflow efficiency; application capacity and performance; and data integrity and interoperability. An oncology data mart (ONCOD) will be used as an example to illustrate a lifecycle of a data warehousing system design.

11:30 Computational Statistical Image Modeling for Lesion Diagnosis and Classification
William O'Neill, Ph.D., Professor, Bioengineering, University of Illinois at Chicago
This presentation describes a method of diagnosing and classifying lesions for cancer and cancer type using only universally available computational software. Multimodal images of brain, breast, and thyroid are modeled by partial difference equations estimated as generalized least squares realizations. Model parameters afford individual lesion statistical diagnosis while Fisher linear discriminants optimally classify models of demographic populations.

12:00 pm Gene Expression Quantification and Variation Detection from RNA-Seq data

Sponsored by
华大基因 BGI

Xin Jin, Group Leader of Genetic Disorder, BGI
RNA-Seq is a promising technique for quantification analysis as well as genome-wide variation analysis. Here we introduce a project that BGI is participating in to demonstrate the utility of RNA-Seq, establish standards and develop better algorithms for the quantification analysis. Also we introduce SOAPsplice and SOAPfusion, to ab initio detect splice junctions and gene fusions at a genome-wide level by RNA-Seq.

12:30 Luncheon Presentation: Enabling Scientific Discovery While Iteratively Cleaning and Standardizing Complex Clinical and Research Data

Sponsored by
BioFortis

Matthew Clark, Ph.D., Senior Application Scientist, BioFortis, Inc.
Today's researchers have access to an ever-expanding treasure trove of electronic data. Traditionally, datasets must be cleaned and standardized before meaningful query and analysis can yield scientific insights. Large scale data cleaning efforts rarely meet desired objectives in time and on budget, delaying scientific discovery. This presentation will describe a new paradigm that allows cross-functional teams to collaboratively diagnose, repair, and circumvent data problems while delivering scientific value every step of the way.

1:40 Chairperson's Remarks
Michael Liebman, Ph.D., President & Managing Director, Strategic Medicine, Inc.
Sabrina Molinaro, Ph.D., Head, Epidemiology and Health Research Services, National Research Council of Italy

1:45 Personalized Medicine: Moving from Correlation to Causality in Breast Cancer
Michael Liebman, Ph.D., President & Managing Director, Strategic Medicine, Inc.
Sabrina Molinaro, Ph.D., Head, Epidemiology and Health Research Services, National Research Council of Italy

Co-authored with Valentina Lorenzoni, Stefania Pieroni, and Fabio Mariani, Unit of Epidemiology and Biostatistics, Institute for Clinical Physiology, National Research Council (Italy)
We have developed a fundamental model of the disease process for breast cancer, from pre-disease through early detection, treatment and outcome, and apply a multi-scalar approach across the risk assessment-enhanced diagnosis-therapeutic decision axis and will present the modeling methodologies. We believe this approach will improve clinical decisions and also drive enhanced development of diagnostics and therapeutic interventions.

GENE EXPRESSION DATA ANALYSIS

2:15 The Allen Mouse Brain Atlas: Towards an Infrastructure for Neuroscience Data
Chinh Dang, Senior Director, Technology, Allen Institute for Brain Science
Launched in 2003, the Allen Mouse Brain Atlas contains genome-wide cellular level gene expression data in the adult mouse brain. Since then, additional gene expression atlases of the developing mouse brain, mouse spinal cord, adult human brain, developing human brain, and non-human primate brain are freely and publicly available with associated visualization and mining tools. Learn how this data can be leveraged by the genomic, bioinformatics, and other research communities.

2:45 Teradata Drug Discovery Analytics Framework
Sponsored by TERADATA Raising Intelligence
Ed Acker, Ph.D., Vice President, Life Sciences, Teradata
The Teradata Drug Discovery Analytics Framework removes data analysis barriers to drug discovery analytics. The barriers include data volume limits, data access limits(semantic, structural,location), data analysis limits (segmentation, aggregation) and analysis performance limits (data movement, application architecture).The major components of this framework are a 3NF Logical Data Model, a Massively Parallel Processing Share Nothing Data Management Architecture, in-database analytics for structured and unstructured data, a SQL interface for unstructured data and shareable virtual data labs self-provisioned by scientists.

3:00 Speaker to be Announced
Sponsored by ELSEVIER

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

3:45 Statistical Issues in the Analysis of Genome-Wide Methylation Arrays as Compared to Gene Expression Data: A Breast Cancer Example
Sandeep Singhal, Bioinformatician, Breast Cancer Translational Research Laboratory J.C. Heuson (BCTL), Jules Bordet Institute
This presentation will highlight some statistical methods for genome wide methylation data analysis with an emphasis on what new information is gained from breast cancer studies for which both DNA methylation and gene expression data are available and what conclusions can be reached about the role of DNA methylation on gene expression.

MOLECULAR PROFILING DATA

4:15 'Omics Interpretation Solutions - A Big Pharma Practical Guide
Jack Pollard, Ph.D., Associate Director, sanofi Oncology, Translational & Experimental Medicine – Bioinformatics
Lars Greiffenberg, Ph.D, sanofi R&D-IS, Health-IT, Biology Solutions
While generating testable hypotheses from 'omics data offers one kind of challenge, implementing informatics solutions company-wide presents a different set of technology, people and process challenges. We will share our recent successful experience and practical insights at specifying and implementing an integrated solution for 'omics data management, analysis, and interpretation for sanofi R&D.

4:45 GenomeSpace: An Environment for Frictionless Bioinformatics
Michael Reich, Director, Cancer Informatics, Broad Institute of MIT and Harvard

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

6:15 Exhibit Hall Closes

THURSDAY, APRIL 26

8:40 Chairperson's Opening Remarks
Justin H. Johnson, Director of Bioinformatics, EdgeBio; Project Lead of Validation Protocol, Archon Genomics X Prize Presented by Express Scripts

BIOINFORMATICS & THE CLOUD

8:45 An Algorithm for Identifying Multiply-Modified Endogenous Proteins Using Both Full-Scan and High Resolution Tandem Mass Spectrometric Data
Ray Fyhr, Project Lead, MRL-IT, Merck
This presentation describes a new top-down proteomics algorithm that runs on Linux clusters either in-house or clouded. This algorithm relies only on a predefined list of 'differential' modifications (i.e., phosphorylation) and a FASTA-formatted protein database, and is not constrained to full-length proteins for identification. The algorithm combines hard core computer science, protein science, and Mass Spectrometry.

9:15 Large-Scale Prediction of Transcription Factor Binding Sites in Multiple Genomes Using Cloud Computing
Chuanbin Du, Ph.D., Post-Doctoral Fellow, Department of Bioinformatics and Genomics, University North Carolina at Charlotte
This presentation describes a computational method to predict transcription factor binding sites (TFBSs) accurately and efficiently using cloud computing. We designed a fast parallel algorithm based on the method GLECLUBS (GLobal Ensemble CLUsters of Binding Sites). The new algorithm is implemented on the Windows Azure platform.

9:45 The Path Toward a Medical Grade Genome
Justin H. Johnson, Director of Bioinformatics, EdgeBio; Project Lead of Validation Protocol, Archon Genomics X Prize Presented by Express Scripts
The Archon Ge3nomics X PRIZE presented by Express Scripts created a "Validation Protocol" that is helping to define for the first time what it means to have a complete and accurate "medical grade" whole human genome sequence. The primary role of the "Validation Protocol" is to enable the X PRIZE Foundation to declare a winner of the $10 Million Competition

in 2013 without controversy. This presentation will describe the Validation protocol in detail, as well as present preliminary data on the methodologies employed to reconstruct the fosmid data, compare sequencing technologies to minimize bias, and develop software for whole genome comparison to fosmid data for contestant grading.

10:15 Coffee Break in the Exhibit Hall and Poster Competition

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

10:50 Plenary Keynote Panel Introduction
Geoffrey Noer, Senior Director, Product Marketing, Panasas

11:00 Plenary Keynote Panel: A special plenary session featuring trends and challenges in cancer research:

Julian Adams, Ph.D., President, Research and Development, Infinity Pharmaceuticals, Inc.

Jose Baselga, M.D., Ph.D., Chief and Bruce A. Chabner Chair, Division of Hematology/Oncology, Massachusetts General Hospital; Associate Director, Massachusetts General Hospital Cancer Center; Professor of Medicine, Harvard Medical School

Sir John Burn, MD, FMedSci, Professor of Clinical Genetics, Institute of Genetic Medicine, Newcastle University, UK; Genetics Lead, National Institute of Health Research, UK; Medical Director, QuantuMDx Ltd

John Quackenbush, Ph.D., Professor, Biostatistics and Computational Biology, Cancer Biology Center for Cancer Computational Biology, Dana-Farber Cancer Institute

12:15 Luncheon in the Exhibit Hall with Poster Viewing

BIOINFORMATICS ADVANCES AND TRENDS

1:55 Chairperson's Remarks
Vishal Rosha, Senior Scientist, Bioprocess Research & Development, Novartis Pharma Ag

2:00 Omics Strategies to Improve Bioprocess Development
Vishal Rosha, Senior Scientist, Bioprocess Research & Development, Novartis Pharma Ag
This presentation describes Omics strategies and various activities to expand cell/process understanding and to further improve/control bioprocessing. The aim of these studies is to systematically collect Omics data from cell lines under various conditions and to investigate the impact of bioprocess parameters such as time viability, stress, pH, temperature, etc. in order to optimize process conditions, cell treatment, and cell line selection towards product quality, quantity, and reproducibility.

2:30 Persephone: Visualizing the Future of Genomics Data Integration
Timothy Swaller, Director, Information Technology and Genomics, Ceres, Inc.
Persephone is a visualization tool currently available that provides the performance and data integration capabilities needed by researchers in this age of high volume data. Persephone integrates both public and private genomic data. Learn how Persephone provides the performance and functionality required by researchers to compare, filter, query through these large, complex datasets through a visual medium.

3:00 Deconvolution of Label-Free Functional Profiles from Native Cells
Roger (Rangjiao) Liu, Ph.D., Research Manager, Bioinformatics, Life Science Development, Corning
Label-free technology is gaining momentum in drug discovery; the interpretation of label-free profiling using bioinformatics algorithms is largely unknown to the scientific world, and will be very valuable to the industry. Learn the development of label-free methods for drug discovery, the understanding and interpretation of label-free data sets, and how to generate hypotheses using pharmacology knowledgebase and bioinformatics algorithms.

3:30 Closing Featured Speaker Introduction
Jonathan Sheldon, Ph.D., Global Senior Director, Translational Medicine, Oracle Health Sciences

3:40 Closing Featured Speaker: GeneStack — Universal Platform for Genomics Application Development
Misha Kapushesky, CEO GeneStack Ltd.

4:00 Conference Adjourns

Track 5 Next-Generation Sequencing Informatics

TUESDAY, APRIL 24

7:00 am Workshop Registration and Morning Coffee

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

- Leveraging SaaS for Next-Gen Sequencing: Case Study with the Galaxy Community
- Cloud Computing

**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
Sanjay Joshi, Solutions Architect, Life Sciences, EMC Isilon Storage Division

4:15 PLENARY KEYNOTES

Martin Leach, Ph.D., CIO, Broad Institute of MIT and Harvard

Jill P. Mesirov, Ph.D., Associate Director and Chief Informatics Officer; Director, Computational Biology and Bioinformatics, Broad Institute of MIT and Harvard

5:00 - 7:00 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 iPod touches® or 1 of 2 Xbox 360s®*!

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WEDNESDAY, APRIL 25

7:00 am Registration and Morning Coffee

7:55 Chairperson's Opening Remarks
Phillips Kuhl, Co-Founder and President, Cambridge Healthtech Institute

8:00 Keynote Introduction
Bas Burger, President, Global Commerce, BT Global Services

8:15 PLENARY KEYNOTE

Eric D. Perakslis, Ph.D., CIO and Chief Scientist of Informatics, U.S. Food and Drug Administration

8:45 Benjamin Franklin Award & Laureate Presentation

9:10 Best Practices Award Program

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

Sponsored by
CYCLE COMPUTING

ORGANIZATIONAL APPROACHES TO NGS INFORMATICS

10:50 Chairperson's Remarks
Kevin Davies, Ph.D., Editor-in-Chief, Bio-IT World

11:00 Washington University Approach to NGS Informatics
David J. Dooling, Ph.D., Assistant Director, The Genome Institute, Washington University, St. Louis

11:30 Broad Approach to NGS Informatics
Toby Bloom, Ph.D., Director, Informatics, Genome Sequencing, Broad Institute

12:00 pm The Informatics of Whole Human Genome Sequencing

Sponsored by
Complete genomics

Jason M. Laramie, Ph.D., Principal Application Scientist, Complete Genomics, Inc.
In the last three years, there has been a deluge of data generated from the advancement of a variety of sequencing technologies. This massive amount of data has created a number of unique informatics challenges. Through numerous examples, this talk will cover the informatics challenges of sequencing over five hundred whole human genomes per month.

12:15 Blind Validation of Omixon Software for Diagnostic Applications: Oncogenes and HLA

Sponsored by
OMIXON BIOCOMPUTING SOLUTIONS

Attila Berces, Ph.D., CEO, Omixon
Omixon presents clinical grade analysis using NGS data for target-specific variants of oncogenes and HLA/MCH genes. The studies are based on Illumina, Ion Torrent and Roche 454 data, and validated by capillary Sanger sequence comparisons. Omixon software correctly identified challenging variants such as indels up to 62 bp. The HLA analysis was validated in collaboration with the Hungarian Blood Services and serves in companion diagnostics development in the clinical trials of Genetic Immunity.

12:30 Luncheon Presentation
Ion Torrent: Open, Accessible, Enabling

Sponsored by
life technologies™

Matt Dyer, Ph.D., Associate Director, Bioinformatics & Community, Ion Torrent, Part of Life Technologies
Ion Torrent has pioneered an entirely new approach to sequencing that enables a direct connection between chemical and digital information and leverage decades of semiconductor technology advances. The result is the first commercial sequencing technology that does not use light, and as a result delivers unprecedented speed, scalability, accuracy, and low cost. In just the first year the Ion Torrent Personal Genome Machine (TM) has become the fastest selling sequencing platform. The throughput scaled 100X, from 10Mb to 1Gb, in just the first year and will scale another 100X in the next year with the new Proton (TM) sequencer, which will enable the single day $1000 human genome. Automated data analysis is driven by Torrent Suite, an open-source software suite that provides a simple and intuitive interface to streamline data analysis and provide results in minutes to hours, not days. Built on top of Torrent Suite is a flexible SDK that allows users to expand the analysis capabilities through the development and utilization of plugins and APIs.

1:40 Chairperson's Remarks
Rick Friedman, Vice President, Marketing & Product Management, Terascala, Inc.

1:45 NGS Informatics - Surnames Leakage, Hacking and Genetic Privacy
Yaniv Erlich, Ph.D., Principal Investigator, Whitehead Fellow, Whitehead Institute for Biomedical Research

2:15 Panel Discussion: Organizational Approaches to NGS Informatics and Privacy
Moderator to be Announced
Panelists:
David J. Dooling, Ph.D., Assistant Director, The Genome Institute, Washington University, St. Louis
Toby Bloom, Ph.D., Director, Informatics, Genome Sequencing, Broad Institute
Yaniv Erlich, Ph.D., Principal Investigator, Whitehead Fellow, Whitehead Institute for Biomedical Research

2:45 Using Tiered Archives to Reduce Storage Costs for Next Gen Instrument Data
Sponsored by Quantum
Will McGrath, Manager, Business Development, Quantum
Next generation genomic sequencers and other instruments are becoming smarter in how they generate data off-instrument, but still data storage requirements grow. Some suggest the cost of managing and analyzing this data will outpace the cost to actually sequence. Research institutions and bio-informatics firms have more aggressively begun to set up tiered storage environments to deal with increasing power and cooling costs and shrinking data center footprint of storing and protecting all this big data. This sponsor session will highlight strategies certain life science customers are using for long-term data tiering, archival, and data protection for handling next gen instrument data using solutions like Quantum's StorNext software and appliances.

3:00 Next Generation Software for Next Generation Sequencing Data
Sponsored by Genedata solutions in silico
Tamas Rujan, Product Manager, Genedata Expressionist
- Genedata Expressionist – data management, processing, and analysis in one powerful enterprise solution
- Data visualization – more than just a nice to have
- Integrative data analysis – better insight into biological systems and superior biomarkers
- No limitations on data size – remove one of the major bottlenecks for NGS

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

CLOUD COMPUTING & COLLABORATIVE TECHNOLOGIES

3:45 NGS Pipelines in the Cloud
Peter J. Tonellato, Ph.D., Visiting Professor, Senior Research Scientist, Pathology, BIDMC & Center for Biomedical Informatics, Harvard Medical School

4:15 Transparent and Public Genomics
Alexander Wait Zaranek, Ph.D., Director, Informatics, Harvard Personal Genome Project, Genetics, Harvard Medical School
At the Personal Genome Project, we are building a transparent and public resource consisting of genomes, detailed phenotypes, as well as cell-lines and other tissue samples for more than 100,000 individuals. With inspiration from the open source and free knowledge movements, we will discuss new ways to benefit from the breathtaking improvements in genomic technologies.

4:45 BaseSpace: A Scalable Cloud Platform for Research and Clinical Sequencing Informatics
Sponsored by illumina
Alex Dickinson, Senior Vice President, Cloud Genomics, Illumina, Inc.
The rapid migration of sequencing from the core lab, to the researcher desktop, to the clinical lab has major implications for bioinformatics. In particular, these new users are looking for solutions that provide ease of use, require no investment in IT infrastructure, and are compliant with the appropriate regulations. Illumina has developed BaseSpace, a cloud computing platform that meets these needs by seamlessly linking on-instrument, local cloud, and public cloud bioinformatics.

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

6:15 Exhibit Hall Closes

THURSDAY, APRIL 26

TRANSLATING GENOMIC DATA AND RESEARCH INTO CLINICAL PRACTICE

8:40 Chairperson's Opening Remarks
Gholson J. Lyon, M.D., Ph.D., Assistant Professor in Human Genetics, Cold Spring Harbor Laboratory; Research Scientist, Utah Foundation for Biomedical Research

8:45 The Gene Partnership
Isaac (Zak) Kohane, M.D., Ph.D., Director, Children's Hospital Informatics Program; Henderson Professor of Pediatrics and Health Sciences and Technology, Harvard Medical School (HMS); Co-Director, HMS Center for Biomedical Informatics and Director of the HMS Countway Library of Medicine

9:15 Carpe Novo & Clinical Genome Sequencing
Elizabeth Worthey, Ph.D., Assistant Professor, Human and Molecular Genetics Center, Department of Pediatrics, Bioinformatics Program, Medical College of Wisconsin

9:45 Embedded NGS Processing with iRODS in DDN SFA Storage Controllers
Sponsored by DataDirect NETWORKS Information in Motion
Jan Jitze Krol, Solutions Architect, Life Sciences, DataDirect Networks, Inc.
NGS pipelines produce vast amounts of data. It has becomes a challenge to manage and process these large data sets. The SFA10KE and SFA12KE line of storage controllers offers the unique capability to embed user processes inside the controller, giving those processes the fastest access to the data. These platforms can facilitate pipeline automation, and reduce the overall time to results.

10:00 Rapid Biological Interpretation of Human NGS Data via Ingenuity® Variant Analysis™
Sponsored by INGENUITY SYSTEMS
Sandeep Sanga, Ph.D., Bioinformatics Product Development Scientist, Ingenuity Systems
Biological interpretation of thousands of potentially causal variants is a bottleneck in extracting valuable insights from NGS studies, often requiring months of effort after completion of read alignment and variant calling steps. Here we demonstrate

Ingenuity® Variant Analysis™ (www.ingenuity.com) as a tool for empowering clinical researchers to quickly zero in on the few variants that are most compelling for follow-up.

10:15 Coffee Break in the Exhibit Hall and Poster Competition

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

10:50 Plenary Keynote Panel Introduction
Geoffrey Noer, Senior Director, Product Marketing, Panasas

11:00 Plenary Keynote Panel: A special plenary session featuring trends and challenges in cancer research:
Julian Adams, Ph.D., President, Research and Development, Infinity Pharmaceuticals, Inc.

Jose Baselga, M.D., Ph.D., Chief and Bruce A. Chabner Chair, Division of Hematology/Oncology, Massachusetts General Hospital; Associate Director, Massachusetts General Hospital Cancer Center; Professor of Medicine, Harvard Medical School

Sir John Burn, MD, FMedSci, Professor of Clinical Genetics, Institute of Genetic Medicine, Newcastle University, UK; Genetics Lead, National Institute of Health Research, UK; Medical Director, QuantuMDx Ltd

John Quackenbush, Ph.D., Professor, Biostatistics and Computational Biology, Cancer Biology Center for Cancer Computational Biology, Dana-Farber Cancer Institute

12:15 Luncheon in the Exhibit Hall with Poster Viewing

SEQUENCING DATA ANALYSIS AND APPLICATIONS

1:55 Chairperson's Remarks
Dawn Van Dam, General Manager, Cambridge Healthtech Associates

2:00 Understanding Adaptive Immune Repertoires by High-Throughput Screening and Next-Generation Sequencing
Roberto Polakiewicz, Ph.D., Chief Scientific Officer, Cell Signaling Technology
The presentation provides insight into how antibody repertoires develop in response to antigen challenges. With the advent of next-generation sequencing, it is now possible to comprehend the vast diversity of Antibody and T cell receptor repertoires. This has important implications for basic science as well as for antibody drug discovery.

2:30 Measurement of T Cell Repertoire Diversity in the Peripheral Blood by Novel Multiplex PCR and Next-Generation Sequencing Methods
Jian Han, Ph.D., Faculty Investigator, Hudson Alpha Institute for Biotechnology
This presentation describes the Repertoire 10K or R10K project – a new method for analysis of the immune repertoire by high-throughput sequencing and informatics, and a new index for measurement of health status and disease prognosis. This method is based on semi-quantitative and comprehensive analysis of the T cell receptor beta CDR3 sequences present in peripheral blood.

3:00 Assess and Minimize False SNVs from RNA-Seq Analysis
Wenming Xiao, Ph.D., Staff Scientist, Division of Computational Biology, Center for Information Technology, National Institutes of Health
RNA-Seq analysis is widely used to discover SNVs in cancer samples. However, many people are struggling with the false results due to software error or mis-mapping of reads. The methodology and process we developed would help researchers to discover SNVs with great accuracy and thus minimize the risk of wasted effect due to analysis error.

3:30 Closing Featured Speaker Introduction
Jonathan Sheldon, Ph.D., Global Senior Director, Translational Medicine, Oracle Health Sciences

3:40 Closing Featured Speaker: GeneStack — Universal Platform for Genomics Application Development
Misha Kapushesky, CEO GeneStack Ltd.

4:00 Conference Adjourns

Track 6 Systems and Multiscale Biology

TUESDAY, APRIL 24

7:00 am Workshop Registration and Morning Coffee

8:00 am - 4:00 pm Pre-Conference Workshops*
Please see page 3 for a list of available 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
Sanjay Joshi, Solutions Architect, Life Sciences, EMC Isilon Storage Division

4:15 PLENARY KEYNOTES

Martin Leach, Ph.D., CIO, Broad Institute of MIT and Harvard

Jill P. Mesirov, Ph.D., Associate Director and Chief Informatics Officer; Director, Computational Biology and Bioinformatics, Broad Institute of MIT and Harvard

5:00 - 7:00 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 iPod touches® or 1 of 2 Xbox 360s®*!

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WEDNESDAY, APRIL 25

7:00 am Registration and Morning Coffee

7:55 Chairperson's Opening Remarks
Phillips Kuhl, Co-Founder and President, Cambridge Healthtech Institute

8:00 Keynote Introduction
Bas Burger, President, Global Commerce, BT Global Services

8:15 PLENARY KEYNOTE

Eric D. Perakslis, Ph.D., CIO and Chief Scientist of Informatics, U.S. Food and Drug Administration

8:45 Benjamin Franklin Award & Laureate Presentation

9:10 Best Practices Award Program

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

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EXPLORING DATASETS AND BIOLOGICAL SYSTEMS

10:50 Chairperson's Remarks
Kip Harry, Associate Producer, Conferences, Cambridge Healthtech Institute

11:00 Featured Speaker
Moving Beyond the Mean: The Role of Variation in Determining Phenotype
John Quackenbush, Ph.D., Professor, Biostatistics and Computational Biology, Cancer Biology Center for Cancer Computational Biology, Dana-Farber Cancer Institute
New datasets have allowed us to explore other properties of biological systems, to embrace natural variation and stochastic effects, and to explore the way in which variation defines phenotypes and the transitions between them. Our work suggests an equally valid and potentially informative question may be: Given two phenotypes, is there a significant difference in the group variance independent of their means.

11:30 From Gene to Function: Understanding Human Variability Using Mechanistic Disease Modeling and Imaginomics in CNS
Hugo Geerts, Ph.D., CSO, Computational Neuropharmacology, In Silico Biosciences
Computer-based mechanistic modeling based upon the physiology of brain networks and the pharmacology of drug-receptor interaction, parametrized with clinical and human imaging data could be a powerful tool to support a variety of decision processes in pre-clinical and clinical CNS R&D. We illustrate an early-stage version of this approach with Alzheimer's disease and schizophrenia that modulate human patient variability in clinical trials and are beyond pre-clinical understanding.

12:00 pm Sponsored Presentation *(Opportunity Available)*

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

1:40 Chairperson's Remarks
Pek Yee Lum, Ph.D., Vice President, Life Sciences, Ayasdi, Inc.

1:45 Chemical-Protein Interactome and its Application in Personalized Medicine and Drug Repositioning
Lun Yang, Ph.D., Principal Investigator, Quantitative Sciences, GlaxoSmithKline
Chemical-Protein Interactome is a computational methodology with a focus on characterizing differential drug efficacy and side effects through the combined analysis of genetic polymorphisms and their impact on chemical-protein interactions and gene expression perturbations. The methodology opens opportunities for developing patient-specific medication in terms of decreasing adverse drug reactions and broadening new uses for old drugs.

2:15 Data Sciences: An Approach to Drug Discovery
Stephen Cleaver, Ph.D., Head, Quantitative Biology, Novartis Institutes for BioMedical Research
The increasing complexity of hypotheses demands not only in depth analysis for each dataset, but also integrative analysis across projects, and groups to realize their full potential for drug discovery. We are developing a multidisciplinary Data Sciences approach by bringing together systems and people of diverse backgrounds to meet the multi-scale and systems challenges.

2:45 Topology as a Novel Approach to Detect Patterns in Complex Data Sets
Pek Yee Lum, Ph.D., Vice President, Life Sciences, Ayasdi, Inc.

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Ayasdi
Mapping worlds of data

We introduce a novel computational platform based on Topological Data Analysis for understanding large and complex biological

datasets. Further, we show how key ideas of topology are uniquely suited to address complex problems for the drug development pipeline. Finally, we demonstrate an application to patient stratification where we identified a new patient subset for breast cancer and the corresponding biomarkers.

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

MULTISCALE MODELING AND SIMULATION

3:45 Featured Speaker
Tying Individual Molecules to Phenotype
Andrew Kasarskis, Ph.D., Vice Chairman, Department of Genetics and Genomic Sciences; Co-Director, Institute for Genomics and Multiscale Biology, Mount Sinai School of Medicine
Technological innovations now allow us to monitor many thousands of individual molecules and their interactions. With this new precision, it is possible to identify distinct sub-populations of molecules in many situations where we could not previously observe them, and we are beginning to probe the relationship between these individual molecular populations and phenotype at both cellular and organismal scales. Progress in both cancer and infectious disease suggests broad and compelling applications for these approaches going forward.

4:15 A Computational Systems Biology Software Platform for Multiscale Modeling and Simulation: Integrating Whole-Body Physiology, Disease Biology, and Molecular Reaction Networks
Thomas Eissing, Ph.D., Head, Systems Biology, Bayer Technology Services GmbH
Diseases are generally a consequence of the dysregulation or malfunction of biological processes on the molecular level. These processes are not isolated, but influence and are influenced by physiology up to whole-body scale. We introduce concepts and show by examples how multiscale models can help to better understand diseases and their progression, as well as potential therapeutic approaches including treatment optimization by a rigorous integration of knowledge, assumptions, and experimental data. Such an approach can also contribute to the personalization of medicine, and is beginning to be applied during drug research and development to rationalize decision making along the development process in the pharmaceutical industry ranging from early target identification to late phase clinical studies.

4:45 Systems Epigenomic Views of Complex Disease Associations Reveal 1000s of Regulatory SNPs.
Manolis Kellis, Ph.D., Associate Professor, MIT Computer Science and Electrical Engineering Department; Head, MIT Computational Biology Group; MIT Computer Science and Artificial Intelligence Laboratory, Broad Institute of MIT and Harvard University
To identify the molecular mechanisms underlying disease-associated variants, we integrate disease studies with large-scale functional genomics studies, including chromatin state maps in multiple human cell types, linking of active enhancers to upstream regulators and downstream targets based on coordinated patterns of activity, and genome-wide brain methylation patterns across hundreds of Alzheimer's patients and healthy controls. These reveal global associations of thousands of enhancer elements with complex human disease that are chromatin-state-specific and cell type-specific, suggesting that thousands of SNPs contribute to the observed disease phenotype.

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

6:15 Exhibit Hall Closes

THURSDAY, APRIL 26

WEB-BASED PLATFORMS FOR SYSTEMS MEDICINE

8:40 Chairperson's Opening Remarks
Subha Madhavan, Ph.D., Director, Clinical Research Informatics, Lombardi Comprehensive Cancer Center; Director, Biomedical Informatics, Georgetown-Howard Universities CTSA, Georgetown University Medical Center

8:45 G-DOC: A Systems Medicine Platform for Personalized Oncology
Subha Madhavan, Ph.D., Director, Clinical Research Informatics, Lombardi Comprehensive Cancer Center; Director, Biomedical Informatics, Georgetown-Howard Universities CTSA, Georgetown University Medical Center
The Georgetown Database of Cancer (G-DOC) is a generic and flexible web-based platform that serves to enable basic, translational, and clinical research activities by integrating patient characteristics and clinical outcome data with a variety of high-throughput research data in a unified environment. Through this modular, extensible, and flexible infrastructure, we can quickly and easily assemble new translational web applications with both analytic and generic administrative features.

9:15 Data Integration around Hierarchically and Modularly Organized Protein-Protein Interaction Network
Bing Zhang, Ph.D., Assistant Professor, Department of Biomedical Informatics, Vanderbilt University School of Medicine
Traditional graph-based network visualization techniques quickly become inadequate as network size and data complexity increase. We propose NetGestalt, a novel web-based data integration framework that exploits the inherent hierarchical modular architecture of protein-protein interaction networks to achieve high scalability. Using multidimensional cancer omics, as an example, we show that Netgestalt allows simultaneous presentation of large scale experimental and annotation data from various sources.

9:45 A Systems Approach to Designing Effective Clinical Trials
Vincent Fusaro, Ph.D., Research Associate, Center for Biomedical Informatics, Harvard Medical School
Randomized clinical trials are unsustainable in the era of personalized medicine due to the exponential number of combinations necessary for evaluating personalized treatment options. Computational methods are necessary to predict the likely outcomes and guide clinical trial designs.

10:15 Coffee Break in the Exhibit Hall and Poster Competition

10:45 Plenary Keynote Panel Chairperson's Remarks
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Jose Baselga, M.D., Ph.D., Chief and Bruce A. Chabner Chair, Division of Hematology/Oncology, Massachusetts General Hospital; Associate Director, Massachusetts General Hospital Cancer Center; Professor of Medicine, Harvard Medical School

Sir John Burn, MD, FMedSci, Professor of Clinical Genetics, Institute of Genetic Medicine, Newcastle University, UK; Genetics Lead, National Institute of Health Research, UK; Medical Director, QuantuMDx Ltd

John Quackenbush, Ph.D., Professor, Biostatistics and Computational Biology, Cancer Biology Center for Cancer Computational Biology, Dana-Farber Cancer Institute

12:15 Luncheon in the Exhibit Hall with Poster Viewing

SYSTEMS PHARMACOLOGY

1:55 Chairperson's Remarks
Avi Ma'ayan, Ph.D., Assistant Professor, Department of Pharmacology and Systems Therapeutics, Mount Sinai School of Medicine

2:00 Data Mining Strategies in Systems Pharmacology and Stem Cell Systems Biology
Avi Ma'ayan, Ph.D., Assistant Professor, Department of Pharmacology and Systems Therapeutics, Mount Sinai School of Medicine
Genome-wide experiments collect data across regulatory layers, including gene expression, transcription factor binding to DNA, epigenetic modifications, as well as protein abundance, protein interactions and protein modifications. Integrating these different types of experimental data is a fundamental challenge of computational systems biology. This presentation describes successful applications of data integration in stem cell systems biology and systems pharmacology.

2:30 Systems Pharmacology Modeling in Drug Research and Development
Oleg Demin, Ph.D., CSO, Institute for Systems Biology SPb
Quantitative Systems Pharmacology (QSP) is an emerging modelling technique that combines the flexibility of systems biology and tractability of compartmental pharmacokinetic–pharmacodynamic modelling techniques. In my presentation the impact of QSP within drug discovery and development is considered by discussing several examples illustrating application of the modeling technique to resolve the problems arising in the field of pharmacology.

3:00 Next-Generation Model-Based Drug Discovery and Development: Quantitative and Systems Pharmacology
Sandy Allerheiligen, Ph.D.,Vice President, Modeling and Simulation, Merck & Co., Inc.

3:30 Closing Featured Speaker:
Platform for Clinical Research Networks: Novel Approach towards Discoveries in Rare Diseases
Alex Sherman, Ph.D., Director, Systems, Neurology, Massachusetts General Hospital
This presentation describes a TREAT ALS™ software platform that is currently deployed to support a clinical research network in Lou Gehrig's disease and allows investigators from 100+ academic institutions around the world to collaborate, share data, and biological specimen. This is a unique solution and approach in managing disease-specific research networks and may serve as a model for academic and industry collaboration in finding cures for rare diseases.

4:00 Conference Adjourns

TUESDAY, APRIL 24

7:00 am Workshop Registration and Morning Coffee

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

- Utilization of EHRs/EMRs for Protocol Design, Site Identification, Patient Recruitment and Real-time Pharmacovigilance
- Information Management and Healthcare Delivery at Point-of-Care

**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

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8:15 PLENARY KEYNOTE

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8:45 Benjamin Franklin Award & Laureate Presentation

9:10 Best Practices Award Program

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

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CYCLE COMPUTING

INTEGRATING SYSTEMS TO IMPROVE TRIAL DESIGN AND OPERATIONS

10:50 Chairperson's Remarks
Aaron Kamauu, M.D., CEO, Healthcare Data Analytics, Anolinx LLC; former Head, Healthcare Data Strategy, Roche and Genentech

11:00 Enabling Innovation and Decision Making Electronically in Clinical Trial Design and Interpretation
Laszlo Vasko, Director, R&D Information, AstraZeneca
What makes innovative companies effective? How can innovation & effective decision making be landed in clinical trial design & interpretation so that it's effective, consistent and repeatable? This session will explore how integrative thinking can be tailored to suit the clinical design & interpretation process, with the help of process execution, collaboration, and search technologies.

11:30 Overcoming Challenges in Integrating Systems (EDC, IVRS, CTMS) and Clinical Operations Data
Christine Gibson, Associate Director, Clinical Business Systems, Biogen Idec and Garen Avetissyan, Senior Manager, Clinical Business Systems, Biogen Idec
As functionalities of different clinical systems expand and intermingle, pharmaceutical companies seek to increase efficiencies and reduce costs by connecting these systems through integrations and data interchanges. At Biogen Idec, integrated solutions have been implemented across clinical platforms: IXRS, EDC, CTMS and internal drug distribution systems, presenting technical and non-technical challenges. This session will explore the integration approaches implemented, along with the development challenges and operational benefits of the strategy.

12:00 pm Collaborating in the Cloud: Breaking Down Silos in Clinical Development
Andrew Grygiel, Chief Marketing Officer, ClearTrial

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Leading life sciences companies are leveraging cloud-based systems as collaboration platforms in clinical development, integrating and connecting siloed functions to ensure data consistency and increase operational efficiency. This presentation will examine real-world examples, such as how a Top 20 biopharmaceutical company is relying on a web-based SaaS application to link clinical operations, finance, outsourcing and project management to compress development cycle-times and reduce project cost and risk.

12:15 The Sepsis Interventions Outcomes Research Project: An Analytics Approach
Mark Adams, Ph.D., Principal, Booz Allen Hamilton

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

DATA INTEGRATION TO ENABLE CLINICAL OPERATIONS AND PHARMA DEVELOPMENT

1:40 Chairperson's Remarks
Mark Adams, Ph.D., Principal, Booz Allen Hamilton

1:45 IxRS & EDC to CDR & MSP: An Integrated Platform to Promote Data Exchange, Collaboration, and Advanced Analytics
Bernd Doetzkies, Director, Informatics, Daiichi Sankyo Pharma Development
Integrating a Modeling & Simulation Platform (MSP) with the Clinical Data Repository (CDR) extends functionality to also support advanced and predictive analytics to optimize clinical trial planning and project execution. This results in a significant competitive advantage by minimizing risks & maximizing benefits to subjects and patients, improving trial design and execution, reducing costs and timelines, scaling back number/size of trials, improving decision making processes and developing effective contingency plans.

2:15 Extension of the Data Warehouse Concept to meet the Needs of Clinical Operations and Pharma Development
Norbert Fritz, Development Leader Business Information Warehouse, Pharma Operations, PDGI, F. Hoffmann-La Roche Ltd.
Data integration for reporting and analysis is generally considered the core task of any data warehouse. In pharma development, however, data warehouses are part of a much wider technical and information landscape. This presentation will examine data quality management across different data sources, as well as management of patient recruitment to clarify the impact of pharma business needs on data warehouse functions.

2:45 Transform Clinical Specimen Management to Empower Clinical Research
Robert Stelling, Program Manager for Clinical Genomics & Biomarker IT, Merck & Co., Inc.
Management of clinical specimen and consent information provides a foundation for translational research. It takes an organization, strategic partners, a process and an IT platform to effectively: plan, collect, monitor, track, govern, and destroy clinical specimen and related information. Benefits include reduced cycle time, reduced compliance risk, reduced inventory costs, and improved decision making ability.

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

OPTIMIZING TRIAL MONITORING AND SAFETY THROUGH TECHNOLOGY

3:45 Impact of New Business Models Made Possible by IT and the Implications for Drug Safety
Michael Celeste, Associate Director, Pharmacovigilance Information Management, Pfizer, Inc.
Healthcare data digitization is a fundamental change in the current drug safety/pharmacovigilance business model. Many industries have felt the impact of adopting digital technologies, and drug safety is finally undergoing its own radical changes. Theoretically framing current changes and observing the recent attempts to formulate new models point us toward a future vision for drug safety, and helps us to discover far-reaching implications for the way we do business and how it's regulated.

4:15 Improving Clinical Trial Monitoring through Technology
Mark Apgar, Senior Manager, Clinical Informatics, Allergan
Intelligent implementation and integration of clinical trial technologies is critical to delivering efficiencies to study monitors. Providing information quickly and conveniently allows monitors to provide better service to the sites and sponsor. The integration of IVR/IWR, CTMS, EDC, and CSMS applications will be discussed as a way to reduce non-value added activities for monitors and allow them to better manage their resources for site activities.

4:45 Optimizing Drug Development: Simulating the Drug Development Process in Order to Optimize Development Choices and Decision Making *Sponsored by* Tessella Technology & Consulting
Tom Parke, Head, Clinical Trial Solutions, Tessella, Plc
More and more drug developers are building models of diseases and their drugs in order to address the increasing difficulties and complexities of drug development. By modeling the process itself we can explore how much these models can be relied on for decision making during the process and we can evaluate different development choices in terms of the likelihood of overall business benefit and risk. This talk will look at what this modeling process involves and the opportunities it offers for better decision making.

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

6:15 Exhibit Hall Closes

THURSDAY, APRIL 26

CLINICAL DATA AGGREGATION AND VISUALIZATION TO IMPROVE TRIAL OPERATIONS

8:40 Chairperson's Opening Remarks
Andrew Grygiel, Chief Marketing Officer, ClearTrial

8:45 Case Study: A Clinical Systems Data Aggregation and Visualization Journey
Ted Snyder, Analyst, Clinical Informatics, Infinity Pharmaceuticals
This talk will share lessons learned from Infinity's efforts to empower clinical development teams with innovative visualizations and integrated data. It will include examples of using data visualization to improve understanding, quality of data, and operational performance, and will provide some tips for gaining adoption with data management, clinical operations, safety, and medical monitors.

9:05 Using Data Visualization to Improve the Efficiency and Quality of Clinical Trial Monitoring
Dimitris Agrafiotis, Vice President, Informatics, Johnson & Johnson PRD
Data visualization is a powerful analytic technique that can greatly enhance the efficiency and quality of the clinical monitoring process. However, many visualization applications are aimed at computer-savvy experts and place a high technical burden on the typical end user. In this talk, we describe the approach to developing such a solution by learning from previous successful efforts in drug discovery and process development.

9:25 Case Study: Electronic Trial Master Files (eTMF)
Jean-Remy Behaeghel, Head, GIS Client Account Management, Vertex

9:45 Leveraging Technology to Achieve Optimal Success at Investigator Sites *Sponsored by* ICON A Symbol of Excellence
Adrian Pencak, Vice President, Strategic Development, Data Technology Services, ICON Clinical Research

10:00 Sponsored Presentation *(Opportunity Available)*

10:15 Coffee Break in the Exhibit Hall and Poster Competition

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

10:50 Plenary Keynote Panel Introduction
Geoffrey Noer, Senior Director, Product Marketing, Panasas

11:00 Plenary Keynote Panel:
A special plenary session featuring trends and challenges in cancer research:

Julian Adams, Ph.D., President, Research and Development, Infinity Pharmaceuticals, Inc.

Jose Baselga, M.D., Ph.D., Chief and Bruce A. Chabner Chair, Division of Hematology/Oncology, Massachusetts General Hospital; Associate Director, Massachusetts General Hospital Cancer Center; Professor of Medicine, Harvard Medical School

Sir John Burn, MD, FMedSci, Professor of Clinical Genetics, Institute of Genetic Medicine, Newcastle University, UK; Genetics Lead, National Institute of Health Research, UK; Medical Director, QuantuMDx Ltd

John Quackenbush, Ph.D., Professor, Biostatistics and Computational Biology, Cancer Biology Center for Cancer Computational Biology, Dana-Farber Cancer Institute

12:15 Luncheon in the Exhibit Hall with Poster Viewing

EHR/EMR DATA & CLINICAL TRIALS

1:55 Chairperson's Remarks
Joel White, Executive Director, Health IT Now Coalition

2:00 Creating World-Class HIT Capabilities for Global Clinical Trials
Gary Keith Mallow, Ph.D., Director, Healthcare Information Technology, Merck Research Labs IT/Global Clinical Development IT
Clinical trial planning includes the potential for improved identification of patients who qualify for a study and subsequent enrollment, improved site identification and assessment of country feasibility, and improved protocol refinement processes. This talk will explore lessons learned from pilots in the area of aggregating and harmonizing EHR suitable for this secondary use of healthcare data in planning trials.

2:30 Facilitating Comparative Effectiveness Research through the Use of EHR Data and Clinical Trial Results
Victor Lobanov, Ph.D., Director, Informatics Center of Excellence, Johnson & Johnson
Mining EHR databases and applying meta-analysis techniques to clinical trial results has a potential of dramatically reducing cost and increasing availability of comparative effectiveness research. This presentation will discuss methods and approaches for leveraging commercial EHR data and publically available clinical trial results for CER purposes.

3:00 Integrating a Clinical Trial into the Electronic Medical Record: The Department of Veterans Affairs Point-of-Care Clinical Trial Program
Leonard D'Avolio, Ph.D., Associate Center Director, Biomedical Informatics, MAVERIC, Department of Veterans Affairs
Louis Fiore, M.D., Executive Director, Massachusetts Veterans Epidemiology Research and Information Center (MAVERIC), Dept of Veterans Affairs
In VA hospitals in Boston and Providence, the first "order" option for physicians ordering insulin regimens is "randomize the patient to a clinical trial." These clinical trials unfold behind the scenes of routine care, combining the scientific power of an RCT with the low cost of an observational study. We believe such a model has the power to transform the way science is conducted.

3:30 Closing Featured Speaker:
Platform for Clinical Research Networks: Novel Approach towards Discoveries in Rare Diseases
Alex Sherman, Director, Systems, Neurology, Massachusetts General Hospital
This presentation describes a TREAT ALS™ software platform that is currently deployed to support a clinical research network in Lou Gehrig's disease and allows investigators from 100+ academic institutions around the world to collaborate, share data, and biological specimen. This is a unique solution and approach in managing disease-specific research networks and may serve as a model for academic and industry collaboration in finding cures for rare diseases.

4:00 Conference Adjourns

TUESDAY, APRIL 24

7:00 am Workshop Registration and Morning Coffee

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

- Utilization of EHRs/EMRs for Protocol Design, Site Identification, Patient Recruitment and Real-Time Pharmacovigilance
- Harnessing Social Media for Health Informatics

**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
Sanjay Joshi, Solutions Architect, Life Sciences, EMC Isilon Storage Division

4:15 PLENARY KEYNOTES

Martin Leach, Ph.D., CIO, Broad Institute of MIT and Harvard

Jill P. Mesirov, Ph.D., Associate Director and Chief Informatics Officer; Director, Computational Biology and Bioinformatics, Broad Institute of MIT and Harvard

5:00 - 7:00 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 iPod touches® or 1 of 2 Xbox 360s®*!

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WEDNESDAY, APRIL 25

7:00 am Registration and Morning Coffee

7:55 Chairperson's Opening Remarks
Phillips Kuhl, Co-Founder and President, Cambridge Healthtech Institute

8:00 Keynote Introduction
Bas Burger, President, Global Commerce, BT Global Services

8:15 PLENARY KEYNOTE

Eric D. Perakslis, Ph.D., CIO and Chief Scientist of Informatics, U.S. Food and Drug Administration

8:45 Benjamin Franklin Award & Laureate Presentation

9:10 Best Practices Award Program

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

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HEALTH INFORMATICS NETWORKS IN CLINICAL DECISION SUPPORT

10:50 Chairperson's Remarks
Mark Hulse, R.N., Vice President, Information Technology & CIO, Moffitt Cancer Center

11:00 Disease Genomics Studies *in situ* in the Health Care System
Isaac Samuel Kohane, M.D., Ph.D., Director, Children's Hospital Informatics Program, Henderson Professor of Pediatrics and Health Sciences and Technology, Harvard Medical School
Large numbers of subjects are needed to obtain reproducible results relating disease characteristics to rare events or weak effects. Tools are now available to conduct such research at lower cost and faster pace by using informational and biological byproducts of healthcare. These are reviewed and examples of previously unrealizable genomic studies are highlighted.

11:30 Perspective of Research and Clinical Data Integration
Keith Perry, Associate Vice President & Deputy CIO, University of Texas MD Anderson Cancer Center
The benefits and obstacles of integrating research data into everyday clinical practice can best be summarized by looking at the perspective of those interested in solving the problem. As the technology and science advances at a rapid pace, addressing the vital needs of the researcher, clinician, administrator, and ultimately the patient, are critical for continued success.

12:00 pm Addressing Big Data Challenges to Accelerate Personalized Medicine Initiatives

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HEALTH SCIENCES

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 improves point of care delivery. This session will discuss the challenges associated with integrating cross platform 'omics' data in a manner that scales to thousands of whole genome sequences and combining with clinical data to provide an integrated view across genotype and phenotype.

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

1:40 Chairperson's Remarks
Jonathan Sheldon, Ph.D., Global Senior Director, Translational Medicine, Oracle Health Sciences

1:45 A Next-Generation Health & Research Informatics Platform
Mark Hulse, R.N., Vice President, Information Technology & CIO, Moffitt Cancer Center
Dana E. Rollison, Ph.D., Vice President & Chief Health Information Officer; Associate Member, Department of Cancer Epidemiology, Moffitt Cancer Center
The Moffitt Cancer Center developed a Health & Research Informatics (HRI) platform to link patient clinical information, molecular profiling and tissue data from one of the world's largest cancer biorepositories. This session will describe Moffitt's HRI and how it is being used for research cohort identification and clinical trial matching.

2:20 Empirical and Pathway-Based Genetic Associations with Subtypes of Metabolic Disorder in the Framingham Heart Study
Marsha Wilcox, Director, Pharmacoepidemiology, Johnson & Johnson
Frank J. DeFalco, Manager, Health Informatics Center of

Excellence, Janssen Pharmaceutical Research & Development, a Johnson & Johnson Company
We examined sets of genes associated with empirically identified cardiovascular subtypes in the Framingham Heart Study. Both biological-pathway and empirical approaches were used to identify gene sets contributing to disease. We discuss the results with respect to the current understanding of cardiovascular and metabolic disorders. Strengths and weakness of the methods are discussed as are the informatics challenges and choices.

2:45 Sponsored Presentation *(Opportunity Available)*

3:00 Patient-Centered Solutions for Translational Medicine *Sponsored by* NEXTBIO

Ilya Kupershmidt, Co-Founder & Vice President, Products, NextBio
High-efficiency 'omics' data generation combined with clinical profiles of patients can potentially transform the current translational medicine paradigm. Here, we describe NextBio's secure, cloud-based platform that integrates the largest collection of patients and cell lines with molecular, clinical and drug sensitivity data to enable discovery of biomarkers, patient stratification for clinical trials and development of more effective, targeted therapies.

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

3:45 Using IT to Improve the Clinical Genetic Testing Process

Sandy Aronson, Executive Director, IT, Partners HealthCare Center for Personalized Genetic Medicine
Genetic testing can introduce powerful new clinical workflows into the care delivery process. However, scaling these workflows requires in-depth IT support. This talk will describe IT infrastructure that has been deployed inside and outside of Partners HealthCare to support the genetic testing process. This infrastructure has been used to gather statistics on the clinical genetic knowledge management process.

4:15 Enterprise-Wide Biobanking: Converging Research and Clinical IT Infrastructure

Natalie Boutin, Director IT - Biobanking & Personalized Medicine, Partners HealthCare
As whole genome sequencing enters the clinical space, the lines between clinical and research efforts are increasingly blurred when it comes to IT infrastructure. The biobanking infrastructure required for broad-based research is proving essential to the translation of genomic data into information for productive clinical use.

4:45 Connected Health meets Personalized Medicine

Joseph C. Kvedar, M.D., Center for Connected Health, Harvard Medical School
As wireless and monitoring technologies become ubiquitous, it is possible to envision a unique phenotypic/behavioral map equivalent to one's genetic map. This presentation will cover the interplay between this unique genetic map and one's unique phenotypic map, a more detailed example using obesity, and the use of communications technology to extend genetic counseling expertise to broad geographies.

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

6:15 Exhibit Hall Closes

THURSDAY, APRIL 26

HIT & PERSONALIZED MEDICINE & HEALTH: REAL WORLD USE OF EHR DATA

8:40 Chairperson's Opening Remarks

Hui Cao, M.D., Ph.D., Director, Personalized Healthcare, Strategic Programs, AstraZeneca Pharmaceuticals LP

8:45 Real World Evidence Data for Real World Insight

Hui Cao, M.D., Ph.D., Director, Personalized Healthcare, Strategic Programs, AstraZeneca Pharmaceuticals LP
Life science companies are looking into Real World Evidence (RWE) data for "real-world" insight into their drug development and product lifecycle strategies. We will discuss expectations for RWE data and examine the breadth and scope of data available. Finally, we will present a case study of mining hospital discharge and claims data for business insight to support R&D, marketing, commercial planning, and HEOR.

9:10 The Role of HIT in Implementing Personalized Medicine

Michael Cantor, M.D., Senior Director, Biomedical Informatics Services, Pfizer; Assistant Professor of Medicine, NYU Medical Center
Healthcare IT is an important tool for translating discoveries related to personalized medicine into clinical practice. This talk will explore the range of HIT's role in PM, including clinical decision support, real world data for evaluating personalized medicine in practice, linking clinical phenotypes to genetic data, and improving patient education.

9:35 Opportunities for Pharmaceutical Application of Real World Healthcare Data

Jason Johnson, Executive Director, Informatics IT, Merck
The rapidly changing healthcare landscape has made it both possible and necessary for pharmaceutical companies to make use of "real world" data outside of clinical trials to position and demonstrate value of new products. Here we will present examples of mature and emerging opportunities for use of health data with accompanying challenges.

9:55 Achieving Personalized Healthcare in Real World using Real World Data

Zhaohui (John) Cai, Ph.D., Biomedical Informatics Director, RWE Biomedical Informatics Lead, AstraZeneca

10:15 Coffee Break in the Exhibit Hall and Poster Competition

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John Quackenbush, Ph.D., Professor, Biostatistics and Computational Biology, Cancer Biology Center for Cancer Computational Biology, Dana-Farber Cancer Institute

12:15 Luncheon in the Exhibit Hall with Poster Viewing

EHR/EMR DATA & CLINICAL TRIALS

1:55 Chairperson's Remarks
Joel White, Executive Director, Health IT Now Coalition

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Gary Keith Mallow, Ph.D., Director, Healthcare Information Technology, Merck Research Labs IT/Global Clinical Development IT
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Leonard D'Avolio, Ph.D., Associate Center Director, Biomedical Informatics, MAVERIC, Department of Veterans Affairs
Louis Fiore, M.D., Executive Director, Massachusetts Veterans Epidemiology Research and Information Center (MAVERIC), Dept of Veterans Affairs
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Alex Sherman, Director, Systems, Neurology, Massachusetts General Hospital
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4:00 Conference Adjourns

Track 9 Drug Discovery Informatics

TUESDAY, APRIL 24

7:00 am Workshop Registration and Morning Coffee

8:00 am - 4:00 pm Pre-Conference Workshops*
Please see page 3 for a list of available 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
Sanjay Joshi, Solutions Architect, Life Sciences, EMC Isilon Storage Division

4:15 PLENARY KEYNOTES

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Jill P. Mesirov, Ph.D., Associate Director and Chief Informatics Officer; Director, Computational Biology and Bioinformatics, Broad Institute of MIT and Harvard

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WEDNESDAY, APRIL 25

7:00 am Registration and Morning Coffee

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Phillips Kuhl, Co-Founder and President, Cambridge Healthtech Institute

8:00 Keynote Introduction
Bas Burger, President, Global Commerce, BT Global Services

8:15 PLENARY KEYNOTE

Eric D. Perakslis, Ph.D., CIO and Chief Scientist of Informatics, U.S. Food and Drug Administration

8:45 Benjamin Franklin Award & Laureate Presentation

9:10 Best Practices Award Program

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

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COLLABORATIVE DRUG DISCOVERY

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

11:00 Introducing eTRIKS: European Translational Information & Knowledge Management Services
Anthony Rowe, Ph.D., Principal Scientist - External Innovation, R&D IT, Janssen
Pre-competitive translational research projects in drug development are highly complex, typically involving virtual organizations, challenging science and research data of many different modalities. The eTRIKS project aims to provide and knowledge management services for such projects that has been designed to meet both the needs of the pharmaceutical industry and academia.

11:30 Library Enhancement through the Wisdom of Crowds
Dimitris Agrafiotis, Ph.D., Vice President, Informatics & Research & Early Development, Johnson & Johnson Pharmaceutical R&D
Motivated by a desire to tap into the collective experience of our global medicinal chemistry community, we developed a novel approach for enhancing the diversity of a chemical library involving the application of chemoinformatics techniques followed by community voting to select the most appropriate chemotypes. The solution was deployed as a plugin to 3DX, a powerful data analysis and visualization platform used by more than 1,000 scientists across J&J to support discovery, clinical, and translational research.

12:00 pm Changing the Landscape of Laboratory Informatics Systems to Enhance Innovation Life Cycle Management (ILM)

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Dominic John, Ph.D., Product Marketing Director, Accelrys
Robert Brown, Ph.D., Senior Director, Product Marketing, Accelrys
Today's R&D stakeholders driving innovation need to execute efficiently in globally distributed project teams. This talk discusses an easy to deploy enterprise-level informatics environment for innovation lifecycle management that allows secure collaboration across global, heterogeneous research teams. New capabilities enable distributed teams to deliver significant productivity enhancements to orchestrate, document , manage and accelerate the innovation lifecycle.

12:30 Luncheon Presentation: The Art of Chemistry:Visualizing Chemical Information

Sponsored by
OpenEye Scientific Software

Krisztina Boda, Ph.D., Senior Scientific Developer, OpenEye Scientific Software
The 2D representation of molecular structures has evolved over the centuries along with our knowledge of chemistry and it is still considered to be the "natural language" of chemists. Grapheme TK, a depiction toolkit, provides a novel way to represent information by visualizing complex molecular interactions and projecting 3D information into a 2D layout that is instantly understandable.

FROM BENCH SIDE TO BEDSIDE AND BACK

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

1:45 Integrating Genomic Data from the Bench & Bedside – Challenges and Opportunities for Advancing the Quality of Care and Improving Treatment Outcomes
Guna Rajagopal, Ph.D., Executive Director, Bioinformatics, Cancer Institute of New Jersey; Adjunct Professor, Radiation Oncology, Robert Wood Johnson Medical School
This presentation will describe ongoing activities of a consortium of academic, government and pharmaceutical industry partners working to address and overcome the many challenges and

barriers that impede translational cancer research, especially existing impediments to the flow of data to/from the bench and bedside, in order to develop personalized cancer therapies.

2:15 Cheminformatic/Bioinformatic Analysis of Large Corporate Databases: Application to Drug Repurposing
Raul Rodriguez-Esteban, Ph.D., Senior Scientist, Computational Biology, Boehringer Ingelheim, Inc.
By using knowledge-driven systems in the form of large data stores and applying rational in silico experimental design, researchers have generated workflows that are capable of identifying novel uses for drugs that span the therapeutic pipeline and beyond. Both broadly accessible data, such as Medline and Chembank, in addition to internal proprietary data of the company in the form of gene chip experiments, compound screening databases, and clinical trial information play an important role in the success of drug repositioning.

2:45 Science at the Bench and the Bedside: Less of a Tightrope, More of a Super Highway *Sponsored by* idbs
Robin Munro, Ph.D., Director, Translational Medicine Solutions, IDBS
Bench to Bedside R&D has become an information science. Increasingly diverse and distributed research and clinical communities are wrestling with higher volumes of highly context-rich data. All researchers in scientific, pre-clinical, clinical and 'real-world' domains expect - and should have - real-time access to scientifically aware, context-rich secured information, delivered in an integrated way to mobile and tethered platforms.

3:00 Boosting Distributed Research & Outsourcing: A Framework for Drug Discovery Decision Support *Sponsored by* wingu THE NEW SPEED OF SCIENCE
Nick Encia, CEO & Co-Founder, Wingu
Pharmaceutical companies continue to distribute costs, risks, and opportunities through outsourcing, but the lack of coordination between R&D centers keeps companies mired in inefficient and costly development cycles. The good news is that a technological underpinning for drug discovery is emerging that overcomes the drawbacks of existing tools and processes and that is extensible and customizable to meet evolving needs.

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

3:45 Leveraging Electronic Health Records for Drug Discovery
Lixia Yao, Ph.D., Investigator, Computational Biology, Quantitative Sciences, GlaxoSmithKline
Pushed by legal mandates, EHR systems have seen increasing adoption of standards, improved medical vocabularies and enhancements in technical infrastructure for data sharing across healthcare providers. This presentation will cover specific applications of EHRs in a drug discovery context, such as finding novel relationships between diseases, re-evaluating drug usage, etc.

4:15 Bruton's Tyrosine Kinase from Bench to Bedside: Covalently Silencing B Cells with AVL-292
Juswinder Singh, Ph.D., Founder & CSO, Avila Therapeutics, Inc.

4:45 Enabling Better Data Interpretation through Content Mashup *Sponsored by* THOMSON REUTERS
Andreas Matern, Vice President, Disruptive Innovation, Thomson Reuters Life Sciences
Life sciences organizations face information overload and are challenged with obtaining proper interpretation of data to achieve actionable results. Accessing content, both public as well as private, through programmatic means can lead to true insights. We will discuss how public and private content can be consumed through a variety of technological means, enabling better, faster decision making.

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

6:15 Exhibit Hall Closes

THURSDAY, APRIL 26

HARMONIZING INFORMATION AND GREEN CHEMISTRY

8:40 Chairperson's Opening Remarks

8:45 Substances and the ISO Identification of Medicinal Product (IDMP) Standards: Streamlining Data for Drug Development and Safety Analysis
Larry Callahan, Ph.D., Chemist, Substance Registration System, Office of Critical Path Programs, Food and Drug Administration
To meet the primary objectives of the regulation of medicines and pharmacovigilance, it is necessary to exchange medicinal product information in a robust and reliable manner. The use of standardized medicinal product information is regarded as one of the key elements of this information flow. This presentation will briefly discuss each of the ISO Identification of Medicinal Product Standards and the role of the standards in harmonizing information and furthering drug utilization and development.

9:15 Use of the Electronic Laboratory Notebook to Faciltate Green Chemistry within the Pharmaceutical Industry
Michael Kopach, Ph.D., Research Advisor, Chemical Product Research and Development, Eli Lilly and Company
For commercial R&D processes, minimization of waste and elimination of hazardous solvents are important environmental objectives. To assist with the green chemistry goals, Process Mass Intensity (PMI) are now reported directly within the ELN. The new ELN tool reports Toxic Release Inventory (TRI) chemicals and classifies all solvents with an environmental rating.

9:45 Are You Ready for 'in litero' Drug Discovery? *Sponsored by* Parthys Reverse Informatics The Art of Generating New Knowledge
Srinivasan Parthiban, Ph.D., CEO & President, Parthys Reverse Informatics
Missing information in drug discovery will cost time, quality and money. Our exhaustive synonym dictionary on drug targets will give you a complete, comprehensive actionable data to work in knowledge rich environment. A search query with our periodically updated synonym dictionary will facilitate interoperability; enabling us to find the unfindable. Our Target Thesaurus aims at empowering Drug Discovery Informatics with a computable knowledge ecosystem.

10:00 Development and Application of Chemical Ontologies *Sponsored by* ontochem

Lutz Weber, Ph.D., Director, OntoChem GmbH

Ontologies have great impact for knowledge and data mining in life sciences, chemical ontologies however are just at their beginning. Thus, we have developed the first chemistry ontology editor, to create chemical ontologies and to annotate databases and scientific literature. Through case study examples, attendees will gain an understanding of how to make use out of chemical ontologies for innovative solutions in their research and product development efforts.

10:15 Coffee Break in the Exhibit Hall and Poster Competition

10:45 Plenary Keynote Panel Chairperson's Remarks

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

10:50 Plenary Keynote Panel Introduction

Geoffrey Noer, Senior Director, Product Marketing, Panasas

11:00 Plenary Keynote Panel: A special plenary session featuring trends and challenges in cancer research:

Julian Adams, Ph.D., President, Research and Development, Infinity Pharmaceuticals, Inc.

Jose Baselga, M.D., Ph.D., Chief and Bruce A. Chabner Chair, Division of Hematology/Oncology, Massachusetts General Hospital; Associate Director, Massachusetts General Hospital Cancer Center; Professor of Medicine, Harvard Medical School

Sir John Burn, MD, FMedSci, Professor of Clinical Genetics, Institute of Genetic Medicine, Newcastle University, UK; Genetics Lead, National Institute of Health Research, UK; Medical Director, QuantuMDx Ltd

John Quackenbush, Ph.D., Professor, Biostatistics and Computational Biology, Cancer Biology Center for Cancer Computational Biology, Dana-Farber Cancer Institute

12:15 Luncheon in the Exhibit Hall with Poster Viewing

DRUG REPOSITIONING

1:55 Chairperson's Remarks

2:00 Next-Generation Connectivity Maps

Justin Lamb, Ph.D., Senior Scientist, Broad Institute

The talk will describe our efforts to greatly expand the Connectivity Map using a novel high-throughput low-cost gene-expression profiling technology we have developed. The idea that a comparable system populated with expression profiles of a pharmaceutical company's proprietary chemical matter could serve as an efficient open-innovation platform will also be discussed.

2:30 Systematic Drug Repositioning

Pankaj Agarwal, Ph.D., Director, Computational Biology & Bioinformatics, GlaxoSmithKline

Drug repositioning offers the potential to create value for patients in a quicker time frame. We will examine some recent methods that can systematically identify disease indications for drugs; in particular 1) genome wide association studies (GWAS), 2) connectivity map (expression based drug signatures), 3) side-effects from drug labels, and 4) electronic health records (EHRs).

3:00 Computational Drug Repurposing Using Mountains of Molecular Data

Joel T. Dudley, Ph.D., Director, Informatics and Co-Founder, NuMedii, Inc.; Consulting Professor of Systems Medicine, Department of Pediatrics, Stanford University School of Medicine

It is now possible to apply large-scale integrative informatics approaches to leverage the aggregate molecular data in these repositories towards evaluating new types of biomedical hypotheses. In this talk, I will present our recent work in developing a systematic computational approach to identify novel drug indication relationships using public gene expression profiles.

3:30 Closing Featured Speaker

Pistoia Alliance: Progress in Pre-Competitive Collaboration

Ramesh Durvasula, Ph.D., Director, Molecular Sciences & Candidate Optimization Informatics, Bristol-Myers Squibb

Since 2009, the Pistoia Alliance has drawn significant interest from across the industry. We are focused on the highest value, most-challenging opportunities for developing technology standards and new capabilities. The industry as a whole benefits from the efforts of Pistoia, not just any single segment. Learn the latest updates and current priorities of the Pistoia Alliance projects and how to become engaged in the Pistoia efforts.

4:00 Conference Adjourns

Track 10 Molecular Diagnostics Informatics

TUESDAY, APRIL 24

7:00 am Workshop Registration and Morning Coffee

8:00 am - 4:00 pm Pre-Conference Workshops*
Please see page 3 for a list of available 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
Sanjay Joshi, Solutions Architect, Life Sciences, EMC Isilon Storage Division

4:15 PLENARY KEYNOTES

Martin Leach, Ph.D., CIO, Broad Institute of MIT and Harvard

Jill P. Mesirov, Ph.D., Associate Director and Chief Informatics Officer; Director, Computational Biology and Bioinformatics, Broad Institute of MIT and Harvard

5:00 - 7:00 Welcome Reception in the Exhibit Hall with Poster Viewing
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WEDNESDAY, APRIL 25

7:00 am Registration and Morning Coffee

7:55 Chairperson's Opening Remarks
Phillips Kuhl, Co-Founder and President, Cambridge Healthtech Institute

8:00 Keynote Introduction
Bas Burger, President, Global Commerce, BT Global Services

8:15 PLENARY KEYNOTE

Eric D. Perakslis, Ph.D., CIO and Chief Scientist of Informatics, U.S. Food and Drug Administration

8:45 Benjamin Franklin Award & Laureate Presentation

9:10 Best Practices Award Program

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

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MDX ENABLED PERSONALIZED CARE

10:50 Chairperson's Remarks
Kevin Krenitsky, M.D., COO, Foundation Medicine

11:00 DNA Testing While You Wait: The Promise of Nanowire Diagnostics
Sir John Burn, MD, FMedSci, Professor of Clinical Genetics, Institute of Genetic Medicine, Newcastle University, UK; Genetics Lead, National Institute of Health Research, UK; Medical Director, QuantuMDx Ltd
We have developed a novel method of performing genotyping and sequencing which involves a simple DNA filtration system, a microfluidic PCR followed by use of nanowires as field effect transistors to detect binding of heavily charged nucleotides to single stranded DNA bound by linker molecules to the nanowires. The result is a feasible method of providing handheld, targeted DNA sequencing for diagnostics at the point of need.

11:30 Genomic Analysis Goes to the Clinic: An Intuitive Interface for a Complex Challenge
Kevin Krenitsky, M.D., COO, Foundation Medicine
When a physician reads a thermometer or blood pressure gauge the results inform their diagnosis almost intuitively. For genomic sequencing advanced computational biology can identify medically relevant mutations out of miles of base pairs, but applying this complex analysis to routine care is far from intuitive. This talk will take us from computational biology to an elegant clinical interface, showing how physicians are now using genomic analysis seamlessly in practice to provide the best possible treatment for individual patients.

12:00 pm The Case for a Completely Outsourced End-to-End Biomarker Discovery Program for Pharma with Regards to Next Generation Sequencing
Premal S. Shah, Ph.D., Director Business Development. Genomic Health Inc.
Multiple forces are converging to support a completely outsourced model. Multi-gene diagnostics companies are growing rapidly and can bring to a partnership a robust global infrastructure and experience in the regulatory and reimbursement environment. At the same time, the rapidly evolving NGS space is conducive to outsourcing to alleviate the investment burden for pharma. Thus, the NGS biomarker discovery space lends itself nicely to a model whereby pharma and advanced diagnostics companies—particularly in oncology—can work together to rapidly advance medicine.

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

CLINICAL APPLICATIONS OF MDX

1:40 Chairperson's Remarks

1:45 Challenges for Clinical Acceptance and Application of Cutting Edge Molecular Diagnostic and Therapeutics by the Medical Community
William G. Loudon, M.D., Ph.D., Assistant Professor, Neurosurgery, University of California Irvine; Section Chief, Neurosurgery, Children's Hospital of Orange County

2:15 Clinical Genomicist Workstation: Analyze, Interpret, and Report NextGen-Based Molecular Diagnostic Studies
Rakesh Nagarajan, Ph.D., Assistant Professor, Pathology & Immunology, Washington University
The advent of genome-wide profiling technologies and their routine use in basic science and translational research is now

promoting their application in the clinical setting. However, there are several potent informatics barriers that must be overcome before clinical sequencing can become routine. Good Laboratory Practice-based quality assurance metrics must be established to guarantee the accuracy required to make medical decisions. Genetic variants identified by sequencing must be systematically annotated and interpreted so that a clinical genomicist can decide which are medically actionable. Software applications and technologies are required to facilitate reporting of genomic results and to transmit these data to the electronic health record (EHR). To address these issues, we have developed the Clinical Genomicist Workstation (CGW), which is a 'soup-to-nuts' solution for processing clinical sequencing orders from specimen accessioning to report finalization, sign out, and submission to the EHR.

2:45 Genalysis: Semiconductor Based True Point-of-Care Nucleic Acid Testing for the Real World
Yan Lin Lye, Business Development Associate, DNA Electronics Ltd.
When it comes to nucleic acid testing, the industry has historically been unable to bring technologies out of the lab to enable rapid, simple, and portable point-of-care testing. That is until now. DNA Electronics has developed Genalysis(R), a true point-of-care, sample-to-answer in 30 minutes USB based platform for nucleic acid testing that requires no expensive instrumentation like heat blocks, optics, or cameras. Moreover since DNA Electronics was established with the goal of bringing the innovation, user friendliness and connectivity of consumer electronics to the life sciences, the entire process only requires simple manual steps that deskills a once arduous process to only 1 minute of hands on time. All this is possible, through our proprietary DNA Logic and CMOS based platform which has already revolutionized the sequencing industry by licensing to Ion Torrent and partnering with Roche 454 for their semiconductor based platforms. DNAe's Genalysis platform is poised to bring an equally significant revolution to the molecular diagnostics industry.

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

3:45 The Role of Evidence Based Medicine in the Adoption of Molecular Diagnostics
Katherine Tynan, Ph.D., Business Development & Strategic Consulting for Diagnostics Companies, Tynan Consulting LLC
The enthusiasm with which personalized medicine is being embraced by healthcare providers, payers and patients is testament to the potential of molecular diagnostics to transform the practice of medicine and thereby improve patient outcomes and healthcare cost-effectiveness. This presentation will present the barriers to realize this potential as well as the different stakeholder perspectives, the levels of evidence that can be generated for molecular diagnostics and how they can drive change in the healthcare system will be discussed.

4:15 Interconnected Drug, Disease & Diagnostics Knowledge to Support Personalized Treatment Decisions
Josef Scheiber, Ph.D., Founder, Biovariance
There is a constantly growing knowledge gap between the opportunities of modern medicine and the approaches that are actually applied by physicians. This talk will show an approach how one could partly remediate this problem by bringing research knowledge to the hand of practitioners in order to benefit patient

4:45 Biomarkers for predicting exacerbations in COPD patients
Raymond Ng, Ph.D., Chief Informatics Officer, Computer Science, Proof Centre of Excellence, University of British Columbia
By employing a computationally-driven biomarker discovery approach on a cohort of 240 patients, clinical as well as genomic and proteomic biomarkers were identified that can predict who will have frequent exacerbations. The area under the receiver operating characteristic curve (AUC) of these biomarkers is between 0.70 and 0.80. Such biomarkers, when validated, will provide valuable information to clinicians for managing COPD patients.

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

6:15 Exhibit Hall Closes

THURSDAY, APRIL 26

GENOMIC AND CLINICAL DATA INTEGRATION AND OPEN PLATFORM

8:40 Chairperson's Opening Remarks

8:45 A Fully Automated, Open Platform for Molecular Differential Diagnoses
Jian Han, Ph.D., President and CSO, iCubate
We (iCubate.com) have developed a patented mPCR (multiplex PCR) technology; a fully integrated molecular diagnostic system, the iCubate system, that can perform extraction, amplification, and detection steps, multiplexed, automatically, and in a closed cassette; and established an open business model, iCubate 2.0 (iCubate2.com).

9:15 Clinical Diagnostics Testing with Next Generation Sequencing: Challenges and Opportunities
Eric Klee, Ph.D., Associate Consultant, HSR, Mayo Clinic & Foundation
The emergence of next generation sequencing has opened numerous opportunities to the field of clinical diagnostic testing, but with it also comes the formidable challenge of managing, processing, and interpreting the data. This deluge of data has resulted in the need for bioinformatics expertise to assist in interpretation of NGS results, and innovative systems to aggregate and integrate disparate data sources for the purpose of the resulting variants. This presentation will discuss the challenges and opportunities we have faced in implementing an NGS based clinical diagnostic test at the Mayo Clinic.

9:45 Linking Together Pharmacogenomics Knowledge: Enabling Diagnostic to be Actionable
Eric Neumann, Ph.D., CTO, PanGenX

10:15 Coffee Break in the Exhibit Hall and Poster Competition

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

10:50 Plenary Keynote Panel Introduction
Geoffrey Noer, Senior Director, Product Marketing, Panasas

11:00 Plenary Keynote Panel:
A special plenary session featuring trends and challenges in cancer research:

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Jose Baselga, M.D., Ph.D., Chief and Bruce A. Chabner Chair, Division of Hematology/Oncology, Massachusetts General Hospital; Associate Director, Massachusetts General Hospital Cancer Center; Professor of Medicine, Harvard Medical School

Sir John Burn, MD, FMedSci, Professor of Clinical Genetics, Institute of Genetic Medicine, Newcastle University, UK; Genetics Lead, National Institute of Health Research, UK; Medical Director, QuantuMDx Ltd

John Quackenbush, Ph.D., Professor, Biostatistics and Computational Biology, Cancer Biology Center for Cancer Computational Biology, Dana-Farber Cancer Institute

12:15 Luncheon in the Exhibit Hall with Poster Viewing

MULTIPLEX ASSAY ACCURACY AND TEST RESULT INTERPRETATION

1:55 Chairperson's Remarks

2:00 Personalized Patient Care through the Use of Multi-Biomarker Diagnostics and Novel Software Applications

Alex Bangs, CIO, Crescendo Bioscience, Inc.

A multi-biomarker blood test has been developed to more comprehensively measure disease activity in RA patients, and provide an objective, quantitative complement to traditional patient and physician assessments. These efforts are complemented by tools that enable physicians to track disease trajectory over time and take a more quantitative and personalized approach to patient care.

2:30 Comparing RNASeq Algorithms for Blood Gene Expression

Stan Letovsky, Ph.D., Vice President and CIO, SynapDx Corporation

Different expression quantitation algorithms for RNASeq data can give suprisingly different results. Here we report on comparisons of several algorithms run on the same dataset. We describe the impact of algorithmic choices on reproducibility and sensitivity to detect expression changes.

3:00 Accelerated Development of Diagnostic Assays Using NGENix™ *in silico* Powered Design

Richard Del Mastro, Vice President, Research and Development, IntelligentMDx

IMDx's proprietary NGENix™ bioinformatics platform powers the design process to rapidly develop qualitative and quantitative multiplexed real time PCR-based solutions to detect all strains of pathogens. NGENix™ utilizes modules that identify unique regions within sequenced genomes, designs oligonucleotide solutions, assesses the thermodynamics of the DNA multiplex and reviews cross-reactivity to other genomes. The process is efficient at generating accurate diagnostic assays with continued clinical relevancy.

3:30 Cloud-Based Development of Molecular Diagnostics Tests for Cancer

Ljubomir Buturovic, Ph.D., Vice President and Chief Scientist, Informatics, Pathwork Diagnostics, Inc.

Development of maximally informative genomics-based cancer diagnostics tests can present informatics challenges due to conceptual and computational complexity of analyzing the high-dimensional genomics data. Pathwork Diagnostics developed a cloud-based software solution to this problem. The system had been used to develop informatics for the FDA-cleared Tissue of Origin cancer classification test currently marketed for clinical use, and can be applied to other prognostic and predictive diagnostic tests.

4:00 Conference Adjourns

Track 11 Open Source Solutions

TUESDAY, APRIL 24

7:00 am Workshop Registration and Morning Coffee

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

- Planning and Structuring Collaborative Innovation and Open Source Deals: Techniques and Lessons from the Leaders
- Cloud Computing

**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
Sanjay Joshi, Solutions Architect, Life Sciences, EMC Isilon Storage Division

4:15 PLENARY KEYNOTES

Martin Leach, Ph.D., CIO, Broad Institute of MIT and Harvard

Jill P. Mesirov, Ph.D., Associate Director and Chief Informatics Officer; Director, Computational Biology and Bioinformatics, Broad Institute of MIT and Harvard

5:00 - 7:00 Welcome Reception in the Exhibit Hall with Poster Viewing
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WEDNESDAY, APRIL 25

7:00 am Registration and Morning Coffee

7:55 Chairperson's Opening Remarks
Phillips Kuhl, Co-Founder and President, Cambridge Healthtech Institute

8:00 Keynote Introduction
Bas Burger, President, Global Commerce, BT Global Services

8:15 PLENARY KEYNOTE

Eric D. Perakslis, Ph.D., CIO and Chief Scientist of Informatics, U.S. Food and Drug Administration

8:45 Benjamin Franklin Award & Laureate Presentation

9:10 Best Practices Award Program

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

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OPEN ACCESS MODELS & TOOLS FOR DATA MANAGEMENT, RESEARCH COMMUNICATIONS, AND COMPUTING RESOURCES

10:50 Chairperson's Remarks
Anil Srivastava, Director, Cancer Collaboratory, Open Health Systems Laboratory

11:00 Panel Discussion: Global Shared Cyberinfrastructure for Medical Research
Moderator: Anil Srivastava, Director, Cancer Collaboratory, Open Health Systems Laboratory
Kenneth Buetow, Ph.D., Director, Computational Sciences and Informatics, Arizona State University
Marcia Kean, Chairman, Strategic Initiatives, Feinstein Kean
George A. Komatsoulis, Ph.D., Deputy Director/Chief Operating Officer (acting)/Chief, Informatics Operations Branch (acting), Center for Biomedical Informatics and Information Technology, National Cancer Institute, National Institutes of Health, Department of Health and Human Services
H. Kim Lyerly, M.D., George Barth Geller Professor of Cancer Research, Duke University; Director, Duke Comprehensive Cancer Center
James G. Williams, Director, International Networking, Indiana University
Physical sciences have created the basic infrastructure of advanced networks and high performance computing for research, however, the life sciences have been lagging behind in spite of the growing need for computational and systems biology; translational and personalized medicine; and the fact that data intensity of medical and life sciences may be many times more than physical sciences. The panel will bring together experts from across the world with use cases and a practical vision to put together a Global Shared Cyberinfrastructure for Medical Research. Hear ideas for a practical roadmap that integrates networks and computing resources in accordance with the best of breed knowledge of interoperable, standard based, open source biomedical informatics into an open system and creating an 'ever widening, never ascending' collaboratory framework.

12:00 pm Sponsored Presentation *(Opportunity Available)*

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

1:40 Chairperson's Remarks
Chris Southan, Ph.D., B.Sc.Hons, M.Sc., Consultant, Knowledge Engineering, ChrisDS Consulting

1:45 Mining Drug Targets, Structures and Activity Data Using Public Full-Text Patent Sources and Open Web Tools
Chris Southan, Ph.D., B.Sc.Hons, M.Sc., Consultant, Knowledge Engineering, ChrisDS Consulting
Historically, the estimated 70% of drug discovery data published in patents has been brokered to the academic community and pharmaceutical companies via subscription databases. Recently this monopoly has been broken by a combination of several factors. This presentation will show how these can be combined to extract targets, key compounds and assay results not only from patents but also from papers.

2:15 The New Frontier of Open Access Research

and Tools: Accelerating the Process and Exchange of Medical Research
Jennifer Lin, Ph.D., Product Manager, Public Library of Science
This presentation will share PLoS's innovations in catalyzing the rapid dissemination of medical research communications. It will also discuss how novel tools for navigating, filtering, aggregating, and assessing research content are integral to the advancement of medicine. It will close with a description of PLoS's efforts to this end (article level metrics, PLoS Currents and PloS Hubs), which focus on post-publication organization and content assessment.

2:45 Bioinformatics Algorithms on Emerging Parallel Architectures *Sponsored by*
Jonathan Cohen, Manager, Emerging Applications, NVIDIA Corporation
NVIDIA graphic processor units (GPUs) are high-performance processors designed for intense computational and high-throughput workloads. I'll review open source bioinformatics algorithms and codes that take advantage of NVIDIA GPUs and applications where GPUs may provide benefit. I will share results from NVIDIA's Emerging Applications group to develop efficient computational building blocks for a variety of genomic processing tasks.

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

OPEN ACCESS AND CLOUD COMPUTING

3:45 Balancing and Augmenting Local Resources with Remote Clouds
Angel Pizarro, Director, ITMAT Bioinformatics Facility, University of Pennsylvania

4:15 Transparent and Public Genomics
Alexander Wait Zaranek, Ph.D., Director, Informatics, Harvard Personal Genome Project, Genetics, Harvard Medical School
At the Personal Genome Project, we are building a transparent and public resource consisting of genomes, detailed phenotypes, as well as cell-lines and other tissue samples for more than 100,000 individuals. With inspiration from the open source and free knowledge movements, we will discuss new ways to benefit from the breathtaking improvements in genomic technologies.

4:45 BaseSpace: A Scalable Cloud Platform for Research and Clinical Sequencing Informatics *Sponsored by*
Alex Dickinson, Senior Vice President, Cloud Genomics, Illumina, Inc.
The rapid migration of sequencing from the core lab, to the researcher desktop, to the clinical lab has major implications for bioinformatics. In particular, these new users are looking for solutions that provide ease of use, require no investment in IT infrastructure, and are compliant with the appropriate regulations. Illumina has developed BaseSpace, a cloud computing platform that meets these needs by seamlessly linking on-instrument, local cloud, and public cloud bioinformatics.

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

6:15 Exhibit Hall Closes

THURSDAY, APRIL 26

OPEN SOURCE PLATFORMS AND COLLABORATIVE TECHNOLOGIES

8:40 Chairperson's Opening Remarks

8:45 A Fully Automated, Open Platform for Molecular Differential Diagnoses
Jian Han, Ph.D., President and CSO, iCubate
We (iCubate.com) have developed a patented mPCR (multiplex PCR) technology; a fully integrated molecular diagnostic system, the iCubate system, that can perform extraction, amplification, and detection steps, multiplexed, automatically, and in a closed cassette; and established an open business model, iCubate 2.0 (iCubate2.com).

9:15 Clinical Diagnostics Testing with NGS: Challenges and Opportunities
Eric W. Klee, Ph.D., Assistant Professor of Medical Informatics, Division of Biomedical Informatics and Statistics, Mayo Clinic Rochester
The emergence of next generation sequencing has opened numerous opportunities to the field of clinical diagnostic testing, but with it also comes the formidable challenge of managing, processing, and interpreting the data. This deluge of data has resulted in the need for bioinformatics expertise to assist in interpretation of NGS results, and innovative systems to aggregate and integrate disparate data sources for the purpose of the resulting variants. This presentation will discuss the challenges and opportunities we have faced in implementing an NGS based clinical diagnostic test at the Mayo Clinic.

9:45 Sponsored Presentation *(Opportunity Available)*

10:15 Coffee Break in the Exhibit Hall and Poster Competition

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

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Geoffrey Noer, Senior Director, Product Marketing, Panasas

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Sir John Burn, MD, FMedSci, Professor of Clinical Genetics, Institute of Genetic Medicine, Newcastle University, UK; Genetics Lead, National Institute of Health Research, UK; Medical Director, QuantuMDx Ltd
John Quackenbush, Ph.D., Professor, Biostatistics and Computational Biology, Cancer Biology Center for Cancer Computational Biology, Dana-Farber Cancer Institute

12:15 Luncheon in the Exhibit Hall with Poster Viewing

OPEN SOURCE PLATFORMS AND COLLABORATIVE TECHNOLOGIES

1:55 Chairperson's Remarks

2:00 User Gateway: A System to Accelerate Molecular Epidemiology

Christopher Farah, Ph.D., Bioinformatics and GIS Specialist, Maine Institute for Human Genetics and Health, Eastern Maine Healthcare Systems

Co-authored with Janet Hock, B.D.S., Ph.D., Senior Investigator, Maine Institute for Human Genetics and Health, Eastern Maine Healthcare Systems

User Gateway is web-based, open source software developed to bridge cancer diagnosis, annotations from banked specimens, and clinical data to outcomes and environmental history. By incorporating GIS technology, existing biobanking functionality is extended through two key functions: advanced specimen requisition and spatiotemporal analysis of patient data. Learn about the core functionality of the software, followed by a software demonstration. Novel use cases will be highlighted.

2:30 A Scientific Spreadsheet for Big Data Analysis, Reporting, and Real-time Collaboration

Mario Morales, Statistician, Simulmedia, Inc.; Programmer, Stanford University School of Medicine

We will present new tools and services that have been designed in collaboration with BD to improve the productivity of biostatisticians, to allow them to work with large volumes of data on a private cloud and on EC2 and to collaborate easily.

3:00 Development and Implementation of Distributed Health Data Networks: Lessons from Medical Product Safety, Public Heath Surveillance, and Comparative Effectiveness Research

Jeffrey Brown, Ph.D., Assistant Professor, Population Medicine, Harvard Pilgrim Health Care Institute/ Harvard Medical School

This presentation describes the development, implementation and selected uses of an open-source software platform (PopMedNetTM) for the creation of distributed health data networks. A distributed health data network advances the secondary use of electronic health information by creating standardized and re-usable data sources in multiple sites, as well as tools to use it. Understand the barriers in creating a distributed health network and approaches for overcoming them.

3:30 Closing Featured Speaker

Pistoia Alliance: Progress in Pre-Competitive Collaboration

Ramesh Durvasula, Ph.D., Director, Molecular Sciences & Candidate Optimization Informatics, Bristol-Myers Squibb

Since 2009, the Pistoia Alliance has drawn significant interest from across the industry. We are focused on the highest-value, most-challenging opportunities for developing technology standards and new capabilities. The industry as a whole benefits from the efforts of Pistoia, not just any single segment. Learn the latest updates and current priorities of the Pistoia Alliance projects and how to become engaged in the Pistoia efforts.

4:00 Conference Adjourns

Track 12 Cancer Informatics

TUESDAY, APRIL 24

7:00 am Workshop Registration and Morning Coffee

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

- Software Development for Clinical Genomics
- Microscopy Imaging Analysis – Quantitative Analysis of Large-Scale Biological Image Data

**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
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WEDNESDAY, APRIL 25

7:00 am Registration and Morning Coffee

7:55 Chairperson's Opening Remarks
Phillips Kuhl, Co-Founder and President, Cambridge Healthtech Institute

8:00 Keynote Introduction
Bas Burger, President, Global Commerce, BT Global Services

8:15 PLENARY KEYNOTE
Eric D. Perakslis, Ph.D., CIO and Chief Scientist of Informatics, U.S. Food and Drug Administration

8:45 Benjamin Franklin Award & Laureate Presentation

9:10 Best Practices Award Program

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

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CYCLE COMPUTING

DATA MODELING AND COMPUTATIONAL INTEGRATIVE TOOLS

10:50 Chairperson's Remarks
William O'Neill, Ph.D., Professor, Bioengineering, University of Illinois at Chicago

11:00 Translational Integrity and Continuity: Individualized Biomedical Data Integration
Xiaoming Wang, Ph.D. Fellow, Computation Institute, University of Chicago and Argonne National Laboratory
This presentation describes an established warehousing system, translational data marts (TraM), to describe the impact of conceptual modeling on the system flexibility, sustainability, and scalability; data integration workflow efficiency; application capacity and performance; and data integrity and interoperability. An oncology data mart (ONCOD) will be used as an example to illustrate a lifecycle of a data warehousing system design.

11:30 Computational Statistical Image Modeling for Lesion Diagnosis and Classification
William O'Neill, Ph.D., Professor, Bioengineering, University of Illinois at Chicago
This presentation describes a method of diagnosing and classifying lesions for cancer and cancer type using only universally available computational software. Multimodal images of brain, breast, and thyroid are modeled by partial difference equations estimated as generalized least squares realizations. Model parameters afford individual lesion statistical diagnosis while Fisher linear discriminants optimally classify models of demographic populations.

12:00 pm Gene Expression Quantification and Variation Detection from RNA-Seq data
Sponsored by
华大基因 BGI
Xin Jin, Group Leader of Genetic Disorder, BGI
In order to better quantify the gene expression levels, BGI is now participating in the Sequencing Quality Control (SEQC) Project launched by the U.S. Food and Drug Administration (FDA), the goal of which is to demonstrate the utility of RNA-Seq technology and further establish standard and develop better algorithm for RNA-Seq quantification analysis. This talk will introduce two softwares, SOAPsplice and SOAPfusion.

12:30 Luncheon Presentation: Enabling Scientific Discovery While Iteratively Cleaning and Standardizing Complex Clinical and Research Data
Sponsored by
BioFortis
Matthew Clark, Ph.D., Senior Application Scientist, BioFortis, Inc.
Today's researchers have access to an ever-expanding treasure trove of electronic data. Traditionally, datasets must be cleaned and standardized before meaningful query and analysis can yield scientific insights. Large scale data cleaning efforts rarely meet desired objectives in time and on budget, delaying scientific discovery. This presentation will describe a new paradigm that allows cross-functional teams to collaboratively diagnose, repair, and circumvent data problems while delivering scientific value every step of the way.

1:40 Chairperson's Remarks
Michael Liebman, Ph.D., President & Managing Director, Strategic Medicine, Inc.
Sabrina Molinaro, Ph.D., Head, Epidemiology and Health Research Services, National Research Council of Italy

1:45 Personalized Medicine: Moving from Correlation to Causality in Breast Cancer
Michael Liebman, Ph.D., President & Managing Director, Strategic Medicine, Inc.
Sabrina Molinaro, Ph.D., Head, Epidemiology and Health Research Services, National Research Council of Italy

Co-authored with Valentina Lorenzoni, Stefania Pieroni, and Fabio Mariani, Unit of Epidemiology and Biostatistics, Institute for Clinical Physiology, National Research Council (Italy)
We have developed a fundamental model of the disease process for breast cancer, from pre-disease through early detection, treatment and outcome, and apply a multi-scalar approach across the risk assessment-enhanced diagnosis-therapeutic decision axis and will present the modeling methodologies. We believe this approach will improve clinical decisions and also drive enhanced development of diagnostics and therapeutic interventions.

GENE EXPRESSION DATA ANALYSIS

2:15 The Allen Mouse Brain Atlas: Towards an Infrastructure for Neuroscience Data
Chinh Dang, Senior Director, Technology, Allen Institute for Brain Science
Launched in 2003, the Allen Mouse Brain Atlas contains genome-wide cellular level gene expression data in the adult mouse brain. Since then, additional gene expression atlases of the developing mouse brain, mouse spinal cord, adult human brain, developing human brain, and non-human primate brain are freely and publicly available with associated visualization and mining tools. Learn how this data can be leveraged by the genomic, bioinformatics, and other research communities.

2:45 Teradata Drug Discovery Analytics Framework
Sponsored by TERADATA Raising Intelligence
Ed Acker, Ph.D., Vice President, Life Sciences, Teradata
The Teradata Drug Discovery Analytics Framework removes data analysis barriers to drug discovery analytics. The barriers include data volume limits, data access limits(semantic, structural,location), data analysis limits (segmentation, aggregation) and analysis performance limits (data movement, application architecture).The major components of this framework are a 3NF Logical Data Model, a Massively Parallel Processing Share Nothing Data Management Architecture, in-database analytics for structured and unstructured data, a SQL interface for unstructured data and shareable virtual data labs self-provisioned by scientists.

3:00 Repurposing Scientific Discovery - Delivering Structured Intelligence from Unstructured Text
Sponsored by ELSEVIER
Ilya Mazo, Ph.D., Director, Product Development, Elsevier
Biological researchers in industry and academia require modern tools that broadly integrate scientific knowledge to reveal new discoveries and to support complex decisions at different stages of drug discovery process. Importantly, the decision at each specific step of this process require access to the information from multiple stages, the trend that poses increased demand on interoperability and to what degree the data needs to be structured. This presentation will describe the approaches towards structuring the information across multiple domains and how Elsevier is supporting researchers today and in the future with tools based on literature-derived intelligence.

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

3:45 Statistical Issues in the Analysis of Genome-Wide Methylation Arrays as Compared to Gene Expression Data: A Breast Cancer Example
Sandeep Singhal, Bioinformatician, Breast Cancer Translational Research Laboratory J.C. Heuson (BCTL), Jules Bordet Institute
This presentation will highlight some statistical methods for genome wide methylation data analysis with an emphasis on what new information is gained from breast cancer studies for which both DNA methylation and gene expression data is available and what conclusions can be reached about the role of DNA methylation on gene expression.

MOLECULAR PROFILING DATA

4:15 'Omics Interpretation Solutions - A Big Pharma Practical Guide
Jack Pollard, Ph.D., Associate Director, sanofi Oncology, Translational & Experimental Medicine – Bioinformatics
Lars Greiffenberg, Ph.D, sanofi R&D-IS, Health-IT, Biology Solutions
While generating testable hypotheses from 'omics data offers one kind of challenge, implementing informatics solutions company-wide presents a different set of technology, people and process challenges. We will share our recent successful experience and practical insights at specifying and implementing an integrated solution for 'omics data management, analysis, and interpretation for sanofi R&D.

4:45 GenomeSpace: An Environment for Frictionless Bioinformatics
Michael Reich, Director, Cancer Informatics, Broad Institute of MIT and Harvard

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

6:15 Exhibit Hall Closes

THURSDAY, APRIL 26

WEB-BASED PLATFORMS FOR SYSTEMS MEDICINE

8:40 Chairperson's Opening Remarks
Subha Madhavan, Ph.D., Director, Clinical Research Informatics, Lombardi Comprehensive Cancer Center; Director, Biomedical Informatics, Georgetown-Howard Universities CTSA, Georgetown University Medical Center

8:45 G-DOC: A Systems Medicine Platform for Personalized Oncology
Subha Madhavan, Ph.D., Director, Clinical Research Informatics, Lombardi Comprehensive Cancer Center; Director, Biomedical Informatics, Georgetown-Howard Universities CTSA, Georgetown University Medical Center
The Georgetown Database of Cancer (G-DOC) is a generic and flexible web-based platform that serves to enable basic, translational, and clinical research activities by integrating patient characteristics and clinical outcome data with a variety of high throughput research data in a unified environment. Through this modular, extensible, and flexible infrastructure, we can quickly and easily assemble new translational web applications with both analytic and generic administrative features.

9:15 Data Integration around Hierarchically and Modularly Organized Protein-Protein Interaction Network
Bing Zhang, Ph.D., Assistant Professor, Department of Biomedical Informatics, Vanderbilt University School of Medicine
Traditional graph-based network visualization techniques quickly become inadequate as network size and data complexity increase. We propose NetGestalt, a novel web-based data integration framework that exploits the inherent hierarchical modular architecture of protein-protein interaction networks to achieve high scalability. Using multidimensional cancer omics, as an example, we show that Netgestalt allows simultaneous presentation of large scale experimental and annotation data from various sources.

9:45 A Systems Approach to Designing Effective Clinical Trials
Vincent Fusaro, Ph.D., Research Associate, Center for Biomedical Informatics, Harvard Medical School
Randomized clinical trials are unsustainable in the era of personalized medicine due to the exponential number of combinations necessary for evaluating personalized treatment options. Computational methods are necessary to predict the likely outcomes and guide clinical trial designs.

10:15 Coffee Break in the Exhibit Hall and Poster Competition

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

10:50 Plenary Keynote Panel Introduction
Geoffrey Noer, Senior Director, Product Marketing, Panasas

11:00 Plenary Keynote Panel: A special plenary session featuring trends and challenges in cancer research:

Julian Adams, Ph.D., President, Research and Development, Infinity Pharmaceuticals, Inc.

Jose Baselga, M.D., Ph.D., Chief and Bruce A. Chabner Chair, Division of Hematology/Oncology, Massachusetts General Hospital; Associate Director, Massachusetts General Hospital Cancer Center; Professor of Medicine, Harvard Medical School

Sir John Burn, MD, FMedSci, Professor of Clinical Genetics, Institute of Genetic Medicine, Newcastle University, UK; Genetics Lead, National Institute of Health Research, UK; Medical Director, QuantuMDx Ltd

John Quackenbush, Ph.D., Professor, Biostatistics and Computational Biology, Cancer Biology Center for Cancer Computational Biology, Dana-Farber Cancer Institute

12:15 Luncheon in the Exhibit Hall with Poster Viewing

MULTIPLEX ASSAY ACCURACY AND TEST RESULT INTERPRETATION

1:55 Chairperson's Remarks
Alex Bangs, CIO, Crescendo Bioscience, Inc.

2:00 Personalized Patient Care through the Use of Multi-Biomarker Diagnostics and Novel Software Applications
Alex Bangs, CIO, Crescendo Bioscience, Inc.
A multi-biomarker blood test has been developed to more comprehensively measure disease activity in RA patients, and provide an objective, quantitative complement to traditional patient and physician assessments. These efforts are complemented by tools that enable physicians to track disease trajectory over time and take a more quantitative and personalized approach to patient care.

2:30 Comparing RNASeq Algorithms for Blood Gene Expression
Stan Letovsky, Ph.D., Vice President and CIO, SynapDx Corporation
Different expression quantitation algorithms for RNASeq data can give suprisingly different results. Here we report on comparisons of several algorithms run on the same dataset. We describe the impact of algorithmic choices on reproducibility and sensitivity to detect expression changes.

3:00 Accelerated Development of Diagnostic Assays Using NGENix™ in silico Powered Design
Richard Del Mastro, Vice President, Research and Development, IntelligentMDx
IMDx's proprietary NGENix™ bioinformatics platform powers the design process to rapidly develop qualitative and quantitative multiplexed real time PCR-based solutions to detect all strains of pathogens. NGENix™ utilizes modules that identify unique regions within sequenced genomes, designs oligonucleotide solutions, assesses the thermodynamics of the DNA multiplex and reviews cross-reactivity to other genomes. The process is efficient at generating accurate diagnostic assays with continued clinical relevancy.

3:30 Cloud-Based Development of Molecular Diagnostics Tests for Cancer
Ljubomir Buturovic, Ph.D., Vice President and Chief Scientist, Informatics, Pathwork Diagnostics, Inc.
Development of maximally informative genomics-based cancer diagnostics tests can present informatics challenges due to conceptual and computational complexity of analyzing the highdimensional genomics data. Pathwork Diagnostics developed a cloud-based software solution to this problem. The system had been used to develop informatics for the FDA-cleared Tissue of Origin cancer classification test currently marketed for clinical use, and can be applied to other prognostic and predictive diagnostic tests.

4:00 Conference Adjourns

HOTEL & TRAVEL

Conference Venue:
Seaport World Trade Center
200 Seaport Boulevard, Boston, MA 02210

Host Hotel:
Seaport Hotel (Located directly across the street)
One Seaport Lane, Boston, MA 02210
T: 617-385-4000
Reservations: Bio-ITWorldExpo.com

Discounted Room Rate: $239 s/d
Discounted Room Rate Cut-off Date: March 30, 2012

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

For information on parking, directions to the Seaport World Trade Center, airport transportation, and visiting Boston and New England, visit www.Bio-ITWorldExpo.com.

CAR RENTAL DISCOUNTS:

Special discount rentals have been established with Hertz for this conference.

- Call Hertz 1-800-654-3131 use our Hertz Convention Number (CV): 04KL0003
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FLIGHT DISCOUNTS:

Special discounts have been established with American Airlines for this conference:

- Call 1-800-433-1790 use Conference code 1942AY
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Bio-IT World is the premier event in North America attracting over 2,100 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. Whether your goal is to showcase a new product in our exhibit hall, or to present your latest technology or solution during a conference session, your sponsorship package will strategically place you in front of hard to reach, high-level decision makers.

BENEFITS OF EXHIBITING & SPONSORING

- *Bio-IT World* is the only life sciences conference that focuses on enabling technologies for predictive biology.
- Positive return on investment for clients who have participated as exhibitors or sponsors. 62% of the companies have resigned for 2012 already!
- Paid delegate audience has grown by 20% each year since 2007. We have been increasing the number of conference programs offered to ensure that you are seeing new prospects and a larger audience each year.
- A high-value business development opportunity that provides direct access to a niche end-user audience, allowing sponsors to: meet new, senior level customer prospects, strengthen existing customer relationships, and shorten the sales cycle.

BEST OF SHOW AWARDS

The Best of Show Awards offer exhibitors an exclusive opportunity to distinguish their new products from the competition. Judged by a joint team of *Bio-IT World* magazine editors and leading industry experts, this awards program will identify exceptional innovation in new product technologies used by life sciences professionals today. Judging and the announcement of the 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 bestofshow@healthtech.com.

As an exhibitor, you have the opportunity to display your new product literature at the showcase at no additional cost. Plus, CHI will promote the New Product Showcase through email, the conference website, press releases, on-site with signage and in the program guide. Ask us about an upgrade! For more information and submission deadline, please contact Elaine Eskedal at 781-972-5430 or email eeskedal@healthtech.com.

For Sponsorship and Exhibit Information, please contact:

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

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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.

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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!

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

INVITATION-ONLY VIP DINNER/HOSPITALITY SUITE
Sponsors will hand-pick 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 or plated dinner, plated dinner with specific conversation focus).

CHI LEAD GENERATION
CHI can help you with lead generation throughout the year. Our internal database includes over 800,000 prospects in the life sciences. By leveraging the database and mining for your specific requirements, we can produce multiple custom projects which will deliver your prospective buyers: Web Symposiums, Podcasts, White Papers, Custom Market Research Surveys and more!

EXHIBIT INFORMATION
Secure your exhibit space by **January 27th & save $300!** Exhibitors will enjoy facilitated networking opportunities with over 2,100 qualified decision makers at **Bio-IT World Conference & Expo**, making it the perfect platform to launch a new product, collect feedback and generate new leads. Exhibit space sells out quickly, so reserve yours today!

OTHER PROMOTIONAL OPPORTUNITIES INCLUDE:

- Pre-Conference Workshops
- Web Symposia (lead generation throughout the year)
- Conference Tote Bags
- Tote Bag Inserts of company Literature
- Padfolios (track specific)
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	Commercial	Academic, Government, Hospital-affiliated
One Half-Day Workshop	$595	$295
Two Half-Day Workshops	$895	$495

Morning Workshops	Afternoon Workshops
(W1) Beyond the Cloud	(W9) Data Visualization in Biology
(W2) Leveraging Saas for Next-Gen Sequencing	(W10) Microscopy Imaging Analysis
(W3) Utilization of EHRs/EMRs for Protocol Design	(W11) Your Cloud, Your Way: How to Choose the Approach that's Best for You (Savvis)
(W4) Building and Using an Ontological Framework	
(W5) Clinical Genomics	(W12) Enhancing R&D Effectiveness through Global ELN Deployment
(W6) Collaborative Innovation and Open Source Deals	(W13) Finding eHealth Savings
(W7) Marketing and Sales: Science Training 101	(W14) Seeking Precise Knowledge
(W8) Best of Breed Informatics	(W15) Social Media Analytics
	(W16) Scientists: Business Training 101

MAIN CONFERENCE PRICING

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Registrations after March 16, 2012, and on-site	$1995	$925

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Track 2: IT Infrastructure - Software	Track 8: eHealth and HIT Solutions for Personalized Medicine
Track 3: Cloud Computing	Track 9: Drug Discovery Informatics
Track 4: Bioinformatics	Track 10: Molecular Diagnostics Informatics
Track 5: Next-Gen Sequencing Informatics	Track 11: Open Source Solutions
Track 6: Systems and Multiscale Biology	Track 12: Cancer Informatics

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Poster Submission-Discount ($50 Off)
Poster abstracts are due by March 9, 2012. 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.

International Society for Computational Biology (ISCB) Member-Discount (10% Off)

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

Please refer to the Registration Code below:

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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.

If you are unable to attend but would like to purchase the Bio-IT World Conference & Expo 2012 CD for $750 (plus shipping), please visit bio-itworldexpo.com. Massachusetts delivery will include sales tax.

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

reg@healthtech.com • P: 781.972.5400 or Toll-free in the U.S. 888.999.6288

Please use keycode **1220F** when registering!