Final Agenda

Record attendance expected at this year's event

Click Here to Register Online!
Bio-ITWorldExpo.com

Cambridge Healthtech Institute,
250 First Avenue, Suite 300,
Needham, MA 02494
www.healthtech.com

Cambridge Healthtech Institute's Thirteenth Annual

Bio-IT World CONFERENCE & EXPO '14

Enabling Technology. Leveraging Data. Transforming Medicine.

APRIL 29 – MAY 1, 2014

SEAPORT WORLD TRADE CENTER
BOSTON, MA

CONFERENCE TRACKS:

1. IT Infrastructure – Hardware
2. Software Development
3. Cloud Computing
4. Bioinformatics
5. Next-Gen Sequencing Informatics
6. Systems Pharmacology
7. eClinical Trials Solutions
8. Data Visualization
9. Pharmaceutical R&D Informatics
10. Clinical Genomics
11. Collaborations and Open Access Innovations
12. Cancer Informatics
13. Data Security

PLENARY KEYNOTE PRESENTERS:

Heather Dewey-Hagborg
Artist, Ph.D. Student, Rensselaer Polytechnic Institute

Yaniv Erlich, Ph.D.
Principal Investigator and Whitehead Fellow, Whitehead Institute for Biomedical Research

Stephen H. Friend, M.D., Ph.D.
President, Co-Founder and Director of Sage Bionetworks

Isaac Samuel Kohane, M.D., Ph.D.
Henderson Professor of Health Sciences and Technology, Children's Hospital and Harvard Medical School; Director, Countway Library of Medicine; Director, i2b2 National Center for Biomedical Computing; Co-Director, HMS Center for Biomedical Informatics.

John Quackenbush, Ph.D.
CEO, Genospace; Professor, Dana-Farber Cancer Institute and Harvard School of Public Health

EVENT FEATURES:

- **Access All 13 Tracks for One Price**
- **Network with 2,500+ Global Attendees**
- **Hear 150+ Technology and Scientific Presentations**
- **Attend Bio-IT World's Best Practices Awards**
- **Connect with Attendees Using CHI's Intro-Net**
- **Participate in the Poster Competition**
- **Choose from 16 Pre-Conference Workshops**
- **See the Winners of the following 2014 Awards:**
  - Benjamin Franklin
  - Best of Show
  - Best Practices
- **View Novel Technologies and Solutions in the Expansive Exhibit Hall**
- **And Much More!**

Platinum Sponsors:

accelrys® · aspera an IBM® company · CYCLE COMPUTING · DataDirect NETWORKS · ELSEVIER · EMC® ISILON · HITACHI Inspire the Next Hitachi Data Systems · IBM · illumina · okta™ · ORACLE HEALTH SCIENCES · sgi · THINKMATE HIGH PERFORMANCE COMPUTING · THOMSON REUTERS · xyratex A Seagate Company

Official Media Partner: Bio-IT World

Official PR Partner: PAN COMMUNICATIONS

Held in Conjunction with: Medical Informatics World Conference April 29, 2014

**IBM and the IBM logo are trademarks of International Business Machines Corp., registered in many jurisdictions worldwide.*

Bio-ITWorldExpo.com

Click Here to Register Online!
Bio-ITWorldExpo.com

Cambridge Healthtech Institute,
250 First Avenue, Suite 300,
Needham, MA 02494
www.healthtech.com

SCHEDULE-AT-A-GLANCE

Tuesday, April 29, 2014

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

Sponsored by IBM

Wednesday, April 30, 2014

8:00 – 9:45am	Plenary Keynote, Benjamin Franklin Award Presentation, and Best Practices Awards Program
9:45am – 6:30pm	Exhibit Hall Open
9:45 – 10:50am	Coffee Break in the Exhibit Hall with Poster Viewing
10:50am – 12:30pm	Tracks 1-13
12:30 – 1:40pm	Luncheon Presentations (Sponsorship Opportunities Available)
1:50 – 3:25pm	Tracks 1-13
3:25 – 4:00pm	Refreshment Break in the Exhibit Hall with Poster Viewing
4:00 – 5:30pm	Tracks 1-13
5:30 – 6:30pm	Best of Show Awards Reception in the Exhibit Hall

Sponsored by DataDirect NETWORKS

Thursday, May 1, 2014

7:00 – 8:00am	Breakfast Presentations (Sponsorship Opportunities Available)
8:00 – 10:00am	Plenary Keynotes
10:00am – 1:55pm	Exhibit Hall Open
10:00 – 10:30am	Coffee Break in the Exhibit Hall and Poster Competition Winners Announced
10:30am – 12:05pm	Tracks 1-13
12:05 – 1:15pm	Luncheon Presentations (Sponsorship Opportunities Available)
1:15 – 1:55pm	Dessert Refreshment Break in the Exhibit Hall with Poster Viewing
1:55 – 4:00pm	Tracks 1-13

Held in Conjunction with

Second Annual **Medical Informatics World Conference** 2014

April 28 - 29, 2014
Seaport World Trade Center
Boston, MA

MedicalInformaticsWorld.com

Exclusive Offer to Attend Medical Informatics World Conference

Bio-IT World and Cambridge Healthtech Institute are proud to announce the Second Annual Medical Informatics World Conference, to be held immediately prior to Bio-IT World Conference & Expo. The two-day conference builds upon last year's successful inaugural launch by delivering timely programming focused on the cross-industry connections and innovative solutions needed to take biomedical research and healthcare delivery to the next level. The 2014 meeting will bring together 300+ senior level executives and industry leaders from each side of the discussion—providers, payers and pharma—in the fields of healthcare, biomedical sciences, health informatics, and IT. Full details are available at MedicalInformaticsWorld.com.

Medical Informatics World and Bio-IT World Expo are being held back-to-back to complete the week of scientific content by bridging the healthcare and life science worlds. Paid attendees of Bio-IT World Conference & Expo can attend Medical Informatics World Conference (April 28-29) for a special discounted rate. See the registration page for details.

Gain Further Exposure and PRESENT A POSTER & SAVE $50

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

- Available to over 2,500 global attendees
- Will be seen by leaders from top pharmaceutical, biotech, academic, government institutes, and technology vendors
- Automatically entered in the Poster Competition, where two winners will each receive an American Express Gift Certificate
- Receive $50 off your registration fee
- Displayed in the Exhibit Hall, which attracts the most number of the event's delegates
- Dedicated poster hours

Please visit Bio-ITWorldExpo.com for poster instructions and deadlines.

ATTENTION STUDENTS!

Student Rate Being Offered to Attend Bio-IT World Conference & Expo!

PRESENT A POSTER & SAVE AN ADDITIONAL $50

Full-time graduate students and PhD candidates can attend Bio-IT World Conference & Expo at a special Student Rate. Students are encouraged to present a research poster and receive an additional $50 off their registration fee. Research posters will be seen by leaders from top pharmaceutical, biotech, academic, government institutes, and technology vendors. Posters will be automatically entered in the Poster Competition, where two winners will each receive an American Express Gift Certificate. Poster abstracts are due by March 7, 2014.

See the Registration Page for student rates and details.

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

Click Here to Register Online!
Bio-ITWorldExpo.com

Cambridge Healthtech Institute,
250 First Avenue, Suite 300,
Needham, MA 02494
www.healthtech.com

2014 SPONSORS

PLATINUM SPONSORS

accelrys® · aspera an IBM® company · CYCLE COMPUTING · DataDirect NETWORKS · ELSEVIER · EMC® ISILON · HITACHI Inspire the Next Hitachi Data Systems · IBM · illumina® · okta™ · ORACLE® HEALTH SCIENCES · sgi · THINKMATE HIGH PERFORMANCE COMPUTING · THOMSON REUTERS · xyratex A Seagate Company

GOLD SPONSORS

Adaptive COMPUTING · AnnaiSystems · ANOLINX GO DEEP · ARISTA · AYASDI · BioFortis · CAMBRIDGE Computer · CAMBRIDGE SEMANTICS · CLC bio A QIAGEN Company · ConvergeHEALTH by Deloitte. · CRAY THE SUPERCOMPUTER COMPANY · EXOSTAR® · GENALICE TECHNOLOGY FOR PEOPLE & SCIENCE · intel · INTERNET 2® · Maverix BIOMICS · METABOLON® · Neural ID® · OpenEye Scientific Software · PerkinElmer For the Better · QIAGEN · QUINTILES · REMEDY INFORMATICS · SABEY Data Centers · SCHRÖDINGER · SILICON MECHANICS SERVERS • STORAGE • HPC · SimulConsult · Tessella Technology & Consulting · Waters THE SCIENCE OF WHAT'S POSSIBLE.™ · YarcData A CRAY COMPANY

BRONZE SPONSORS

bina TECHNOLOGIES · databiology · DELL · epharmasolutions · GGA GGA Software Services LLC · Linguamatics · eClinicalOS

CORPORATE SUPPORT SPONSORS

adaptive clinical SYSTEMS · SevenBridges genomics · tranSMART Foundation · UMT

*IBM and the IBM logo are trademarks of International Business Machines Corp., registered in many jurisdictions worldwide.

Click Here to Register Online!
Bio-ITWorldExpo.com

Cambridge Healthtech Institute,
250 First Avenue, Suite 300,
Needham, MA 02494
www.healthtech.com

PLENARY KEYNOTE PRESENTATIONS:

TUESDAY, APRIL 29 | 4:00 – 5:00 PM

Keynote Introduction:
Dave Wilson, Senior Director, Business Development Manager, Global Channels, Hitachi Data Systems

Sponsored by HITACHI Inspire the Next
Hitachi Data Systems

John Quackenbush, Ph.D.
CEO, GenoSpace; Professor, Dana-Farber Cancer Institute and Harvard School of Public Health

John Quackenbush received his Ph.D. in 1990 in theoretical physics from UCLA working on string theory models. Following two years as a postdoctoral fellow in physics, Dr. Quackenbush applied for and received a Special Emphasis Research Career Award from the National Center for Human Genome Research to work on the Human Genome Project. He spent two years at the Salk Institute and two years at Stanford University working at the interface of genomics and computational biology. In 1997 he joined the faculty of The Institute for Genomic Research (TIGR) where his focus began to shift to understanding what was encoded within the human genome. Since joining the faculties of the Dana-Farber Cancer Institute and the Harvard School of Public Health in 2005, his work has focused on decoding and modeling the networks of interacting genes that drive disease. In 2011 he and partner Mick Correll launched GenoSpace to facilitate genomic data analysis and interpretation, focused on accelerating research and delivering relevant and actionable solutions for personalized medicine.

WEDNESDAY, APRIL 30 | 8:00 – 9:45 AM

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

Sponsored by EMC® ISILON

Stephen H. Friend, M.D., Ph.D.
President, Co-Founder and Director of Sage Bionetworks

Dr. Friend is the President of Sage Bionetworks. He was previously Senior Vice President and Franchise Head for Oncology Research at Merck & Co., Inc. where he led Merck's Basic Cancer Research efforts. He led the Advanced Technologies and Oncology groups to firmly establish molecular profiling activities throughout Merck's laboratories around the world, as well as to coordinate oncology programs from Basic Research through phase IIA clinical trials. Prior to joining Merck, Dr. Friend along with Dr. Leland Hartwell founded and co-led the Fred Hutchinson Cancer Research Center's "Seattle Project", an advanced institute for drug discovery. While there Drs. Friend and Hartwell developed a method for examining large patterns of genes that led them to co-found Rosetta Inpharmatics in 1997. Dr. Friend has also held faculty positions at Harvard Medical School from 1987 to 1995 and at Massachusetts General Hospital from 1990 to 1995. He received his B.A. in philosophy, his Ph.D. in chemistry and his M.D. from Indiana University. Dr. Friend was named an Ashoka Fellow for his work at Sage Bionetworks.

Benjamin Franklin Award Presentation and Best Practices Awards Program follows

2014 Benjamin Franklin Award Laureate:

Helen Berman, Ph.D.
Board of Governors Professor of Chemistry and Chemical Biology, Rutgers University; Founding Member, Worldwide Protein Data Bank (wwPDB); Director, Research Collaboratory for Structural Bioinformatics PDB (RCSB PDB)

THURSDAY, MAY 1 | 8:00 – 10:00 AM

Keynote Introduction:
Fred Lee, M.D., MPH, Director, Healthcare Strategy and Business Development, Oracle Health Sciences

Sponsored by ORACLE HEALTH SCIENCES

Heather Dewey-Hagborg
Artist, Ph.D. Student, Rensselaer Polytechnic Institute

Heather Dewey-Hagborg is an interdisciplinary artist, programmer and educator who explores art as research and public inquiry. She recreates identity from strands of human hair in an entirely different way. Collecting hairs she finds in random public places – bathrooms, libraries, and subway seats – she uses a battery of newly developing technologies to create physical, life-sized portraits of the owners of these hairs. Her fixation with a single hair leads her to controversial art projects and the study of genetics. Traversing media ranging from algorithms to DNA, her work seeks to question fundamental assumptions underpinning perceptions of human nature, technology and the environment. Examining culture through the lens of information, Heather creates situations and objects embodying concepts, probes for reflection and discussion. Her work has been featured in print, television, radio, and online. Heather has a BA in Information Arts from Bennington College and a Masters degree from the Interactive Telecommunications Program at Tisch School of the Arts, New York University. She is currently a Ph.D. student in Electronic Arts at Rensselaer Polytechnic Institute.

Yaniv Erlich, Ph.D.
Principal Investigator and Whitehead Fellow, Whitehead Institute for Biomedical Research

Dr. Yaniv Erlich is Andria and Paul Heafy Family Fellow and Principal Investigator at the Whitehead Institute for Biomedical Research. He received a bachelor's degree from Tel-Aviv University, Israel and a PhD from the Watson School of Biological Sciences at Cold Spring Harbor Laboratory in 2010. Dr. Erlich's research interests are computational human genetics. Dr. Erlich is the recipient of the Burroughs Wellcome Career Award (2013), Harold M. Weintraub award (2010), the IEEE/ACM-CS HPC award (2008), and he was selected as one of 2010 Tomorrow's PIs team of Genome Technology.

Isaac Samuel Kohane, M.D., Ph.D.
Henderson Professor of Health Sciences and Technology, Children's Hospital and Harvard Medical School; Director, Countway Library of Medicine; Director, i2b2 National Center for Biomedical Computing; Co-Director, HMS Center for Biomedical Informatics

Isaac Kohane, MD, PhD, co-directs the Center for Biomedical Informatics at Harvard Medical School. He applies computational techniques, whole genome analysis, and functional genomics to study human diseases through the developmental lens, and particularly through the use of animal model systems. Kohane has led the use of whole healthcare systems, notably in the i2b2 project, as "living laboratories" to drive discovery research in disease genomics (with a focus on autism) and pharmacovigilance (including providing evidence for the cardiovascular risk of hypoglycemic agents which ultimately contributed to "black box"ing by the FDA) and comparative effectiveness with software and methods adopted in over 84 academic health centers internationally. Dr. Kohane has published over 200 papers in the medical literature and authored a widely used book on Microarrays for an Integrative Genomics. He has been elected to multiple honor societies including the American Society for Clinical Investigation, the American College of Medical Informatics, and the Institute of Medicine. He leads a doctoral program in genomics and bioinformatics within the Division of Medical Science at Harvard University. He is also an occasionally practicing pediatric endocrinologist.

AWARDS PROGRAMS

Cambridge Healthtech Institute and Bio-IT World will again be recognizing and celebrating leaders in innovation through the following Awards Programs.

Best of Show Awards
The Best of Show Awards offer exhibitors an opportunity to distinguish their products from the competition. Judged by a team of leading industry experts and Bio-IT World editors, this award identifies exceptional innovation in technologies used by life science professionals today. Judging and the announcement of winners is conducted live in the Exhibit Hall. Winners will be announced on Wednesday, April 30 at 5:30pm. The deadline for product submissions is February 21, 2014. To learn more about this program, contact Ryan Kirrane at 781-972-1354 or email rkirrane@healthtech.com.

Best Practices Awards - Call for Entries!
Add value to your Conference & Expo attendance, sponsorship or exhibit package, and further heighten your visibility with the creative positioning offered as a Best Practices participant. Winners will be selected by a peer review expert panel in early 2014. Bio-IT World will present the Awards in the Amphitheater at 9:30am on Wednesday, April 30 during the Plenary Keynote and Awards Program. Early bird deadline (no fee) for entry is December 16, 2013 and final deadline (fee) for entry is February 10, 2014. Full details including previous winners and entry forms are available at Bio-ITWorldExpo.com.

2014 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! The winner will be announced in the Ampitheater at 9:00am on Wednesday, April 30 during the Plenary Keynote and Awards Program. Full details including previous laureates and entry forms are available at www.bioinformatics.org/franklin.

Click Here to Register Online!
Bio-ITWorldExpo.com

Cambridge Healthtech Institute,
250 First Avenue, Suite 300,
Needham, MA 02494
www.healthtech.com

PRE-CONFERENCE WORKSHOPS*

#BioIT14

TUESDAY, APRIL 29, 2014

MORNING WORKSHOPS | 8:00 - 11:30 AM

W1: Genome Assembly and Annotation
Jeremy Bruestle, Co-Founder and CTO, Spiral Genetics
Deming Chen, Ph.D., Associate Professor, Electrical and Computer Engineering, University of Illinois, Urbana-Champaign
Kim D. Pruitt, Ph.D., Senior Staff Scientist, National Institutes of Health, National Center for Biotechnology Information (NCBI)
Carlos P. Sosa, Ph.D., Applications Engineer, HPC Lead, Cray, Inc.

W2: Data Visualization in Biology: From the Basics to Big Data
Nils Gehlenborg, Ph.D., Research Associate, Center for Biomedical Informatics, Harvard Medical School

W3: Biologics, Bioassay, and Biospecimen Registration Systems
Arturo J. Morales, Ph.D., Vice President, Informatics, Emerald Bio; former Global Lead, Biology Platform Informatics, Novartis Institutes for Biomedical Research
Josh Bittker, Ph.D., Director, Lead Discovery, The Broad Institute
Stefan Klostermann, Ph.D., Senior Principal Scientist, Roche pRED Informatics
Olivier Roche, Ph.D., Data Quality Coordinator, F. Hoffmann-La Roche Ltd.
Beth Basham, Ph.D., Director, Account Management, Biologics Discovery & IT Site Lead, Merck

W4: Analyzing NGS Data in Galaxy
Anushka Brownley, Senior Scientific Consultant, BioTeam
Nate Coraor, System Administrator, Galaxy Team
Adam Kraut, Senior Scientific Consultant, BioTeam
Tristan Lubinski, Consultant, BioTeam

W5: Aligning Projects with Organization Strategy
Gurpreet Kanwar, Senior Project Manager, Information Management, Nav Canada

W6: An Embarrassment of Riches: Choosing and Implementing Cloud Infrastructure to Replace On-Premises HPC for Next-Generation Sequence Analysis
R. Mark Adams, Ph.D., CIO, Good Start Genetics
Benjamin Breton, Bioinformatics Software Engineer, Good Start Genetics
Rajeshwar Malathker, IT Manager, Johnson & Johnson
Jason Stowe, CEO and Founder, Cycle Computing

W7: Simplify Informatics, Simplify Life - Taming Quality and Complexity of Big Data and IT Solutions
Rich Lysakowski, Ph.D., Director of R&D, Informatics Engineer and Consultant, Collaborative Electronic Notebook Systems Association, Inc.

AFTERNOON WORKSHOPS | 12:30 - 4:00 PM

W9: Advancing the Use of EHR/EMR for Clinical Research and Drug Development: Breaking Down Barriers & Building Up Bridges
Andreas Schmidt, Manager European External Collaborations, Product Development Innovation Management, F. Hoffmann–La Roche AG
Dipak Kalra, Professor, Health Informatics, University College London
David Voets, Project Manager, Custodix NV, Belgium

W10: Determining Genome Variation and Clinical Utility
Caleb J. Kennedy, Ph.D., Manager, Translational Bioinformatics, Be The Match
Vasisht Tadigotla, Ph.D., Senior Bioinformatics Scientist, Courtagen Life Sciences
Elizabeth Worthey, Ph.D., Assistant Professor, Pediatrics & Bioinformatics Program, Human & Molecular Genetics Center, Medical College of Wisconsin

W11: UCSC Genome Browser Interactive Workshop
Robert Kuhn, Ph.D., Associate Director, UCSC Genome Browser, Center for Biomolecular Science and Engineering, University of California, Santa Cruz
Participants should bring a fully-charged laptop.

Sponsored by SevenBridges genomics UMT

W12: IT & Informatics in Support of Collaboration and Externalization
Martin Leach, Ph.D.,Vice President, R&D IT, Biogen Idec
Robert J. Boland, Senior Manager, External Innovation R&D IT, Janssen, Pharmaceutical Companies of Johnson & Johnson
David Sedlock, Ph.D., Senior Director, R&D Systems, Millennium Pharmaceuticals, Inc.
Anastasia (Khoury) Christianson, Ph.D., Head, Translational R&D IT, Bristol-Myers Squibb
Scott Sutherland, Head, Alliance & Operations, Information Technology, Moderna Therapeutics
John Koch, Director, Scientific Information Architecture & Search, Merck
Benoit Millet, Partner, UMT Consulting
Sebastian Wernicke, Ph.D., Director, Seven Bridges Genomics
Sebastien Lefebvre, Director, R&D IT Platform, Biogen Idec

W13: Big Data Analytics
Vas Vasiliadis, Computation Institute, University of Chicago and Argonne National Laboratory
Ravi K. Madduri, Fellow, Computation Institute, University of Chicago; Project Manager, Mathematics and Computer Science Division, Argonne National Laboratory

Sponsored by sgi

W14: Running a Local Galaxy Instance
Adam Kraut, Principal Investigator, BioTeam
Nate Coraor, System Administrator, Galaxy Team
Anushka Brownley, Senior Scientific Consultant, BioTeam
Tristan Lubinski, Consultant, BioTeam
James Reaney, Senior Director, Research Markets, SGI

Sponsored by tranSMART Foundation

W15: The tranSMART Platform Today and Tomorrow
Brian Athey, Ph.D., Co-CEO, tranSMART Foundation
Keith Elliston, Ph.D., CSO, tranSMART Foundation
Yike Guo, Ph.D., CTO, tranSMART Foundation
Paul Avillach, M.D., Ph.D., Research Associate, Center for Biomedical Informatics atCountway, Harvard Medical School
Sherry Cao, Associate Director, Scientific Computing, Genzyme Sanofi

W16: A Bar Code for Chemical Structures: Using the InChI to Transform Connectivity between Chemistry, Biology, Biomedicine, and Drug Discovery
Steve Heller, Ph.D., Project Director, InChI Trust; Scientific Information Consultant
Antony Williams, Ph.D., Vice President, Strategic Development; Head, Cheminformatics for the Royal Society of Chemistry (RSC)
Stephen K. Boyer, Ph.D., Research Solutions for the ChemPharma Industry, IBM Almaden Research Center
Evan Bolton, Ph.D., Lead Scientist, National Center for Biotechnology Information (NCBI), National Library of Medicine (NLM), and National Institutes of Health (NIH)
Christopher Southan, Ph.D., Curator for IUPHARdb/Guide to PHARMACOLOGY, Queen's Medical Research Institute, University of Edinburgh

**Separate Registration Required*

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

Click Here to Register Online!
Bio-ITWorldExpo.com

Cambridge Healthtech Institute,
250 First Avenue, Suite 300,
Needham, MA 02494
www.healthtech.com

Track 1

IT Infrastructure – Hardware

Big Data Solutions and End-User Perspectives

TUESDAY, APRIL 29

7:00 am Workshop Registration and Morning Coffee

8:00 - 11:30 Recommended Morning Pre-Conference Workshops*

Aligning Projects with Organization Strategy

12:30 - 4:00 pm Recommended Afternoon Pre-Conference Workshops*

IT & Informatics in Support of Collaboration and Externalization

**Separate Registration Required. See page 5 for additional workshops.*

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 PLENARY KEYNOTE SESSION

Please see page 4 for details.

5:00 – 7:00 Welcome Reception in the Exhibit Hall with Poster Viewing

Sponsored by IBM

WEDNESDAY, APRIL 30

7:00 am Registration Open and Morning Coffee

8:00 Chairperson's Opening Remarks

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

» 8:05 PLENARY KEYNOTE SESSION

Please see page 4 for details.

9:00 Benjamin Franklin Award & Laureate Presentation

9:30 Best Practices Awards Program

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

10:50 Chairperson's Remarks

Rick Friedman, HPC Research Computing & Big Data Specialist, Dell

» 11:00 FEATURED PRESENTATION: HPC Trends in the Trenches 2014

Chris Dagdigian, Founding Partner & Director, Technology, BioTeam, Inc.

In one of the most popular presentations of the Expo, Chris delivers a candid assessment of the best, the worthwhile, and the most overhyped information technologies (IT) for life sciences. The presentation time for this talk has been extended from 30 to 60 minutes to accommodate the amount of information that is shared. Plus, Chris won't feel pressured to speak so fast!

12:00 pm The Pan-Cancer Analysis of Whole Genomes Project

Sponsored by HITACHI Inspire the Next ©Hitachi Data Systems

Lincoln Stein, Ph.D., Director, Informatics and Bio-Computing, Ontario Institute of Cancer Research; Professor, Molecular Genetics, University of Toronto

The Pan-Cancer Analysis of Whole Genomes project aims to understand common and distinguishing patterns of variation among a diverse set of cancer types. We are performing uniform computational processing of the whole genome sequencing data from the tumors and normal control DNA of more than 2000 donors in order to eliminate differences that are due to different ways of analyzing the data.

12:40 Luncheon Presentation I: Cloud Networking Agility Drives Biotech Innovation & Discovery

Sponsored by ARISTA

Chris Campbell, Data Center Specialist, Arista Networks, Inc.

BigData-methods for BioTech now require new hybrid-use of map/reduce & SQL techniques to achieve ever more meaningful correlations across more varied forms of data and across more locations where data resides. Arista and best-of-breed technology partners deliver one simple, leaf-spine, open-standard network topology to span and to scale, to support all applications across all the datastores that scientists wish to combine. Driven by automation-enabled Software-Defined Cloud Networking, Arista applies cloud-like agility and scale for lowest OPEX and unprecedented innovation potential.

1:10 Luncheon Presentation II: IBM's Comprehensive Reference Architecture for Genomic Medicine

Sponsored by IBM

Frank Lee, Ph.D., Senior Certified Solution Architect, Technical Advisor for Life Sciences, IBM Technical & Platform Computing Worldwide

Dr. Frank N. Lee will describe IBM's open and extensible reference architecture for genomic medicine, including integration of genomic data within a translational platform. The architecture describes a unique, converged platform for high-throughput genomics and analytics through on-premise, cloud and hybrid delivery. It includes a scalable data repository, powerful workload engine and genomics application center for commonly used applications.

Infrastructure and Platforms for Big Data: Capabilities and Solutions

1:50 Chairperson's Remarks

Jacob Farmer, CTO, Cambridge Computer

1:55 How to Bridge the Gap Between Corporate and Research IT: Leveraging the Best of Two Worlds for Bioinformatics

Thomas Schilling, Ph.D., Director, IT Portfolio Management, R&D, Bayer Business Services GmbH

We will discuss the implementation of our Bayer IT-Innovation Lab which consists of in-house cloud solutions linked to HPC clusters in the R&D ecosystem as well to our external clouds. This platform allows for fast evaluation of innovative IT solutions, prototyping and staging into the productive R&D IT landscapes. This lab was established with a long-term interdisciplinary program with skilled and experienced participants from science and IT.

2:25 High-Performance Integrated Virtual Environment (HIVE) Infrastructure for Big-Data Analysis: Applications to Next-Gen Sequencing Informatics

Vahan Simonyan, Ph.D., Lead Scientist - HIVE, CBER, FDA

The High-Performance Integrated Virtual Environment (HIVE) is a distributed cloud-based environment optimized for the secure storage and parallelized analysis of extra-large Next-Generation Sequencing (NGS) data. Learn about the HIVE infrastructure and technical aspects of implementation which facilitate deposition, retrieval, annotation and computation on NGS data, and analysis of outcomes using visual web environments appropriately built in collaboration with research scientists and regulatory personnel.

Click Here to Register Online!
Bio-ITWorldExpo.com

Cambridge Healthtech Institute,
250 First Avenue, Suite 300,
Needham, MA 02494
www.healthtech.com

2:55 Bridging the Worlds of Files, Objects, NAS, and Cloud: A Blazing Fast Crash Course in Object Storage
Sponsored by CAMBRIDGE Computer

Jacob Farmer, CTO, Cambridge Computer

This session is the world's fastest-paced tutorial on object-based storage. It starts by defining the term "object" and lists various ways object technology manifests itself in data storage. Topics covered include: object stores, HPC file systems such as Lustre, cloud storage, cloud file systems, NAS accelerators and gateways, erasure codes, and rules-based metadata systems such as IRODS and Starfish.

3:10 Accelerating Biomedical Research Discovery: The 100G Internet2 Network – Built and Engineered for the Most Demanding Big Data Science Collaborations
Sponsored by INTERNET2

Christian Todorov, Director, Network Services Management, Internet2

Genomic & biomedical researchers have been forced to exchange big data via physical drives as advanced network connectivity was previously unavailable or cost prohibitive. Hear how colleagues are improving big data workflows using the 100G Internet2 Network, which provides the highest data transport rates available, along with dynamic cloud and trust applications that are interconnecting research and accelerating discovery.

3:25 Refreshment Break in the Exhibit Hall with Poster Viewing

4:00 Innovative Data Storage Approaches of a Start-Up

Mark Kapel, Director, Information Technologies & Data Management, Technology Platform, Evogene

Evogene is a plant genomics company utilizing a proprietary integrated technology infrastructure to enhance seed traits underlying crop productivity. This presentation will demonstrate how Evogene's IT group can be driven by the need for innovation and motivated to provide added value and enterprise grade services by focusing on risk management and agile project approaches which are second nature to Israeli start-ups.

4:30 Lessons Learned: Deploying Very Low Cost Cloud Storage Technology in a Traditional Research HPC Environment

Dirk Petersen, Manager, Scientific Computing, Fred Hutchinson Cancer Research Center

When implementing storage chargebacks we wanted to offer researchers an alternative storage solution that would not cost more than AWS Glacier. We also wanted it to be long term durable, self-protecting, easy to manage, store petabytes, survive the loss of an entire datacenter and deliver predictable performance. Learn how to avoid pitfalls and be able to determine if a solution like this makes sense for your organization.

5:00 Co-Presentation: Speeding up Genomic Software on Modern Computer Hardware
Sponsored by intel

Paolo Narvaez, Ph.D., Principal Engineer, Intel Corporation, Data Center Group

Mauricio Carneiro, Ph.D., Broad Institute

In this talk we will review the collaborative work between the Broad Institute and Intel to improve the computational performance of genomic software. We will look at the GATK best practices DNA pipeline and identify areas where computational improvements are being targeted. We will focus on the recent optimizations released with GATK 3.1 and demonstrate how computational kernels can be accelerated with standard Intel hardware. We will show the 5x improvements made to the GATK's variant caller without using any additional cores by taking advantage of new instructions in recent processors. Finally, we will discuss how genomics software can leverage current and future hardware improvements to deliver maximum performance.

5:30 - 6:30 Best of Show Awards Reception in the Exhibit Hall
Sponsored by DataDirect NETWORKS

THURSDAY, MAY 1

7:00 am Registration Open

7:00 Breakfast Presentation Panel: Enabling Technology. Leveraging Data. Transforming Personalized Medicine.
Sponsored by intel

Panelists:

Ketan Paranjape, Global Director, Healthcare and Life Sciences, Intel Corporation

Sanjay Joshi, CTO, Life Sciences, EMC Isilon

Steve Schwartz, Vice President, Business Development & Strategy, 23&Me

Hans Karten, CEO & CTO, GENALICE

Jason Stowe, CEO and Founder, Cycle Computing

Adam Berrey, CEO, Curoverse

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. Learn how Intel is working with a broad range of ecosystem partners & industry experts to accelerate scientific discovery, translate results into clinical practice, and achieve the vision of personalized medicine today.

8:00 Chairperson's Opening Remarks

Kevin Davies, Ph.D., Vice President Business Development & Publisher C&EN, American Chemical Society; Founding Editor, Bio-IT World

» 8:05 PLENARY KEYNOTE SESSION
Please see page 4 for details.

10:00 Coffee Break in the Exhibit Hall and Poster Competition Winners Announced

File System Optimization

10:30 Chairperson's Opening Remarks

Zachary Giles, HPC Administrator, Scientific Computing, Icahn School of Medicine at Mount Sinai

10:35 File System Optimization for Genomics Workload using SSDs and File System Tiering

Zachary Giles, HPC Administrator, Scientific Computing, Icahn School of Medicine at Mount Sinai

The audience will gain an understanding of current cluster file system technologies used within the genomics community and possibly changes that can be made to make better use of the file system hardware and software to provide better service for their users. A case study will be presented on usage patterns and new concepts for file system optimization such as "hot files" and SSDs.

11:05 How to Build a Genomics Platform that Addresses Performance, Data Management and Translational Medicine
Sponsored by IBM

Janis Landry Lane, Executive, Life Sciences Industry, IBM Technical & Platform Computing Worldwide

Data used in next generation sequencing is doubling every five months, and HPC computing resources are required to analyze and store it. Attend this session and learn IBM's best practices for HPC data management and archiving. We will describe new ways to integrate genomics data into translational platforms, and help researchers manage the analytics required to realize the genomics promise.

11:35 Converged Infrastructure for Life Science Research and Communities
Sponsored by DataDirect NETWORKS

George Vacek, Ph.D., Global Business Director, Life Sciences, DataDirect Networks

Dr. Vacek will discuss the recent infrastructure adoption and trends among many of the world's largest big data sites in Life Science. Topics covered will include architectural elements like iRODs, converged parallel file systems, object storage, secure research communities and specific examples of leading research center use cases.

11:50 Resilient, Compliant, High Performance IT Environments through Flexible Design
Sponsored by SABEY Data Centers

John Sabey, President, Sabey Data Center Properties

Sabey Data Centers brings 42 years of experience building and operating critical environments for healthcare and life sciences. Our geo-diverse, energy-efficient, highly robust facilities enable our partners to build and maintain compliant systems through end to end control and redundant architecture.

12:15 pm Luncheon Presentations *(Sponsorship Opportunities Available)* **or Lunch on Your Own**

1:15 Dessert Refreshment Break in the Exhibit Hall with Poster Viewing

Cambridge Healthtech Institute,
250 First Avenue, Suite 300,
Needham, MA 02494
www.healthtech.com

Managing Big Data and Security Strategies

1:55 Chairperson's Remarks

Toby Bloom, Ph.D., Deputy Scientific Director, Informatics, New York Genome Center

2:00 Data and Intellectual Property Security in a Global Cyber Environment

Russ Brown, Supervisory Special Agent, Boston Division Criminal Cyber Squad, FBI

Data security is a very significant issue faced by businesses in today's electronically connected environment. Data "owned" or controlled by a business, as well as applications developed by a business, are categorized as Intellectual Property. The security and protection of Intellectual Property is critical to conducting, maintaining and growing a secure business in the current global environment.

2:30 Information Classification: The Key to a Sane Security Strategy

William Telford, Director, R&D IS Security, Sanofi R&D

Understanding your information is key to your security success and enables collaboration. This talk will address the key topics to consider and challenges that must be overcome.

3:00 PANEL DISCUSSION: The Big Data Storage and Security Maze: Balancing Collaboration and Privacy

Moderator: Toby Bloom, Ph.D., Deputy Scientific Director, Informatics, New York Genome Center

Russ Brown, Supervisory Special Agent, Boston Division Criminal Cyber Squad, FBI

Yaniv Erlich, Ph.D., Principal Investigator and Whitehead Fellow, Whitehead Institute for Biomedical Research

Philip Groth, Ph.D., IT Business Partner, CoE Research, Bayer HealthCare Pharmaceuticals

John Sabey, President, Sabey Data Center Properties

William Telford, Director, R&D IS Security, Sanofi R&D

Big data has led to organizations turning to virtual networks for information storage and processing. Thus, unauthorized access to data and implementation of effective governance structures are growing concerns. To balance knowledge sharing and respect for confidentiality, researchers must consider how and where to store and secure data – plus what data and why. This panel gathers representatives from academia, pharma and IT to discuss these issues. Topics include:

- How secure is your data?
- When should you favor data sharing and when should you restrict data flow?
- What data actually needs to be protected in the first place?
- What security systems and practices are most appropriate for specific research needs?

4:00 Conference Adjourns

Cambridge Healthtech Institute,
250 First Avenue, Suite 300,
Needham, MA 02494
www.healthtech.com

Track 2

Software Development

Technologies and Applications for Managing and Sharing Data

TUESDAY, APRIL 29

7:00 am Workshop Registration and Morning Coffee

8:00 - 11:30 Recommended Morning Pre-Conference Workshops*

Aligning Projects with Organization Strategy

12:30 - 4:00 pm Recommended Afternoon Pre-Conference Workshops*

IT & Informatics in Support of Collaboration and Externalization

**Separate Registration Required. See page 5 for additional workshops.*

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 PLENARY KEYNOTE SESSION

Please see page 4 for details.

5:00 – 7:00 Welcome Reception in the Exhibit Hall with Poster Viewing

Sponsored by IBM

WEDNESDAY, APRIL 30

7:00 am Registration Open and Morning Coffee

8:00 Chairperson's Opening Remarks

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

» 8:05 PLENARY KEYNOTE SESSION

Please see page 4 for details.

9:00 Benjamin Franklin Award & Laureate Presentation

9:30 Best Practices Awards Program

**IBM and the IBM logo are trademarks of International Business Machines Corp., registered in many jurisdictions worldwide.*

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

10:50 Chairperson's Remarks

Rick Friedman, HPC Research Computing & Big Data Specialist, Dell

» 11:00 FEATURED PRESENTATION: HPC Trends in the Trenches 2014

Chris Dagdigian, Founding Partner & Director, Technology, BioTeam, Inc.

In one of the most popular presentations of the Expo, Chris delivers a candid assessment of the best, the worthwhile, and the most overhyped information technologies (IT) for life sciences. The presentation time for this talk has been extended from 30 to 60 minutes to accommodate the amount of information that is shared. Plus, Chris won't feel pressured to speak so fast!

12:00 pm The Pan-Cancer Analysis of Whole Genomes Project

Sponsored by HITACHI Inspire the Next Hitachi Data Systems

Lincoln Stein, Ph.D., Director, Informatics and Bio-Computing, Ontario Institute of Cancer Research; Professor, Molecular Genetics, University of Toronto

The Pan-Cancer Analysis of Whole Genomes project aims to understand common and distinguishing patterns of variation among a diverse set of cancer types. We are performing uniform computational processing of the whole genome sequencing data from the tumors and normal control DNA of more than 2000 donors in order to eliminate differences that are due to different ways of analyzing the data.

12:40 Luncheon Presentation I: Cloud Networking Agility Drives Biotech Innovation & Discovery

Sponsored by ARISTA

Chris Campbell, Data Center Specialist, Arista Networks, Inc.

BigData-methods for BioTech now require new hybrid-use of map/reduce & SQL techniques to achieve ever more meaningful correlations across more varied forms of data and across more locations where data resides. Arista and best-of-breed technology partners deliver one simple, leaf-spine, open-standard network topology to span and to scale, to support all applications across all the datastores that scientists wish to combine. Driven by automation-enabled Software-Defined Cloud Networking, Arista applies cloud-like agility and scale for lowest OPEX and unprecedented innovation potential.

1:10 Luncheon Presentation II: IBM's Comprehensive Reference Architecture for Genomic Medicine

Sponsored by IBM

Frank Lee, Ph.D., Senior Certified Solution Architect, Technical Advisor, Life Sciences, IBM Technical & Platform Computing Worldwide

Dr. Frank N. Lee will describe IBM's open and extensible reference architecture for genomic medicine, including integration of genomic data within a translational platform. The architecture describes a unique, converged platform for high-throughput genomics and analytics through on-premise, cloud and hybrid delivery. It includes a scalable data repository, powerful workload engine and genomics application center for commonly used applications.

Harnessing Data & Standards

1:50 Chairperson's Remarks

John A. Norris, J.D., MBA, Chairman, Norris Capital, Inc. and FDDH, Inc.; Senior US Advisor to Kanagawa, Japan, Governor Kuroiwa and GCC

1:55 HELM: An Open Standard for the Representation of Complex Biomolecules

Sergio Rotstein, Ph.D., Director, Research Business Technology, Pfizer, Inc.

This presentation will describe the HELM standard and associated toolkit, its origins and use at Pfizer, and the Pistoia Alliance HELM project that has transitioned the technology into the open source, making it available freely and openly to the biopharmaceutical industry at large.

2:15 Looking at Clouds from Both Sides Now: Systems, Dataflow and the Future of Drug Development

Greg Koski. M.D., Ph.D., President and Co-Founder, Executive Office, Alliance for Clinical Research Excellence and Safety

2:35 Summary: FDA Software-Tools Reform

John A. Norris, J.D., MBA, Chairman, Norris Capital, Inc. and FDDH, Inc.; Senior US Advisor to Kanagawa, Japan, Governor Kuroiwa and GCC

This presentation discusses the efforts of the Global Collaborative Center (GCC) in helping to reform the U.S. FDA'S review methods and standards relating to data/business intelligence analytics and decision-support software tools for new medical device products.

2:55 Metabolync™: A Cloud-Based Solution for Sharing, Visualizing and Analyzing Metabolomics Data

Sponsored by METABOLON

Corey DeHaven, Vice President, Information Systems, Metabolon, Inc.

Metabolomics experiments may generate a large amount of data including both named and unnamed metabolites, group statistical analysis and biological pathway annotations. Data visualization and analytical tools are required to aid in understanding the data and relationships among detected metabolites and their effects on the underlying biology. Metabolync™ leverages cloud-based resources and web service API's to enable these functions.

Click Here to Register Online!
Bio-ITWorldExpo.com

Cambridge Healthtech Institute,
250 First Avenue, Suite 300,
Needham, MA 02494
www.healthtech.com

3:10 Accelerate Insights – Processing Intense Simulations and Big Data Analysis

Sponsored by Adaptive Computing

Nick Ihli, Senior Systems Engineer, Adaptive Computing

Adaptive powers the world's largest and most robust datacenters with its scheduling and optimization software, Moab. Moab plays a huge role in accelerating insights for researchers and IT professionals. Learn about how Big Workflow accelerates insights by efficiently procession intensesimulation and big data analysis- unifyingHPC, cloud and datacenterresources, optimizing the analysis process and guaranteeing services to the business -speeding time to discovery.

3:25 Refreshment Break in the Exhibit Hall with Poster Viewing

Data Integration and Business Intelligence

4:00 Transforming Scientific Information into Business Intelligence through Search-Based Applications

Robert Hernandez, Informatics Scientist, AstraZeneca

The inability to harness data for scientific decision-making is a problem that negatively impacts organizations worldwide. The AstraZeneca R&D search vision is to leverage internal and external data and create insights that deliver novel search-based business applications. This presentation demonstrates the power of building search-based applications that leverage 200 million scientific documents as a solution.

4:30 In Pursuit of Knowledge Management: The Implementation of a Highly Adopted Database within a Drug Substance Process Development Department

Russell Van Buskirk, Senior Associate Scientist, Purification Process Development, Amgen

As development timelines decrease, knowledge management of drug substance development data becomes essential. The time savings inherent in electronic lab notebook templates with automatic report generation capabilities is perceived by the scientific staff as a benefit to their daily work flow and increases adoption with the added benefit that the template doubles as a future searchable database.

5:00 Utilizing Amazon Web Services for Data Collection, Integration, and Analysis in the Life Sciences

Angel Pizarro, Solutions Architect, Amazon Web Services

Setting up proper infrastructure for data ingestion, integration and analysis can be daunting, especially in the life science space where data sources are varied, dense and complex. Amazon Web Services provides a rich set of services that can be combined for creating cost-effective solutions for ingestion, integration, and analysis of life science data sources. In this talk we will describe these processes using AWS services such as Kinesis, Elastic Map Reduce, and Redshift.

5:30 - 6:30 Best of Show Awards Reception in the Exhibit Hall

Sponsored by DataDirect Networks

THURSDAY, MAY 1

7:00 am Registration Open

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

8:00 Chairperson's Opening Remarks

Kevin Davies, Ph.D., Vice President Business Development & Publisher C&EN, American Chemical Society; Founding Editor, Bio-IT World

» 8:05 PLENARY KEYNOTE SESSION

Please see page 4 for details.

10:00 Coffee Break in the Exhibit Hall and Poster Competition Winners Announced

Integrating and Implementing Analysis Platforms and Data Workflows

10:30 Chairperson's Opening Remarks

Brian Bissett, IT Specialist, Office of Systems, Social Security Administration

10:35 From Animal to Image - Integrating a Research Pathology Lab Environment at Roche pRED

Angelika Fuchs, Ph.D., Senior Scientist, pRED Informatics, Roche pRED

We present an exemplary case study where several components (in-house implemented tools as well as customized commercial platforms) have been successfully integrated into a departmental system landscape for the pathology department in Roche pRED, leading to a strong increase in transparency as well as efficiency.

10:55 Navigator Workbench - An Integrated Analysis Platform for Modeling & Simulation

Alexandra Grebe de Barron, Ph.D., Consultant, R&D IT Early Development, Bayer Pharma AG

We will present an integrated platform for modeling and simulation (population PK/PD analysis) in a regulated environment. The first results of the proof-of-concept at Bayer Pharma AG will be shown. The solution includes an internal high-performance cluster for routine analysis and a private external cloud for peak computing demands. Data security and validation approach will also be presented.

11:15 Enterprise Level SharePoint Administration for Program Management

Brian Bissett, IT Specialist, Office of Systems, Social Security Administration

Using InfoPath, SharePoint's capabilities can be expanded to design, distribute, file, and submit electronic forms containing structured XML data. Numerous third party tools can expand both SharePoint and InfoPath's capabilities far beyond their original scope to include functions such as Project Management, Dashboarding, and Asset Management. Limitations, pros and cons, and cost effective solutions will be discussed.

11:35 Implementation and Deployment of a Workflow Management System for Abbvie's Antibody Engineering Groups

Ankita Bhan, PMP, Scientist Informatics, Scientific Informatics and Automation, AbbVie

In order to address the existing and anticipated needs of Antibody engineering groups across the sites at Abbvie, we need to deploy technology based platforms covering the next gen biologics research. Here, we will focus on the successful management of an implementation and deployment project for Abbvie's antibody lead discovery group leveraging the solution offered by Genedata Biologics.

Sponsored by Thomson Reuters

12:15 Luncheon Presentation: BI-SMART - A Work-Flow Based tranSMART System Enabling Scientists for Fast and Reliable Genomic Analysis

Will Loging, Director of Computational Biology, Boehringer Ingelheim

1:15 Dessert Refreshment Break in the Exhibit Hall with Poster Viewing

Managing Big Data and Security Strategies

1:55 Chairperson's Remarks

Toby Bloom, Ph.D., Deputy Scientific Director, Informatics, New York Genome Center

2:00 Data and Intellectual Property Security in a Global Cyber Environment

Russ Brown, Supervisory Special Agent, Boston Division Criminal Cyber Squad, FBI

Data security is a very significant issue faced by businesses in today's electronically connected environment. Data "owned" or controlled by a business, as well as applications developed by a business, are categorized as Intellectual Property. The security and protection of Intellectual Property is critical to conducting, maintaining and growing a secure business in the current global environment.

2:30 Information Classification: The Key to a Sane Security Strategy

William Telford, Director, R&D IS Security, Sanofi R&D

Understanding your information is key to your security success and enables collaboration. This talk will address the key topics to consider and challenges that must be overcome.

3:00 PANEL DISCUSSION: The Big Data Storage and Security Maze: Balancing Collaboration and Privacy

Moderator: Toby Bloom, Ph.D., Deputy Scientific Director, Informatics, New York Genome Center

Russ Brown, Supervisory Special Agent, Boston Division Criminal Cyber Squad, FBI

Yaniv Erlich, Ph.D., Principal Investigator and Whitehead Fellow, Whitehead Institute for Biomedical Research

Philip Groth, Ph.D., IT Business Partner, CoE Research, Bayer HealthCare Pharmaceuticals

John Sabey, President, Sabey Data Center Properties

William Telford, Director, R&D IS Security, Sanofi R&D

Big data has led to organizations turning to virtual networks for information storage and processing. Thus, unauthorized access to data and implementation of effective governance structures are growing concerns. To balance knowledge sharing and respect for confidentiality, researchers must consider how and where to store and secure data – plus what data and why. This panel gathers representatives from academia, pharma and IT to discuss these issues. Topics include:

- How secure is your data?
- When should you favor data sharing and when should you restrict data flow?
- What data actually needs to be protected in the first place?
- What security systems and practices are most appropriate for specific research needs?

4:00 Conference Adjourns

Cambridge Healthtech Institute,
250 First Avenue, Suite 300,
Needham, MA 02494
www.healthtech.com

Track 3

Cloud Computing

Riding the Cloud to Next-Generation Computing

TUESDAY, APRIL 29

7:00 am Workshop Registration and Morning Coffee

8:00 - 11:30 Recommended Morning Pre-Conference Workshops*

An Embarrassment of Riches: Choosing and Implementing Cloud Infrastructure to Replace On-Premises HPC for Next-Generation Sequence Analysis

Analyzing NGS Data in Galaxy

12:30 - 4:00 pm Recommended Afternoon Pre-Conference Workshops*

IT & Informatics in Support of Collaboration

Running a Local Galaxy Instance and Externalization

**Separate Registration Required. See page 5 for additional workshops.*

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 PLENARY KEYNOTE SESSION

Please see page 4 for details.

5:00 – 7:00 Welcome Reception in the Exhibit Hall with Poster Viewing

Sponsored by IBM

WEDNESDAY, APRIL 30

7:00 am Registration Open and Morning Coffee

8:00 Chairperson's Opening Remarks

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

» 8:05 PLENARY KEYNOTE SESSION

Please see page 4 for details.

9:00 Benjamin Franklin Award & Laureate Presentation

9:30 Best Practices Awards Program

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

Collaborations

10:50 Chairperson's Remarks

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

11:00 tranSMART – A Rapidly Evolving Community-Driven Open Source Platform for Translational Research

Michael Braxenthaler, Ph.D., Global Head, Strategic Alliances, F. Hoffmann-La Roche; VP, Industry Relations, tranSMART Foundation

One year after its inception, the tranSMART Foundation releases version 1.2 of the open source translational research platform tranSMART. Major new features across all key functional areas were contributed by many members of a vibrant community spanning academic, not-profit and commercial sectors. We present a success story for pre-competitive collaborative efforts.

11:30 Improving Multi-Organization Collaboration – Using the Best the World Has to Offer

Sponsored by EXOSTAR

Andrew Porter, Director, IT Architecture, Merck

In today's environment, successful life science organizations are looking outside their four walls to engage the best resources available. EngageZone is a collaboration platform powered by a secure cloud-based life sciences identity hub which allows companies across the industry to utilize a shared infrastructure to facilitate better collaboration while delivering improved usability, ease of deployment, security of intellectual property, and information accountability.

12:00 pm New Cloud-Based Workflows Power Global Life Science Innovation

Sponsored by aspera, an IBM® company

Michelle Munson, President, CEO & Co-Founder, Aspera

Cloud-based tools for life sciences are driving innovation and enabling advancements like never before. High-speed transport technology was the first step in removing the inherent bottlenecks of cloud infrastructure. Now life sciences workflows have been transformed. High-speed transport and powerful, high-performance cloud computing sit behind a new generation of transport, analysis, transformation and sharing of big data.

12:40 Luncheon Presentation I: Bringing the Big Brain Computer to the Cloud: SGI UV for Cloud-Based Genomics Workflows

Sponsored by SGI

James Reaney, Director, Research Markets, SGI

Building on years of experience with Cyclone™, SGI announces a new collaborative project to bring cloud-based computational resources to genomics workflows worldwide. SGI will showcase several of its computational and storage technologies in the project but chief among these is the SGI UV platform: the "Big Brain" supercomputing system which already powers several large genomics research facilities worldwide. A brief, high-level overview of the project and its collaborative approach will be given, along with a discussion of the initial goals and anticipated benefits for researchers.

1:10 Luncheon Presentation II: Embrace the Inevitable: Six Imperatives to Prepare Your Company for Cloud Computing

Sponsored by okta

Vadim Parizher, Senior Director of Enterprise Architecture, Allergan

In today's digital economy, speed and agility are the keys to winning in business. This session outlines Allergan, Inc.'s (NYSE: AGN) journey from a traditional on-premise IT landscape into a Hybrid IT environment and the role Cloud computing has played in enabling a "second" speed delivery capability. This session will detail experiences, lessons learned, and required changes – including the requirements for identity management - as part of this evolution and share specific challenges in the Pharmaceutical industry.

Healthcare and Security

1:50 Chairperson's Remarks

R. Mark Adams, Ph.D., CIO, Good Start Genetics

1:55 Riding the Cloud to Big Data Analytics in and for Healthcare

Nitesh Chawla, Ph.D., Associate Professor, Computer Science and Engineering, University of Notre Dame

Faced with unsustainable costs and huge amounts of under-utilized data, healthcare needs more efficient practices, research and tools to harness the full benefits of personal health and healthcare-related data. In this talk, I will present the foundations of work that takes a Big Data approach, leveraging cloud computing, towards population health management and personalized healthcare.

2:25 Bursting through to the Cloud – Migrating On-Premises High-Performance Computing to the Cloud in a Clinically Validated, HIPAA-Regulated Setting

R. Mark Adams, Ph.D., CIO, Good Start Genetics

High-performance computing is a critical component of the emerging clinical next-generation sequencing field. This talk addresses the processes involved with taking a custom-developed, in-house pipeline supporting a unique exon-capture NGS approach and acquiring/developing the necessary refinements, tools and processes to implement a clinically validated system in the cloud.

2:55 Gov't, Pharma, and BioTech Case Studies: Implementing Cloud for Computational Life Sciences

Sponsored by CYCLE COMPUTING

Jason Stowe, CEO and Founder, Cycle Computing

From HIPAA, to Genomics, and Drug Design, this session will review Science-on-Cloud implementations, and provide thoughts on future directions. Case studies will represent a variety of applications, and workload sizes from 128 cores, up to runs of more than 156,000 cores. Bring your questions about Cloud HPC, your thinking caps, and we'll review several real examples from the past year.

Click Here to Register Online!
Bio-ITWorldExpo.com

Cambridge Healthtech Institute,
250 First Avenue, Suite 300,
Needham, MA 02494
www.healthtech.com

3:25 Refreshment Break in the Exhibit Hall with Poster Viewing

4:00 GenoSpace – Integrated Data Services for Genomic Medicine Delivery

Niall O'Connor, Head, Engineering, GenoSpace

Genomic data generation has become a commodity and the challenge of managing, analyzing and interpreting results for clinically actionable findings remains a growing problem. We present a secure cloud-based data architecture and service model that integrates vast, disparate knowledge collections. It empowers pathologists, clinicians and patients to harness precision medicine's promise.

4:30 New Approaches around Security and Cloud-Based Orchestration of Genomic Workflows

Charles Schmitt, Ph.D., CTO, RENCI, University of North Carolina at Chapel Hill

Executing genomic workflows in the cloud allows convenience and financial savings over traditional approaches. But users must deal with issues of security and potentially complex workflow orchestration to take full advantage of cloud offerings. We present work from NSF- and NIH-funded projects that provide a cloud-based trust fabric to securely execute cloud-based genomic workflows.

5:00 Enabling Secure Global Genomic Data Exchanges

Sponsored by AnnaiSystems

Stuart Young, Director, Bioinformatics, Annai Systems

Research and healthcare organizations are facing the challenge of finding and exchanging genomic information. Annai Systems provides a solution: Annai-GNOS, a Repository as a Service platform that provides secure access to conduct metadata searches and execute encrypted, accelerated downloads of genomic information. GNOS enables global genomic data exchanges of public and private partners to increase the use and value of genomic information.

5:15 Sponsored Presentation *(Opportunity Available)*

5:30 - 6:30 Best of Show Awards Reception in the Exhibit Hall

Sponsored by DataDirect NETWORKS

THURSDAY, MAY 1

7:00 am Registration Open

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

8:00 Chairperson's Opening Remarks

Kevin Davies, Ph.D., Vice President Business Development & Publisher C&EN, American Chemical Society; Founding Editor, Bio-IT World

» **8:05 PLENARY KEYNOTE SESSION**
Please see page 4 for details.

10:00 Coffee Break in the Exhibit Hall and Poster Competition Winners Announced

NGS Analysis

10:30 Chairperson's Opening Remarks

Jason Stowe, CEO and Founder, Cycle Computing

10:35 Implementations of Cloud-Based Pipelines for Large-Scale DNA-Seq and RNA-Seq Data Analyses

Shanrong Zhao, Ph.D., Senior Scientist, Informatics, Johnson & Johnson

Due to reduced sequencing costs, more NGS data are produced by small research groups. Data storage and CPU resources required for large-scale whole-genome sequencing and RNA-Seq data analyses are too large for many individual laboratories to provide. To meet these challenges, we developed *Rainbow* and *Stormbow*: cloud-based software packages for large-scale DNA-Seq and RNA-Seq analyses.

10:55 Analyzing DNA-Seq Data Using DRAW: Lessons Learned from Using Amazon EC2 for Next-Generation Sequencing Studies

Li-San Wang, Ph.D., Assistant Professor, Pathology and Laboratory Medicine, University of Pennsylvania

DNA-Seq studies pose enormous challenges to many researchers who have limited access to dedicated IT support or high-performance computing. Cloud computing is a promising solution to address these needs. This talk covers our experience using the DNA Resequencing Analysis Workflow (DRAW) software to process >800 samples and our strategy to use Amazon EC2 effectively for DNA-Seq analysis.

11:15 Globus Genomics: An End-to-End NGS Analysis Service on the Cloud for Researchers and Core Labs

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

We describe the Globus Genomics platform. Globus Genomics provides an integrated platform for end-to-end data management using Globus Online and scalable analysis using the Galaxy framework and Amazon Web Services. We will walk through case studies of researchers and core labs at various universities that are leveraging the service to meet their rapidly growing genomics analysis needs.

11:35 Technology Advancements in High Density Compute and Storage that Power the Next Generation of Cloud Infrastructure

Sponsored by THINKMATE HIGH PERFORMANCE COMPUTING

Brian Corn, Vice President, Marketing, Thinkmate

Thinkmate solutions accelerate discovery while reducing TCO, expanding scalability and enabling business continuity. Exciting new solutions from names like Intel, Supermicro, and Western Digital will be covered. This presentation is a "must see" for any attendees involved in hardware infrastructure design, testing, and procurement.

12:15 pm Luncheon Presentation I: Turn-Key RNA-Seq Analysis for the Biologist Using the Maverix Analytic Platform

Sponsored by Maverix BIOMICS

Dan Kearns, Director, Software Development, Maverix Biomics, Inc.

Studies leveraging RNA-seq data are commonly limited by the tools, infrastructure, and trained bioinformaticians necessary to process, interpret and manage the data. The Maverix Analytic Platform addresses these challenges through a unique environment designed for biologists. This cloud-based platform leverages best-in-class tools and provides an integrated UCSC-genome browser endpoint to enable visualization and interpretation of results.

12:45 Luncheon Presentation II: Biotech Self-Service Agility in Public and Private Clouds

Sponsored by ADVIZEX TECHNOLOGIES A ROLTA COMPANY

Dennis Faucher, Director, Presales, AdvizeX Technologies, a Rolta Company

Biotech requires fast time to market with high quality, high compliance and lowered cost. The correct mix of private and public cloud enables: reduced costs to significantly lower Total Cost of Ownership (TCO), on-demand application and service provisioning in hours rather than weeks, increasing business agility, supporting business growth and accelerating time-to-market, and increased service levels and business continuity via an in-built disaster recovery capability.

1:15 Dessert Refreshment Break in the Exhibit Hall with Poster Viewing

Pharma Strategies

1:55 Chairperson's Remarks

Jason Stowe, CEO and Founder, Cycle Computing

2:00 Data Sciences: Cloud Compute and New Graph Compute Models

Jeremy Chambers, Senior Data/IT Architect, Data Science, R&D IT, Biogen Idec

2:20 The Path to Establishing a Global Data Analysis Infrastructure at AstraZeneca

Justin H. Johnson, Principal Scientist, Translational Oncology, AstraZeneca, Inc.

NGS technologies are evolving, the data is growing, data is subject to artifacts and NGS moves toward the clinic. It is imperative that we build tools and methods to translate NGS data into knowledge for target discovery, patient selection and translational medicine through a flexible, scalable and secure infrastructure. The hybrid cloud / local solution and novel data warehousing strategies being built at AstraZeneca will allow for a global streamlined ability to analyze, store and interpret NGS data. Ultimately, it will provide the ability to identify variation responsible in tumorigenesis and stratify the disease as well as identify mechanisms of resistance and correlate preclinical drug response with genome data.

2:40 SHERPA: A Service to Utilize ScienceCloud for Integration of Collaboration Data at Sanofi

James Connelly, Ph.D., Head, Research Data Management, Sanofi

In recent years, there has been a great increase in collaborative research that requires integration and analysis of compound and bioactivity data from multiple sources. This is necessary to enable efficient cycle time for compound optimization and effective project decisions. ScienceCloud/HEOS was an ideal platform to enable secure collaborative data sharing in a "Cloud" and to facilitate pipelining of data to and from our internal data systems. At Sanofi, we have built a service, called SHERPA, to support drug discovery research projects data sharing with external collaborators. Expansion is also planned to support Biologics Research.

3:00 From Nebula to Cloud: A Critical Assessment of Cloud Technologies in R&D Informatics

Alain Nanzer, Ph.D., Global Head, Safety and Development Workflows, Pharma Research and Early Development Informatics (pREDi), F. Hoffmann-La Roche Ltd.

Migration of R&D computer systems and services to "The Cloud" are considered an important step to reduce costs while increasing flexibility, availability and service quality. The presentation will assess a series of cloud implementations in R&D informatics to define the success of these projects along the predicted gains. A special focus will be put on cloud implementations in regulated environments.

3:30 PANEL DISCUSSION: Optimizing Cloud Computing for Scientific Research

Moderator: Jason Stowe, CEO and Founder, Cycle Computing

Jeremy Chambers, Senior Data/IT Architect, Data Science, R&D IT, Biogen Idec

James Connelly, Ph.D., Head, Research Data Management, Sanofi

Justin H. Johnson, Principal Scientist, Translational Oncology, AstraZeneca, Inc.

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

Alain Nanzer, Ph.D., Global Head, Safety and Development Workflows, Pharma Research and Early Development Informatics (pREDi), F. Hoffmann-La Roche Ltd.

Thomas Schilling, Ph.D., IT Portfolio Manager, R&D, Bayer Business Services GmbH

In this big data age, researchers rely more heavily on cloud computing to store, share and analyze data. It is thus important to understand the options, potential uses and best practices for optimizing this technology. This panel of IT infrastructure experts, software development pros and end users will address the possibilities and perils of working in the cloud, now and in the future.

4:00 Conference Adjourns

Cambridge Healthtech Institute,
250 First Avenue, Suite 300,
Needham, MA 02494
www.healthtech.com

Track 4

Bioinformatics

Utilizing Massive Quantities of –omic Information across Research Initiatives

TUESDAY, APRIL 29

7:00 am Workshop Registration and Morning Coffee

8:00 - 11:30 Recommended Morning Pre-Conference Workshops*

Data Visualization in Biology: From the Basics to Big Data

Analyzing NGS Data in Galaxy

12:30 - 4:00 pm Recommended Afternoon Pre-Conference Workshops*

Big Data Analytics

Running a Local Galaxy Instance

**Separate Registration Required. See page 5 for additional workshops.*

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 PLENARY KEYNOTE SESSION
Please see page 4 for details.

5:00 – 7:00 Welcome Reception in the Exhibit Hall with Poster Viewing

Sponsored by IBM

WEDNESDAY, APRIL 30

7:00 am Registration Open and Morning Coffee

8:00 Chairperson's Opening Remarks

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

» 8:05 PLENARY KEYNOTE SESSION
Please see page 4 for details.

9:00 Benjamin Franklin Award & Laureate Presentation

9:30 Best Practices Awards Program

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

Bioinformatics for Big Data

10:50 Chairperson's Remarks

Les Mara, Founder, Databiology, Ltd.

11:00 Data Management Best Practices for Genomics Service Providers

Vas Vasiliadis, Director, Products, Computation Institute, University of Chicago and Argonne National Laboratory

Genomics research teams in academia and industry are increasingly limited at all stages of their work by large and unwieldy datasets, poor integration between the computing facilities they use for analysis, and difficulty in sharing analysis results with their customers and collaborators. We will discuss issues with current approaches and describe emerging best practices for managing genomics data through its lifecycle.

11:30 NGS Analysis to Drug Discovery: Impact of High-Performance Computing in Life Sciences

Bhanu Rekepalli, Ph.D., Assistant Professor and Research Scientist, Joint Institute for Computational Sciences, The University of Tennessee, Oak Ridge National Laboratory

We are working with small-cluster-based applications most widely used by the scientific community on the world's premier supercomputers. We incorporated these parallel applications into science gateways with user-friendly, web-based portals. Learn how the research at UTK-ORNL will help to bridge the gap between the rate of big data generation in life sciences and the speed and ease at which biologists and pharmacists can study this data.

12:00 pm The Future of Biobank Informatics

Sponsored by REMEDY INFORMATICS

Bruce Pharr, Vice President, Product Marketing, Laboratory Systems, Remedy Informatics

As biobanks become increasingly essential to basic, translational, and clinical research for genetic studies and personalized medicine, biobank informatics must address areas from biospecimen tracking, privacy protection, and quality management to pre-analytical and clinical collection/identification of study data elements. This presentation will examine specific requirements for third-generation biobanks and how biobank informatics will meet those requirements.

12:15 Learn How YarcData's Graph Analytics Appliance Makes It Easy to Use Big Data in Life Sciences

Sponsored by YarcData

Ted Slater, Senior Solutions Architect, Life Sciences, YarcData, a division of Cray

YarcData, a division of Cray, offers high performance solutions for big data graph analytics at scale, finally giving researchers the power to leverage all the data they need to stratify patients, discover new drug targets, accelerate NGS analysis, predict biomarkers, and better understand diseases and their treatments.

12:40 Luncheon Presentation I: The Role of Portals for Managing Biostatistics Projects at a CRO

Sponsored by QUINTILES

Les Jordan, Director, Life Sciences IT Consulting, Quintiles

This session will focus on how portals and other tools are used within Quintiles and at other pharmas to manage projects within the biostatistics department.

1:10 Luncheon Presentation II *(Sponsorship Opportunity Available)* **or Lunch on Your Own**

1:50 Chairperson's Remarks

Michael Liebman, Ph.D., Managing Director, IPQ Analytics, LLC

Sabrina Molinaro, Ph.D., Head of Epidemiology, Institute of Clinical Physiology, National Research Council - CNR Italy

1:55 Integration of Multi-Omic Data Using Linked Data Technologies

Aleksandar Milosavljevic, Ph.D., Professor, Human Genetics; Co-Director, Program in Structural & Computational Biology and Molecular Biophysics; Co-Director, Computational and Integrative Biomedical Research Center, Baylor College of Medicine

By virtue of programmatic interoperability (uniform REST APIs), Genboree servers enable virtual integration of multi-omic data that is distributed across multiple physical locations. Linked Data technologies of the Semantic Web provide an additional "logical" layer of integration by enabling distributed queries across the distributed data and by bringing multi-omic data into the context of pathways and other background knowledge required for data interpretation.

2:25 Building Open Source Semantic Web-Based Biomedical Content Repositories to Facilitate and Speed Up Discovery and Research

Bhanu Bahl, Ph.D., Director, Clinical and Translational Science Centre, Harvard Medical School

Douglas MacFadden, CIO, Harvard Catalyst at Harvard Medical School

Eagle-i open source network at Harvard provides a state-of-the-art informatics

Click Here to Register Online!
Bio-ITWorldExpo.com

Cambridge Healthtech Institute,
250 First Avenue, Suite 300,
Needham, MA 02494
www.healthtech.com

platform to support the quality control and annotation of resources establishing a sound foundation for a well-curated resource collection in accordance with Semantic Web and Linked Open Data principles. Learn how this ontology-centric architecture is used to efficiently store, create, and search data.

2:55 Analysis of Disease and Drug Interactions in the Elderly: An Application of Big Data

Michael Liebman, Ph.D., Managing Director, IPQ Analytics, LLC

Sabrina Molinaro, Ph.D., Head of Epidemiology, Institute of Clinical Physiology, National Research Council - CNR Italy

Diagnosis and treatment in elderly patients presents a unique set of challenges because of their extensive clinical history, altered physiology and physiological response both to diseases and treatments, patterns of behavior and access to appropriate medical care. Although certain characteristics can be present in patients at any age, several are particularly prevalent among the elderly: active co-morbid conditions; extended history of taking multiple medications; utilization of multiple physicians/specialists without a single point of coordination of care; presentation of signs and symptoms that could result from undiagnosed disease, side-effects of current medications, interactions among current medications, failure to adhere to prescribing directions, cognitive decline and confusion which can lead to drug misuse/abuse, etc. This study highlights application of big data to address the complexity in treatment of elderly patients with diabetes and hypertension.

3:25 Refreshment Break in the Exhibit Hall with Poster Viewing

Biological Networks

4:00 Network Verification Challenge: A Reputation-Based Crowd-Sourced Peer Review Platform for Network Biology

William Hayes, Ph.D., Senior Vice President, Platform Development, IT/ Informatics, Selventa

Anselmo DiFabio, Vice President, Technology, Applied Dynamic Solutions

The Network Verification Challenge proposes a new approach for peer review for Network biology. The use of a reputation-based crowd-sourced platform can make previously overwhelming efforts in capturing large-scale network biology and validating it possible. The same approach for peer review can also be applied inside bioPharma for internal collaboration and validation of network biology in and across therapeutic areas.

4:30 NDEx, the Network Data Exchange: Bridging the Knowledge Gap for Commercial and Academic Collaboration on Biological Networks

Dexter Pratt, Project Director, NDEx, Cytoscape Consortium

NDEx is a public portal for collaboration and publication for scientists and organizations working with biological networks of multiple types and in multiple formats. This talk presents key features of the NDEx portal and the underlying open-source server software. The status of NDEx in collaborations with other organizations and the use (or development) of standards will be summarized.

5:00 MINE: A Novel Computational Approach for Gene Network Identification

Diane Joseph-McCarthy, Ph.D., Vice President, Chemistry & Computational Science, EnBiotix, Inc.

A perturbation to a biological system results in changes to molecular processes, signaling networks, and the constituent genes. These changes reflect the mode-of-action (MOA) of the perturbation and, if properly characterized, can be used to gain insights into how the perturbation acts. Our novel MINE approach (Mode-of-action by Iterative Network Expansion), leverages the strengths of two well-established computational methods: MNI (Mode-of-action by Network Identification) and CLR (Context Likelihood of Relatedness). MINE iteratively uses both methods to allow for enhanced characterization of the biological processes underlying a perturbation. Details of this approach as well as initial results in mammalian datasets will be presented.

5:30 - 6:30 Best of Show Awards Reception in the Exhibit Hall

Sponsored by DataDirect NETWORKS

THURSDAY, MAY 1

7:00 am Registration Open

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

8:00 Chairperson's Opening Remarks

Kevin Davies, Ph.D., Vice President Business Development & Publisher C&EN, American Chemical Society; Founding Editor, Bio-IT World

» 8:05 PLENARY KEYNOTE SESSION

Please see page 4 for details.

10:00 Coffee Break in the Exhibit Hall and Poster Competition Winners Announced

Bioinformatics Across Multiple Research Initiatives

10:30 Chairperson's Opening Remarks

Subha Madhavan, Ph.D., Director, Innovation Center for Biomedical Informatics, Oncology, Georgetown University

10:35 Analysis of Genomics Data in an Internal Cloud Computing Environment

Philip Groth, Ph.D., IT Business Partner Genomics, R&D IT - Research, Bayer HealthCare

This talk presents the technical set-up of vCloud, an in-house cloud solution, maintenance and running an internal cloud-computing environment, and how this set-up enables fast & secure analysis of large-scale genomics data. Results of analyzing genomic data from over 4,000 cancer patients will be presented.

11:05 Genome-Wide Multi-Omics Profiling of Colorectal Cancer Identifies Immune Determinants Strongly Associated With Relapse

Subha Madhavan, Ph.D., Director, Innovation Center for Biomedical Informatics, Oncology, Georgetown University

This presentation demonstrates the use of novel informatics methods and data integration approaches in identifying prognostic markers of cancer. The use and benefit of adjuvant chemotherapy to treat patients with state II colorectal cancer (CRC) is not well understood since the majority of these patients are cured by surgery alone.

11:35 Bioinformatics Initiatives Spanning Academia, Biotech and Pharma

Gerry Higgins, M.D., Ph.D., Vice President, Pharmacogenomic Science, AssureRx Health, Inc.

12:15 pm Luncheon Presentations *(Sponsorship Opportunities Available)* **or Lunch on Your Own**

1:15 Dessert Refreshment Break in the Exhibit Hall with Poster Viewing

1:55 Chairperson's Remarks

Simon Berkovich, Ph.D., Professor, Computer Science, The George Washington University

2:00 An Algorithm to Access Human Memory Showing Alzheimer Symptoms When Distorted

Simon Berkovich, Ph.D., Professor, Computer Science, The George Washington University

This talk presents a novel theoretical framework for bioinformatics. Access to a holographic model of the brain encounters a particular problem of multiple responses resolution. For the given milieu, we employ a digital-analog adjustment of a streaming algorithm for finding a predominant element. Receptacles deterioration incurs preferential recall of prior life stages akin to Alzheimer's disease.

Machine Learning Models

2:30 Accurate Prediction of Clinical Stroke Scales from Robotic Measurements

Dimitris K. Agrafiotis, Ph.D., FRSC, Vice President and Chief Data Officer, Covance

Here, we describe a novel approach that combines robotic devices and advanced machine learning algorithms to derive predictive models of clinical assessments of motor function following stroke. We show that it is possible to derive sensitive biomarkers of motor impairment using a few easily obtained robotic measurements, which can then be used to improve the efficiency and cost of clinical trials.

3:00 GPS Engineering: Machine Learning Approaches to Biological Engineering

Drew Regitsky, Scientist, Bioengineering, Calysta Energy

This talk presents a potential new approach to computational representations of biological systems and applying multidimensional analysis to predicting the behavior of complex systems. Several case studies will be presented to demonstrate applications of the methods and examples of the output of data analysis.

3:30 A Multiclass Extreme-Learning-Machine Approach to the Discovery of Multiple Cancer Biomarkers: Using Binary Coded Genetic Algorithm and IPA Analysis

Saras Saraswathi, Ph.D., Clinical Instructor, Pediatrics, Ohio State University; Postdoctoral Research Associate, Battelle Center for Mathematical Medicine, Research Institute, Nationwide Children's Hospital

The neural network-based Extreme Learning Machine is combined with a Binary Coded Genetic Algorithm to select a small set of 92 genes which simultaneously classify 14 different types of cancers simultaneously, to high accuracy. IPA analysis of the selected genes reveals that over 60% of the selected genes are related to many cancers that are being classified.

4:00 Conference Adjourns

Click Here to Register Online!
Bio-ITWorldExpo.com

Cambridge Healthtech Institute,
250 First Avenue, Suite 300,
Needham, MA 02494
www.healthtech.com

Track 5

Next-Gen Sequencing Informatics

Advances in Analysis and Interpretation of NGS Data

TUESDAY, APRIL 29

7:00 am Workshop Registration and Morning Coffee

8:00 - 11:30 Recommended Morning Pre-Conference Workshops*

Analyzing NGS Data in Galaxy

12:30 - 4:00 pm Recommended Afternoon Pre-Conference Workshops*

Running a Local Galaxy Instance

**Separate Registration Required. See page 5 for additional workshops.*

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 PLENARY KEYNOTE SESSION
Please see page 4 for details.

5:00 – 7:00 Welcome Reception in the Exhibit Hall with Poster Viewing

Sponsored by IBM

WEDNESDAY, APRIL 30

7:00 am Registration Open and Morning Coffee

8:00 Chairperson's Opening Remarks

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

» 8:05 PLENARY KEYNOTE SESSION
Please see page 4 for details.

9:00 Benjamin Franklin Award & Laureate Presentation

9:30 Best Practices Awards Program

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

NGS Bioinformatics Marketplace: Emerging Trends and Predictions

10:50 Chairperson's Remarks

Narges Baniasadi, Ph.D., Founder & CEO, Bina Technologies, Inc.

11:00 Global Next-Generation Sequencing Informatics Markets: Inflated Expectations in an Emerging Market

Greg Caressi, Senior Vice President, Healthcare and Life Sciences, Frost & Sullivan

This presentation evaluates the global next-generation sequencing (NGS) informatics markets from 2012 to 2018. Learn key market drivers and restraints, key highlights for many of the leading NGS informatics services providers and vendors, revenue forecasts, and the important trends and predictions that affect market growth.

Organizational Approaches to NGS Informatics

11:30 High-Performance Databases to Manage and Analyze NGS Data

Joseph Szustakowski, Ph.D., Head, Bioinformatics, Biomarker Development, Novartis Institutes for Biomedical Research

The size, scale, and complexity of NGS data sets call for new data management and analysis strategies. High-performance database systems combine the advantages of both established and cutting edge technologies. We are using high performance database systems to manage and analyze NGS, clinical, pathway, and phenotypic data with great success. We will describe our approach and concrete success stories that demonstrate its efficiency and effectiveness.

12:00 pm Taming Big Science Data Growth with Converged Infrastructure

Sponsored by DataDirect Networks

Aaron D. Gardner, Senior Scientific Consultant, BioTeam, Inc.

Many of the largest NGS sites have identified IO bottlenecks as their number one concern in growing their infrastructure to support current and projected data growth rates. In this talk Aaron D. Gardner, Senior Scientific Consultant, BioTeam, Inc. will share real-world strategies and implementation details for building converged storage infrastructure to support the performance, scalability and collaborative requirements of today's NGS workflows.

12:15 Next Generation Sequencing: Workflow Overview from a High-Performance Computing Point of View

Sponsored by Cray The Supercomputer Company

Carlos P. Sosa, Ph.D., Applications Engineer, HPC Lead, Cray, Inc.

Next Generation Sequencing (NGS) allows for the analysis of genetic material with unprecedented speed and efficiency. NGS increasingly shifts the burden from chemistry done in a laboratory to a string manipulation problem, well suited to High- Performance Computing. We explore the impact of the NGS workflow in the design of IT infrastructures. We also present Cray's most recent solutions for NGS workflow.

12:40 Luncheon Presentation I: Erasing the Data Analysis Bottleneck with BaseSpace

Sponsored by illumina

Jordan Stockton, Ph.D., Marketing Director, Enterprise Informatics, Illumina, Inc.

Since the inception of next generation sequencing, great attention has been paid to challenges such as storage, alignment, and variant calling. We believe that this narrow focus has distracted many biologists from higher-level scientific goals, and that simplifying this process will expedite the discovery process in the field of applied genomics. In this talk we will show that applications in BaseSpace can empower a new class of researcher to go from sample to answer quickly, and can allow software developers to make their tools accessible to a vast and receptive audience.

1:10 Luncheon Presentation II: The Empowered Genome Community: First Insights from Shareable Joint Interpretation of Personal Genomes for Research

Sponsored by QIAGEN

Nathan Pearson, Ph.D. Principal Genome Scientist, QIAGEN

Genome sequencing is becoming prevalent however understanding each genome requires comparing many genomes. We launched the Empowered Genome Community, consisting of people from programs such as the Personal Genome Project (PGP) and Illumina's Understand Your Genome. Using Ingenuity Variant Analysis, members have identified proof of principle insights on a common complex disease (here,myopia) derived by open collaborative analysis of PGP genomes.

Click Here to Register Online!
Bio-ITWorldExpo.com

Cambridge Healthtech Institute,
250 First Avenue, Suite 300,
Needham, MA 02494
www.healthtech.com

1:50 Chairperson's Remarks
Georges Heiter, Founder, Databiology, Ltd.

1:55 High-Performance *de novo* Transcript Reconstruction Leveraging Distributed Memory and Massive Parallelization
Brian Haas, Senior Computational Biologist, Broad Institute
Exemplifying collaborative software development between industry and academia to tackle computational challenges in manipulating large volumes of next-gen sequence data, leveraging advances in algorithm development and compute hardware, we describe our efforts to optimize the performance of the Trinity RNA-Seq *de novo* assembly software. We explore a massively parallel computing architecture to tackle more efficient assembly of RNA-Seq data in the context of the Trinity assembly workflow.

2:25 'Titan' Supercomputer Helps Identify Pathogenic Bacteria in the Human Microbiome for Biosurveillance
Tae-Hyuk Ahn, Ph.D., Research Associate, Computer Science and Mathematics Division, Oak Ridge National Laboratory
This talk will present a new algorithm, SIGMA (http://sigma.omicsbio.org), for metagenomic biosurveillance. SIGMA has the unique capability of identifying the correct strain of a pathogen in a complex metagenomic background from many closely related candidates in the reference genome database. Using a top open-science supercomputer, Titan, pathogenic bacteria strains can be identified in an hour from the 100 million human microbiome sequences.

2:55 GENALICE MAP: The New Gateway for Whole Genome Sequencing to the Clinic
Sponsored by GENALICE
Hans Karten, CEO, CTO, GENALICE
The ever-increasing output of Next Generation Sequencing (NGS) puts equally increasing demands on IT resources such as computing power, network bandwidth and data storage capacity. GENALICE MAP is an NGS short read alignment and variant calling solution using a novel alignment algorithm, efficient storage structure and a state-of-the-art high performance software design. It is faster, better and extremely cost-effective.

3:25 Refreshment Break in the Exhibit Hall with Poster Viewing

NGS Data Computing and Management Structures and Workflows

4:00 Multitier Infrastructure for NGS Data Computing and Management
Xiang Yao, Ph.D., Principal Scientist, Translational Informatics, the Janssen Pharmaceutical Companies of Johnson & Johnson
Pipelines having all NGS functions have provided us conveniences. But this bundling approach is inefficient in addressing different needs of the users ranging from IT professionals to biologists, and is difficult for frequent software and hardware upgrades. This talk describes a multitier infrastructure that is modular and interconnected, to accommodate different computing, storage and access needs of the users, and to maximize return on investments.

4:30 HIVE Integrated Tools for NGS Bioinformatics: Detection Pipeline, Assembly Pipeline, Metagenomic Discovery Tools, Sequence Toolbox and More

Bio-IT 2013 Poster Winner

Raja Mazumder, Ph.D., Associate Professor, Biochemistry and Molecular Biology, The George Washington University
HIVE (High-Performance Integrated Virtual Environment: hive.biochemistry.gwu.edu) is an implementation of a multicomponent cloud infrastructure where distributed storage and computational powerhouse are linked seamlessly to provide a secure Big Data analysis platform. Development of HIVE-based pipelines for NGS analytics has been the focus of collaborative efforts by FDA and GWU research groups.

5:00 Understanding NGS Variant Data Using Pathway Analysis
Sponsored by ELSEVIER
Nikolai Daraselia, Ph.D., Director of Research, Life Science Solutions, Elsevier
Next generation sequencing data is a tremendous resource for researchers studying the underlying genetic basis for diseases, and will be a key driver in the development of personalized medicine. However the large data sets generated by NGS also present significant analysis and interpretation challenges. To assist researchers in these tasks, Elsevier is developing a Variation Analysis module for its Pathway Studio product. This new capability will make use of Pathway Studio's industry-leading biological knowledgebase to provide researchers with the literature-based evidence they need to understand the significance of genetic variants. We will discuss sample workflows and examples of variation data analysis in the context of protein biological functions.

5:30 - 6:30 Best of Show Awards Reception in the Exhibit Hall
Sponsored by DataDirect NETWORKS

THURSDAY, MAY 1

7:00 am Registration Open

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

8:00 Chairperson's Opening Remarks
Kevin Davies, Ph.D., Vice President Business Development & Publisher C&EN, American Chemical Society; Founding Editor, Bio-IT World

» 8:05 PLENARY KEYNOTE SESSION
Please see page 4 for details.

10:00 Coffee Break in the Exhibit Hall and Poster Competition Winners Announced

Cloud Computing and Collaborative Technologies

10:30 Chairperson's Opening Remarks
Jason Stowe, CEO and Founder, Cycle Computing

10:35 Implementations of Cloud-Based Pipelines for Large-Scale DNA-Seq and RNA-Seq Data Analyses
Shanrong Zhao, Ph.D., Senior Scientist, Informatics, Johnson & Johnson
Due to reduced sequencing costs, more NGS data are produced by small research groups. Data storage and CPU resources required for large-scale whole-genome sequencing and RNA-Seq data analyses are too large for many individual laboratories to provide. To meet these challenges, we developed *Rainbow* and *Stormbow*: cloud-based software packages for large-scale DNA-Seq and RNA-Seq analyses.

10:55 Analyzing DNA-Seq Data Using DRAW: Lessons Learned from Using Amazon EC2 for Next-Generation Sequencing Studies
Li-San Wang, Ph.D., Assistant Professor, Pathology and Laboratory Medicine, University of Pennsylvania
DNA-Seq studies pose enormous challenges to many researchers who have limited access to dedicated IT support or high-performance computing. Cloud computing is a promising solution to address these needs. This talk covers our experience using the DNA Resequencing Analysis Workflow (DRAW) software to process >800 samples and our strategy to use Amazon EC2 effectively for DNA-Seq analysis.

11:15 Globus Genomics: An End-to-End NGS Analysis Service on the Cloud for Researchers and Core Labs
Ravi K. Madduri, Fellow, Computation Institute, University of Chicago; Project Manager, Mathematics and Computer Science Division, Argonne National Laboratory
We describe the Globus Genomics platform. Globus Genomics provides an integrated platform for end-to-end data management using Globus Online and scalable analysis using the Galaxy framework and Amazon Web Services. We will walk through case studies of researchers and core labs at various universities that are leveraging the service to meet their rapidly growing genomics analysis needs.

11:35 Technology Advancements in High Density Compute and Storage that Power the Next Generation of Cloud Infrastructure
Sponsored by THINKMATE HIGH PERFORMANCE COMPUTING
Brian Corn, Vice President, Marketing, Thinkmate
Thinkmate solutions accelerate discovery while reducing TCO, expanding scalability and enabling business continuity. Exciting new solutions from names like Intel, Supermicro, and Western Digital will be covered. This presentation is a "must see" for any attendees involved in hardware infrastructure design, testing, and procurement.

Cambridge Healthtech Institute,
250 First Avenue, Suite 300,
Needham, MA 02494
www.healthtech.com

Sponsored by Maverix BIOMICS

12:15 pm Luncheon Presentation I: Turn-Key RNA-Seq Analysis for the Biologist Using the Maverix Analytic Platform

Dan Kearns, Director, Software Development, Maverix Biomics, Inc.

Studies leveraging RNA-seq data are commonly limited by the tools, infrastructure, and trained bioinformaticians necessary to process, interpret and manage the data. The Maverix Analytic Platform addresses these challenges through a unique environment designed for biologists. This cloud-based platform leverages best-in-class tools and provides an integrated UCSC-genome browser endpoint to enable visualization and interpretation of results.

12:45 Luncheon Presentation II: *(Sponsorship Opportunity Available)* **or Lunch on Your Own**

1:15 Dessert Refreshment Break in the Exhibit Hall with Poster Viewing

NGS Variants & Gene Mapping and Expression

1:55 Chairperson's Remarks

2:00 Characterization and Benchmarking of NGS Workflow Methods on Various Platform Architectures

Anthony Costa, Ph.D., Computational Scientist, Scientific Computing, Mount Sinai School of Medicine

We target numerically expensive pieces of the Next-Generation Sequencing (NGS) pipeline and investigate performance of many codes against a variety of CPU architectures and file systems. We further compare more recent methods implemented on non-traditional or heterogeneous architectures such as GPUs. The quality of the results from each method is also considered.

2:30 Avoiding Nonsense Results in your NGS Variant Studies

James Lyons-Weiler, Ph.D., Scientific Director, Bioinformatics Analysis Core Genomics and Proteomics Core Laboratory, University of Pittsburgh

This talk presents an information-theory based paradigm that allows the objective performance comparison of pipeline components such as variant callers, study designs, read filters, and mapping algorithms. Our method solves the problem of concordance, increasing agreement among methods in one case from 32% to 86%. The evaluation methods I will present generalize to provide advanced quality control over sample prep protocols and will be useful for comparing sequencing platforms.

3:00 Bridger: A New Framework for *de novo* Transcriptome Assembly Using RNA-Seq Data

Guojun Li, Ph.D., Senior Research Scientist, Biochemistry and Molecular Biology, The University of Georgia

Full-length transcriptome assembly is highly challenging and not a well-solved problem. The most important broad impact of the study will be that our new capability for transcriptome assembly will lead to a new level of understanding about the detailed mechanism of alternative splicing in eukaryotic genomes, hence facilitating new studies of transcriptional mechanism. This talk presents a new *de novo* assembler Bridger that takes advantage of techniques employed in the reference based assembler Cufflinks to overcome limitations of the existing *de novo* assemblers.

3:30 Analysis of Transgene Sequence and Integration Site in the CHO Genome by Next-Generation Sequencing and Use to Improve Expression

Nic Mermod, Ph.D., Professor and Director, Institute of Biotechnology, University of Lausanne

This talk presents information on how to validate protein-expressing cell lines taking an NGS approach. We have sequenced the genomes of several CHO cell clones producing therapeutic proteins and compared them to the parental genome sequence. This yielded information on the transgene sequence integrity as well as on the genomic integration locus and sequence. In turn, this gave information on the molecular mechanisms allowing the genomic integration of the vector and provided approaches to further optimize transgene integration and expression from transiently or stably engineered CHO cells.

4:00 Conference Adjourns

Cambridge Healthtech Institute,
250 First Avenue, Suite 300,
Needham, MA 02494
www.healthtech.com

Track 6

Systems Pharmacology

Pathways to Patient Response

TUESDAY, APRIL 29

7:00 am Workshop Registration and Morning Coffee

8:00 - 11:30 Recommended Morning Pre-Conference Workshops*

Biologics, Bioassay, and Biospecimen Registration Systems

12:30 - 4:00 pm Recommended Afternoon Pre-Conference Workshops*

Determining Genome Variation and Clinical Utility

**Separate Registration Required. See page 5 for additional workshops.*

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 PLENARY KEYNOTE SESSION

Please see page 4 for details.

5:00 – 7:00 Welcome Reception in the Exhibit Hall with Poster Viewing

Sponsored by IBM*

**IBM and the IBM logo are trademarks of International Business Machines Corp., registered in many jurisdictions worldwide.*

WEDNESDAY, APRIL 30

7:00 am Registration Open and Morning Coffee

8:00 Chairperson's Opening Remarks

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

» 8:05 PLENARY KEYNOTE SESSION

Please see page 4 for details.

9:00 Benjamin Franklin Award & Laureate Presentation

9:30 Best Practices Awards Program

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

Modeling: Novel Tools

10:50 Chairperson's Remarks

Avi Ma'ayan, Ph.D., Associate Professor, Pharmacology and Systems Therapeutics, Icahn School of Medicine at Mount Sinai

11:00 The Human Avatar: Quantitative Systems Pharmacology to Support Physician Decision Making in Neurology and Psychiatry

Hugo Geerts, Ph.D., MBA, BA, CSO, In Silico Biosciences; Adjunct Associate Professor, Perelman School of Medicine, University of Pennsylvania

CNS Quantitative Systems Pharmacology uses computer-based mechanistic modeling integrating brain network neurophysiology, functional imaging of genetics, pharmacology of drug-receptor interactions and parameterization with clinical data. A patient model ("human avatar") can be developed accounting for polypharmacy and life history of traumatic events to help identify optimal treatments.

11:30 VisANT: An Integrative Network Platform to Connect Genes, Drugs, Diseases and Therapies

Zhenjun Hu, Ph.D., Research Associate Professor, Center for Advanced Genomic Technology, Bioinformatics Program, Boston University

With the rapid accumulation of our knowledge on diseases, disease-related genes and drug targets, network-based analysis plays an increasingly important role in systems biology, systems pharmacology and translational science. The new release of VisANT aims to provide new functions to facilitate the convenient network analysis of diseases, therapies, genes and drugs.

12:00 pm Selected Oral Poster Presentation: Individualized PK/PD Biosimulations for Precision Drug Dosing: Diabetes Mellitus

Clyde Phelix, Ph.D., Associate Professor, Biology, University of Texas San Antonio

Individualized biosimulations offer many advantages to precision medicine. Using one's transcriptome to determine parameters of kinetic models of metabolism reanimates that individual for *in silico* testing. The Transcriptome-To-Metabolome™ Model is multiorgan and multicompartmental, including over 30 primary and secondary metabolic pathways and transport processes. Thus pharmacokinetics/pharmacodynamics studies can be performed *in silico* before treating each patient.

12:40 Luncheon Presentations *(Sponsorship Opportunities Available)* **or Lunch on Your Own**

Modeling: Cancer

1:50 Chairperson's Remarks

Hugo Geerts, Ph.D., MBA, BA, CSO, In Silico Biosciences; Adjunct Associate Professor, Perelman School of Medicine, University of Pennsylvania

» 1:55 FEATURED PRESENTATION

Identifying Drug Targets from Drug-Induced Changes in Genome-Wide mRNA Expression

Avi Ma'ayan, Ph.D., Associate Professor, Pharmacology and Systems Therapeutics, Icahn School of Medicine at Mount Sinai

We collected and organized publicly available genome-wide gene expression data where hundreds of drugs were used to treat mammalian cells and changes in expression were compared to a control. We then developed computational methods that try to find the drug targets from the expression changes. We show that different steps in the analysis can contribute to approaching the right answer.

2:25 Tools for Comparison of Systematically Generated Cancer Networks vs. Literature Models

Dexter Pratt, Project Director, NDEx, Cytoscape Consortium

Cancer subtype genetic networks can be generated by systematic analysis of patient somatic mutation data. Comparison to existing models of cancer mechanisms is an important step in investigating these data-derived models. Recent work on Network Based Stratification (NBS) at the Ideker Lab will be described along with tools for network comparison under development in the NDEx project.

Click Here to Register Online!
Bio-ITWorldExpo.com

Cambridge Healthtech Institute,
250 First Avenue, Suite 300,
Needham, MA 02494
www.healthtech.com

2:55 Integration of Text Mining and High Throughput Screening to Identify Candidate Targets for Cancer Therapy: Focus on the Autophagy Pathway

Sponsored by ELSEVIER

Philip L. Lorenzi, M.D., Anderson Cancer Center

Autophagy, a programmed process in which cell contents are delivered to lysosomes for degradation, appears to have both tumor-suppressive and tumor-promoting functions; both stimulation and inhibition of autophagy have been reported to induce cancer cell death, and particular genes and proteins have been associated both positively and negatively with autophagy. To provide a basis for incisive analysis of those complexities and ambiguities and to guide development of new autophagy-targeted treatments for cancer, we have compiled a comprehensive, curated inventory of autophagy modulators by integrating information from published siRNA screens, multiple pathway analysis algorithms, and extensive text-mining of the literature. The resulting inventory includes 739 proteins and 385 chemicals (including drugs, small molecules, and metabolites). Because autophagy is still at an early stage of investigation, we provide extensive analysis of our sources of information and their complex relationships with each other. We conclude with a discussion of novel strategies that could potentially be used to target autophagy for cancer therapy.

3:25 Refreshment Break in the Exhibit Hall with Poster Viewing

4:00 Using Multiscale Systems Modeling to Design and Develop New Protein Therapeutics

Matthew Onsum, Ph.D., President, Silver Creek Pharmaceuticals

In this talk, I will present an approach to building multiscale systems models that capture drug pharmacokinetics and their effects on cell-signaling networks. I will then present two case studies that illustrate how these models can be used to design new therapies.

4:30 Biomarker Discovery to Predict Antitumor Activity through Systems Pharmacology in Drug Development and Cancer Therapy

Yasuhiro Funahashi, Ph.D., Senior Director, Biomarkers and Personalized Medicine Core Function Unit, Eisai, Inc.

NGS promotes molecular profiling of cancer and provides novel gene alterations to be targeted. But many cancer types cannot be caused by a single driver gene. A systematic approach based on pharmacology data combining PD and PG will be effective to identify biomarkers for anticancer agents targeting tumor microenvironments like angiogenesis inhibitors and chemotherapeutic agents.

5:00 A Pharmacogenomic View of the NCI-60 Cell Lines and Beyond

Ogan D. Abaan, Ph.D., Research Fellow, Genetics Branch, National Cancer Institute, National Institutes of Health (NIH)

In this talk, we will present findings from our next-generation sequencing efforts using the NCI-60 cell lines and the pharmacogenomic data we have generated. In addition, we will discuss some new directions we have taken to mine the sequence data.

5:30 - 6:30 Best of Show Awards Reception in the Exhibit Hall

Sponsored by DataDirect NETWORKS

THURSDAY, MAY 1

7:00 am Registration Open

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

8:00 Chairperson's Opening Remarks

Kevin Davies, Ph.D., Vice President Business Development & Publisher C&EN, American Chemical Society; Founding Editor, Bio-IT World

» 8:05 PLENARY KEYNOTE SESSION

Please see page 4 for details.

10:00 Coffee Break in the Exhibit Hall and Poster Competition Winners Announced

Modeling: Biotherapeutics

10:30 Chairperson's Opening Remarks

John M. Burke, Ph.D., Co-Founder, President and CEO, Applied BioMath, LLC

10:35 Mechanistic Models to Guide Development of Novel Biotherapeutics

Bruce Gomes, Ph.D., Senior Translational Modeler, Novartis Institutes for BioMedical Research

Novel biotherapeutic modalities are being created at an ever-growing pace. Due to their novelty, many design parameters and questions about feasibility and safety are unknown. The "design-test-redesign" cycle is often daunting. Modeling of the basic mechanisms that apply to these novel strategies can shorten the time to produce valuable, life-saving new drugs. We explore such issues.

11:05 Systems Pharmacology: Enabling Quantitative Decision Making from Early Discovery to Phl

John M. Burke, Ph.D., Co-Founder, President and CEO, Applied BioMath, LLC

Systems Pharmacology modeling has been used successfully at several pharmaceutical companies. Here we present several case studies that saved an estimated $175M by enabling earlier quantitative decisions that could not be easily addressed by traditional methods. Unlike traditional PK/PD models, Systems Pharmacology models leverage known biophysical interactions and integrate data from a variety of sources (*in vitro*, *in vivo* and clinical). These models act as a central repository of data and knowledge of human pathomechanisms, allowing for the exploration of hypotheses that cannot be fully tested prior to dosing patients.

11:35 Turning -Omic Data into Therapeutic Insights

Ernest Fraenkel, Ph.D., Associate Professor, Biological Engineering, Massachusetts Institute of Technology

Biology has been transformed by new technologies that provide detailed descriptions of the molecular changes that occur in diseases. However, it has been difficult to use these data to reveal new therapeutic insights. I will show how specific network modeling approaches reveal previously undetected pathways linking disparate -omic observations. We have used these methods to analyze how oncogenic mutations alter signaling and transcription and to prioritize experiments aimed at discovering therapeutic targets.

12:15 pm Luncheon Presentations *(Sponsorship Opportunities Available)* **or Lunch on Your Own**

1:15 Dessert Refreshment Break in the Exhibit Hall with Poster Viewing

Modeling: Drug/Dose Response

1:55 Chairperson's Remarks

Birgit Schoeberl, Ph.D., Vice President, Research, Merrimack Pharmaceuticals

» 2:00 FEATURED PRESENTATION

Systems Approaches to Risk Assessment

Lawrence J. Lesko, Ph.D., FCP, Clinical Professor and Director, Center for Pharmacometrics and Systems Pharmacology, University of Florida

"Idiosyncratic" adverse drug events (ADEs) are a substantial societal burden in terms of morbidity, mortality and healthcare costs. Predicting who will suffer ADEs from what medications is extremely difficult with current observational or surveillance approaches. A new mechanistic approach to drug safety science is sorely needed. Systems approaches may address this unmet medical need.

2:30 Pharmacodynamic Characterization of Compounds in Drug Discovery

Rui-Ru Ji, Ph.D., Principal Scientist, Genomics, Bristol-Myers Squibb

The transcriptome reacts in a dose-dependent manner to compound treatment. We will present methodology and will discuss multiple applications of dose response profiling of the whole transcriptome.

Modeling: Drug Discovery

3:00 Bringing Quantitative Systems Pharmacology into Drug Discovery: Implementation, Examples and Challenges

Sandra A.G. Visser, Ph.D., Principal Scientist, Modeling and Simulation, Merck Research Labs

Model-based drug discovery uses systems pharmacology to more quantitatively understand relations between drug exposure, target engagement, efficacy and safety for target validation; define compound properties in lead-optimization and safety margins; and predict human dose and scheduling for clinical candidates. We discuss drug discovery implementation, impact examples and challenges.

3:30 Applying Systems Biology from Bench to Bedside

Birgit Schoeberl, Ph.D., Vice President, Research, Merrimack Pharmaceuticals

We will discuss how Systems Biology can be applied throughout the drug discovery and development process: from drug target identification to therapeutic design and, ultimately, to the clinical development strategy.

4:00 Conference Adjourns

Click Here to Register Online!
Bio-ITWorldExpo.com

Cambridge Healthtech Institute,
250 First Avenue, Suite 300,
Needham, MA 02494
www.healthtech.com

Track 7

eClinical Trials Solutions

Innovative Management in Clinical Trials

TUESDAY, APRIL 29

7:00 am Workshop Registration and Morning Coffee

8:00 - 11:30 Morning Pre-Conference Workshops*

12:30 - 4:00 pm Recommended Afternoon Pre-Conference Workshops*

Advancing the Use of EHR/EMR for Clinical Research and Drug Development: Breaking Down Barriers & Building Up Bridges

**Separate Registration Required. See page 5 for additional workshops.*

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 PLENARY KEYNOTE SESSION
Please see page 4 for details.

5:00 – 7:00 Welcome Reception in the Exhibit Hall with Poster Viewing

Sponsored by IBM

WEDNESDAY, APRIL 30

7:00 am Registration Open and Morning Coffee

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

» 8:05 PLENARY KEYNOTE SESSION
Please see page 4 for details.

9:00 Benjamin Franklin Award & Laureate Presentation

9:30 Best Practices Awards Program

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

New Tools For Advancing Clinical Trials

10:50 Chairperson's Remarks
Lisa La Luna, Senior Vice President, Corporate Development & Implementation, ePharmaSolutions

11:00 CAT: Collaborative Authoring Tool -- A New Way of Authoring and Reviewing Documents for Clinical Development
David Twomey, Associate Director, Software Architecture, Information Science for Translational Medicine, Novartis Institute for Biomedical Research

11:30 eClinical Platform vs. Point Solutions for Clinical Trial Workflow Management
Brian Mundy, eClinical Product Manager/ Solutions Consultant, ePharmaSolutions

12:00 pm Seeing is Believing: Interactive Analysis for Clinical Data Exploration and Safety Review

Sponsored by PerkinElmer For the Better

Josh Patel, CFA, Team Leader, Clinical Informatics, PerkinElmer

TIBCO Spotfire interactive visualizations and predictive analytics enables proactive, responsive decision making, rather than retrospective tracking of results. Such proactive decision making can shorten the time between critical development gates and enable key milestones to be met sooner, while simultaneously managing safety risk. The platform allows for the development of solutions without significant strain on biostatistics and IT resources.

12:15pm Sponsored Presentation *(Opportunity Available)*

12:40 Luncheon Presentations *(Sponsorship Opportunities Available)* **or Lunch on Your Own**

Ensuring Data Quality while Improving Clinical Trial Monitoring

1:50 Chairperson's Remarks

1:55 Case Study in Risk-Based Monitoring
Thomas Verish, Group Director, Data Operations Services, Bristol-Myers Squibb

A recent pilot has shown that the use of remote monitoring of clinical trials using trained staff and analytics can detect inconsistencies in data, which drives a site visit from the monitor. We will discuss the methodology followed, examples of tools that were used and what we learned from this experience.

2:25 Managing Risk in Clinical Trials: A Case Study of Quality by Design and Central Statistical Monitoring
Brian Nugent, Associate Director, Clinical Operations & Process, Gilead Sciences

Today's clinical research professional is faced with an overwhelming amount of data and an increasingly sophisticated choice of analytic tools, all constructed to help us focus on what matters. This presentation will concentrate on a case study emphasizing how two common analytic approaches (Quality by Design and Central Statistical Monitoring) were incorporated into routine practice, and how risk is managed through a standard Quality and Risk Management plan.

2:55 Smart Trials: Novel "Scientific Intelligence" Tools to Enable Advanced Clinical Trial Data Monitoring

Sponsored by BioFortis

Mark A Collins, Ph.D, Director, Marketing, BioFortis, Inc

Modern clinical trials are data rich but often knowledge poor. Leveraging clinical trial data in innovative ways can lead to improved trial outcomes, quality improvements and reductions in cost. Using a series of case studies we will demonstrate how novel data exploration tools that harmonize disparate clinical trial data streams and provide real-time monitoring can significantly impact trial outcomes.

3:10 Sponsored Presentation *(Opportunity Available)*

3:25 Refreshment Break in the Exhibit Hall with Poster Viewing

Cambridge Healthtech Institute,
250 First Avenue, Suite 300,
Needham, MA 02494
www.healthtech.com

Using Real-World Healthcare Data for Clinical Research

4:00 Identification of Patient Populations Using Natural Language Processing on Real-World Healthcare Data

Scott DuVall, Associate Director, VA Informatics and Computing Infrastructure (VINCI), VA Salt Lake City Health Care System

Clinical research targets specific patient populations based on a distinct set of eligibility criteria. Some of these criteria can be queried using coded structured electronic healthcare data; however, in many cases the codes are not specific enough for the target medical condition. I will present specific examples of developing natural language processing to extract the relevant information directly from narrative clinical notes at high levels of accuracy to identify the target patient population.

4:30 Secondary Uses of Healthcare Data: Improving Clinical Trials

Steven Labkoff, M.D., FACP, Head, Strategic Programs, R&D Information, AstraZeneca

5:00 Sponsored Presentations *(Opportunities Available)*

5:30 - 6:30 Best of Show Awards Reception in the Exhibit Hall

Sponsored by DataDirect NETWORKS

THURSDAY, MAY 1

7:00 am Registration Open

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

8:00 Chairperson's Opening Remarks

Kevin Davies, Ph.D., Vice President Business Development & Publisher C&EN, American Chemical Society; Founding Editor, Bio-IT World

» 8:05 PLENARY KEYNOTE SESSION

Please see page 4 for details.

10:00 Coffee Break in the Exhibit Hall and Poster Competition Winners Announced

Collaborative Approaches to Clinical Data

10:30 Chairperson's Opening Remarks

Thomas Verish, Group Director, Data Operations Services, Bristol-Myers Squibb

10:35 PANEL DISCUSSION: Forming a Collaborative Approach to Develop a Data and Technology Blueprint

Muzafar Mirza, Director, Information Strategy and Analytics, Clinical Informatics and Innovation, Pfizer, Inc.

Georgina Wood, Global Head, Technology Innovations, Novartis

Francis Kendall, Global Head, Statistical Programming and Analysis, Roche

Matt Smith, Director, Bristol-Myers Squibb

Brooke Hinkson, Global Head, Clinical Information Governance, Clinical Sciences & Operations, Sanofi

This panel is a read-out of a collaboration between several pharma companies with the prime objective of devising solutions to the challenges that we face as an industry. This cross-pharma consortium focused discussions on technology, standards and data with a view to creating a common framework for how we process data, especially in the changing data landscape. Key focus areas included: Transition to CDSIC, Data Aggregation (including broad categories of data - Clinical Trial data, Payer databases, Registry data, Electronic Medical Records Genome data, Biomarker data and Legacy data), key technologies related to data warehousing/data reporting, validation of data analysis tools and open source approaches.

12:15 pm Luncheon Presentations *(Sponsorship Opportunities Available)* **or Lunch on Your Own**

1:15 Dessert Refreshment Break in the Exhibit Hall with Poster Viewing

New Ways of Looking at Clinical Data

1:55 Chairperson's Remarks

Thomas Verish, Group Director, Data Operations Services, Bristol-Myers Squibb

2:00 The 3R's of Clinical Data in a Humanizing Drug Discovery World: Re-Use, Re-Analyze, and Reveal New Science

Catherine Marshall, Director, Information Strategy & Analytics, Clinical Informatics and Innovations, Pfizer

There is a significant opportunity to capitalize on the science that can be obtained from the results of clinical studies alone. This session explores three case studies demonstrating how clinical data is being re-used for exploratory research, some of the key challenges we face in making the most relevant data discoverable for scientific analytics, and how we might enable this type of research in a more efficient and automated manner than is possible today.

2:30 Roche's Approach in Selecting a New Data Reporting Environment

Francis Kendall, Global Head, Statistical Programming and Analysis, Roche

Roche used a traditional approach to selecting a new data reporting environment; due to difficulties with the original project, a more novel approach in selection and assessment was adopted. This presentation explains Roche's need to look for a new data reporting environment and provides an overview of the selection process and the current status of the project.

3:00 Co-Presentation: Establishing a PKPD Data Flow across a Multi-Vendor Framework

Stuart Pearce, Associate Director, Information Strategy and Analytics, Development Operations, Worldwide Research & Development, Pfizer, Inc.

Muzafar Mirza, Director, Information Strategy and Analytics, Clinical Informatics and Innovation, Pfizer, Inc.

This presentation demonstrates the importance of collaborating across vendors on a standard file format and process flow in the provision of PK and PD data for data modeling, clinical trial simulation and clinical reporting activities. Following the change in operating model in Pfizer it was essential that the timely deliverable of key data was delivered to a standard format whilst protecting the blind. This presentation will cover the challenges, solution and benefits of a standardized approach.

3:30 Ending the Clinical IT Lifecycle with Decommissioning of GCP Clinical Data

Jesper Ilm, Senior Consultant, Compliance & Validation, NNIT

Any clinical IT system will eventually end the journey in its lifecycle. When decommissioning the IT system a big question is what to do with data that are managed and controlled by the system? Companies do not know what to do to stay in compliance with GCP. This presentation covers an approach to define which clinical data can be deleted and which should be migrated when ending the lifecycle of GCP clinical data.

4:00 Conference Adjourns

Cambridge Healthtech Institute,
250 First Avenue, Suite 300,
Needham, MA 02494
www.healthtech.com

Track 8

Data Visualization and Exploration Tools

From Genomics to the Discovery

TUESDAY, APRIL 29

7:00 am Workshop Registration and Morning Coffee

8:00 - 11:30 Recommended Morning Pre-Conference Workshops*

Data Visualization in Biology: From the Basics to Big Data

12:30 - 4:00 pm Recommended Afternoon Pre-Conference Workshops*

UCSC Genome Browser Interactive Workshop

**Separate Registration Required. See page 5 for additional workshops.*

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 PLENARY KEYNOTE SESSION
Please see page 4 for details.

5:00 – 7:00 Welcome Reception in the Exhibit Hall with Poster Viewing

Sponsored by IBM

WEDNESDAY, APRIL 30

7:00 am Registration Open and Morning Coffee

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

» 8:05 PLENARY KEYNOTE SESSION
Please see page 4 for details.

9:00 Benjamin Franklin Award & Laureate Presentation

9:30 Best Practices Awards Program

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

Visualization and Analysis of Genomic Data

10:50 Chairperson's Remarks
Jeremy Goecks, Ph.D., Computational Biology Institute, George Washington University

» 11:00 FEATURED PRESENTATION

Variant View: Visualizing Sequence Variants in their Gene Context
Tamara Munzner, Ph.D., Professor, Computer Science, University of British Columbia

The Variant View visualization tool supports variant impact assessment with an information-dense visual encoding that provides maximal information at the overview level, in contrast to the extensive navigation required by currently-prevalent genome browsers. We discuss design considerations, and show how the tool simplified and accelerated workflows through four case studies.

» 11:30 FEATURED PRESENTATION

A Compendium of Next-Generation Clustered Heat Maps for Interactive Exploration of TCGA Data
John N. Weinstein, M.D., Ph.D., Professor & Chair, Bioinformatics & Computational Biology, Division of Quantitative Sciences, The University of Texas MD Anderson Cancer Center

The Cancer Genome Atlas (TCGA) program is generating comprehensive molecular profiles of more than 25 clinical tumor types. A challenge is the visual detective work necessary to explore individual genes, pathways and patterns in the data. We have developed "next-generation" clustered heat maps (NG-CHMs), which use a Google-maps-like tiling technology for extreme zooming and navigation without loss of resolution. The result is a visually rich, dynamic environment for exploration of the masses of data produced by TCGA.

12:00 pm Choose the Right: The Right Information to the Right Person in the Right Way to Support Clinical Research Decision Making

Sponsored by ANOLINX GO DEEP

Aaron Kamauu, M.D., M.S., M.P.H., CEO, Anolinx LLC

Use of healthcare data as real world evidence has become a forefront for clinical research. However, this "big data" is very complex and difficult to interpret. This presentation will describe the representation of analysis results conducted on big patient-level electronic health records data to support drug development and clinical research.

12:15 pm Sponsored Presentations *(Opportunities Available)*

12:40 Luncheon Presentation I: Big Data & Little Data in the Pharma Industry

Sponsored by THOMSON REUTERS

Andreas Matern, Vice President, Disruptive Innovation, Thomson Reuters

Big Data is quickly becoming an overused, and poorly understood, term in technology. This talk will focus on Big Data for the life sciences. What role does visualization have in Big Data? How do we resolve gaps in life sciences data? How can we spot trends, and effectively ask questions and monitor the amount of structured and unstructured content?

1:10 Luncheon Presentation II: *(Sponsorship Opportunity Available)*

1:50 Chairperson's Remarks
John N. Weinstein, M.D., Ph.D., Professor & Chair, Bioinformatics & Computational Biology, Division of Quantitative Sciences, The University of Texas MD Anderson Cancer Center

1:55 Making the UCSC Genome Browser Work for You
Robert Kuhn, Ph.D., Associate Director, UCSC Genome Browser, Center for Biomolecular Science and Engineering University of California, Santa Cruz

The UCSC Genome Browser provides visualization tools for a large genomic database spanning more than 100 animals. New features include a tool to analyze sequence variant data and hosting organisms not part of the UCSC infrastructure. Browser views of user data may be saved and shared with colleagues.

2:25 Visualizing the Broad Institute's Connectivity Map
Bang Wong, Creative Director, Broad Institute of MIT & Harvard; Adjunct Assistant Professor, Art as Applied to Medicine, Johns Hopkins University School of Medicine

The CMap is a catalog of a gene-expression data generated by exposing cells to chemical and genetic modifiers. Depicting findings from this 26 trillion point dataset requires thoughtful decisions about data presentation. I will describe how we apply design principles to develop user-friendly tools to explore the data.

Click Here to Register Online!
Bio-ITWorldExpo.com

Cambridge Healthtech Institute,
250 First Avenue, Suite 300,
Needham, MA 02494
www.healthtech.com

Novel Visualizations in Pharma & Life Science Companies

2:55 Visualization of Heterogeneous, Multidimensional Data to Support Lead Discovery

Anne Mai Wassermann, Ph.D., Researcher, Novartis Institutes for BioMedical Research, Inc.

Integrating and providing easy access to complex, multidimensional data is crucial for success. Therefore, many different visualization tools have been developed to facilitate data analysis at the early stages of drug discovery. In this presentation, an overview is given about different visual analysis approaches to lead discovery at Novartis.

3:25 Refreshment Break in the Exhibit Hall with Poster Viewing

4:00 GWAVA: Genome-Wide Association Visual Analyzer

Peter Henstock, Ph.D., Senior Principal Scientist, Research Business Technology Group, Pfizer, Inc.

GWAVA serves as our new corporate standard tool for the visual analysis of genome-wide association studies data loaded into the tranSMART platform. GWAVA provides an interactive visualization of the study-SNP data extracted both from queries using tranSMART's native interface, or through GWAVA's own query interface. GWAVA has been recently been made available as open source software.

4:30 Navigating to the Needle in the Haystack – Interactive SAR Analysis Tools

Lisa Sach-Peltason, Ph.D., Cheminformatics and Statistics, Pharma Research & Early Development Informatics, F. Hoffmann-La Roche Ltd.

At Roche, we created an innovative application for chemical data visualization and analysis of structure-activity relationships. Built on top of our small-molecule assay data warehouse, cutting-edge visualization approaches have been implemented and enhanced with interactive drill-down capabilities. The tool provides complementary views on a data landscape.

5:00 Select Poster Presentation: GenCloud: A Modular Genomics Data Organization, Analytics and Visualization Platform

Nejc Skoberne, Faculty of Computer and Information Science, University of Ljubljana

Various methods and scripting tools for analysis, visualization and interpretation of NGS data are available. In order to have the data ready for further analysis, a secure system for data storage, sharing and organization is required. GenCloud is a web platform with intuitive interface for securely storing, sharing and organizing NGS data. It is also a development platform for web applications that enable interactive analysis and visualization of NGS data.

5:30 - 6:30 Best of Show Awards Reception in the Exhibit Hall

Sponsored by DataDirect NETWORKS

THURSDAY, MAY 1

7:00 am Registration Open

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

8:00 Chairperson's Opening Remarks

Kevin Davies, Ph.D., Vice President Business Development & Publisher C&EN, American Chemical Society; Founding Editor, Bio-IT World

» 8:05 PLENARY KEYNOTE SESSION
Please see page 4 for details.

10:00 Coffee Break in the Exhibit Hall and Poster Competition Winners Announced

10:30 Chairperson's Opening Remarks

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

10:35 Merck's Information Landscape Knowledgebase

Kelly Clark, Lead Analyst, Scientific Information Architecture, Merck & Co., Inc.

Merck's Informatics IT team has developed the Information Landscape Knowledgebase, a semantically rich, intuitively accessible repository of information sources across Merck. In this talk, we will discuss how the solution takes advantage of underlying semantic models and novel visualizations to address the needs of both scientists and data stewards while providing valuable insights for IT resourcing.

11:05 Persephone: Enabling Real-Time Exploration across Genomes

Stanislav Freidin, Senior Software Engineer, Persephone, Ceres, Inc.

Our tool allows the user to quickly navigate between different genomes, as well as between different areas of a single genome, in real time. It allows a user to explore a genome even when the user has no particular destination in mind, to view different genomes side by side, and to zoom in and out of regions of interest very quickly.

11:35 Cross-Organizational Data Visualization and Correlation to Design Drug and Process in the Pharmaceutical Industry

Jean-Etienne Fortier, Knowledge Management Specialist, GPS, UCB PHARMA

At UCB, the Knowledge Management department recently implemented a system to provide scientists and managers an easy access to scientific data and visualization tools, to support decisions during drug and process development. This platform uses a very simple architecture and allows mixing any type of data, associated with any metadata.

12:15 pm Luncheon Presentations *(Sponsorship Opportunities Available)* **or Lunch on Your Own**

1:15 Dessert Refreshment Break in the Exhibit Hall with Poster Viewing

Visualization and Analysis of Genomic Data

1:55 Chairperson's Remarks

Alexander Lex, Ph.D., Researcher, Harvard School of Engineering & Applied Sciences

2:00 Integrated Analysis and Visualization of Large-Scale Biological Data with the Refinery Platform

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

The development of visualization tools for large and complex data sets require extensive software infrastructure. To address these challenges, we developed the Refinery Platform, a web-based data visualization and analysis system powered by an ISA-Tab-compatible data repository for public and private data sets. Analyses are implemented as Galaxy workflows and executed through the Galaxy API.

2:30 Web-Based Visualization and Visual Analysis for High-Throughput Genomics with Galaxy

Jeremy Goecks, Ph.D., Computational Biology Institute, George Washington University

Learn about how to use the popular, web-based Galaxy platform to analyze and visualize your high-throughput genomics data. Galaxy visualizations require only a web browser to use and no software or data downloads. Galaxy visualizations include a genome browser, Circos plot, phylogenetic tree, and a parameter sweeping application.

Pathway Analysis & Cancer Data Visualization

3:00 NetGestalt: Integrating Multidimensional Omics Data over Biological Networks

Bing Zhang, Ph.D., Associate Professor, Biomedical Informatics, Vanderbilt University School of Medicine

NetGestalt exploits the inherent hierarchical modular architecture of biological networks to achieve high scalability. It allows simultaneous presentation of large-scale experimental and annotation data from various sources in the context of biological networks to facilitate data visualization, analysis, interpretation and hypothesis generation.

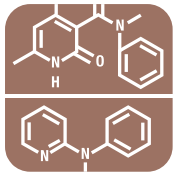
3:40 Caleydo Entourage: Visualizing Relationships between Biological Pathways

Alexander Lex, Ph.D., Researcher, Harvard School of Engineering & Applied Sciences

This talk will present three case studies showing how Entourage, a visualization technique for analyzing interrelationships between multiple related biological pathways, can be used to judge potential side-effects of compounds, to find potential targets for drug-repositioning and how it can be combined with visualization of experimental data to reason about varying effects of compounds on samples.

4:00 Conference Adjourns

Cambridge Healthtech Institute,
250 First Avenue, Suite 300,
Needham, MA 02494
www.healthtech.com



Track 9

Pharmaceutical R&D Informatics

Collaboration, Data Science and Biologics

TUESDAY, APRIL 29

7:00 am Workshop Registration and Morning Coffee

8:00 - 11:30 Recommended Morning Pre-Conference Workshops*

Biologics, Bioassay, and Biospecimen Registration Systems

12:30 - 4:00 pm Recommended Afternoon Pre-Conference Workshops*

IT & Informatics in Support of Collaboration and Externalization

**Separate Registration Required. See page 5 for additional workshops.*

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 PLENARY KEYNOTE SESSION

Please see page 4 for details.

5:00 – 7:00 Welcome Reception in the Exhibit Hall with Poster Viewing

Sponsored by IBM

WEDNESDAY, APRIL 30

7:00 am Registration Open and Morning Coffee

8:00 Chairperson's Opening Remarks

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

» 8:05 PLENARY KEYNOTE SESSION

Please see page 4 for details.

9:00 Benjamin Franklin Award & Laureate Presentation

9:30 Best Practices Awards Program

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

Big Data and Data Science in R&D and Translational Research

10:50 Chairperson's Remarks

Ralph Haffner, Local Area Head, Research Informatics, F. Hoffmann-La Roche AG

11:00 Can Data Science Save Pharmaceutical R&D?

Jason M. Johnson, Ph.D., Associate Vice President, Scientific Informatics & Early Development and Discovery Sciences IT, Merck

Although both premises - that the viability of pharmaceutical R&D is mortally threatened and that modern "data science" is a relevant superhero - are suspect, it is clear that R&D productivity is progressively declining and many areas of R&D suboptimally use data in decision-making. We will discuss some barriers to our overdue information revolution, and our strategy for overcoming them.

11:30 Enabling Data Science in Externalized Pharmaceutical R&D

Sándor Szalma, Ph.D., Head, External Innovation, R&D IT, Janssen Research & Development, LLC

Pharmaceutical companies have historically been involved in many external partnerships. With recent proliferation of hosted solutions and the availability of cost-effective, massive high-performance computing resources there is an opportunity and a requirement now to enable collaborative data science. We discuss our experience in implementing robust solutions and pre-competitive approaches to further these goals.

12:00 pm Co-Presentation: Collaborative Waveform Analytics: How New Approaches in Machine Learning and Enterprise Analytics will Extend Expert Knowledge and Improve Safety Assessment

Sponsored by Neural ID

Tim Carruthers, CEO, Neural ID

Matt Clifford, Healthcare Consultant, IDBS

Neural ID's Intelligent Waveform Service (IWS) delivers the only enterprise biosignal analysis solution combining machine learning with human expertise. A collaborative platform supporting all phases of research and development, IWS addresses a significant unmet need, delivering scalable analytics and a single interoperable data format to transform productivity in life sciences. By enabling analysis from BioBook (IDBS) to original biosignals, IWS enables users of BioBook to evaluate cardio safety assessment across the R&D lifecycle.

12:15 Building a Life Sciences Data Lake: A Useful Approach to Big Data

Sponsored by Cambridge Semantics

Ben Szekely, Director & Founding Engineer, Cambridge Semantics

The promise of Big Data is in its ability to give us technology that can cope with overwhelming volume and variety of information that pervades R&D informatics. But the challenges are in practical use of disconnected and poorly described data. We will discuss: Linking Big Data from diverse sources for easy understanding and reuse; Building R&D informatics applications on top of a Life Sciences Data Lake; and Applications of a Data Lake in Pharma.

12:40 Luncheon Presentation I: Chemical Data Visualization in Spotfire

Sponsored by OpenEye Scientific Software

Matthew Stahl, Ph.D., Senior Vice President, OpenEye Scientific Software

Spotfire deftly facilitates the analysis and interrogation of data sets. Domain specific data, such as chemistry, presents a set of challenges that general data analysis tools have difficulty addressing directly. Fortunately, Spotfire is an extensible platform that can be augmented with domain specific abilities. Spotfire has been augmented to naturally handle cheminformatics and chemical data visualization through the integration of OpenEye toolkits. The OpenEye chemistry extensions for Spotfire will be presented.

1:10 Luncheon Presentation II *(Sponsorship Opportunity Available)*

1:50 Chairperson's Remarks

Yuriy Gankin, Ph.D., Co. Founder and CSO, GGA Software Services

1:55 Enable Translational Science by Integrating Data across the R&D Organization

Christian Gossens, Ph.D., Global Head, pRED Development Informatics Team, pRED Informatics, F. Hoffmann-La Roche Ltd.

Multi-national pharmaceutical companies face an amazingly complex information management environment. The presentation will show that a systematic system landscaping approach is an effective tool to build a sustainable integrated data environment. Data integration is not mainly about technology, but the use and implementation of it.

2:25 The Role of Collaboration in Enabling Great Science in the Digital Age: The BARD Data Science Case Study

Andrea DeSouza, Director, Informatics & Data Analysis, Broad Institute

BARD (BioAssay Research Database) is a new, public web portal that uses a standard representation and common language for organizing chemical biology data. In this talk, I describe how data professionals and scientists collaborated to develop BARD, organize the NIH Molecular Libraries Program data, and create a new standard for bioassay data exchange.

Click Here to Register Online!
Bio-ITWorldExpo.com

Cambridge Healthtech Institute,
250 First Avenue, Suite 300,
Needham, MA 02494
www.healthtech.com

2:55 Enhancing Research Productivity through Integrated Informatics Sponsored by accelrys

Rob Brown, Ph.D., Senior Director, Product Marketing, Accelrys

This talk will discuss the use of the Accelrys Cheminformatics Suite to enhance research productivity and innovation. Managing end-to-end scientific workflows in a unified informatics platform allows research organizations to streamline their operations and reduce operating costs, increase the potential for innovation through timely capture of information, enhanced collaboration and informed decision making and make effective decisions in an environment that crosses internal and external research.

3:10 GSK's Next Generation Collaborative Design Platform, Powered by Schrödinger's LiveDesign Sponsored by SCHRÖDINGER.

Jeffrey Axten, Ph.D., Director, Medicinal Chemistry, Virtual Proof of Concept DPU, GlaxoSmithKline

The majority of small molecule drugs originate from an idea created based on knowledge of SAR, molecular properties, DMPK, and pharmacology. We believe that the availability of design tools and integration of modern design principles into the daily practice of chemists are critical factors influencing the conception of high quality new molecular entities. We set out to build a layer on-top of our existing software to help scientists digitize and improve their design process, simultaneously providing a collaborative working environment to complement today's research culture. By leveraging Schrodinger's LiveDesign, GSK is enhancing its chemistry design software capabilities to provide drug discovery chemists a unified software platform. This talk will discuss what we have built and our vision for the future.

3:25 Refreshment Break in the Exhibit Hall with Poster Viewing

COLLABORATION AND EXTERNALIZATION IN R&D

4:00 Co-Presentation: Informatics Paradox: Separating and Collaborating in Life Science

Sarah Blendermann, Senior Director, Chemistry & Pharmacology, Business Technology, Pfizer

Rick Somes, Senior Director, Acquisitions, Divestitures and Restructuring R&D Business Technology, Pfizer

Pfizer is in the process of completing the largest ever divestiture of an animal health organization spanning both commercial and research and development. The organization was faced with running operations and discovery while separating data and systems. Collaboration and segregation were key components of the informatics required to successfully meet an IPO timeline. A long-term collaboration agreement means ties between the organizations will remain, requiring longer-term technical solutions for granular security, collaboration, and data sharing.

4:30 Towards the Intelligent and Automated Analytical Laboratory

Dave Hartsough, Ph.D., Executive Director, Research & Development Informatics, Amgen

This presentation will provide an update on the progress of the Allotrope Foundation towards delivering an open framework solution for managing analytical data throughout its lifecycle and will include details on the deliverables, timelines, and results from completed proof-of-concept applications based upon the initial proposal and analysis presented in 2013.

5:00 Growing our Innovation Capability from the Inside-Out: AstraZeneca's Journey to a New Way of Working

Scott Wilkins, Ph.D., Enterprise Innovation Director, AstraZeneca

5:30 - 6:30 Best of Show Awards Reception in the Exhibit Hall Sponsored by DataDirect NETWORKS

THURSDAY, MAY 1

7:00 am Registration Open

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

8:00 Chairperson's Opening Remarks

Kevin Davies, Ph.D., Vice President Business Development & Publisher C&EN, American Chemical Society; Founding Editor, Bio-IT World

» 8:05 PLENARY KEYNOTE SESSION
Please see page 4 for details.

10:00 Coffee Break in the Exhibit Hall and Poster Competition Winners Announced

BIG DATA AND DATA SCIENCE IN R&D AND TRANSLATIONAL RESEARCH

10:30 Chairperson's Opening Remarks

John Koch, Director, Scientific Information Architecture & Search, Merck

10:35 The Role of a Data Scientist in Drug Discovery and Development

Anastasia (Khoury) Christianson, Ph.D., Head, Translational R&D IT, Bristol-Myers Squibb

A major challenge in drug discovery and development is finding all the relevant data, information, and knowledge to ensure informed, evidence-based decisions in drug projects, including meaningful correlations between preclinical observations and clinical outcomes. This presentation will describe where and how data scientists can support pharma R&D.

11:05 Designing and Building a Data Sciences Capability to Support R&D and Corporate Big Data Needs

Shoibal Datta, Ph.D., Director, Data Sciences, Biogen Idec

To achieve Biogen Idec's strategic goals, we have built a cross-disciplinary team to focus on key areas of interest and the required capabilities. To provide a reusable set of IT services we have broken down our platform to focus on the Ingestion, Digestion, Extraction and Analysis of data. In this presentation, we will outline how we brought focus and prioritization to our data sciences needs, our data sciences architecture, lessons learned and our future direction.

11:35 Data Experts: Improving Translational Drug-Development Efficiency Sponsored by Tessella

Jamie MacPherson, Ph.D., Consultant, Tessella

We report on a novel approach to translational informatics support: embedding 'Data Experts' within drug-project teams. Data experts combine first-line informatics support and Business Analysis. They help teams exploit data sources that are diverse in type, scale and quality; analyse user-requirements and prototype potential software solutions. We then explore scaling this approach from a specific drug development team to all.

12:15 pm Luncheon Presentations *(Sponsorship Opportunities Available)* **or Lunch on Your Own**

1:15 Dessert Refreshment Break in the Exhibit Hall with Poster Viewing

Biologics R&D Data Management – From Collaboration to Registration Systems

1:55 Chairperson's Remarks

Sándor Szalma, Ph.D., Head, External Innovation, R&D IT, Janssen Research & Development, LLC

2:00 Registration Systems: Applications or Data Stores?

Arturo J. Morales, Ph.D., Vice President, Informatics, Emerald Bio; former Global Lead, Biology Platform Informatics, Novartis Institutes for Biomedical Research

Registration systems are not applications that usually stand on their own. Their value comes from the enablement of downstream data analysis and sample tracking through proper management of concept and sample metadata. As such, most registration systems offer little intrinsic value to those that use it directly and user compliance can be a challenge. Thus, it is important to adapt to workflows, as opposed to making users adapt to them.

2:30 Development and Implementation of a Biologics Data Platform

Kai Herrmann, Ph.D., R&D IT Project Manager, BBS-ITS-R&D-HCR-BIO, Bayer Business Services GmbH

We report our experience over the last five years of developing and implementing an innovative turn-key solution for biologics R&D data management. The goal of the new platform was to increase the number and throughput of large-molecule R&D projects, to establish a shared collaboration platform for data exchange, and to improve the quality of results.

3:00 Building the Biomolecules Management Platform

Monica Wang, Ph.D., Lead System Engineer, Project and Program Manager, R&D Systems, Takeda Boston

Building a comprehensive Biomolecules Management Platform is a very challenging task. We are building an enterprise solution to track individual biomolecules in different drug development workflows and visualize their relationships. This platform will improve user efficiency, data quality, data exchange and collaboration for both research and preclinical development departments.

3:30 Peptide Informatics – Bridging the Gap between Small- and Large-Molecule Systems

Lisa Sach-Peltason, Ph.D., Cheminformatics and Statistics, Pharma Research & Early Development Informatics, F. Hoffmann-La Roche Ltd.

We established an informatics infrastructure for registering and analyzing peptide data. By introducing an intuitive sequence nomenclature and implementing tailored registration processes, peptide sequence and structure data are captured in a consistent way, enabling computational analysis, interfaces with other bioinformatics and cheminformatics systems, and preserving valuable data.

4:00 Conference Adjourns

Cambridge Healthtech Institute,
250 First Avenue, Suite 300,
Needham, MA 02494
www.healthtech.com

Track 10

Clinical Genomics

Tools for Interrogation, Integration and Implementation

TUESDAY, APRIL 29

7:00 am Workshop Registration and Morning Coffee

8:00 - 11:30 Recommended Morning Pre-Conference Workshops*

Genome Assembly and Annotation

12:30 - 4:00 pm Recommended Afternoon Pre-Conference Workshops*

Determining Genome Variation and Clinical Utility

**Separate Registration Required. See page 5 for additional workshops.*

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 PLENARY KEYNOTE SESSION

Please see page 4 for details.

5:00 – 7:00 Welcome Reception in the Exhibit Hall with Poster Viewing

Sponsored by IBM

WEDNESDAY, APRIL 30

7:00 am Registration Open and Morning Coffee

8:00 Chairperson's Opening Remarks

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

» 8:05 PLENARY KEYNOTE SESSION

Please see page 4 for details.

9:00 Benjamin Franklin Award & Laureate Presentation

9:30 Best Practices Awards Program

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

**IBM and the IBM logo are trademarks of International Business Machines Corp., registered in many jurisdictions worldwide.*

Implementing NGS in the Clinic

10:50 Chairperson's Remarks

Jonathan Sheldon, Ph.D., Global Vice President, Oracle Health Sciences Product Strategy

11:00 Projected Clinical Utility of NGS Screening in the General Population

Joseph V. Thakuria, M.D., Medical Geneticist, Massachusetts General Hospital

Clinical utility of NGS in patients suspected of rare Mendelian disorders is now generally accepted, but mounting evidence also supports medical utility of NGS screening in the general populace. We explore opportunities and challenges in NGS's transition from research and clinical use in subsets of genetic patients to genomic health screening strategies on asymptomatic individuals.

11:30 Rapid Tumor Evolution Propagating across the Genome, Epigenome, Transcriptome and Epitranscriptome

Christopher Mason, Ph.D., Assistant Professor, Computational Biomedicine, Weill Cornell Medical College

We have identified the evolution of molecular changes in tumors at diagnosis and relapse stages in acute myeloid leukemia patients spanning the genome, epigenome, transcriptome and epitranscriptome, with NGS revealing 1000s of relapse-specific molecular changes driving chemo-resistance. Integrating these data can validate mutations, reveal regulatory dynamics and build predictive models.

12:00 pm Clinical Genomics 2013: Lessons Learned – A Summary

Sponsored by EMC® ISILON

Sanjay Joshi, CTO, Life Sciences, EMC Isilon

A lot has happened in the past year: clinically, ethically, infrastructurally, methodologically and regulatorily. We will look at a summary of the happenings in 2013 and their effects on scalable infrastructures moving forward.

12:40 Luncheon Presentation I: Harnessing the Power of Patient Cohort Data with NextBio

Sponsored by illumina

Ilya Kupershmidt, Head, Products, Enterprise Informatics, Illumina Inc.

Advances in genomic and other molecular technologies have vastly expanded the richness of the information available to investigators in drug development, cancer, and other biomedical research. Until recently the myriad opportunities to use this data for patient stratification, to understand differential patient response, to predict adverse events, and to drive a better mechanistic understanding were limited by a number of factors. In this talk we will show how NexBio removes many of these barriers by standardizing, normalizing and integrating patient molecular and phenotype information. More importantly, we will focus on how simple interfaces make these data useful to a broader set of participants in both medical and pharmaceutical settings.

1:10 Luncheon Presentation II *(Sponsorship Opportunity Available)* **or Lunch on Your Own**

From Genome Variation to Clinical Utility

1:50 Chairperson's Remarks

Elizabeth Worthey, Ph.D., Assistant Professor, Pediatrics & Bioinformatics Program, Human & Molecular Genetics Center, Medical College of Wisconsin

1:55 Mapping Disease Risk to the Human Variome

Yana Bromberg, Ph.D., Assistant Professor, Biochemistry and Microbiology, School of Environmental and Biological Sciences, Rutgers University

The drop in sequencing cost and its increased speed and accuracy are bringing genome-based evaluation of individual disease risk to the bedside. Personalized medicine research today is tasked with developing techniques to connect human phenotypes with individual variomes. We discuss building computational pipelines bridging these new tools for predicting "variome"-defined disease risk.

Software Spotlights *(Sponsorship Opportunities Available)*

Next-generation sequencing has made obtaining A, C, T, Gs relatively easy; making sense of and interpreting them is hard. There are commercial software solutions and pipelines for managing raw genome sequence data. However, providing the medical interpretation and delivering a clinical diagnosis is critical in making good on the promise of personalized medicine. This session showcases how genomic data analysis companies are streamlining the genomic diagnostic process.

2:25 Topological Data Analysis for Translational Research and Development

Sponsored by AYASDI

Pek Lum, Ph.D., Vice President, Solutions & Chief Data Scientist, Ayasdi

There is an urgent need for modern analytical techniques to couple myriad data sources such as molecular, genetic and phenotypic to drive discoveries related to clinical outcomes of interest. In this session, we generalize methods of Topological Data Analysis (TDA) past the basic research phase and discuss how this approach permits rapid exploration of multi-modal clinical data.

2:40 Pertinence Metric Enables Hypothesis-Independent Genome-Phenome Analysis in Seconds

Sponsored by SimulConsult

Michael M. Segal, M.D., Ph.D., Chief Scientist, SimulConsult

Genome-phenome analysis uses a genomic variant table and compares patient's findings to those of known diseases ("phenome"). Accuracy was 100% with trios with family-aware calling, and close to that with only probands. The gene pertinence metric calculated in the analysis was 99.9% for the causal genes, and the analysis took seconds and was hypothesis-independent.

Click Here to Register Online!
Bio-ITWorldExpo.com

Cambridge Healthtech Institute,
250 First Avenue, Suite 300,
Needham, MA 02494
www.healthtech.com

2:55 Clinician-Friendly Diagnostic Tools for Using Whole-Genome Sequence Data in Real Time

Jeffrey R. Gulcher, M.D., Ph.D., President and CSO, NextCODE Health

NextCODE offers informatics solutions we first developed at deCODE genetics to store, query and analyze whole-genome sequence data on 300,000 individuals. These are built on the genomic ordered relational (GOR) data architecture that allows for real-time queries of massive variant and raw sequence datasets for clinical diagnosis and quality control. Our clinically-intuitive, web-based tools can be used for the analysis of individual patients, families or cohorts.

3:15 Selected Oral Poster Presentation: A Robust and Versatile MiSeq Data Analysis Pipeline to Support Translational Projects

Aleksandra Markovets, Ph.D., Senior Scientist, Oncology, AstraZeneca, Inc.

Next-generation sequencing (NGS) is increasingly important in oncology drug development. The MiSeqDX is becoming a commonly adopted platform for next-generation sequencing of targeted gene panels in patient samples, achieving FDA approval for *in vitro* diagnostic use. To overcome the challenges associated with processing, analysis and interpretation of vast amounts of data returned by a sequencing platform, we have developed an effective and versatile analytical pipeline. This pipeline enables quality assessment of sequencing runs, disambiguation of sequencing data from animal models and precise identification of various DNA aberrations. The application of this pipeline to accurately measure genetic biomarkers in patients and preclinical samples has provided impactful data to a number of drug projects.

3:25 Refreshment Break in the Exhibit Hall with Poster Viewing

4:00 Returning Genomic Results to Physicians and Patients: Where the Rubber Meets the Road

Elissa Levin, MS, CGC, Head, Genomics and Integrative Health Innovations; Assistant Professor, Genetics and Genomic Sciences, Icahn Institute for Genomics and Multiscale Biology, Mount Sinai School of Medicine

There is much discussion on how to responsibly deliver complex, probabilistic genomic information into clinical practice in our current system. We review innovative approaches being applied in research, clinical and consumer settings that strive to further enable access and personalization of genomic information, with the goal of making it useful and relevant for patients and providers.

4:30 Integrating Genomics into Medicine

Heidi L. Rehm, Ph.D., FACMG, Director, Laboratory for Molecular Medicine, Partners HealthCare Center for Personalized Genetic Medicine; Associate Professor of Pathology, Harvard Medical School

We will discuss the integration of genomic sequencing into medical practice for both diagnostic purposes and screening of healthy adults and newborns. Systems to enable patients, physicians, clinical laboratories and researchers to all interact and support data sharing and genomic knowledge curation will be discussed as they relate to the new NIH-funded Clinical Genome Resource Program.

5:00 Clinical Interpretation Tools

Matthew Lebo, Ph.D., Instructor, Pathology, Brigham & Women's Hospital and Harvard Medical School; Assistant Laboratory Director, Senior IS Domain Specialist, Laboratory for Molecular Medicine

5:30 - 6:30 Best of Show Awards Reception in the Exhibit Hall

Sponsored by DataDirect NETWORKS

THURSDAY, MAY 1

7:00 am Registration Open

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

8:00 Chairperson's Opening Remarks

Kevin Davies, Ph.D., Vice President Business Development & Publisher C&EN, American Chemical Society; Founding Editor, Bio-IT World

» 8:05 PLENARY KEYNOTE SESSION

Please see page 4 for details.

10:00 Coffee Break in the Exhibit Hall and Poster Competition Winners Announced

Ensuring Genomic Privacy and Security

10:30 Chairperson's Opening Remarks

Mary Ann Brown, Executive Director, Conferences, Cambridge Healthtech Institute

» 10:35 FEATURED PRESENTATION

A Global Alliance for Interoperability of Genomic and Clinical Data

David Altshuler, M.D., Ph.D., Deputy Director and Chief Academic Officer, Broad Institute of Harvard and MIT; Professor, Genetics and Medicine, Harvard Medical School and Massachusetts General Hospital; Adjunct Professor, Biology, Massachusetts Institute of Technology

Analysis of large-scale data on genome sequence and clinical outcomes holds great promise for medicine. Learning requires access to datasets and to methods beyond the scope of any single institution. I will discuss a global alliance created to nurture a common framework of international standards for how genomic and clinical data are shared in a responsible and effective manner.

» 11:05 FEATURED PRESENTATION

Incorporating Security Infrastructure from the Beginning at the New York Genome Center

Toby Bloom, Ph.D., Deputy Scientific Director, Informatics, New York Genome Center

As genomic data falls under more regulations governing personally identifiable information and more clinical genomics studies combine deep clinical data with genomic data, privacy and security requirements integrated into genome centers' informatics infrastructures become increasingly complex. We discuss how NYGC is addressing these challenges.

11:35 Architecture of Omics-Aware Clinical Decision Support Systems

Sponsored by ORACLE HEALTH SCIENCES

Andrew Boudreau, Principal Product Strategist, Oracle Health Sciences

While many EMR implementations include some form of configurable decision support, the demands of genome data – gene panels as well as whole-exome and whole-genome data – make molecular decision support in the EMR a significant challenge. We propose architectures for decision support systems external to but integrated with an EMR, along with analytical tools and scalability appropriate for genome-wide personalized medicine.

12:15 pm Luncheon Presentations *(Sponsorship Opportunities Available)* **or Lunch on Your Own**

1:15 Dessert Refreshment Break in the Exhibit Hall with Poster Viewing

Integrating Genomics into the Clinic

1:55 Chairperson's Remarks

John Quackenbush, CEO, Genospace; Professor, Dana-Farber Cancer Institute and Harvard School of Public Health

2:00 Enterprise-Wide Support for Individualized Treatment at a Cancer Center: Dana-Farber's Profile Project

Barrett J. Rollins, M.D., Ph.D., CSO, Dana-Farber Cancer Institute; Linde Family Professor of Medicine, Harvard Medical School

Bringing the promise of precision medicine to cancer patients requires overcoming scientific and operational impediments. Dana-Farber Cancer Institute's Profile project attempts to address these problems. It seeks to obtain broad genetic profiles on every patient who visits our hospital, link the data to their clinical information and make it available for research and clinical care.

2:30 PANEL DISCUSSION: From Data to Knowledge, from Research to Care – Meeting the Challenges of Genomic Medicine

Moderator: John Quackenbush, CEO, Genospace; Professor, Dana-Farber Cancer Institute and Harvard School of Public Health

Walter M. Capone, President, Multiple Myeloma Research Foundation

Andy Corts, Chief Information Officer, Sarah Cannon Research Institute

Pranil Chandra, DO, FCAP, FASCP, Director, Molecular Pathology Services, PathGroup

Joe Donahue, Senior Vice President, Thomson Reuters

While delivering actionable personalized medicine reports to physicians seems, on the surface, like a relatively straight-forward exercise, there are many stakeholders who play a role in making the endeavor successful. Key elements in building a truly successful program include collecting and managing clinical and genomic data, integrating these in a decision support system, creating an appropriate knowledgebase to support data interpretation, and effectively delivering the data at the point of care. This panel brings together representatives from GenoSpace, Sarah Cannon Research Institute, Multiple Myeloma Research Foundation, PathGroup, and Thomson Reuters to discuss strategies to meet the challenges of genomic medicine.

4:00 Conference Adjourns

Cambridge Healthtech Institute,
250 First Avenue, Suite 300,
Needham, MA 02494
www.healthtech.com

Track 11

Collaborations and Open Access Innovations

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

TUESDAY, APRIL 29

7:00 am Workshop Registration and Morning Coffee

8:00 - 11:30 Recommended Morning Pre-Conference Workshops*

Analyzing NGS Data in Galaxy

12:30 - 4:00 pm Recommended Afternoon Pre-Conference Workshops*

Running a Local Galaxy Instance

The tranSMART Platform Today and Tomorrow

IT & Informatics in Support of Collaboration and Externalization

**Separate Registration Required. See page 5 for additional workshops.*

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 PLENARY KEYNOTE SESSION

Please see page 4 for details.

5:00 – 7:00 Welcome Reception in the Exhibit Hall with Poster Viewing

Sponsored by IBM

WEDNESDAY, APRIL 30

7:00 am Registration Open and Morning Coffee

8:00 Chairperson's Opening Remarks

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

» 8:05 PLENARY KEYNOTE SESSION

Please see page 4 for details.

9:00 Benjamin Franklin Award & Laureate Presentation

9:30 Best Practices Awards Program

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

Collaborating in Chronic and Rare Diseases

10:50 Chairperson's Remarks

Marcia Kean, Chairman, Strategic Initiatives, Feinstein Kean Healthcare

11:00 PANEL DISCUSSION: Patient-Powered Research Networks: Surge in the War against MS and other Diseases

Marcia Kean, Chairman, Strategic Initiatives, Feinstein Kean Healthcare

Joe Laferrera, Partner, J.D., Gesmer Updegrove LLP

Sara Loud, MSEE, MBA, Repository and Operations Director, Accelerated Cure Project for Multiple Sclerosis

Kenneth Buetow, Ph.D., Director of Computational Sciences and Informatics, Complex Adaptive Systems Initiative (CASI), Arizona State University

Dave King, Founder and CEO, Exaptive, Inc.

Driven by increasing consumer demand for knowledge, as well as the mandate of the Patient-Centered Outcomes Research Institute (PCORI), a new model for collection, integration, aggregation and analysis of data is emerging in which the patient is central. With an award from PCORI, the Accelerated Cure Project for MS, with its members and partners, are launching the iConquerMS portal for such patient empowerment, to speed and enhance research into MS and then to apply the model to other neurological diseases.

12:00 Collaboration to Support Translational Research to Transform R&D

Sponsored by ConvergeHEALTH by Deloitte.

Hongyue Dai, Ph.D., Chief Bioinformatics Officer, M2Gen

Asif Dhar, Ph.D., M.D., Executive Vice President, Solutions, ConvergeHEALTH by Deloitte

Join M2Gen and Deloitte as they discuss their collaboration to support personalized medicine and review case studies leveraging informatics to transform the industry.

12:15 Analysis of TCGA Data with User-Friendly Tools for Cancer Genomics

Sponsored by CLC bio A QIAGEN Company

M. Michael Barmada, Ph.D., Associate Professor, Human Genetics and Biomedical Informatics, University of Pittsburgh

Next-generation sequencing enables cancer researchers to identify biomarker, which can be used as new drug targets, prognosis, and diagnosis. However, facilitating the data analysis in a user-friendly way is still a bottleneck. Here we present the analysis of TCGA data using an intuitive and customizable software solution as an example for rapid and accurate interpretation of advanced NGS sequencing data.

12:40 Luncheon Presentations *(Sponsorship Opportunities Available)* **or Lunch on Your Own**

1:50 Chairperson's Remarks

Alexander Wait Zaranek, Ph.D., Director Informatics, Personal Genome Project, Harvard Medical School

1:55 Collaborating in Rare Diseases through Technology

Alex Sherman, Director, Strategic Development and Systems, Neurological Clinical Research Institute, Massachusetts General Hospital

Rare diseases have to self-organize to become attractive to pharma/biotech industry. Collaborative technology and methodology allow information to be aggregated and harmonized from heterogeneous sources, including patient registries, Electronic Health Records, biorepositories, and clinical and research databases. Global Patient Identifier helps to link it all together. Evolving crowd-sourcing and crowd-funding initiatives allow multiply number of people participating in medical research and data analyses.

2:25 Accelerating Rare and Chronic Disease Research with Transparent Informatics

Alexander Wait Zaranek, Ph.D., Director Informatics, Personal Genome Project, Harvard Medical School

Rapid improvements in DNA sequencing and synthesis could usher in a new era of precision medicine. The Personal Genome Project is building a transparent and public resource consisting of genomes, detailed phenotypes, software, as well as cell-lines and other tissue samples for more than 100,000 individuals. However, the effort to address computational and storage needs created by genomic and other types of molecular data are not well served by a fragmented landscape of homegrown solutions and proprietary technologies. An open-source foundation can help coordinate the efforts of stakeholders around open biomedical infrastructure. The open data, interactive applications and cloud infrastructure developed at the PGP can provide the initial seed for the initiative.

**IBM and the IBM logo are trademarks of International Business Machines Corp., registered in many jurisdictions worldwide.*

Click Here to Register Online!
Bio-ITWorldExpo.com

Cambridge Healthtech Institute,
250 First Avenue, Suite 300,
Needham, MA 02494
www.healthtech.com

2:55 Accelrys ScienceCloud: A Hosted Strategy for Collaborative R&D

Sponsored by accelrys®

Matt Hahn, Ph.D., CTO, Accelrys

The life sciences industry has been undergoing dramatic changes and effective global collaboration has become a key success factor in this new age. Accelrys is providing a hosted and comprehensive solution stack for externalized, collaborative research for pharma/biotech and CROs to address these new challenges.

3:25 Refreshment Break in the Exhibit Hall with Poster Viewing

Collaboration and Externalization in R&D

4:00 Co-Presentation: Informatics Paradox: Separating and Collaborating in Life Science

Sarah Blendermann, Senior Director, Chemistry & Pharmacology, Business Technology, Pfizer

Rick Somes, Senior Director, Acquisitions, Divestitures and Restructuring R&D Business Technology, Pfizer

The organization was running operations and discovery while separating data and systems. Collaboration and segregation were key components of the informatics required to successfully meet an IPO timeline. A long-term collaboration agreement means ties between the organizations will remain, requiring longer-term technical solutions for granular security, collaboration, and data sharing.

4:30 Towards the Intelligent and Automated Analytical Laboratory

Dave Hartsough, Ph.D., Executive Director, Sites, Benchtop, & Validation R&D Informatics, Amgen

This presentation will provide an update on the progress of the Allotrope Foundation towards delivering an open Framework solution for managing analytical data throughout its lifecycle and will include details on the deliverables, timelines, and results from completed proof-of-concept applications based upon the initial proposal and analysis presented in 2013.

5:00 Growing our Innovation Capability from the Inside-Out: AstraZeneca's Journey to a New a Way of Working

Scott Wilkins, Ph.D., Enterprise Innovation Director, AstraZeneca

5:30 - 6:30 Best of Show Awards Reception in the Exhibit Hall

Sponsored by DataDirect NETWORKS

THURSDAY, MAY 1

7:00 am Registration Open

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

8:00 Chairperson's Opening Remarks

Kevin Davies, Ph.D., Vice President Business Development & Publisher C&EN, American Chemical Society; Founding Editor, Bio-IT World

» 8:05 PLENARY KEYNOTE SESSION

Please see page 4 for details.

10:00 Coffee Break in the Exhibit Hall and Poster Competition Winners Announced

Collaborative Approaches to Clinical Data

10:30 Chairperson's Opening Remarks

Thomas Verish, Group Director, Data Operations Services, Bristol-Myers Squibb

10:35 PANEL DISCUSSION: Forming a Collaborative Approach to Develop a Data and Technology Blueprint

Muzafar Mirza, Director, Information Strategy and Analytics, Clinical Informatics and Innovation, Pfizer, Inc.

Georgina Wood, Global Head, Technology Innovations, Novartis

Francis Kendall, Global Head, Statistical Programming and Analysis, Roche

Matt Smith, Director, Bristol-Myers Squibb

William Turner, Global Head, Programming, Biometrics and Information Sciences, Global Medicines Development, AstraZeneca

Brooke Hinkson, Global Head, Clinical Information Governance, Clinical Sciences & Operations, Sanofi

This panel is a read-out of a collaboration between several pharma companies with the prime objective of devising solutions to the challenges that we face as an industry. This cross-pharma consortium focused discussions on technology, standards and data with a view to creating a common framework for how we process data especially in the changing data landscape. Key focus areas included: Transition to CDSIC, Data Aggregation (including broad categories of data - Clinical Trial data, Payer databases, Registry data, Electronic Medical Records Genome data, Biomarker data and Legacy data), key technologies related to data warehousing/data reporting, validation of data analysis tools and open source approaches.

12:15 pm Luncheon Presentations *(Sponsorship Opportunities Available)* **or Lunch on Your Own**

1:15 Dessert Refreshment Break in the Exhibit Hall with Poster Viewing

1:55 Chairperson's Remarks

Scott Wilkins, Ph.D., Enterprise Innovation Director, AstraZeneca

2:00 Interactive Medical Literature: ITN TrialShare for Open Access in Clinical Trials

Adam Asare, Ph.D., Senior Director, Bioinformatics, Immune Tolerance Network

The Immune Tolerance Network (ITN) recently achieved an unprecedented milestone in clinical trial transparency through a high profile publication in the New England Journal of Medicine. The presentation includes lessons learned in creating interactive publications with embedded URL links and its impact on the manuscript development and review process. Metrics on system usage will also be highlighted along with scientific collaborations developed.

Consortia Efforts: Updates, Opportunities, Discussion

Speakers will give a 15-20 minute presentation about their consortia efforts and then convene for a panel discussion.

2:30 Open PHACTS: Practical Semantics for Drug Discovery

Lee Harland, Ph.D., CTO, Open PHACTS, Connected Discovery

The Open PHACTS project is a €20 Million collaboration between major pharma and a range of top academic institutes. Its mission it to create an open, pre-competitive, cloud-based data integration and analysis platform. This talk will describe the journey and the outcome of a major effort in applying semantic technologies to drug discovery and provide a vision for future collaboration across pharma and biotech in this area.

2:50 Enable Unified Analysis and Mining of Biological and Chemical Data from Various Sources

Daniel Stoffler, Ph.D., Senior Principal Scientist, Group Leader Cheminformatics & Statistics, F. Hoffmann-La Roche Ltd, Basel

Computational methods that rely on historical activity data such as target identification in phenotypic screens or virtual screenings based on biological profiles, compound repurposing or pathway identification have been limited due to the inaccessibility or fragmentation of the various data sources. This undertaking will capitalize on the IMI 'OpenPHACTS' initiative and will use novel approaches to allow scientist accessing internal and external Chemical and Biological data sources through one interface.

3:10 The European Translational Research Information and Knowledge Management Services (eTRIKS): 18 Months into a Novel IMI Project to Support Translational Research Data Management

Jay Bergeron, Director, Translational and Bioinformatics, Pfizer

eTRIKS has delivered substantial value to the translational data management community including acting as the key development partner for creating a fully open source version of the tranSMART platform (using PostgreSQL). eTRIKS has released (Nov 2013) a public server including clinical and molecular studies and is continuing to implement a tranSMART-based roadmap that includes emerging security, analytic and semantic capabilities.

3:30 tranSMART: Enabling Rapid Exploratory Analyses and Hypothesis Generation at Pfizer

Angela Gaudette, Business Analyst, Research Business Technology, Pfizer

We will share our experience at Pfizer with our adoption of tranSMART, an open source platform. Learn how Pfizer has contributed to this open source initiative by enabling the search and visualization of Genome Wide Association Studies within the tranSMART platform and discover the potential of such a platform through a neuroscience case study.

3:50 PANEL DISCUSSION with Speakers

4:00 Conference Adjourns

Cambridge Healthtech Institute,
250 First Avenue, Suite 300,
Needham, MA 02494
www.healthtech.com

Track 12

Cancer Informatics

Applying Computational Biology to Cancer Research & Care

TUESDAY, APRIL 29

7:00 am Workshop Registration and Morning Coffee

8:00 - 11:30 Morning Pre-Conference Workshops*

12:30 - 4:00 pm Afternoon Pre-Conference Workshops*

**Separate Registration Required. See page 5 for additional workshops.*

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 PLENARY KEYNOTE SESSION
Please see page 4 for details.

5:00 – 7:00 Welcome Reception in the Exhibit Hall with Poster Viewing

Sponsored by IBM

WEDNESDAY, APRIL 30

7:00 am Registration Open and Morning Coffee

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

» 8:05 PLENARY KEYNOTE SESSION
Please see page 4 for details.

9:00 Benjamin Franklin Award & Laureate Presentation

9:30 Best Practices Awards Program

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

Collaborating in Chronic and Rare Diseases

10:50 Chairperson's Remarks

11:00 PANEL DISCUSSION: Data Liquidity: New "Surge" in the War against Cancer, Diabetes and MS

Marcia Kean, Chairman, Strategic Initiatives, Feinstein Kean Healthcare

Gwen Darien, Executive Vice President, Programs and Services, Cancer Support Community

Robert McBurney, Ph.D., Neuroscientist; CEO, Accelerated Cure Project for MS

Kenneth Buetow, Ph.D., Director, Computational Sciences and Informatics, Complex Adaptive Systems Initiative (CASI), Arizona State University

Dave King, Founder and CEO, Exaptive, Inc.

Data that could be applied to fuel biomedical research has been siloed, inaccessible, and often incomprehensible across disciplines. New initiatives, often driven by patients, are demanding standards-based collection of data that can be facilely integrated, analyzed and shared. The Data Liquidity Coalition is a collaboration comprised of a wide spectrum of stakeholders in the biomedical community – including providers, payers, patients, researchers and others—who are deeply committed to actualizing a common vision of data liquidity to achieve personalized medicine. This panel of Coalition members will present three collaborative projects underway to combat killer and chronic diseases. Each project puts patients at the center, and uses open source technology to enable the seamless usage of data from multiple sources to accelerate basic, translational, clinical and psychosocial research, as well as to lay the groundwork for a national system of data liquidity in biomedicine.

12:00 Co-Presentation: Collaboration to Support Translational Research to Transform R&D

Sponsored by ConvergeHEALTH by Deloitte.

Bill Dalton, Ph.D., M.D., Founder and CEO, M2Gen

Asif Dhar, Executive Vice President

M2Gen and Deloitte will discuss their collaboration to support translational research and review case studies leveraging informatics to transform Research and Development.

12:15 Analysis of TCGA Data with User-Friendly Tools for Cancer Genomics

Sponsored by CLC bio, A QIAGEN Company

M. Michael Barmada, Ph.D., Associate Professor, Human Genetics and Biomedical Informatics, University of Pittsburgh

Next-generation sequencing enables cancer researchers to identify biomarker, which can be used as new drug targets, prognosis, and diagnosis. However, facilitating the data analysis in a user-friendly way is still a bottleneck. Here we present the analysis of TCGA data using an intuitive and customizable software solution as an example for rapid and accurate interpretation of advanced NGS sequencing data.

12:40 Luncheon Presentations *(Sponsorship Opportunities Available)* **or Lunch on Your Own**

Modeling: Cancer

1:50 Chairperson's Remarks
Hugo Geerts, Ph.D., MBA, BA, CSO, In Silico Biosciences; Adjunct Associate Professor, Perelman School of Medicine, University of Pennsylvania

» 1:55 FEATURED PRESENTATION
Identifying Drug Targets from Drug-Induced Changes in Genome-Wide mRNA Expression

Avi Ma'ayan, Ph.D., Associate Professor, Pharmacology and Systems Therapeutics, Icahn School of Medicine at Mount Sinai

We collected and organized publicly available genome-wide gene expression data where hundreds of drugs were used to treat mammalian cells and changes in expression were compared to a control. We then developed computational methods that try to find the drug targets from the expression changes. We show that different steps in the analysis can contribute to approaching the right answer.

2:25 Tools for Comparison of Systematically Generated Cancer Networks vs. Literature Models

Dexter Pratt, Project Director, NDEx, Cytoscape Consortium

Cancer subtype genetic networks can be generated by systematic analysis of patient somatic mutation data. Comparison to existing models of cancer mechanisms is an important step in investigating these data-derived models. Recent work on Network Based Stratification (NBS) at the Ideker Lab will be described along with tools for network comparison under development in the NDEx project.

2:55 Integration of Text Mining and High Throughput Screening to Identify Candidate Targets for Cancer Therapy: Focus on the Autophagy Pathway

Sponsored by ELSEVIER

Philip L. Lorenzi, M.D., Anderson Cancer Center

Autophagy, a programmed process in which cell contents are delivered to lysosomes for degradation, appears to have both tumor-suppressive and tumor-promoting functions; both stimulation and inhibition of autophagy have been reported to induce cancer cell death, and particular genes and proteins have been associated both positively and negatively with autophagy. To provide a basis for incisive analysis of those complexities and ambiguities and

Cambridge Healthtech Institute,
250 First Avenue, Suite 300,
Needham, MA 02494
www.healthtech.com

to guide development of new autophagy-targeted treatments for cancer, we have compiled a comprehensive, curated inventory of autophagy modulators by integrating information from published siRNA screens, multiple pathway analysis algorithms, and extensive text-mining of the literature. The resulting inventory includes 739 proteins and 385 chemicals (including drugs, small molecules, and metabolites). Because autophagy is still at an early stage of investigation, we provide extensive analysis of our sources of information and their complex relationships with each other. We conclude with a discussion of novel strategies that could potentially be used to target autophagy for cancer therapy.

3:25 Refreshment Break in the Exhibit Hall with Poster Viewing

4:00 Using Multiscale Systems Modeling to Design and Develop New Protein Therapeutics

Matthew Onsum, Ph.D., President, Silver Creek Pharmaceuticals

This talk presents an approach to building multiscale systems models that capture drug pharmacokinetics and their effects on cell-signaling networks. Two case studies will be presented that illustrate how these models can be used to design new therapies.

4:30 Biomarker Discovery to Predict Antitumor Activity through Systems Pharmacology in Drug Development and Cancer Therapy

Yasuhiro Funahashi, Ph.D., Senior Director, Biomarkers and Personalized Medicine Core Function Unit, Eisai, Inc.

NGS promotes molecular profiling of cancer and provides novel gene alterations to be targeted. But many cancer types cannot be caused by a single driver gene. A systematic approach based on pharmacology data combining PD and PG will be effective to identify biomarkers for anticancer agents targeting tumor microenvironments like angiogenesis inhibitors and chemotherapeutic agents.

5:00 A Pharmacogenomic View of the NCI-60 Cell Lines and Beyond

Ogan D. Abaan, Ph.D., Research Fellow, Genetics Branch, National Cancer Institute, National Institutes of Health (NIH)

In this talk, we will present findings from our next-generation sequencing efforts using the NCI-60 cell lines and the pharmacogenomic data we have generated. In addition, we will discuss some new directions we have taken to mine the sequence data.

5:30 - 6:30 Best of Show Awards Reception in the Exhibit Hall

Sponsored by DataDirect NETWORKS

THURSDAY, MAY 1

7:00 am Registration Open

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

8:00 Chairperson's Opening Remarks

Kevin Davies, Ph.D., Vice President Business Development & Publisher C&EN, American Chemical Society; Founding Editor, Bio-IT World

» **8:05 PLENARY KEYNOTE SESSION**
Please see page 4 for details.

10:00 Coffee Break in the Exhibit Hall and Poster Competition Winners Announced

Bioinformatics across Multiple Research Initiatives

10:30 Chairperson's Opening Remarks

10:35 Analysis of Genomics Data in an Internal Cloud Computing Environment

Philip Groth, Ph.D., IT Business Partner Genomics, R&D IT - Research, Bayer HealthCare

This talk presents the technical set-up of vCloud, an in-house cloud solution, maintenance and running an internal cloud-computing environment, and how this set-up enables fast & secure analysis of large-scale genomics data. Results of analyzing genomic data from over 4,000 cancer patients will be presented.

11:05 Genome-Wide Multi-Omics Profiling of Colorectal Cancer Identifies Immune Determinants Strongly Associated with Relapse

Subha Madhavan, Ph.D., Director, Innovation Center for Biomedical Informatics, Oncology, Georgetown University

This presentation demonstrates the use of novel informatics methods and data integration approaches in identifying prognostic markers of cancer. The use and benefit of adjuvant chemotherapy to treat patients with state II colorectal cancer (CRC) is not well understood since the majority of these patients are cured by surgery alone.

11:35 Sponsored Presentations *(Opportunities Available)*

12:15 pm Luncheon Presentations *(Sponsorship Opportunities Available)* **or Lunch on Your Own**

1:15 Dessert Refreshment Break in the Exhibit Hall with Poster Viewing

Integrating Genomics into the Clinic

1:55 Chairperson's Remarks

John Quackenbush, CEO, Genospace; Professor, Dana-Farber Cancer Institute and Harvard School of Public Health

2:00 Enterprise-Wide Support for Individualized Treatment at a Cancer Center: Dana-Farber's Profile Project

Barrett J. Rollins, M.D., Ph.D., CSO, Dana-Farber Cancer Institute; Linde Family Professor of Medicine, Harvard Medical School

Bringing the promise of precision medicine to cancer patients requires overcoming scientific and operational impediments. Dana-Farber Cancer Institute's Profile project attempts to address these problems. It seeks to obtain broad genetic profiles on every patient who visits our hospital, link the data to their clinical information and make it available for research and clinical care.

2:30 PANEL DISCUSSION: From Data to Knowledge, from Research to Care – Meeting the Challenges of Genomic Medicine

Moderator: John Quackenbush, CEO, Genospace; Professor, Dana-Farber Cancer Institute and Harvard School of Public Health

Walter M. Capone, President, Multiple Myeloma Research Foundation

Andy Corts, Chief Information Officer, Sarah Cannon Research Institute

Pranil Chandra, DO, FCAP, FASCP, Director, Molecular Pathology Services, PathGroup

Joe Donahue, Senior Vice President, Thomson Reuters

While delivering actionable personalized medicine reports to physicians seems, on the surface, like a relatively straight-forward exercise, there are many stakeholders who play a role in making the endeavor successful. Key elements in building a truly successful program include collecting and managing clinical and genomic data, integrating these in a decision support system, creating an appropriate knowledgebase to support data interpretation, and effectively delivering the data at the point of care. This panel brings together representatives from GenoSpace, Sarah Cannon Research Institute, Multiple Myeloma Research Foundation, PathGroup, and Thomson Reuters to discuss strategies to meet the challenges of genomic medicine.

4:00 Conference Adjourns

Click Here to Register Online!
Bio-ITWorldExpo.com

Cambridge Healthtech Institute,
250 First Avenue, Suite 300,
Needham, MA 02494
www.healthtech.com

Track 13

Data Security

Meeting the Challenge in a Data-Centric World

TUESDAY, APRIL 29

7:00 am Workshop Registration and Morning Coffee

8:00 - 11:30 Recommended Morning Pre-Conference Workshops*

12:30 - 4:00 pm Recommended Afternoon Pre-Conference Workshops*

**Separate Registration Required. See page 5 for additional workshops.*

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 PLENARY KEYNOTE SESSION**
Please see page 4 for details.

5:00 – 7:00 Welcome Reception in the Exhibit Hall with Poster Viewing

Sponsored by IBM

WEDNESDAY, APRIL 30

7:00 am Registration Open and Morning Coffee

8:00 Chairperson's Opening Remarks

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

» **8:05 PLENARY KEYNOTE SESSION**
Please see page 4 for details.

9:00 Benjamin Franklin Award & Laureate Presentation

9:30 Best Practices Awards Program

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

Collaborating in a Secure Environment

10:50 Chairperson's Remarks

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

11:00 tranSMART – A Rapidly Evolving Community-Driven Open Source Platform for Translational Research

Michael Braxenthaler, Ph.D., Global Head, Strategic Alliances, F. Hoffmann-La Roche; VP, Industry Relations, tranSMART Foundation

One year after its inception, the tranSMART Foundation releases version 1.2 of the open source translational research platform tranSMART. Major new features across all key functional areas were contributed by many members of a vibrant community spanning academic, not-profit and commercial sectors. We present a success story for pre-competitive collaborative efforts.

11:30 Improving Multi-Organization Collaboration – Using the Best the World Has to Offer

Sponsored by EXOSTAR

Andrew Porter, Director, IT Architecture, Merck

In today's environment, successful life science organizations are looking outside their four walls to engage the best resources available. EngageZone is a collaboration platform powered by a secure cloud-based life sciences identity hub which allows companies across the industry to utilize a shared infrastructure to facilitate better collaboration while delivering improved usability, ease of deployment, security of intellectual property, and information accountability.

12:00 pm New Cloud-Based Workflows Power Global Life Science Innovation

Sponsored by aspera an IBM company

Michelle Munson, President, CEO & Co-Founder, Aspera

Cloud-based tools for life sciences are driving innovation and enabling advancements like never before. High-speed transport technology was the first step in removing the inherent bottlenecks of cloud infrastructure. Now life sciences workflows have been transformed. High-speed transport and powerful, high-performance cloud computing sit behind a new generation of transport, analysis, transformation and sharing of big data.

12:40 Luncheon Presentation I: Bringing the Big Brain Computer to the Cloud: SGI UV for Cloud-Based Genomics Workflows

Sponsored by sgi

James Reaney, Director, Research Markets, SGI

Building on years of experience with Cyclone™, SGI announces a new collaborative project to bring cloud-based computational resources to genomics workflows worldwide. SGI will showcase several of its computational and storage technologies in the project but chief among these is the SGI UV platform: the "Big Brain" supercomputing system which already powers several large genomics research facilities worldwide. A brief, high-level overview of the project and its collaborative approach will be given, along with a discussion of the initial goals and anticipated benefits for researchers.

1:10 Luncheon Presentation II: Embrace the Inevitable: Six Imperatives to Prepare Your Company for Cloud Computing

Sponsored by okta

Vadim Parizher, Senior Director of Enterprise Architecture, Allergan

In today's digital economy, speed and agility are the keys to winning in business. This session outlines Allergan, Inc.'s (NYSE: AGN) journey from a traditional on-premise IT landscape into a Hybrid IT environment and the role Cloud computing has played in enabling a "second" speed delivery capability. This session will detail experiences, lessons learned, and required changes – including the requirements for identity management - as part of this evolution and share specific challenges in the Pharmaceutical industry.

Securing the Cloud for Healthcare

1:50 Chairperson's Remarks

R. Mark Adams, Ph.D., CIO, Good Start Genetics

1:55 Riding the Cloud to Big Data Analytics in and for Healthcare

Nitesh Chawla, Ph.D., Associate Professor, Computer Science and Engineering, University of Notre Dame

Faced with unsustainable costs and huge amounts of under-utilized data, healthcare needs more efficient practices, research and tools to harness the full benefits of personal health and healthcare-related data. In this talk, I will present the foundations of work that takes a Big Data approach, leveraging cloud computing, towards population health management and personalized healthcare.

2:25 Bursting through to the Cloud – Migrating On-Premises High-Performance Computing to the Cloud in a Clinically Validated, HIPAA-Regulated Setting

R. Mark Adams, Ph.D., CIO, Good Start Genetics

High-performance computing is a critical component of the emerging clinical next-generation sequencing field. This talk addresses the processes involved with taking a custom-developed, in-house pipeline supporting a unique exon-capture NGS approach and acquiring/developing the necessary refinements, tools and processes to implement a clinically validated system in the cloud.

Click Here to Register Online!
Bio-ITWorldExpo.com

Cambridge Healthtech Institute,
250 First Avenue, Suite 300,
Needham, MA 02494
www.healthtech.com

2:55 Gov't, Pharma, and BioTech Case Studies: Implementing Cloud for Computational Life Sciences

Sponsored by CYCLE COMPUTING

Jason Stowe, CEO and Founder, Cycle Computing

From HIPAA, to Genomics, and Drug Design, this session will review Science-on-Cloud implementations, and provide thoughts on future directions. Case studies will represent a variety of applications, and workload sizes from 128 cores, up to runs of more than 156,000 cores. Bring your questions about Cloud HPC, your thinking caps, and we'll review several real examples from the past year.

3:25 Refreshment Break in the Exhibit Hall with Poster Viewing

4:00 GenoSpace – Integrated Data Services for Genomic Medicine Delivery

Niall O'Connor, Head, Engineering, GenoSpace

Genomic data generation has become a commodity and the challenge of managing, analyzing and interpreting results for clinically actionable findings remains a growing problem. We present a secure cloud-based data architecture and service model that integrates vast, disparate knowledge collections. It empowers pathologists, clinicians and patients to harness precision medicine's promise.

4:30 New Approaches around Security and Cloud-Based Orchestration of Genomic Workflows

Charles Schmitt, Ph.D., CTO, RENCI, University of North Carolina at Chapel Hill

Executing genomic workflows in the cloud allows convenience and financial savings over traditional approaches. But users must deal with issues of security and potentially complex workflow orchestration to take full advantage of cloud offerings. We present work from NSF- and NIH-funded projects that provide a cloud-based trust fabric to securely execute cloud-based genomic workflows.

5:00 Enabling Secure Global Genomic Data Exchanges

Sponsored by AnnaiSystems

Stuart Young, Director, Bioinformatics, Annai Systems

Research and healthcare organizations are facing the challenge of finding and exchanging genomic information. Annai Systems provides a solution: Annai-GNOS, a Repository as a Service platform that provides secure access to conduct metadata searches and execute encrypted, accelerated downloads of genomic information. GNOS enables global genomic data exchanges of public and private partners to increase the use and value of genomic information.

5:15 Sponsored Presentation *(Opportunity Available)*

5:30 - 6:30 Best of Show Awards Reception in the Exhibit Hall

Sponsored by DataDirect NETWORKS

THURSDAY, MAY 1

7:00 am Registration Open

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

8:00 Chairperson's Opening Remarks

Kevin Davies, Ph.D., Vice President Business Development & Publisher C&EN, American Chemical Society; Founding Editor, Bio-IT World

» 8:05 PLENARY KEYNOTE SESSION

Please see page 4 for details.

10:00 Coffee Break in the Exhibit Hall and Poster Competition Winners Announced

Ensuring Genomic Privacy and Security

10:30 Chairperson's Opening Remarks

Mary Ann Brown, Executive Director, Conferences, Cambridge Healthtech Institute

» 10:35 FEATURED PRESENTATION

A Global Alliance for Interoperability of Genomic and Clinical Data

David Altshuler, M.D., Ph.D., Deputy Director and Chief Academic Officer, Broad Institute of Harvard and MIT; Professor, Genetics and Medicine, Harvard Medical School and Massachusetts General Hospital; Adjunct Professor, Biology, Massachusetts Institute of Technology

Analysis of large-scale data on genome sequence and clinical outcomes holds great promise for medicine. Learning requires access to datasets and to methods beyond the scope of any single institution. I will discuss a global alliance created to nurture a common framework of international standards for how genomic and clinical data are shared in a responsible and effective manner.

» 11:05 FEATURED PRESENTATION

Incorporating Security Infrastructure from the Beginning at the New York Genome Center

Toby Bloom, Ph.D., Deputy Scientific Director, Informatics, New York Genome Center

As genomic data falls under more regulations governing personally identifiable information and more clinical genomics studies combine deep clinical data with genomic data, privacy and security requirements integrated into genome centers' informatics infrastructures become increasingly complex. We discuss how NYGC is addressing these challenges.

11:35 Architecture of Omics-Aware Clinical Decision Support Systems

Sponsored by ORACLE HEALTH SCIENCES

Andrew Boudreau, Principal Product Strategist, Oracle Health Sciences

While many EMR implementations include some form of configurable decision support, the demands of genome data – gene panels as well as whole-exome and whole-genome data – make molecular decision support in the EMR a significant challenge. We propose architectures for decision support systems external to but integrated with an EMR, along with analytical tools and scalability appropriate for genome-wide personalized medicine.

12:15 pm Luncheon Presentations *(Sponsorship Opportunities Available)* **or Lunch on Your Own**

1:15 Dessert Refreshment Break in the Exhibit Hall with Poster Viewing

Three Cs of Security: Confidentiality, Classification, Collaboration

1:55 Chairperson's Remarks

Toby Bloom, Ph.D., Deputy Scientific Director, Informatics, New York Genome Center

2:00 Data and Intellectual Property Security in a Global Cyber Environment

Russ Brown, Supervisory Special Agent, Boston Division Criminal Cyber Squad, FBI

Data security is a very significant issue faced by businesses in today's electronically connected environment. Data "owned" or controlled by a business, as well as applications developed by a business, are categorized as Intellectual Property. The security and protection of Intellectual Property is critical to conducting, maintaining and growing a secure business in the current global environment.

2:30 Information Classification: The Key to a Sane Security Strategy

William Telford, Director, R&D IS Security, Sanofi R&D

Understanding your information is key to your security success and enables collaboration. This talk will address the key topics to consider and challenges that must be overcome.

3:00 PANEL DISCUSSION: The Big Data Storage and Security Maze: Balancing Collaboration and Privacy

Moderator: Toby Bloom, Ph.D., Deputy Scientific Director, Informatics, New York Genome Center

Russ Brown, Supervisory Special Agent, Boston Division Criminal Cyber Squad, FBI

Yaniv Erlich, Ph.D., Principal Investigator and Whitehead Fellow, Whitehead Institute for Biomedical Research

Philip Groth, Ph.D., IT Business Partner, CoE Research, Bayer HealthCare Pharmaceuticals

John Sabey, President, Sabey Data Center Properties

William Telford, Director, R&D IS Security, Sanofi R&D

Big data has led to organizations turning to virtual networks for information storage and processing. Thus, unauthorized access to data and implementation of effective governance structures are growing concerns. To balance knowledge sharing and respect for confidentiality, researchers must consider how and where to store and secure data – plus what data and why. This panel gathers representatives from academia, pharma and IT to discuss these issues. Topics include:

- How secure is your data?
- When should you favor data sharing and when should you restrict data flow?
- What data actually needs to be protected in the first place?
- What security systems and practices are most appropriate for specific research needs?

4:00 Conference Adjourns

Click Here to Register Online!
Bio-ITWorldExpo.com

Cambridge Healthtech Institute,
250 First Avenue, Suite 300,
Needham, MA 02494
www.healthtech.com

HOTEL & TRAVEL

Conference Venue:

Seaport World Trade Center
200 Seaport Boulevard
Boston, MA 02210

Host Hotel:

Seaport Hotel *(Located directly across the street)*
One Seaport Lane
Boston, MA 02210
T: 617-385-4514
Reservations: Bio-ITWorldExpo.com

Discounted Room Rate: $251 s/d
Discounted Room Rate Cut-off Date: March 21, 2014

Please visit Bio-ITWorldExpo.com to make your reservations online or you may also call the hotel directly to reserve your sleeping accommodations. You will need to identify yourself as a Bio-IT World Conference attendee to receive the discounted room rate with the host hotel. Reservations made after the cut-off date or after the group room block has been filled (whichever comes first) will be accepted on a space and rate availability basis. Rooms are limited, so please book early.

For information on parking, directions, airport transportation, and visiting Boston and New England, visit the Hotel & Travel page at **Bio-ITWorldExpo.com.**

MEDIA PARTNERS

Official Media Partner: Bio-IT World

Official PR Partner: PAN COMMUNICATIONS

Lead Sponsoring Publications: Clinical Informatics News, Drug Discovery Today, GEN Genetic Engineering & Biotechnology News, nature, Science AAAS

Sponsoring Publications: Assay and Drug Development Technologies, DDNews, Epigenomics, FierceBiotech, FierceBiotech IT, FiercePharma, genomeweb, Insight Pharma Reports, Personalized Medicine, Pharmaceutical Outsourcing, Pharmacogenomics, PharmaVOICE, scientific computing world

Sponsoring Organizations: Bioinformatics Organization, ISCB International Society for Computational Biology Affiliated Conference, Massachusetts High Technology Council, Massachusetts Life Sciences Center

Web Partners: Biocompare, BioSpace.com, CanBiotech, mendelspod.com, www.PharmCast.com – Pharmaceutical Internet –

Click Here to Register Online!
Bio-ITWorldExpo.com

Cambridge Healthtech Institute,
250 First Avenue, Suite 300,
Needham, MA 02494
www.healthtech.com

SPONSORSHIP, EXHIBIT, AND LEAD GENERATION OPPORTUNITIES

CHI offers comprehensive sponsorship packages which include presentation opportunities, exhibit space, branding and networking with specific prospects. Sponsorship allows you to achieve your objectives before, during, and long after the event. Any sponsorship can be customized to meet your company's needs and budget. Signing on early will allow you to maximize exposure to qualified decision-makers.

Podium Presentations – *Within the Main Agenda!*

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

Breakfast & Luncheon Podium Presentations

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

Invitation-Only VIP Dinner/Hospitality Suite

Sponsors will select their top prospects from the conference pre-registration list for an evening of networking at the hotel or at a choice local venue. CHI will extend invitations and deliver prospects, helping you to make the most out of this invaluable opportunity. Evening will be customized according to sponsor's objectives i.e.:

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

Exhibit

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

New Product Showcase

Exhibitors have the opportunity to showcase their new product in the main exhibit hall. CHI will promote your new product through the event website, program guide, pre-show marketing campaigns, press releases and more.

Additional branding and promotional opportunities are available, including:

- Mobile App
- Hotel Room Keys (SOLD)
- Footprint Trails
- Staircase Ads
- Conference Tote Bags (SOLD)
- Badge Lanyards (SOLD)
- Padfolios
- Program Guide Advertisement

Looking for additional ways to drive leads to your sales team? One move can make all the difference!

CHI's Lead Generation Programs will help you obtain more targeted, quality leads throughout the year. We will mine our database of 800,000+ life science professionals to your specific needs. We guarantee a minimum of 100 leads per program! Opportunities include:

- Whitepapers
- Web Symposia
- Custom Market Research Surveys
- Podcasts

For sponsorship and exhibit information, please contact:

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

Companies L-Z:
Elizabeth Lemelin
Business Development Manager
781-972-1342
elemelin@healthtech.com

2014 EXHIBITORS & SPONSORS (As of December 2, 2013)

Accelrys
Accunet Solutions
Annai Systems Inc.
Arxspan
Aspera
Avere Systems
Bina Technologies
BioDatomics
BioFortis, Inc
Biomatters
BioTeam
BSI
Cambridge Computer
Cambridge Semantics
Ceiba Solutions
Certara
ChemAxon
CLC bio
Core Informatics
Cray
Cycle Computing LLC
DataDirect Networks Inc
Deloitte.
DeltaSoft
DNAnexus
Dotmatics
Edico Genome
EMC Isilon
ePharmaSolutions
Exostar
Experis IT
Freezerworks
Gene by Gene
Genedata, Inc.
GenoSpace, LLC
GGA Software Services LLC
Globus Online
Hewlett Packard
Hitachi Data Systems
HoloInfo, Inc.
IBM
IDBS
Intel
Internet2
LabAnswer
LABVANTAGE Solutions, Inc.
Liaison Healthcare Informatics
Linguamatics
Metrum Research Group
Microway, Inc.
Neural ID
OnX Enterprise Solutions
OpenEye Scientific Software
Optra Systems Inc
Oracle Health Sciences
Panasas, Inc.
Partek Incorporated
Parthys Reverse Informatics
PointCross Life Sciences, Inc.
Primesoft
Qlucore
RAID Incorporated
RCH Solutions, Inc.
Remedy Informatics
RURO Inc.
SABEY Data Centers
Sapio Sciences
SAS Institute Inc., JMP Division
Scigilian Software, Inc.
Scilligence
Seven Bridges Genomics
SGI
Sidus BioData
Silicon Mechanics
Simulations Plus, Inc.
Sinequa
STaCsDNA
Studylog Animal Study Workflow Suite
Tessella
Thinkmate
Thomson Reuters
TimeLogic, a division of Active Motif
Titian Software
TopQuadrant, Inc.
tranSMART Foundation
Waters Corporation
Y Prime
YarcData

Click Here to Register Online!
Bio-ITWorldExpo.com

Cambridge Healthtech Institute,
250 First Avenue, Suite 300,
Needham, MA 02494
www.healthtech.com

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 1420 F when registering

Pricing and Registration Information

PRE-CONFERENCE WORKSHOPS

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

Please refer to Workshop list on page 5.

CONFERENCE PRICING (excludes workshops)

	Commercial	Academic, Government, Hospital-affiliated	Student*
sRegistrations after March 21, 2014, and on-site	$2045	$950	$325

Conference Tracks	
Track 1: IT Infrastructure - Hardware	Track 8: Data Visualization
Track 2: Software Development	Track 9: Pharmaceutical R&D Informatics
Track 3: Cloud Computing	Track 10: Clinical Genomics
Track 4: Bioinformatics	Track 11: Collaborations and Open Access Innovations
Track 5: Next-Gen Sequencing Informatics	Track 12: Cancer Informatics
Track 6: Systems Pharmacology	Track 13: Data Security
Track 7: eClinical Trials Solutions	

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

CONFERENCE DISCOUNTS

Exclusive Offer to Attend Medical Informatics World Conference**

Paid attendees of Bio-IT World Conference & Expo can attend the co-located Medical Informatics World Conference (April 28-29) for a special discounted rate (20% discount off the registration fee for the main conference). Medical Informatics World and Bio-IT World Expo are being held back-to-back to complete the week of scientific content by bridging the healthcare and life science worlds.

To receive this exclusive 20% discount, mention keycode **1420BITXP** when registering for Medical Informatics World Conference.
Please note: Our records must indicate you are a paid attendee of Bio-IT World Conference & Expo 2014 to qualify.

*** Discount applies to paid attendees of Bio-IT World Conference & Expo 2014 only. Applies to new registrations only and cannot be combined with other discount offers, except poster discount. Discount does not apply to workshops.*

Poster Submission-Discount ($50 Off)
Poster abstracts are due by March 7, 2014. 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

If you are unable to attend but would like to purchase the Bio-IT World Conference & Expo 2014 conference CD for $750 (plus shipping), please visit Bio-ITWorldExpo.com. Massachusetts delivery will include sales tax.

ADDITIONAL REGISTRATION DETAILS

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

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

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

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