Cambridge Healthtech Institute's Ninth Annual

Bio·IT World

CONFERENCE & EXPO '10

April 20 – 22, 2010 • World Trade Center • Boston, MA

ENABLING TECHNOLOGY. LEVERAGING DATA. TRANSFORMING MEDICINE.

CONCURRENT TRACKS:

1. IT Infrastructure – Hardware
2. IT Infrastructure – Software
3. Bioinformatics and Next-Gen Data
4. Systems and Predictive Biology
5. Cheminformatics and Computer-Aided Modeling
6. eClinical Trials Technology
7. eHealth Solutions

EVENT FEATURES:

- Access All Seven Tracks for One Price
- Network with 1,500+ Attendees
- Hear 100+ 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
- See the Winners of the following 2010 Awards:
  - Benjamin Franklin
  - Best of Show
  - Best Practices
- View Novel Technologies and Solutions in the Expansive Exhibit Hall
- And Much More!

KEYNOTE PRESENTATIONS BY:

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

Christoph Westphal, M.D., Ph.D.,
CEO, Sirtris Pharmaceuticals; Senior Vice President, Centre of Excellence for External Drug Discovery, GlaxoSmithKline

Deepak Singh, Ph.D.,
Business Development Manager, Amazon Web Services

KEYNOTE PANEL:

The Future of Personal Genomics

A special plenary panel discussion featuring:

James Heywood, Co-founder and Chairman, PatientsLikeMe

Dan Vorhaus, J.D., M.A., Attorney, Robinson, Bradshaw & Hinson; Editor, Genomics Law Report

Dietrich Stephan, Ph.D., President & CEO, Ignite Institute

Kári Stefánsson, MD, Dr Med, Executive Chairman and President of Research, deCODE genetics

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

And More...

Bio-ITWorldExpo.com

Organized & Managed by:
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Bio-IT World

SCHEDULE-AT-A-GLANCE

Tuesday, April 20, 2010	
7:00-8:00am	Pre-Conference Registration and Morning Coffee
8:00am-4:00pm	Pre-Conference Workshops
2:00-6:00pm	Main Conference Registration
4:00pm	Keynote Presentation
5:00-7:00pm	Welcome Reception in Exhibit Hall
Wednesday, April 21, 2010	
7:30am	Registration and Morning Coffee
8:20am	Keynote Presentations & 2010 Benjamin Franklin Award
9:30am	Exhibit Hall Opens
9:30-10:50am	Coffee Break, Exhibit and Dedicated Poster Viewing
10:50am-12:30pm	Main Conference Tracks 1-7
12:30-1:40pm	Luncheon Presentation *(Sponsorship Opportunity Available)* or Lunch on Your Own
1:40-3:15pm	Main Conference Tracks 1-7
3:15-3:45pm	Refreshment Break, Exhibit and Dedicated Poster Viewing
3:45-5:15pm	Main Conference Tracks 1-7
5:15-6:15pm	2010 Best of Show Awards in Exhibit Hall
6:15pm	Exhibit Hall Closes
6:30-10:00pm	2010 *Bio-IT World*'s Best Practices Awards Reception & Dinner
Thursday, April 22, 2010	
8:00am	Registration and Morning Coffee
8:45am	Keynote Presentation & Plenary Panel
10:30am	Exhibit Hall Opens
10:30-10:55am	Coffee Break, Exhibit Viewing and Poster Competition
10:55am-12:30pm	Main Conference Tracks 1-7
12:30-2:00pm	Luncheon in the Exhibit Hall
2:00pm	Exhibit Hall Closes
2:00-4:00pm	Main Conference Tracks 1-7
4:00pm	Conference Adjourns

KEYNOTE SPEAKERS:

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

John D. Halamka, M.D., M.S. is Chief Information Officer of Beth Israel Deaconess Medical Center, Chief Information Officer of Harvard Medical School, Chairman of the New England Healthcare Exchange Network (NEHEN), Chair of the US Healthcare Information Technology Standards Panel (HITSP), co-Chair of the HIT Standards Committee, and a practicing Emergency Physician. As Chief Information Officer of Beth Israel Deaconess Medical Center, he is responsible for all clinical, financial, administrative and academic information technology serving 3000 doctors, 14000 employees and two million patients. As Chief Information Officer of Harvard Medical School, he oversees all educational, research and administrative computing for 18000 faculty and 3000 students. As Chairman of NEHEN he oversees clinical and administrative data exchange in Massachusetts. As Chair of HITSP/co-Chair of the HIT Standards Committee he coordinates the process of electronic standards harmonization among stakeholders nationwide.

Christoph Westphal, *M.D., Ph.D., CEO, Sirtris Pharmaceuticals; Senior Vice President, Centre of Excellence for External Drug Discovery, GlaxoSmithKline*

Christoph Westphal, M.D., Ph.D., co-founded Sirtris Pharmaceuticals, Inc. in 2004 and has since served as Chief Executive Officer. In addition to leading Sirtris as an independent discovery performance unit within GlaxoSmithKline (GSK), Dr. Westphal serves as the Senior Vice President of GSK's Centre of Excellence for External Drug Discovery (CEEDD). Dr. Westphal was previously co-founder and CEO of Alnylam Pharmaceuticals, Momenta Pharmaceuticals and Acceleron Pharma. He was also co-founder of Concert Pharmaceuticals. Dr. Westphal earned his M.D. from Harvard Medical School and Ph.D. in genetics from Harvard University; and he graduated with a B.A. summa cum laude and Phi Beta Kappa from Columbia University. Dr. Westphal currently serves on the Board of Directors for Alnara Pharmaceuticals, Inc., the Board of Fellows of Harvard Medical School and the Board of Overseers of the Boston Symphony Orchestra. Dr. Westphal has been the lead or senior author on several patent applications and scientific papers in journals.

Deepak Singh, *Ph.D., Business Development Manager, Amazon Web Services*

Dr. Deepak Singh manages business development for Amazon EC2 at Amazon Web Services (AWS) where he works with customers carrying out large scale computing, scientific research, and data analytics on the AWS cloud. Prior to AWS, Deepak managed strategic planning for Rosetta Biosoftware, a business unit at a subsidiary of Merck & Co. Deepak came to Rosetta Biosoftware from Accelrys where he was product manager for the life sciences modeling and simulation portfolio and subsequently Director of the Accelrys NanoBiology Initiative, an effort to investigate multiscale modeling technologies for biological applications of nanosystems. He started his career as a scientific programmer at GeneFormatics, where was responsible for the maintenance and development of algorithms for protein structure and function prediction. Deepak has a Ph.D. in Physical Chemistry from Syracuse University where he used electronic structure theory and molecular dynamics to study the photophysics of opsins.

AWARDS PROGRAMS

Cambridge Healthtech Institute and *Bio-IT World* will again be recognizing and celebrating leaders in innovation through the "Best of Show Award" and "Best Practices Award" Programs. Finalists in the Best of Show Awards will be recognized on-site, and winners will be honored in a ceremony on the exhibit hall floor. The Best Practices Awards take place at a gala dinner, playing host to more than 100 thought-leaders hailing from Biotech, Pharma, and IT.

Best of Show Awards

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

Best Practices Awards - Call for Entries!

Add value to your Conference & Expo attendance, sponsorship or exhibit package, and further heighten your visibility with the creative positioning offered as a Best Practices participant. The Best Practices Awards identify and showcase outstanding examples of innovative partnerships, technologies and strategies impacting research and drug development. Winners will be selected by a peer review expert panel in early 2010. *Bio-IT World* will present the Awards for its 2010 competition at a special gala dinner ceremony on April 21, 2010. Early bird deadline (no fee) for entry is December 18, 2009 and final deadline (fee) is January 18, 2010. Full details including previous winners and entry forms are available at www.Bio-ITWorldExpo.com .

2010 Benjamin Franklin Award

The Benjamin Franklin Award for Open Access in the Life Sciences is a humanitarian/bioethics award presented annually by the Bioinformatics Organization to an individual who has, in his or her practice, promoted free and open access to the materials and methods used in the life sciences. Nominations are now being accepted! Full details including previous laureates and entry forms are available at www.bioinformatics.org/franklin/. The winner will be announced Wednesday, April 21.

CHI's INTRONET Networking at its Best

CHI'S INTRO-NET: NETWORKING AT ITS BEST! Maximize Your Experience Onsite at the Bio-IT World Conference & Expo!

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

PRE-CONFERENCE WORKSHOPS*

TUESDAY, APRIL 20

* Separate Registration Required

HALF-DAY WORKSHOPS

MORNING WORKSHOPS (8:00-11:30AM)

Workshop 3: Visualization (8:00-11:30am)

Data visualization is a powerful tool for communicating quantitative information and facilitating effective decision making among researchers, management, healthcare funders, providers, insurers, and policy makers, as well as physicians. Data visualization is a critical component for leveraging data, enabling technology, and transforming medicine. Unfortunately, our visualizations often obscure the reality in the data and may be the cause of naïve, or intentional, miscommunication or distortion. One of the goals of this course is to prevent such unfortunate outcomes by enhancing the 'graphicacy' skills of those who use, or prepare, data visualizations for decision making. Additional goals are to deliver the benefits of improving the efficacy of decision making a s well as enhancing the productivity of meetings and written communications. This workshop has proven particularly valuable for senior management, who enhance their knowledge to explain exactly how, and why, they want their data presented in new ways.

Instructor:

Howard A. Spielman, Ph.D., M.B.A., Management Semiotics International, Inc.

Workshop 4: Knowledge Management (8:00-11:30am)

This workshop focuses on the integration and application of data to improve R&D productivity and decision making across an organization. Speakers will discuss how they are leveraging informatics to drive innovation and productivity.

Instructor:

Dan Housman, Managing Director, Analytical Applications, Recombinant

Griffin M. Weber, M.D., Ph.D., Chief Technology Officer, Harvard Medical School

AFTERNOON WORKSHOPS (12:30-4:00PM)

Workshop 1: Agile Answers from Literature: Using Text Mining and Analytics to Drive Decision Support (12:30-4:00pm)

The scientific literature captures the learnings of over a $100 billion investment in biomedical research per year. Our ability to access the knowledge buried in the literature has been limited at best. This workshop will present strategies on using the scientific literature to answer questions that have previously been unanswerable. A comprehensive view of utilizing the literature will be presented and how text mining fits into the overall approach. Everything from accessing the literature, legal issues, text analytics technologies and tools, visualization of results and curation strategies will be covered. Key topics to be covered:

- What types of questions can be answered using text mining
- How to source literature to mine and the complications of copyright and licensing
- What tools are available for text mining and how to get started using them
- Best practice in curation for extracted information
- Visualization and results distribution strategies

William Hayes, Ph.D., Director, Decision Support, R&D IT, Biogen Idec

Phoebe Roberts, Ph.D., Sr Principal Scientist, Computational Sciences Center of Emphasis, Pfizer,Inc

Larry Hunter, Ph.D., Director, Center for Computational Pharmacology & Computational Bioscience Program; Professor, Pharmacology, University of Colorado

Workshop 5: Imaging Informatics: Optimizing Image Collection, Management and Analysis (12:30-4:00pm)

The richness of information in images has made it one of the most popular readouts for high throughput screening in recent years. This increasing amount of images requires the development of tools to automatically analyze and interpret them. However, neither the infrastructure nor the development of image analysis has been able to keep up with the fast growth of image data. This workshop offers you some solutions including data management, image analysis algorithm, image and metadata integration, etc. The main focus of this workshop is to share available resources, experiences and promote discussion for current needs in the HCS community.

Estelle Glory Afshar, Ph.D., Postdoctoral Fellow, Murphy Lab, Center for Bioimage Informatics, Carnegie Mellon University

Tom Hasaka, Ph.D., Senior Automation Engineer, Broad Institute

Vebjorn Ljosa, Ph.D., Computational Biologist, Broad Institute

Matthew Silva, Ph.D., Head, Imaging Science, Millennium Pharmaceuticals, Inc.

Tiao Xie, Ph.D., Image Analyst, ICCB-Longwood, Systems Biology, Harvard

PRE-CONFERENCE WORKSHOPS*

TUESDAY, APRIL 20

* Separate Registration Required

ALL DAY WORKSHOPS

Workshop 2: Cloud Computing (8:00am - 4:00pm)

Sponsored by

CYCLE COMPUTING

parascale Powering Cloud Storage

Cycle Computing is leading the efforts for many life science organizations in using the cloud, helping research labs and companies leverage internal and external clouds for collaboration, calculations, and storage. We'll cover real-world use cases across drug discovery & design, collaboration, next generation sequencing, proteomics, software as a service, and bioinformatics, to explore how life sciences are using cloud computing, its challenges and effectiveness, how money can be saved by an organization, and regulatory compliance. Join thought leaders in this day long workshop to examine how cloud computing can be used effectively as an external IT service and an internal computing model.

Instructors:

Jason Stowe, Founder, CEO, Cycle Computing

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

Jack Norris, M.B.A., Vice President, Marketing and Corporate Development, ParaScale, Inc.

Andrew Kaczorek, Information Consultant and HPC Specialist, Eli Lilly

Jeremy Lawrence, CIO, The Mind Research Network

Steve Phillpott, CIO, Amylin

Angel Pizarro, Director, University of Pennsylvania ITMAT Bioinformatics Facility

Simon N. Twigger, Ph.D., Assistant Professor, Department of Physiology, Medical College of Wisconsin

Peter S. Shenkin, Vice President, Schrodinger

Workshop 6: Next-Gen Sequencing (8:00am - 4:00pm)

Sponsored by

DNAnexus

ion torrent

ISILON SYSTEMS

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BioTeam has been on the frontlines of next-generation sequencing integration, having helped several organizations with their unique next-gen IT, storage, and data management challenges. This workshop will present real-world customer experiences straight from the trenches. You'll get practical information about the analysis, assessment, design, implementation, testing, and support needed to bring a research organization from technology adoption to publication in the next-gen world.

Phil Butcher, Head of IT, The Wellcome Trust Sanger Institute

George Church, Ph.D., Professor of Genetics at Harvard Medical School and Director of the Center for Computational Genetics

Jurgen Eils, Bioinformatic Database Group Leader, German Cancer Research Center

William Van Etten, Ph.D., Founding Partner, BioTeam, Inc.

Carter George, VP Products, Ocarina Networks Carter George, VP Products, Ocarina Networks

John M. Greally, M.B.A, Ph.D., Director of Center for Epigenomics, Chief of Division of Computational Genetics, Department of Genetics, Albert Einstein College of Medicine

Rod Wing, Director of the Arizona Genomics Institute, University of Arizona

Giles Day, Senior Director, R&D Informatics, Pfizer, Inc.

Michael Reich, Director of Cancer Informatics Development, Broad Institute of MIT and Harvard

Paul Rutherford, Chief Technology Officer, Isilon Systems

Jonathan Rothberg, Ph.D., Founder and Chief Executive Officer, Ion Torrent

Andreas Sundquist, Ph.D., CEO, DNAnexus

Luncheon Presentation:

Sponsored by

ISILON SYSTEMS

Finding Clarity in the Cloud—Separating Fact from Fiction in Cloud Computing for Life Sciences

Paul Rutherford, Chief Technology Officer, Isilon Systems

IDC recently stated revenues from Cloud IT services will increase by a 26% CAGR through 2013, compared to only 4% for traditional IT services. These statistics demonstrate actual momentum that is driving the Cloud's hype. In the same study, however, respondents noted security, availability, performance, and concern of the "pay what you use model" may be more expensive than building your own infrastructure. They are serious impediments to cloud adoption. It's no wonder that many of us are still unsure of what to make of the Cloud - fact or fiction? As with many new IT trends, the answer lies somewhere in between. This presentation will detail exactly what the Cloud is - and isn't - and what best practices life science organizations can follow to ensure they make the right IT investment. We will also discuss how the Cloud can save moy, accelerate application performance, and increase IT efficiency.

TRACK 1:
IT INFRASTRUCTURE – HARDWARE

Track 1 will delve into high performance computing and computing platforms, including grid computing, datacenter design and data storage (storing solutions, data security, standards & regulations, access issues, system interoperability).

TUESDAY, APRIL 20

2:00 - 6:00 pm Main Conference Registration

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

4:05 KEYNOTE INTRODUCTION:
Ronald Ranauro, Chief Executive Officer, GenomeQuest, Inc. *Sponsored by* GenomeQuest

4:15 PLENARY KEYNOTE: Drug Discovery Opportunities and Challenges—VC, Biotech and Pharma Perspectives
Christoph Westphal, M.D., Ph.D., CEO, Sitris Pharmaceuticals; Senior Vice President, Center of Excellence for External Drug Discovery, GlaxoSmithKline

5:00 - 7:00 pm Welcome Reception in the Exhibit Hall
****Drop off your business card at the CHI Sales Re-Sign Booth for a chance to win an Apple® - iPod nano®! 2 Winners will be announced at 6:45pm in the Exhibit Hall*

WEDNESDAY, APRIL 21

7:30 am Registration and Morning Coffee

8:15 Event Chairperson's Opening Remarks
Phillips Kuhl, Co-founder and President, Cambridge Healthtech Institute
Keynote Introduction: *Jamie Wyatt, Vice President and General Manager Health and Life Sciences, Netezza* *Sponsored by* NETEZZA

8:20 PLENARY KEYNOTE: Impact of HIT Stimulus on Novel Sources of Data for Research
John Halamka, M.D., M.S., CIO, Harvard Medical School

9:00 Keynote Presentation & 2010 Benjamin Franklin Award
Alex Bateman, Ph.D., Senior Investigator, Pfam Database Project, Wellcome Trust Sanger Institute

9:30 Coffee Break, Poster and Exhibit Viewing *Sponsored by* SCYNEXIS
****Drop off your business card at the CHI Sales Re-Sign Booth for a chance to win 1 of 2 Prizes! (Nintendo® Wii™ System or Apple® - iPod touch®)*

SCALING UP FOR THE DATA DELUGE

10:50 Track Chairperson's Remarks "HPC from the Trenches"
Chris Dagdigian, Founding Partner and Director of Technology, BioTeam, Inc.

11:00 Sanger Centre's Perspective on Data Storage Challenges
Phil Butcher, Head of Systems, Sanger Centre
As the largest sequencing centre in Europe, the Sanger Institute makes a massive contribution to the worldwide collection of genomic information. A key challenge is identifying an appropriate storage infrastructure to manage the onslaught of raw data that continues to be generated. This talk will present Sanger Institute's perspective on scaling techniques and practical issues they are considering that address the data storage challenge.

11:30 Adjusting to the New Scale of Research Data Management
Matthew Trunnell, Acting Director, Advanced IT, Broad Institute of MIT and Harvard
One of the Broad Institute's core missions is to discover, develop and optimize the critical technologies needed to obtain and analyze the massive amounts of genomic data being generated by scientists at the Broad and around the world. Much of our attention in recent years has been focused on scaling our IT infrastructure to accommodate the influx of data resulting from second-generation sequencing and other high-throughput technologies, but it is only recently that we have started to come to terms with some of the secondary impacts of the data scale-out. In this talk I will discuss how the Broad been exploring new approaches to the challenges of data protection and long-term data management at our current multi-petabyte scale with particular emphasis on the increased responsibility of researchers in the data management process.

12:00 pm Maximizing Research and Minimizing Storage Expenditure: Analyzing a Production Deployment of Deduplication & Compression for Bioinformatics *Sponsored by* ocarinanetworks
Carter George, Vice President of Products, Ocarina Networks
In all Bioinformatics disciplines, rich data is the platform from which all discovery is made, and rapid throughput growth of highly anticipated next-generation scanning systems means faster time-to-discovery. However, with each increase in scanner throughput comes a corresponding requirement for additional storage. Because scanner throughput is out-pacing disk system density, bioinformatics organizations may be allocating more and more of their budgets to IT and less to research. The deployment of cheaper disk is attractive, but imposes higher administrative costs.

This presentation will review various solutions to keeping IT expenditures in check, without sacrificing on enterprise-class reliability and scalability features. Much of the presentation will be devoted to reviewing the process of selection, deployment, and results of a major bioinformatics institution's deployment of deduplication and compression to improve utilization of existing storage and reduce costs

12:30 Luncheon Presentation : Enabling World Class Research through Innovative Data Management Strategies *Sponsored by* hp
Peter Brey, WW Business Development Manager, Scalable NAS, HP Storage
Brent Richter, Director, Enterprise IS, Partners HealthCare Systems
In the past five years, Partners HealthCare Center for Personalized Genetic Medicine focused its efforts on building an IT foundation with the right hardware and software to support their vision of personalized medicine, where clinicians are able to make treatment and medication decisions based on patient's genetic profile.

For organizations like Partners HealthCare Center for Personalized Genetic Medicine there is an on-going concern that IT must keep pace with the biology, especially in terms of storage capabilities. As the costs of sequencing technologies continue to fall and the volumes of data from those technologies continue to rise, that concern becomes a reality that IT must grapple with daily.

IT continues to play a significant role in supporting the vision of personalized medicine, implementing a scalable storage solution is an important component in realizing the benefits of next generation sequencing technologies.

1:40 Track Chairperson's Remarks
David Medina, Worldwide Life Science and Pharma Segment Executive, Hewlett Packard

Apple® - iPod touch®, Nano®, Nintendo® Wii™, are not sponsors or participants in this program.

TRACK 1:
IT INFRASTRUCTURE — HARDWARE

1:45 IT Infrastructure Strategy in Support of Next-Gen Biological Research

Gregg TeHennepe, Senior Manager, Research Liaison, Information Technology, The Jackson Laboratory

The Jackson Laboratory is a leading genetics laboratory. This talk presents our 2009 Research Information Technology Whitepaper documenting The Jackson Laboratory's five-year IT infrastructure plan. Attendees will learn about the methods behind the whitepaper and understand the key research drivers. This talk will review the current status of Jackson's IT infrastructure supporting research today, how the institution compares to its peers, and provide recommendations for meeting the five year needs of its research programs.

2:15 Improving Storage Efficiency for Unstructured Research Data

Richard Shaginaw, Project Manager, Scientific Computing Services, Bristol Meyers Squibb

This presentation offers insight into an infrastructure approach that expedites growth and change in the research environment while containing costs. The fire hose of data from discovery-related sources requires rapid storage provisioning, manageable yet flexible access controls, and reliable data protection. Supplying these needs by way of a central file service -- large networks of applications using a common file server -- allows us to be more responsive to research requirements, to protect data more effectively, and to reduce management overhead. The novelty of this approach lies in removing the need to manage disk and freeing us to work with the researcher to address data challenges. The audience will learn that for many research purposes, central file-based storage with unified access control is empowering and more efficient than older approaches.

2:45 Teradata's Agile Analytic Cloud for Research & Development

Sponsored by TERADATA

Joy King, Senior Pharmaceutical Industry Consultant, Teradata3:00 Sponsored Presentation

Teradata's Private Agile Analytic Cloud solution and its new "Elastic Mart" functionality allows end-users (scientists, statisticians, data analysts) to integrate data that may reside on public web sites, or their own desktop, with data that resides in the data warehouse -- with no IT intervention. The solution supports agile, iterative analyses using commonly available statistical and visualization tools. Results can easily be published to the data warehouse when ready since all work takes place inside the private cloud and takes full advantage of the power and performance of the Teradata MPP Data Warehouse Platform. Elastic Marts can also easily be monitored and managed by IT via a web tool that is part of the solution. Teradata clients are generating results faster and at a higher capacity. They are able to share and reuse data and results in near real-time. Our customers are realizing business value on day one after they implement our Agile Analytic Cloud solution!

3:00 IBM Research Solutions for Life Sciences *Sponsored by* IBM

Michael Hehenberger, Ph.D., Life Sciences Business Development Executive, IBM

3:15 Refreshment Break, Poster and Exhibit Viewing

****Drop off your business card at the CHI Sales Re-Sign Booth for a chance to win 1 of 2 Prizes! (Nintendo® Wii™ System or Apple® - iPod touch®) Winners will be announced at 3:30pm in the Exhibit Hall*

3:45 ResearchStation: A Bioinformatics Platform for Research Collaboration in Translational Medicine

Lynn H. Vogel, Ph.D., FHIMSS, FCHIME, Vice President and CIO, Associate Professor, Bioinformatics and Computational Biology, The University of Texas M. D. Anderson Cancer Center

M.D. Anderson's IT division developed a unique SOA-based IT platform to easily access, integrate and analyze genomic and clinical data. This application, called ResearchStation, enables collaboration between life science researchers utilizing disparate data sources and the analytic tools of their choice, and demonstrates the effectiveness of a SOA-based architecture in enabling interoperability in support of translational research. Learn how life science research organizations are dealing with the challenges of data explosion, how industry partnerships are essential to increase probability of successful outcomes for patients, and how IT continues to contribute to the understanding of translational medicine.

4:15 Building a Translational Biomarker Data Mining Platform: What Does it Take?

Daniel Ingber, Senior Manager, Information Systems, MedImmune

Biomarker Data Mining (BDM) will lead to a better understanding of drug action, an improved ability to understand physiological responses, and better overview of interrelationships between research and clinical data. MedImmune just completed building a BDM platform to extract, transform, and load (ETL) data from various disparate storage locations and formats such as current databases and spreadsheets, and assemble and present correlated data for exploratory analyses. This talk presents how this flexible data model supports a scalable, industrial-strength scientific data pipeline.

4:45 Breaking Through the Real World Data Storage Barriers *Sponsored by* BLUE ARC

Björn Andersson, Director of Product Marketing, BlueArc Corporation

Shared storage environments in the real world need broad and robust performance that can deliver through crunch times and scale as necessary when the characteristics of the application workload change over time. Flexibility, open architectures and the tools to support smart data migration and efficient operation are key for a well functioning system. Knowing your application characteristics is more important than relying on narrow benchmark numbers

The session will cover:

- How the unique BlueArc architecture provides the foundation needed for real world data intensive applications
- How smart tools enable you to migrate your data to storage technologies optimized for your applications
- Experience from application level testing with real world data sets

5:15 – 6:15 2010 Best of Show Awards in the Exhibit Hall

6:15 Exhibit Hall Closes

6:30 – 10:00 2010 Best Practices Awards Reception & Dinner *Sponsored by* GenomeQuest, Tessella

THURSDAY, APRIL 22

8:00 am Registration and Morning Coffee

8:45 Event Chairperson's Opening Remarks *Sponsored by* imprivata

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

Keynote Introduction: *Eric Blatte, Vice President of Sales, Commercial & Public Sector, Imprivata*

8:50 PLENARY KEYNOTE: There is No Magic, There is Only Awesome: Scientific Computing with Amazon Web Services

Deepak Singh, Ph.D., Business Development Manager, Amazon Web Services

Presentation delivered via a live, interactive videoconferencing platform.

9:30 KEYNOTE PANEL

The Future of Personal Genomics

A special plenary panel discussion featuring:

James Heywood, Co-founder and Chairman, PatientsLikeMe
Dan Vorhaus, J.D., M.A., Attorney, Robinson, Bradshaw & Hinson; Editor, Genomics Law Report
Dietrich Stephan, Ph.D., President & CEO, Ignite Institute
Kári Stefánsson, MD, Dr Med, Executive Chairman and President of Research, deCODE genetics
Kevin Davies, Ph.D., Editor-in-Chief, Bio-IT World

TRACK 1:
IT INFRASTRUCTURE — HARDWARE

10:30 Coffee Break, Poster Competition, Vendor Theater Presentations and Exhibit Viewing

****Drop off your business card at the CHI Sales Re-Sign Booth for a chance to win 1 of 2 Prizes! (Nintendo® Wii™ System or Apple® - iPod touch®)*

SEQUENCING, GENETICS DATA MANAGEMENT & GRID COMPUTING

10:55 Track Chairperson's Remarks

Bob Schoettle, Chief Marketing Officer, Panasas, Inc.

11:00 Pallas, a Computational Analysis Network

Daniel McGoldrick, Associate Bioinformatics Scientist, Information Sciences, St. Jude Children's Research Hospital

The focus of this talk will center on the development and implementation of a computational analysis network (Pallas) at St. Jude Children's Research Hospital. This system is being developed to facilitate data collection, correlation, and computation using a virtualized storage system and standards based pipeline and workflow architecture. The primary driver of this project is a proposed 'Pediatric Genome Project', in which 120 complete genomes will be sequenced using high throughput next-gen technologies. This, along with the validation studies will produce an estimated two to four pedabytes of data and tens of thousands of human interactions with this data. Attendees will understand the approach used to integrate research data and workflows across the many disciplines.

11:30 The Use of Grid Computing to Drive Data-Intensive Genetic Research

Jorge Andrade, Ph.D., Research Scientist, Bioinformatics, Lilly Singapore Center for Drug Discovery

This talk discusses the implementation of a grid computing approach that executes thousands of genotype simulations in parallel, tremendously reducing computational time. A high-resolution genetic study will be used as a case example.

12:00 pm Enabling World Class Research through Innovative Data Management Strategies

Sponsored by

Patrick Osborne, WW Business Development Manager, Scalable NAS, HP Storage

Krishna Sankavaran, Director for Research Information Systems & Technology Development, MD Anderson Cancer Center

12:15 CycleCloud: Boosting Productivity with HPC as a Service on the Cloud

Sponsored by CYCLE COMPUTING

Jason Stowe, Chief Executive Officer, Cycle Computing

Now/Next generation Sequencers, spectrometers, and other medical instruments give scientists access to larger amounts of data at cheaper costs. The cloud offers easy, inexpensive access to computing for sequence alignment, SNP detection, proteomics, and other scientific pipelines. For researchers that rely on computation to analyze these data sets, cloud computing can change the way science gets done by making it faster and more cost effective.

But successfully deploying applications to use the cloud efficiently involves a number of technical challenges. These include making applications scale, securing the clusters, and focusing on ease of use. CycleCloud makes this easy by pre-engineering clusters/pipelines to work optimally and securely on the Cloud.

With a focus on improving researcher productivity, CycleCloud creates fully-managed HPC clusters as a service with key applications pre-installed, the ability to quickly develop new analysis workflows, shared filesystems, and auto-scaling to size clusters to the multi-user workloads you place on them. This session will focus on:

- Bandwidth/data considerations for using the Cloud
- Productivity, ease of use, and security requirements
- Example walkthroughs of pre-engineered pipelines for drug discovery with Schrodinger, proteomics, and genome analysis use cases

12:30 Luncheon in the Exhibit Hall

****Drop off your business card at the CHI Sales Re-Sign Booth for a chance to win 1 of 2 Prizes! (Nintendo® Wii™ System or Apple® - iPod touch®) Winners will be announced at 1:45pm in the Exhibit Hall*

2:00 Exhibit Hall Closes

DATA STORAGE AND USAGE FOR COMPUTATIONAL TASKS

1:55 Track Chairperson's Remarks

Ercan Kamber, Ph.D., Director HPC Engineering, RAID, Inc.

2:00 Elastic-R, Toward an International Portal for On-Demand Scientific Computing, Collaboration and Resources Sharing

Karim Chine, Software Architect and Coordinator, Biocep

Elastic-R is a new portal built using the Biocep-R platform. It enables life scientists to use cloud resources seamlessly; to work with virtual scientific computing environments such as R and Scilab within the browser; to collaborate, share and reuse functions, algorithms, user interfaces, and servers; and to perform elastic distributed computing with any number of virtual machines to solve heavily computational problems. This talk will show the new Elastic-R portal in production and present the first results of that next experience

2:30 Making Systems and Services Easy: Secure File Sharing and Computational Portals

Shawn Houston, Technical Lead, Life Science Informatics, University of Alaska Fairbanks

Life Science Informatics at the University of Alaska Fairbanks provides a secure file share and a web based computational portal as interfaces to storage and computational resources. The two complimentary services are designed for ease of use, global access, and to foster research collaborations. Learn how our secure file shares and computational portal are designed with scientific research as their primary drivers.

3:00 Talk Title to be Announced

George Talbot, Senior Software Engineer, Scientific Computation, Ansaris, Inc.

4:00 Conference Adjourns

TRACK 2:
IT INFRASTRUCTURE – SOFTWARE

This Track will explore data handling and integration activities, including new approaches to collaborative data sharing, cloud computing, social networking, enterprise 2.0, open-source, Wikis, and SOA, as well as semantic web/linked data solutions for knowledge management.

TUESDAY, APRIL 20

2:00 - 6:00 pm Main Conference Registration

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

4:05 KEYNOTE INTRODUCTION:
Ronald Ranauro, Chief Executive Officer, GenomeQuest, Inc. *Sponsored by* GenomeQuest

4:15 PLENARY KEYNOTE: Drug Discovery Opportunities and Challenges—VC, Biotech and Pharma Perspectives
Christoph Westphal, M.D., Ph.D., CEO, Sitris Pharmaceuticals; Senior Vice President, Center of Excellence for External Drug Discovery, GlaxoSmithKline

5:00 - 7:00 pm Welcome Reception in the Exhibit Hall
****Drop off your business card at the CHI Sales Re-Sign Booth for a chance to win an Apple® - iPod nano®! 2 Winners will be announced at 6:45pm in the Exhibit Hall*

WEDNESDAY, APRIL 21

7:30 am Registration and Morning Coffee

8:15 Event Chairperson's Opening Remarks
Phillips Kuhl, Co-founder and President, Cambridge Healthtech Institute
Keynote Introduction: *Jamie Wyatt, Vice President and General Manager Health and Life Sciences, Netezza* *Sponsored by* NETEZZA

8:20 PLENARY KEYNOTE: Impact of HIT Stimulus on Novel Sources of Data for Research
John Halamka, M.D., M.S., CIO, Harvard Medical School

9:00 Keynote Presentation & 2010 Benjamin Franklin Award
Alex Bateman, Ph.D., Senior Investigator, Pfam Database Project, Wellcome Trust Sanger Institute

9:30 Coffee Break, Poster and Exhibit Viewing *Sponsored by* SCYNEXIS
****Drop off your business card at the CHI Sales Re-Sign Booth for a chance to win 1 of 2 Prizes! (Nintendo® Wii™ System or Apple® - iPod touch®)*

COLLABORATION & OPEN SOURCE TOOLS

10:50 Track Chairperson's Remarks *Sponsored by* GenomeQuest
Richard Resnick, Vice President, Software and Professional Services, GenomeQuest, Inc.

11:00 Test to Best - Evidence for Collaboration and Science Driven IT as Criteria for Personalized Medicine
Michael Berens, Ph.D., Director of the Cancer and Cell Biology Division, Brain Tumor Research Lab, Translational Genomics Research Institute
The Ivy Genomics-Based Medicine (Ivy G.B.M.) Project links nine U.S. research institutions and one web-applications developer, empirically testing whether genomic characteristics in individual brain tumors can inform optimal treatment options for individual patients. Learn how a combination of established platforms, open source applications, and custom software were fused to meet challenges and support the science to be performed.

11:30 Data Generation, Validation, Interpretation, & Consecration
Brian Bissett, Staff Scientist, Structural Sciences, Pfizer Global R&D
Scientists are challenged today with the multitude of data collected. Many software packages exist to analyze data. Most are designed to satisfy the requirements of the mass market. Scientists desire improvement in software packages to better reflect the needs of their laboratory. Common data analysis techniques which can improve the quality and accuracy of determinations will be discussed using tools such as Excel, as well as free open source tools.

12:00 pm caBIG® in the Trenches: Deploying an Infrastructure that Enables Collaboration *Presented by* caBIG
Mark Adams, Ph.D., National Institute of Neurological Disorder, NIH
Vast amounts of data generated by sophisticated research techniques and millions of clinical interactions represent an un-mined opportunity for collaborative research and discovery. Realization of this potential is predicated upon an interoperable IT environment to facilitate data integration and exchange in support of a wide variety of basic and clinical research efforts. This talk will describe how caBIG® (the cancer Biomedical Informatics Grid®) infrastructure enables such endeavors and discuss ongoing deployment efforts and lessons learned.

12:30 Luncheon Presentation: Microsoft BioIT Alliance: An Update *Sponsored by* Microsoft
Les Jordan, Director, BioIT Alliance & Chief Technology Strategist, Life Sciences, Microsoft Corporation
This talk will present the latest activities of the BioIT Alliance, a cross-industry group working to further integrate science and technology as a first step toward making personalized medicine a reality.

1:40 Chairperson's Remarks NOVARTIS MOLECULAR DIAGNOSTICS
Charles Lee, DVM, Ph.D., Associate Director, Diagnostics Development, Novartis Molecular Diagnostics

1:45 How myExperiment Supports Social Curation, Workflow & Protocols
Carol Goble, Ph.D., Professor of Computer Science, University of Manchester; Principal Investigator (PI), myGrid Project
myExperiment is a collaborative environment where scientists can safely publish and share data and analytical pipelines, computational workflows and experiment plans. Workflows, and other scientific objects and collections can be swapped, sorted and searched for. This talk describes why myExperiment is an extraordinary resource for bio-developers developing workflows and protocols, how we have incentivised and protected contributors of content, and how myExperiment can be embedded in a workflow platform.

GENOMICS DATA & WIKIS

2:15 Wiki-Based Data Management System for Toxicogenomics
Stephen Edwards, Ph.D., Systems Biologist, National Health and Environmental Effects Research Laboratory (NHEERL), U.S. Environmental Protection Agency
We are developing a data management system to enable systems-based toxicology at the U.S. EPA. This is built upon the WikiLIMS™ platform and is capable of housing not just genomics data but also a wide variety of toxicology data and associated experimental design information. This promotes the joint analysis of gene expression and toxicology endpoints

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TRACK 2:
IT INFRASTRUCTURE – SOFTWARE

enriching for genes associated with the outcomes of interest. A brief discussion of the system and a case study using the system will be discussed. This talk does not reflect EPA policies or EPA endorsement of any products.

2:45 Featured Presentation

The BIG Idea: Strategies to Achieve a Rapid-Learning Health System

Presented by caBIG

(Joint Talk with Tracks 2, 3, 4, 6, and 7)

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

Considerable momentum has been building in government, academe and the commercial sector towards implementation of a "rapid-learning health system". In this approach to biomedicine, research and clinical care are seamlessly linked in a virtuous circle that enables the collection and analysis of information on clinical outcomes of large populations. This talk will outline the requisite components of such a system—including a mega-community called the BIG Health Consortium™ encompassing the various sectors of biomedicine and electronic interoperability that enables the liquidity of information—and will showcase this new model in action.

3:15 Affordable and Sustainable Long Term Data Storage: A Case Study from the National Center for Biotechnology Information (NCBI)

Sponsored by

Jacob Farmer, Chief Technology Officer, Cambridge Computer Services

3:30 Refreshment Break, Poster and Exhibit Viewing

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SEMANTIC WEB & LINKED DATA TECHNOLOGIES

3:45 Talk Title to be Announced

Elgar Pichler, Ph.D., Principal Scientist, Discovery Information, AstraZeneca Pharmaceuticals, Inc.

4:15 Answering Translational Questions in Neuroscience Using Linked Data Techniques

Susie Stephens, Ph.D., Director, Biomedical Informatics, Johnson & Johnson; Co-chair, W3C Semantic Web for Health Care & Life Sciences

Researchers frequently face challenges in being able to answer translational questions of interest because data is held in disparate stores across discovery, development, and clinical practice. Linked Data has the potential to ease access to these data for scientists and managers by making the connections between the data sets explicit in the form of data links. This talk will describe how the Linked Data approach has been used to integrate a number of data sources in the area of neuroscience.

4:45 Evolution of the Electronic Lab Environment: How End-to-end Information Management Improves Communication and Collaboration to Drive Efficient R&D

Sponsored by Symyx

John McCarthy, Ph.D., Vice President Product Management Strategy, Symyx Technologies, Inc

R&D labs often spend too much time and resource collecting, managing and distributing information to scientists. As a result, many organizations are investing in multi-disciplinary electronic laboratory notebooks (ELNs) that can be used internally across the enterprise or worldwide across business ventures. The latest generation of ELNs serves as a fulcrum supporting the convergence of instruments, software and workflows. This enables scientists and project teams to share methods, samples, analysis and ideas without disrupting the way the lab works today.

5:00 Now-Generation Data Transport Technology for Life Sciences: Keeping Pace with Innovation

Sponsored by aspera

Michelle Munson, President and Co-Founder, Aspera, Inc.

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

5:15 – 6:15 2010 Best of Show Awards in the Exhibit Hall

6:15 Exhibit Hall Closes

6:30 – 10:00 2010 Best Practices Awards Reception & Dinner

Sponsored by GenomeQuest, Tessella

THURSDAY, APRIL 22

8:00 am Registration and Morning Coffee

8:45 Event Chairperson's Opening Remarks

Sponsored by imprivata

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

Keynote Introduction: *Eric Blatte, Vice President of Sales, Commercial & Public Sector, Imprivata*

8:50 PLENARY KEYNOTE: There is No Magic, There is Only Awesome: Scientific Computing with Amazon Web Services

Deepak Singh, Ph.D., Business Development Manager, Amazon Web Services

Presentation delivered via a live, interactive videoconferencing platform.

9:30 KEYNOTE PANEL

The Future of Personal Genomics

A special plenary panel discussion featuring:

James Heywood, Co-founder and Chairman, PatientsLikeMe
Dan Vorhaus, J.D., M.A., Attorney, Robinson, Bradshaw & Hinson; Editor, Genomics Law Report
Dietrich Stephan, Ph.D., President & CEO, Ignite Institute
Kári Stefánsson, MD, Dr Med, Executive Chairman and President of Research, deCODE genetics
Kevin Davies, Ph.D., Editor-in-Chief, Bio-IT World

10:30 Coffee Break, Poster Competition, Vendor Theater Presentations and Exhibit Viewing

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INFORMATION EXCHANGE, INTEGRATION & SECURITY

10:55 Track Chairperson's Remarks

Sponsored by biogen idec

Rainer Fuchs, Ph.D., VP IT R&D & Executive Director, Innovation Incubator, Biogen Idec, Inc.

11:00 Annotating Personal Genomes with SNPedia and Promethease

Mike Cariaso, Founder, SNPedia.com

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TRACK 2:
IT INFRASTRUCTURE — SOFTWARE

11:30 A Pioneer Electronic Patient Imaging Transferring and Archive System in the Pharmaceutical Industry

Judy Huang, Project Leader , Application Service, Basic Research and Biomarker Program, Merck & Co.

i-SCORE (Imaging Solution for Compliance in a Regulated Environment) is a web based software customized jointly by a technology vendor and Merck based on Merck's clinical imaging experience. This solution provides a lean and effective system for managing images in biomarker and clinical studies. In addition, Merck is the first in the pharmaceutical industry that uses this innovative on-line electronic transfer and management technology. This talk will present out experience learned throughout the entire process and how we applied sigma methodology to resolve issues.

12:00 pm Developing and Implementing caBIG® Enterprise Services

Presented by caBIG

George Komatsoulis, Ph.D., Deputy Director & Acting COO & Chief Department Informatics Operations, NIH NCI

NCI CBIIT is evolving and expanding the capabilities of its caBIG® (Cancer Bioinformatics Grid®) program and IT infrastructure by launching its first set of four enterprise services. These efforts draw on five years of experience providing software components and an infrastructure to support information exchange and integration as well as guidance from key industry standards organizations. This talk will describe benefits of the caBIG® approach as well as provide a trajectory for the overall service tapestry being developed by NCI CBIIT.

12:30 Luncheon in the Exhibit Hall

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2:00 Exhibit Hall Closes

1:55 Track Chairperson's Remarks

2:00 Pharma Informatics: Looking Beyond Our Walls

(Joint with Tracks 2 and 3)

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

Matteo di Tommas, Vice President, Research Informatics, Pfizer, Inc.

The pharmaceutical industry is under increasing pressure to increase the output from research pipelines in an environment of increasing regulatory oversight, and need for significant cost-containment. Across pharma R&D IT the trend is to focus on greater business value and partnership and lower cost. Both Pfizer & Merck are increasingly looking outside our walls to leverage expertise and develop capabilities for R&D scientists. Our joint presentation will highlight lessons learned and innovative approaches to meeting the challenge of delivering better outcomes at lower costs by changes in governance, sourcing, collaboration and architecture.

2:30 Sharing Data while Keeping Control

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

Even when appropriate data exchange standards for the integration of electronic health records, clinical trial databases and research repositories are available and adequately implemented, legal, economic and cultural issues may still be barriers for useful information exchange. Fear is everywhere: patients are concerned about insurability and employment, pharma companies want to keep a competitive advantage, researchers want to be the first to publish new results, and clinicians fear more malpractice suits. We propose an information architecture for which there is no basis for these fears.

3:00 How Federated Identity Trust Hubs Improve Identity Management in the Global Biopharmaceutical Community

Mollie Shields-Uehling, President and CEO, Headquarters Office, SAFE-BioPharma Association

Industry-wide Federated identity trust hubs are supplanting identity management within individual enterprises. Public key technology-based trust hubs assert participants' identity across the entire federation, allowing for trusted interoperability between disparate systems, sectors and geographies. This talk will describe the role of identity trust hubs in the biopharmaceutical sector and how the SAFE-BioPharma digital standard is being used for authentication and for digital signing of contracts, regulatory filings and other documents.

3:30 Safeguarding Electronic Lab Notebooks: Using Digital Timestamps to Both "Sign and Seal" Your Content Protects Its Integrity and Defends Its Authenticity

Chaka Benson, BioInformatics Developer, Scientific Computation, Ansaris, Inc.

This talk will explain how to protect data integrity within an electronic lab informatics environment. A digital time-stamping solution integrated into an electronic lab notebook (ELN) can both sign and "seal" scientific intellectual property and can irrefutably provide the exact format that a record existed in at any given point in time, proving its authenticity and ownership. This presentation will profile Ansaris Pharmaceutical's approach toward protecting its scientific intellectual property.

4:00 Conference Adjourns

GAIN FURTHER EXPOSURE: PRESENT A POSTER AND SAVE $50

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

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

Poster authors will be available to talk about their research and answer questions during the following times:

Wednesday, April 21 | 9:30-10:45am
Wednesday, April 21 | 3:15-3:45pm
Thursday, April 22 | 10:30-11:00 am

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

TRACK 3:
BIOINFORMATICS AND NEXT-GEN DATA

Themes covered in this Track include the handling of next-generation sequencing data, combining markers/tests for usage in personal genomics, GWAS, genotyping, Gene ID, biological databases, and microarrays.

TUESDAY, APRIL 20

2:00 - 6:00 pm Main Conference Registration

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Cindy Crowninshield, Conference Director, Cambridge Healthtech Institute

4:05 KEYNOTE INTRODUCTION:
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WEDNESDAY, APRIL 21

7:30 am Registration and Morning Coffee

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

9:00 Keynote Presentation & 2010 Benjamin Franklin Award
Alex Bateman, Ph.D., Senior Investigator, Pfam Database Project, Wellcome Trust Sanger Institute

9:30 Coffee Break, Poster and Exhibit Viewing *Sponsored by* SCYNEXIS
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DRIVING BIOMARKER DISCOVERY AND TRANSLATIONAL RESEARCH THROUGH EMERGING GENOMICS TECHNOLOGIES

10:50 Track Chairperson's Remarks Quantum
Chris Duffy, Product Marketing Manager, Quantum

11:00 Leverage Emerging Technologies to Manage Genomic and Clinical Data
Stephen Friend, M.D., Ph.D., President, Sage Bionetworks
Why are we blindly assuming linear data sets and pathways will be sufficient to navigate the coming onslaught of genomic and clinical data? Many remain pleased with narrative approaches to diseases where like in the middle ages their favorite gene must be at the center of the universe. This is likely to prove insufficient. Many also are assuming GWAS data sets will provide the treasure maps to understanding disease risks. Further, those starting efforts in collecting clinical data are wooed by the scale and scope of the data. All evidence from more mature "big science" efforts in other sciences like Physics would say "hold on-wait a minute." This lecture will frame four tenets on which we will need to operate if we are going to leverage the emerging genomics technologies coupled to robust clinical datasets.

11:30 Enabling Translational Research and Biomarker Discovery through Informatics and Genomics
Jacob de Vlieg, Ph.D., Global Head, Molecular Design & Informatics, Schering-Plough/MSD
Genomics and bioinformatics are well-established scientific disciplines in pharmaceutical research. Vast amounts of structural information on targets and target-ligand complexes and the availability of complete genome sequences have stimulated tremendous efforts to rationalize the drug design process.

While it's believed that 'omics' and informatics may create opportunities to speed up the process and provide novel design processes, a concern of low productivity and high late stage attrition will continue to challenge the industry. This talk will explore how R&D approaches and genomics-based methods can be integrated efficiently to address these concerns. Advances in bioinformatics, cheminformatics, and genomics technologies in drug discovery and development will be discussed.

12:00 pm Pipelining Your NGS Data *Sponsored by* accelrys
Nancy Miller Latimer, M.S., Senior Product Manager, Biological Sciences and Analytics, Accelrys
Has data pipelining become the darling of next-generation sequencing (NGS) analysis challenges? We present a web-based NGS workbench for variation detection on reads data generated from 3 different NGS platforms, Illumina, SOLiD, and 454, that caters to the novice but also has the flexibility required for the expert. We will look underneath the covers at a popular common pipelining software application that drives the workbench. We also discuss a model for deployment of the workbench to the cloud environment.

12:15 RISe: An Approach to Combine Online Transaction Processing and Semantic Information in a Research Informatics Platform *Sponsored by* Infosys
Ajay Shah, Ph.D., MBA, PMP, Director of Research Informatics, Elan Pharmaceuticals Inc.
Elan and Infosys are building an integrated research data integration platform called RISe (Research Informatics System at élan). RISe enables integration of diverse experimental, computational, in-house and external data for registration, inventory tracking, workflow and analysis. RISe enables research analytics dashboards, collaboration and knowledge management to enhance research productivity. RISe utilizes a unique software architecture that combines multiple approaches to database schemas to achieve the integration. Flexibility of the definition of biological entities is accommodated via Entity-Attribute-Value model, efficiency-prioritized OLTP schema is used for inventory management and RDF schema is used for semantic data integration. RISe utilizes a workflow driven, multi-tiered, SOA based architecture built on the Microsoft.NET platform and SharePoint client.

12:30 Luncheon Presentation: Empowering Researchers with Hypothesis-Driven Data Exploration
Jian Wang, Ph.D., CEO, BioFortis Inc. *Sponsored by* BioFortis
A significant bottleneck on productivity in translational research is the inability for researchers to directly interrogate data by themselves. Instead, the standard workflow is often to rely heavily on informatics specialists to answer questions, which has limitations in many ways. As a repeatable, best-practice measure, we present a novel process & case study to demonstrate how, with the right tools, translational researchers can be more self-sufficient, efficient and productive, while enabling informatics specialists to focus more on higher value contributions instead of mundane ad hoc data manipulations.

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TRACK 3: BIOINFORMATICS AND NEXT-GEN DATA

DATA MANAGEMENT AND INTEGRATION STRATEGIES

1:40 Chairperson's Remarks

Richard Golob, President and Chief Executive Officer, GGA Software Services, LLC

1:45 CASTOR QC - A Database Approach for Handling Large Genomic Data Sets

Marc Bouffard, M.Sc., Senior Bioninformatician, Montreal Heart Institute and Genome Quebec Pharmacogenomics Center

Current genetic analysis solutions are overwhelmed by the large volume of data produced by current generation sequencing and genotyping technologies. Next generation sequencing is significantly increasing the amount of data produced. New solutions must be developed to transform this data into useful knowledge. The CASTOR QC (Comprehensive Analysis and STORage) project uses a novel database-centric approach to leverage both data structures and database technologies to enable rapid analysis of genotypic and phenotypic data. Attendees will learn about data and data processing, how data converts into knowledge, and what steps can be taken in order to transform this data into a storage and analysis friendly format.

2:15 Success Strategies in Translational Medicine: The Best Decisions Are Made with the Best Information

Jonathan Usuka, Ph.D., M.B.A., Director, Research & Development, Celgene Corporation

In this discussion, we will examine specific commercial successes in translational research for the inflammation and oncology therapy areas. We will review the ingredients for success as indicated in the underlying strategies - emerging criteria for a successful biomarker effort, such as diagnostic partnering, clinical sample repositories, patient consent, and increased reimbursement for increased efficacy or safety. The economic effects of a fragmented market resulting from personalized therapy will be examined in the context of the declining blockbuster model.

2:45 Featured Presentation

The BIG Idea: Strategies to Achieve a Rapid-Learning Health System

Presented by caBIG

(Joint Talk with Tracks 2, 3, 4, 6, and 7)

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

Considerable momentum has been building in government, academe and the commercial sector towards implementation of a "rapid-learning health system". In this approach to biomedicine, research and clinical care are seamlessly linked in a virtuous circle that enables the collection and analysis of information on clinical outcomes of large populations. This talk will outline the requisite components of such a system—including a mega-community called the BIG Health Consortium™ encompassing the various sectors of biomedicine and electronic interoperability that enables the liquidity of information—and will showcase this new model in action.

3:15 Refreshment Break, Poster and Exhibit Viewing

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3:45 Cancer Pharmacogenomics Data Integration: Challenges, Promises and its Application to Cancer Drug Discovery

Lihua Yu, Ph.D., Principal Scientist II, Cancer Discovery, AstraZeneca R&D

AstraZeneca Cancer has developed a cancer pharmacogenomics data integration system. The system manages multi-dimensional data (compound profiling data across cancer cell lines, gene expression, aCGH and mutation data of cancer cell lines) and is widely used across cancer drug discovery. We will discuss the system's design principles and key functionalities, drug discovery projects where this system has been used, and challenges & lessons learned.

4:15 Engineering Hope: Conducting Successful Translational Medicine in Oncology and Immunology Biopharmaceutical Development

Eric Perakslis, Ph.D., Vice President, R&D Informatics, Johnson & Johnson Pharmaceutical R&D

Delivering successfully on the promise of translational medicine and science, the Johnson & Johnson Pharmaceutical group has reinvented the approach to informatics. By centralizing the function and bringing all data into scope for a single team, significant strides have been made in systems, processes and value delivery. One technical outcome is the tranSMART data warehouse and analytics system, enabling superior decision support across the R&D process. The process, social engineering and systems methodology approaches will be detailed in this talk.

4:45 NGS: The Bioinformatics Bottleneck *Sponsored by* GenomeQuest

Richard Resnick, Vice President, Software and Professional Services, GenomeQuest, Inc.

Next-generation sequencing instruments are being placed by the hundreds while their throughput increases every quarter. Massive disk arrays, hundreds of thousands of cores of processing power, and tens of new mapping algorithms have been introduced to keep up. And yet the vast majority of researchers still wait months after their sequencing runs to get analyses to drive their science forward, while bioinformaticians scurry to keep pace. We will briefly present a free online NGS sequence data management (SDM) platform on the cloud produces interactive, mineable, shareable NGS analyses on not one but thousands of genomes, with an open API to allow bioinformaticians to develop and publish their own workflows for some or all to use.

5:15 – 6:15 2010 Best of Show Awards in the Exhibit Hall

6:15 Exhibit Hall Closes

6:30 – 10:00 2010 Best Practices Awards Reception & Dinner *Sponsored by* GenomeQuest, Tessella

THURSDAY, APRIL 22

8:00 am Registration and Morning Coffee

8:45 Event Chairperson's Opening Remarks *Sponsored by* imprivata

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

Keynote Introduction: *Eric Blatte, Vice President of Sales, Commercial & Public Sector, Imprivata*

8:50 PLENARY KEYNOTE: There is No Magic, There is Only Awesome: Scientific Computing with Amazon Web Services

Deepak Singh, Ph.D., Business Development Manager, Amazon Web Services

Presentation delivered via a live, interactive videoconferencing platform.

9:30 KEYNOTE PANEL

The Future of Personal Genomics

A special plenary panel discussion featuring:

James Heywood, Co-founder and Chairman, PatientsLikeMe
Dan Vorhaus, J.D., M.A., Attorney, Robinson, Bradshaw & Hinson; Editor, Genomics Law Report
Dietrich Stephan, Ph.D., President & CEO, Ignite Institute
Kári Stefánsson, MD, Dr Med, Executive Chairman and President of Research, deCODE genetics
Kevin Davies, Ph.D., Editor-in-Chief, Bio-IT World

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TRACK 3:
BIOINFORMATICS AND NEXT-GEN DATA

10:30 Coffee Break, Poster Competition, Vendor Theater Presentations and Exhibit Viewing

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APPLICATION OF DATA

10:55 Track Chairperson's Remarks *Sponsored by* GenomeQuest

Richard Resnick, Vice President, Software and Professional Services, GenomeQuest, Inc.

11:00 Unbiased Prioritization of Mutations in Cancer Genomes

David Dooling, Ph.D., Director, Analysis Developers, Laboratory Information Management Systems (LIMS), and the Information Systems Groups, The Genome Center at Washington University in St. Louis School of Medicine

With the advent of massively-parallel sequencing technologies, the rate of discovery of mutations in cancer genomics far outstrips our ability to attribute functional significance to the mutations. Short of a breakthrough in functional genomics, other methods will be needed to, at the very least, narrow down the massive number of potentially important mutations into a more manageable set of mutations that are clinically relevant, i.e., so-called driver mutations. Using massive data sets on dozens of tumors and matched normals, a highly-scalable information management system, and machine learning algorithms, we have developed a system that can integrate sequence reads, array data, clinical information, phenotypic data, genomic annotation, and cellular pathway databases to assign significance scores to the millions of mutations found in cancer genomes.

11:30 Combining Multiple Signals to Identify the Causal Variant within Regions Under Positive Natural Selection

Pardis Sabeti, M.D., D.Phil., M.Sc., Assistant Professor, Center for Systems Biology and Department of Organismic and Evolutionary Biology, Harvard University

The genomes of humans and other species contain hundreds of regions with evidence of recent positive natural selection, yet, for all but a handful of cases, the underlying advantageous mutation remains unknown. This talk illustrates the Composite of Multiple Signals (CMS), a novel method developed and validated, that combines tests for multiple signals of selection and provides 10-100x better positional resolution than any individual signal.

12:00 pm Integrative Biological Analysis of Public and Proprietary Microarray, GWAS and Nextgen Sequencing Dat *Sponsored by* NEXTBIO

Ilya Kupershmidt, Cofounder and VP Products, NextBio

Ability to integrate and mine public and proprietary datasets from microarray and next-gen technologies is central to modern day biology. In this talk I will describe the latest evolution of NextBio platform to support integrative biological analysis and correlation of data from gene expression, DNA copy-number, resequencing, epigenetic and genotyping studies in order to explore gene function and mechanisms of disease development. Meta-analysis techniques combining these diverse data types within the context of genome structure and pathway information will be explored.

12:15 Highly Efficient Bioinformatics Solutions on Amazon Web Services offered by Omixon Biocomputing Solutions *Sponsored by* OMIXON BIOCOMPUTING SOLUTIONS

Miklos Csuros, Ph.D., Associate Professor, Informatics Department and Operations Research, Université de Montréal

Omixon offers computationally and cost efficient NGS analysis web services such as a highly sensitive short read gapped alignment application called Crema. BAYGEN Research Institute used this tool to analyze genome sequences from 14 P. acnes isolates sequenced by ABI SOLiD V3.5 sequencer. The attendees will learn how this tool is used to find SNPs, insertions and deletions, in a number of genes encoding putative virulence factors. We present a comparative study to align 135 million reads from Ciona savigny with Crema as well.

Omixon aims to provide the most cost efficient solutions for the most computationally intensive problems.

12:30 Luncheon in the Exhibit Hall

****Drop off your business card at the CHI Sales Re-Sign Booth for a chance to win 1 of 2 Prizes! (Nintendo® Wii™ System or Apple® - iPod touch®) Winners will be announced at 1:45pm in the Exhibit Hall*

2:00 Exhibit Hall Closes

1:55 Track Chairperson's Remarks

2:00 Pharma Informatics: Looking Beyond Our Walls

(Joint with Tracks 2 and 3)

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

Matteo di Tommas, Vice President, Research Informatics, Pfizer, Inc.

The pharmaceutical industry is under increasing pressure to increase the output from research pipelines in an environment of increasing regulatory oversight, and need for significant cost-containment. Across pharma R&D IT the trend is to focus on greater business value and partnership and lower cost. Both Pfizer & Merck are increasingly looking outside our walls to leverage expertise and develop capabilities for R&D scientists. Our joint presentation will highlight lessons learned and innovative approaches to meeting the challenge of delivering better outcomes at lower costs by changes in governance, sourcing, collaboration and architecture.

2:30 What is Still Required for Semantic Linked Data to Advance Biomedical & Pharmaceutical R&D?

Eric Neumann, Ph.D., Director, Clinical Semantics Group; Former Chair, W3C Healthcare and Life Sciences Interest Group

Linked Data standards have been quite successful in some areas recently (UK public data), and many powerful demonstrations have been compiled around Linked Open Data (LOD). However, for them to be practical and powerful in scientific and enterprise R&D, some additional features and capabilities need to be developed and utilized. They will also need to align with existing installed technologies in order to provide a way forwards and to gain vendor acceptance. These issues will be further elaborated on and proposed solutions to help realize the vision of semantic integration through Linked Data will be offered.

3:00 Toward Meaningful Whole-Genome Interpretation with Open Access Tools from the Genome Commons

Reece Hart, Ph.D., Chief Scientist, Genome Commons, UC Berkeley QB3 and Center for Computational Biology

The widespread availability of personal genomic data is imminent, yet we are ill-prepared to reap the full personal, scientific, clinical, and social benefits from these data. Among the many barriers to holistic genome interpretation, four are prominent: 1) isolation of genotype and phenotype data; 2) lack of tools that are easily interoperable; 3) insufficient scientific methods for the analysis of variants; and 4) unsettled ethical and social policy issues. The Genome Commons is a nascent collaboration among faculty from UC Berkeley and UC San Francisco that will provide freely accessible databases, analytical tools, and scientific methods for the interpretation of human genomic data. Our collaborators bring expertise in computational biology, computer science, statistics, clinical genetics, and ethics. While scientific utility is our immediate goal, we envision that the Genome Commons will provide a foundation for clinical tools and a repository for studies of human variation. In this talk, I will introduce the Genome Commons, describe our preliminary results, and present the outlook for this project.

4:00 Conference Adjourns

TRACK 4:
SYSTEMS AND PREDICTIVE BIOLOGY

The explosion of "omic" data has energized mathematical modeling and simulation of biological systems. Track 4 provides in-depth modeling approaches from *in silico* to *in vivo* with an emphasis on drug discovery, ADME predictions, and systems medicine.

TUESDAY, APRIL 20

2:00 - 6:00 pm Main Conference Registration

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

4:05 KEYNOTE INTRODUCTION:
Ronald Ranauro, Chief Executive Officer, GenomeQuest, Inc. *Sponsored by* GenomeQuest

4:15 PLENARY KEYNOTE: Drug Discovery Opportunities and Challenges—VC, Biotech and Pharma Perspectives
Christoph Westphal, M.D., Ph.D., CEO, Sitris Pharmaceuticals; Senior Vice President, Center of Excellence for External Drug Discovery, GlaxoSmithKline

5:00 - 7:00 pm Welcome Reception in the Exhibit Hall
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WEDNESDAY, APRIL 21

7:30 am Registration and Morning Coffee

8:15 Event Chairperson's Opening Remarks
Phillips Kuhl, Co-founder and President, Cambridge Healthtech Institute
Keynote Introduction: *Jamie Wyatt, Vice President and General Manager Health and Life Sciences, Netezza* *Sponsored by* NETEZZA

8:20 PLENARY KEYNOTE: Impact of HIT Stimulus on Novel Sources of Data for Research
John Halamka, M.D., M.S., CIO, Harvard Medical School

9:00 Keynote Presentation & 2010 Benjamin Franklin Award
Alex Bateman, Ph.D., Senior Investigator, Pfam Database Project, Wellcome Trust Sanger Institute

9:30 Coffee Break, Poster and Exhibit Viewing *Sponsored by* SCYNEXIS
****Drop off your business card at the CHI Sales Re-Sign Booth for a chance to win 1 of 2 Prizes! (Nintendo® Wii™ System or Apple® - iPod touch®)*

DATA MODELING: ENABLING SYSTEMS MEDICINE

10:50 Track Chairperson's Remarks

11:00 Featured Speaker

A Roadmap for Systems Medicine of Pulmonary Diseases
Charles Auffray, Ph.D., Research Director, Functional Genomics and Systems Biology for Health, CNRS Institute of Biological Sciences
Complex inflammatory diseases such as chronic obstructive pulmonary disease and asthma represent a major health burden worldwide. The primary causes and mechanisms of these diseases remain to a large extent unknown, preventing the development of more efficient diagnosis and treatment. An integrative systems biology research strategy is being developed to overcome these limitations. It relies on careful experimental design for the collection and integration of relevant data amenable to computational modeling and simulation, complying with the roadmap for systems medicine.

11:30 Systems Neuromedicine: Connecting the Periphery to the CNS
Timothy Mhyre, Ph.D., Assistant Professor, Neuroscience, Georgetown University
Many neurological disorders are systemic but such peripheral features often elude detection. We are exploiting a systems approach to define the peripheral characteristics of neurological disorders by analyzing blood. In the presentation our work on Alzheimer and Parkinson disease will be discussed to illustrate the approach. The scientific and clinical impact of the systems neuromedicine approach will be discussed.

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

12:30 Luncheon Presentation *Sponsored by* GLS GenoLogics
A Multi-Center Translational Research Informatics Platform Based on Cloud and Semantic Web Technologies for NCI EDRN Early Detection Cancer Research Program
Daniel Crichton, Informatics PI, NASA's Jet Propulsion Laboratories
James DeGreef, Vice President Market Strategy, GenoLogics Life Sciences Software
An end-to-end translational research informatics solution from discovery to validation to knowledge management, provisioned by NASA JPL and GenoLogics for NCI EDRN and Canary Foundation Lung Cancer Research Program, leveraging cloud computing and semantic web technologies.

DATA GENERATION: GOOD MODELS START WITH GOOD DATA

1:40 Chairperson's Remarks

1:45 Advancing Predictive and Quantitative Personalized Medicine by Inferring Cause and Effect in Clinical and Molecular Data
Paul McDonagh, Ph.D., VP, Discovery Biology, Gene Network Sciences
With a simple blood test, newborn infants are tested for harmful metabolic conditions that aren't apparent at birth. These simple and effective personalized medicine tests prevent future suffering. We show that they can also be used to illustrate logic that can be captured in mathematics and consistently applied to 10,000's of variables, including genetics, gene expression and clinical outcomes collected from existing patients. The insights that come from this integrated data analysis include the ability to find new therapeutic targets, surrogate endpoints and patient stratification markers.

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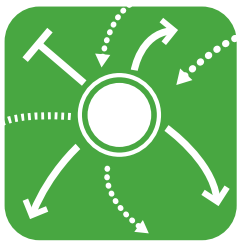
TRACK 4:
SYSTEMS AND PREDICTIVE BIOLOGY



2:15 Data Integration not Isolation: The Role of Computational Systems Biology in the Discovery of Antibody Therapeutics

John M. Burke, Ph.D., Associate Director, Systems Biology, Boehringer Ingelheim Pharmaceuticals

Using this validated model, simulations predict that the effective half-life of higher binding affinity antibodies assumes the half-life of mechanistically irrelevant compartment and is insensitive to half-life extension, while the effective half-life of lower binding affinity antibodies are sensitive to half-life extension. This suggests that increasing affinities would make candidates less efficacious by reducing effective half-life, while half-life extension and affinity 'de-maturation' of low affinity therapeutics could potentially enhance efficacy. In an integrated fashion, Computational Systems Biology analysis offers suggestions to the project team to determine optimal binding affinities, doses, and optimal dosing strategies to maintain high efficacy, low cost of good and shorten timelines.

2:45 Featured Presentation

The BIG Idea: Strategies to Achieve a Rapid-Learning Health System

Presented by caBIG

(Joint Talk with Tracks 2, 3, 4, 6, and 7)

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

Considerable momentum has been building in government, academe and the commercial sector towards implementation of a "rapid-learning health system". In this approach to biomedicine, research and clinical care are seamlessly linked in a virtuous circle that enables the collection and analysis of information on clinical outcomes of large populations. This talk will outline the requisite components of such a system—including a mega-community called the BIG Health Consortium™ encompassing the various sectors of biomedicine and electronic interoperability that enables the liquidity of information—and will showcase this new model in action.

3:15 Refreshment Break, Poster and Exhibit Viewing

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DATA INTEGRATION: MODELING DISPARATE "OMIC" SOURCES

3:45 Multi-Scale Cancer Modeling

Thomas S. Deisboeck, M.D., Associate Professor, Radiology, Massachusetts General Hospital, Harvard Medical School

This talk will focus on modeling cancer as a complex dynamic, multi-scaled biosystem where macroscopic behavior is determined by microscopic cell-cell and cell-microenvironment interactions that in turn are guided by dynamics on the sub-cellular level.

4:15 Controlling the Human Proteome: What do we Know and What can we do?

Florian Nigsch, Ph.D., Postdoctoral Fellow, Lead Discovery Informatics, Novartis Institute for Biomedical Research

Our efforts to unite several chemical biology sources of compound activity information led to a repository that holds 20 million activity records of 3 million distinct compounds. This data was placed into a rich biological context through extensive target normalization and the use of GeneGo MetaBase to provide pathways, regulatory network, disease and other relevant information for drug discovery. An in-depth analysis reveals pharmacological hotspots and provides information on the global coverage of the human proteome, as well as new opportunities for drug discovery.

4:45 Knowledge Management: Issues and Solutions from the Vendor's Perspective

Sponsored by GeneGo

Yuri Nikolsky, Ph.D., CEO, GeneGo, Inc.

The shift of life science IT focus to "knowledge management" involves alignment of terms, vocabularies and ontologies between different fields and sources, development of novel visualization and analytical tools and standardization of semantics and annotation procedures throughout drug discovery. I will describe the challenges and possible solutions from a vendor's perspective.

5:00 – 5:15 Sponsored Presentation *(Opportunity Available)*

5:15 – 6:15 2010 Best of Show Awards in the Exhibit Hall

6:15 Exhibit Hall Closes

6:30 – 10:00 2010 Best Practices Awards Reception & Dinner

Sponsored by GenomeQuest, Tessella

THURSDAY, APRIL 22

8:00 am Registration and Morning Coffee

8:45 Event Chairperson's Opening Remarks

Sponsored by imprivata

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

Keynote Introduction: *Eric Blatte, Vice President of Sales, Commercial & Public Sector, Imprivata*

8:50 PLENARY KEYNOTE: There is No Magic, There is Only Awesome: Scientific Computing with Amazon Web Services

Deepak Singh, Ph.D., Business Development Manager, Amazon Web Services

Presentation delivered via a live, interactive videoconferencing platform.

9:30 KEYNOTE PANEL

The Future of Personal Genomics

A special plenary panel discussion featuring:

James Heywood, Co-founder and Chairman, PatientsLikeMe
Dan Vorhaus, J.D., M.A., Attorney, Robinson, Bradshaw & Hinson; Editor, Genomics Law Report
Dietrich Stephan, Ph.D., President & CEO, Ignite Institute
Kári Stefánsson, MD, Dr Med, Executive Chairman and President of Research, deCODE genetics
Kevin Davies, Ph.D., Editor-in-Chief, Bio-IT World

10:30 Coffee Break, Poster Competition, Vendor Theater Presentations and Exhibit Viewing

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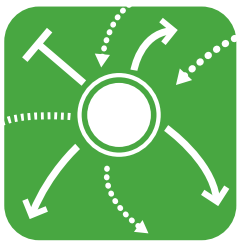
TRACK 4:
SYSTEMS AND PREDICTIVE BIOLOGY



DATA INTEGRATION: MODELING DISPARATE "OMIC" SOURCES

10:55 Track Chairperson's Remarks

11:00 Integrative Genomics Approach Identifies Candidate Causal Gene Mediators of Sleep/Wake Phenotypes

Joshua Millstein, Ph.D., Biostatistics, Senior Scientist, Statistical Genetics, Sage Bionetworks

Despite the high prevalence of sleep disorders and overwhelming evidence linking sleep to a myriad of diverse diseases, including diabetes, cardiovascular disease, obesity, and depression, there has been slow progress identifying biomolecular determinants of sleep/wake patterns. We have broken new ground with a data-driven integrative genomics approach investigating the underlying genetics of sleep in mammals by measuring sleep phenotypes, genome-wide genotypes, and transcriptome-wide expression in three brain regions, frontal cortex, hypothalamus, and thalamus in over 300 mice.

11:30 Developing Combinatorial Biomarker Panels for End-Stage Organ Failures

Raymond Ng, CIO, PROOF Centre; Professor of Computer Science, University of British Columbia

The PROOF Centre is a Canadian National Centre of Excellence, with a mandate to develop biomarker panels for clinical use. In this talk, we will give an overview of our projects for heart, kidney and lung failures. We describe a general combinatorial approach which involves transciptomics, proteomics and metabolomics data. If time permits, we will highlight the importance of data cleansing in biomarker discovery.

12:00pm Informatics Best Practices for Pre-GLP Safety Assessment: Results of Pharma R&D Expert Interviews and Industry Survey

Ernest D. Bush, Ph.D., VP & Research Director, Cambridge Healthtech Associates (CHA)

In order to better understand current strategies and define best or optimal practices in pre-GLP safety assessment, CHA recently conducted a project to explore standard and emerging procedures in safety assessment before the initiation of expensive and resource consuming in vivo GLP toxicology studies. Of particular interest were the use and/or non-use of informatics tools to help predict safety outcomes very early in the drug discovery process. This presentation will focus on the results from interviews of industry experts and the complementary findings from a broad survey of current practitioners in the field; with special focus on what informatics approaches have demonstrated value added insights to pre-GLP safety evaluation.

12:30 Luncheon in the Exhibit Hall

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2:00 Exhibit Hall Closes

DATA VALIDATION: FROM BENCHTOP TO CLINICAL OUTCOMES

1:55 Track Chairperson's Remarks

2:00 Systems Biology & Mode of Action Based Risk Assessment

Stephen Edwards, Ph.D., Systems Biologist, National Health and Environmental Effects Research Laboratory (NHEERL), U.S. Environmental Protection Agency

The application of systems biology for risk assessment of environmental chemicals is a natural extension of its use in pharmaceutical research. The basis for this is the concept of a key event network that builds on existing mode of action frameworks for risk assessment. The application of molecular networks derived from gene expression data for prediction of susceptible subpopulations of asthmatics and for characterization of disruption of the hypothalamic-pituitary-gonadal axis in fish will be presented.

2:30 Using Computational Neuropharmacology to Support Research & Development in CNS Disorders

Hugo Geerts, Ph.D., COO, Computational Neuropharmacology, In Silico Biosciences

Computational Neuropharmacology is a mathematical and mechanistic CNS disease model, based upon the physiology of brain targets, the interaction of drugs with these targets and the introduction of human pathology from imaging, genotypic and postmortem data. This platform for schizophrenia and cognitive disorders is retrospectively validated by correlating the model outcomes with actual clinical effects of antipsychotics on well-defined clinical scales. This technology is a powerful tool to support a variety of decision processes in preclinical and clinical CNS R&D.

3:00 Design of Surrogate Safety Biomarkers Using Pre-Clinical Poly Pharmacology and *in vivo* Data by a Novel Multi-Dimensional Data Mining Technology (KEM)

Mohammad Afshar, M.D., Ph.D., CEO, Management, Ariana Pharmaceuticals

Development of surrogate Safety Markers is a key driver to increasing success in clinical trials. The contrast between the small number of patients versus the large number of parameters observed pushes existing statistical methods to their limits. Logic based data mining techniques such as KEM has been shown to be effective in early identification of robust safety signatures. Examples will be shown.

3:30 Safety Informatics: Enhancing Quality of Integrated Risk Assessment

Dmitri Mikhailov, Ph.D., Center for Proteomic Chemistry, Novartis Institutes for Biomedical Research, Inc.

Novartis has established informatics approaches to enable integrated safety assessment in discovery phase. These include decision support applications for prospective risk evaluation based on broad in vitro safety pharmacology panel. In addition, we have developed and applied predictive chemogenomics methods to generate off-target mechanistic hypotheses for compounds that have shown toxicity in preclinical and clinical studies and to suggest possible follow up studies. The talk will include several case studies.

4:00 Conference Adjourns

TRACK 5: CHEMINFORMATICS AND COMPUTER-AIDED MODELING

Track 5 explores partnerships and collaborations to further drug discovery, open source chemistry, recent advances in cheminformatics, modeling for safety, using biological and chemical information to guide hit-to-lead phase and lead optimization, and repurposing drugs by applying 21st century tools to find new targets.

TUESDAY, APRIL 20

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Cindy Crowninshield, Conference Director, Cambridge Healthtech Institute

4:05 KEYNOTE INTRODUCTION:
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4:15 PLENARY KEYNOTE: Drug Discovery Opportunities and Challenges—VC, Biotech and Pharma Perspectives
Christoph Westphal, M.D., Ph.D., CEO, Sitris Pharmaceuticals; Senior Vice President, Center of Excellence for External Drug Discovery, GlaxoSmithKline

5:00 - 7:00 pm Welcome Reception in the Exhibit Hall
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WEDNESDAY, APRIL 21

7:30 am Registration and Morning Coffee

8:15 Event Chairperson's Opening Remarks
Phillips Kuhl, Co-founder and President, Cambridge Healthtech Institute
Keynote Introduction: *Jamie Wyatt, Vice President and General Manager Health and Life Sciences, Netezza* *Sponsored by* NETEZZA

8:20 PLENARY KEYNOTE: Impact of HIT Stimulus on Novel Sources of Data for Research
John Halamka, M.D., M.S., CIO, Harvard Medical School

9:00 Keynote Presentation & 2010 Benjamin Franklin Award
Alex Bateman, Ph.D., Senior Investigator, Pfam Database Project, Wellcome Trust Sanger Institute

9:30 Coffee Break, Poster and Exhibit Viewing *Sponsored by* SCYNEXIS
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PARTNERSHIPS AND COLLABORATIONS: A NEW PARADIGM IN DRUG DISCOVERY

10:50 Track Chairperson's Remarks
John Overington, Ph.D., Team Leader, Computational Chemical Biology, EMBL-EBI

11:00 Partnerships and Collaborations: A New Paradigm in Drug Discovery
Barbara Mittleman, M.D., Director, Program on Public-Private Partnerships, Office of Science Policy, NIH
Dr. Mittleman will discuss how the NIH views and implements partnerships with entities in industry, in the non-profit sector, and with other government agencies to accomplish the NIH's mission to improve the public health through biomedical research. Drug development is an important component of accomplishing our mission. Partnerships focused on developing and qualifying biomarkers, in developing high throughput screening methods, in identifying novel disease targets and development schemata, etc. will be discussed in the setting of both pre-competitive and competitive approaches.

11:30 Precompetitive Collaborative Opportunities in Cheminformatics
Ramesh Durvasula, Ph.D., Director, Chemistry Informatics, Research Informatics & Automation, Bristol-Myers Squibb
In early 2008, work began in earnest on the creation of a precompetitive collaboration legal construct, the Pistoia Alliance. Initially targeted toward the identification of cross-pharma opportunities in chemistry informatics (common processes, data models, etc.), the focus rapidly expanded to include all components of the research workflow as the group expanded. Currently, there are active work streams spanning chemistry, biology, and knowledge management. This talk will review past, present, and emerging pre-competitive cheminformatics opportunities within and outside the Pistoia Alliance construct.

12:00 pm Scientific Informatics Outsourcing – New Trend in the Life Sciences Industry
Richard Golob, CEO, GGA Software Services LLC
The historical paradigm in the life sciences industry has been to use outsourcing companies primarily for non-scientific informatics activities. However, with the advent of outsourcing companies that have strong scientific and mathematical expertise, this paradigm is shifting towards scientific informatics outsourcing, from software engineering, algorithm development, and knowledge management to testing, support and maintenance, and scientific BPO. Through scientific informatics outsourcing, life science companies have an opportunity to extend their workbench in a cost-effective way and to complement and supplement their internal teams.

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

OPEN ACCESS CHEMISTRY AND BIOLOGY

1:40 Chairperson's Remarks
Antony Williams,Ph.D., FRSC, VP, Strategic Development, ChemSpider, Royal Society of Chemistry

1:45 Linking Biology and Chemistry Spaces - Prospects for Improved Drug Discovery and Development
John Overington, Ph.D., Team Leader, Computational Chemical Biology, EMBL-EBI
Large-scale databases of small molecule and target interactions can now be analyzed to uncover fundamental patterns and constraints in drug-like and druggable target space. These rules can be used to prioritize likely successful targets, to identify compounds for screening studies, and also provide the basis for data integration tools for translational drug discovery.

2:15 Chemical Information Mining Today & Tomorrow
Debra Banville, Ph.D., Information Analyst, Discovery Information, AstraZeneca Pharmaceuticals
Chemical information mining is rapidly developing in the public sector as a way to find and share key information about chemical entities within a broad community. This talk will focus on the latest developments and project into the future the potential paradigm shift we could expect. This presentation will give the audience an update on what's currently available and will offer insight into how these developments will change the way we search and interact with scientific literature in general.

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TRACK 5: CHEMINFORMATICS AND COMPUTER-AIDED MODELING

2:45 Machine Learning Approaches for Molecular Modeling

Ramgopal Mettu, Assistant Professor, Electrical and Computer Engineering, UMass Amherst

Often in molecular modeling we wish to study a particular target under a number of different simulation conditions (e.g. testing a database of ligands, or probing for binding sites). In recent years, mining and inference techniques from the machine learning community have become widely used for molecular modeling. In this talk, I will give a overview of the technical ideas behind these methods, and discuss their application to ligand-binding prediction, computational mutagenesis, and protein design.

3:15 Refreshment Break, Poster and Exhibit Viewing

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RECENT ADVANCES IN CHEMINFORMATICS AND SCREENING

3:45 Knowledge-Based Compound Perturbation of Biological Networks

Meir Glick, Ph.D., Research Investigator II, Center for Proteomic Chemistry, Novartis

Literature-curated networks of biological interactions are traditionally used to expand our understanding of cellular and pathway biology. In this work, networks are used as the organizing principle for target and compound selection to create focused screening libraries. We demonstrate the use of network-focused libraries in assay development, tool compound selection, lead discovery, and potential chemical combinations.

4:15 Integration with PubChem Biological Activity Reporting on Small Molecules for Better Project Decision Making

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

We will present how a programmatic integration with PubChem compound, assay and activity data has enabled faster and better decision making on which hits to take forward in a small molecule probe development campaign. There is a wealth of data being deposited in PubChem and manually browsing through is really time consuming and cumbersome. A unique pivot report of compounds against known assays for biological activity that is generated in real-time on your hits allows this process to be efficient and effective.

4:45 Bioassay Ontology and Software Tools to Integrate and Analyze Diverse Data Sets

Stephan Schurer, Ph.D., Assistant Professor, Pharmacology and Center for Computational Sciences, University of Miami

Increasingly large and diverse data sets are being generated by publically funded screening centers using various high- and low-throughput screening technologies. Much of this data is accessible, for example via PubChem, the largest public repository of small molecule screening results, currently covering over 1,500 assays for 370,000 compounds. The number of assays can be expected to grow more than 10 fold during the next five years. The utility of this invaluable resource is currently limited, because the knowledge contained in complex and diverse bioassay data sets is not formalized and therefore cannot be accessed for comprehensive computational analysis or integration with other data sources. This proposal is to attack this limitation. For the past ten years ontologies have been developed by biologists to facilitate the analysis and discussion of the massive amounts of information emerging from the various genome projects. An ontology is a controlled vocabulary representation of the objects and concepts and their properties and relationships. The purpose is to model and share domain-specific knowledge so that software agents can automatically extract and associate information. The aim of this proposal is to develop a bioassay ontology, software tools, and to demonstrate their utility. The bioassay ontology will coherently describe diverse biological assays (such as those in PubChem) with a focus on complex cell-based assays and in particular high-content screening data. Software support and development includes modules to build ontology terms and to curate data sets, tools to map the ontology onto screening experiments and other ontologies, and tools to standardize, reformat, and aggregate data sets in the context of the ontology. We will demonstrate the utility of our approach by creating a PubChemderived database and making it available to the community via a search interface. The ontology and software tools will facilitate the analysis of bioassay screening data in various contexts, for example signaling or metabolic pathways and indirectly human disease. The tools will enable one to extract data sets for modeling specific interactions between perturbing agents and biological targets (or pathways), or to model assay technology-dependent interferences. End user software needs to provide ease of use for biologists and chemical biologists to utilize the ontology in the context of their own and external data sets. It will be modular and open source. We will develop various collaborations to disseminate the bioassay ontology and software in the community and to facilitate their ongoing development.

5:15 – 6:15 2010 Best of Show Awards in the Exhibit Hall

6:15 Exhibit Hall Closes

Sponsored by

6:30 – 10:00 2010 Best Practices Awards Reception & Dinner

THURSDAY, APRIL 22

8:00 am Registration and Morning Coffee

8:45 Event Chairperson's Opening Remarks

Sponsored by

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

Keynote Introduction: *Eric Blatte, Vice President of Sales, Commercial & Public Sector, Imprivata*

8:50 PLENARY KEYNOTE: There is No Magic, There is Only Awesome: Scientific Computing with Amazon Web Services

Deepak Singh, Ph.D., Business Development Manager, Amazon Web Services

Presentation delivered via a live, interactive videoconferencing platform.

9:30 KEYNOTE PANEL

The Future of Personal Genomics

A special plenary panel discussion featuring:

James Heywood, Co-founder and Chairman, PatientsLikeMe
Dan Vorhaus, J.D., M.A., Attorney, Robinson, Bradshaw & Hinson; Editor, Genomics Law Report
Dietrich Stephan, Ph.D., President & CEO, Ignite Institute
Kári Stefánsson, MD, Dr Med, Executive Chairman and President of Research, deCODE genetics
Kevin Davies, Ph.D., Editor-in-Chief, Bio-IT World

10:30 Coffee Break, Poster Competition, Vendor Theater Presentations and Exhibit Viewing

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STRUCTURE-INFORMED MODELING

10:55 Track Chairperson's Remarks

11:00 Improving Proteochemometrics Modeling for GPCRs and HIV Reverse Transcriptase Using Protein Fingerprints

Andreas Bender, Ph.D., Assistant Professor for Cheminformatics and Pharmaceutical IT, Medicinal Chemistry Division, Leiden/Amsterdam Center for Drug Research

Proteochemometrics Modeling is a recently introduced valuable technique in computer-aided drug design that uses both ligand and target features to predict ligand activity also against

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TRACK 5: CHEMINFORMATICS AND COMPUTER-AIDED MODELING

novel receptor subtypes or protein mutants. In this work we describe how rationally useful protein/amino acid descriptors can be chosen, and we present prospective validations on selecting active ligands of G-Protein Coupled Receptors and HIV Reverse Transcriptase. Given that proteochemometrics models more fully exploit information given in ligand-target bioactivity matrices than conventional QSAR models, this leads to improved predictive models as we will show here.

11:30 PRDB: A Protein Relational Database and Protein Family Knowledge Bases to Facilitate Structure-Based Design Analyses

Dominick Mobilio, Ph.D., Director, Cheminformatics, Pfizer, Inc.

The Protein Data Bank is the most comprehensive source of experimental structures. However, it can be difficult to locate relevant structures with its search interface, particularly when searching for protein–ligand complexes containing specific intermolecular interactions. We describe three new databases, Protein Relational Database (PRDB), Kinase Knowledge Base and Matrix Metalloproteinase Knowledge Base, containing protein structures from the PDB. In PRDB, atom-atom distances between protein and ligand are pre-calculated allowing for retrieval based on these data in less than one second.

12:00 pm Predicting Multiple Ligand Binding Modes Using Self-Consistent

Ryan Lilien, Ph.D., Assistant Professor, Department of Computer Science and Banting & Best Department of Medical Research, Faculty of Medicine, University of Toronto

We present a step toward improving protein-ligand binding mode prediction for a set of ligands known to interact with a common protein. There is thus an important distinction between this work and traditional virtual screening algorithms. Whereas traditional approaches attempt to identify binding ligands from a large database of available compounds, our approach aims to more accurately predict the binding mode for a set of ligands which are already known to bind the target protein. The approach is based on the hypothesis that each active site contains a set of interaction points which binding ligands tend to exploit. In a more traditional context, these interaction points make up a pharmacophoric map. Our algorithm first performs traditional protein-ligand docking for each known binder. The ranked lists of candidate binding modes are then evaluated to identify a set of poses maximally self-consistent with respect to a pharmacophoric map generated from the same poses. We have extensively demonstrated the application of the algorithm to four protein systems (thrombin, cyclin-dependent kinase 2, dihydrofolate reductase, and HIV-1 protease) and attained predictions with an average RMSD < 2.5 A for all tested systems. This represents a typical improvement of 0.5-1.0 A (up to 25%) RMSD over the naive virtual docking predictions. Our algorithm is independent of the docking method and may significantly improve binding mode prediction of virtual docking experiments.

12:30 Luncheon in the Exhibit Hall

****Drop off your business card at the CHI Sales Re-Sign Booth for a chance to win 1 of 2 Prizes! (Nintendo® Wii™ System or Apple® - iPod touch®) Winners will be announced at 1:45pm in the Exhibit Hall*

2:00 Exhibit Hall Closes

APPLYING 21ST CENTURY TOOLS TO FIND NEW TARGETS FOR OLD COMPOUNDS

1:55 Track Chairperson's Remarks

Andreas Bender, Ph.D., Assistant Professor for Cheminformatics and Pharmaceutical IT, Medicinal Chemistry Division, Leiden/Amsterdam Center for Drug Research

2:00 Pharmacography: The Art of Mapping Drug-Target Interactions

Tudor I. Oprea, Ph.D., Professor & Chief, Biochemistry & Molecular Biology Biocomputing, Health Sciences Center, University of New Mexico

Our understanding of drug-target interactions has been limited by the amount of experimental evidence, and by our ability to attribute drug-target interactions to clinical relevance. Dubbed polypharmacology or secondary pharmacology, this emerging area challenges our notions of drugs selectivity. We will place the relationship between documented drug-target interactions and clinical relevance, within the context of several pharmacokinetic parameters such as MRTD (the maximum recommended therapeutic dose), plasma protein binding, and availability. Extensions to a CNS-centric model of ligand-protein interactions will be discussed as will some of our preliminary results and conclusions. Some of these efforts may serve as the rational basis for drug repurposing, i.e., identifying novel modes of action and therapeutic applications for already-approved drugs, and may have a profound effect on the way drug design will be conducted in the future.

2:30 Predicting Drug Off-Targets

Michael Keiser, Ph.D., Postdoctoral Scholar, Pharmaceutical Chemistry, University of California San Francisco

Whereas drugs are intended to be selective, at least some bind to several physiologic targets, explaining both side effects and efficacy. We compared ~3,700 drugs against hundreds of targets, defining each target by its ligands, using the Similarity Ensemble Approach. Chemical similarities between drugs and ligand sets predicted thousands of unanticipated associations. Thirty were tested experimentally, including GPCR off-targets of the transporter inhibitor Prozac and the enzyme inhibitor Rescriptor. Overall, 23 new drug-target associations were confirmed, five below 100 nM.

3:00 Recent Results in Network Pharmacology

Philip E. Bourne, Ph.D., Professor of Pharmacology, Associate Director Protein Data Bank, Editor-in-Chief, PLoS Computational Biology, University of California San Diego, Department of Pharmacology

We have developed a strategy for determining off-targets to a number of major pharmaceuticals. Finding off-targets presents the possibility of better understanding side effects, repositioning drugs and better defining dirty drugs. Beyond the targets we infer phenotypic effect through both static and dynamic network analysis. Recent results will be presented for a multi-target strategy in treating TB and in offering reasons for the failure of the CETP inhibitor Torcetrapib.

3:30 Case Study: Is There a Link Between Structure-Rich Information and Improving Potency and Selectivity?

Jose Duca, Senior Principal Scientist, 3D - Drug Design Department, Schering Plough

Serine and threonine kinases play an important role in signal transduction pathways. Within this kinase family, cyclin-dependent 2 kinase (CDK2) is an attractive oncology target involved in cell cycle regulation. In recent years, kinase inhibition has become a major area for therapeutic involvement. As we discuss here, these efforts have resulted in a considerable increase in the number of available high resolution structures of CDK2-inhibitor complexes. A large amount of structural-based and computational work has allowed identifying novel chemical scaffolds and structural motifs to design potent CDK2 inhibitors. Of any kinase, CDK2 has the most structures available from the Protein Data Bank (PDB), averaging 22 new structures per year since 2002. A protein-ligand interaction fingerprint analysis of the available CDK2 protein-ligand complexes indicates that structural diversity is attainable from structure-based design of CDK2 inhibitors. Since the first CDK2 structure was published on 1996, seven new chemical entities (NCE) have been advanced to clinical stages. To date, only three of these NCE have their complexes published in the PDB. This review summarizes the structurally-informed efforts in the field of CDK2 inhibitor design.

4:00 Conference Adjourns

TRACK 6:
eCLINICAL TRIALS TECHNOLOGY

Track 6 explores how to leverage technology to optimize speed, quality and cost of clinical trials. Themes covered include best practices in data collection and analysis, systems integration, recruiting and engaging patient communities using Web 2.0 technologies, pharmacovigilance, and utilization of EHR data for drug development.

TUESDAY, APRIL 20

2:00 - 6:00 pm Main Conference Registration

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

4:05 KEYNOTE INTRODUCTION:
Ronald Ranauro, Chief Executive Officer, GenomeQuest, Inc. *Sponsored by* GenomeQuest

4:15 PLENARY KEYNOTE: Drug Discovery Opportunities and Challenges—VC, Biotech and Pharma Perspectives
Christoph Westphal, M.D., Ph.D., CEO, Sitris Pharmaceuticals; Senior Vice President, Center of Excellence for External Drug Discovery, GlaxoSmithKline

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WEDNESDAY, APRIL 21

7:30 am Registration and Morning Coffee

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Phillips Kuhl, Co-founder and President, Cambridge Healthtech Institute
Keynote Introduction: *Jamie Wyatt, Vice President and General Manager Health and Life Sciences, Netezza* *Sponsored by* NETEZZA

8:20 PLENARY KEYNOTE: Impact of HIT Stimulus on Novel Sources of Data for Research
John Halamka, M.D., M.S., CIO, Harvard Medical School

9:00 Keynote Presentation & 2010 Benjamin Franklin Award
Alex Bateman, Ph.D., Senior Investigator, Pfam Database Project, Wellcome Trust Sanger Institute

9:30 Coffee Break, Poster and Exhibit Viewing *Sponsored by* SCYNEXIS
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PATIENT-CENTERED CLINICAL TRIALS AND ECOLLECTION

10:50 Track Chairperson's Remarks *Presented by* Ariana Pharma
Mohammad Afshar, M.D., Ph.D., CEO, Ariana Pharmaeuticals

11:00 Patient-Centered Clinical Trials – Engaging Patients Through On-line Communities and Novel Trial Data Capture
Craig H. Lipset, Director/Commercial Lead (Molecular Medicine) and eHealth Team Member, Pfizer, Inc.
Web 2.0 technologies enable unprecedented engagement of patients in managing their health and wellness. In the emerging age of participatory medicine, the active role of the e-patient as an informed participant is encouraged. Patient communities expand beyond discussion forums into vehicles for patient-generated research. Clinical trials are often characterized by their extensive regulation and legacy processes. Can we shift from our current "site-centric" model to more actively engage the patient in clinical research? Can telemedicine and mobile technology enable a less burdensome and more accessible trial? The session will present a novel integration of mobile and internet-based technologies, along with principles of telemedicine and tools of health information technology, to demonstrate the potential for a disruptive new model, a patient-centered clinical trial. Tools to enable this model will be presented in the context of an ongoing pilot designed to demonstrate the value of patient-centered trials in improving patient engagement while reducing the time, cost, and complexity of clinical research.

11:30 eCollaboration: A Case Study on the Challenges in Building an Internet Collaborative Platform for Study Teams and Investigators
Laszlo Vasko, Director, Business Relationship Management, Global Drug Development IS, AstraZeneca
This presentation will provide an overview of AstraZeneca's Clinical Partners Portal - an internet platform to support collaboration both within AZ and externally with investigators. The case study will present the challenges with technology and project management that were encountered. The presentation will educate on the complexity of the technologies, advise on pitfalls to avoid, and help anyone looking to either build or buy such capabilities.

12:00 pm Powering Collaborations in Clinical Research *Presented by* caBIG
John Speakman, Clinical Science Program Manager/Associate Director, National Cancer Institute Center for Biomedical Informatics and Information Technology (NCI CBIIT)
William T. Dyer, Jr., Clinical Trials Management Systems Representative, NCI CBIIT
Umit Topaloglu, Ph.D., IT Bioinformatics Manager, University of Arkansas for Medical Sciences
Large-scale, multi-site collaborations are a growing trend in clinical research, creating a need for the means to seamlessly exchange and integrate data between various departments and institutions. This approach is powered by the use of a standards-based infrastructure and interoperable tools that simplify data exchange and facilitate collaborative research. This session will provide an overview of caBIG® capabilities in support of clinical research as well as real-world examples of how standards and tools are being deployed and integrated with existing systems to streamline and enhance clinical trial activation and conduct.

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

RECRUITING PATIENTS AND ENGAGING PATIENT COMMUNITIES

1:40 Chairperson's Remarks *Presented by* caBIG
Ken Buetow, Ph.D., Associate Director for Bioinformatics and Information Technology, National Cancer Institute

1:45 How Patients Are Transforming Clinical Trials
Paul Wicks, Ph.D., R&D Director, Research & Development, PatientsLikeMe
Today, patients are playing the central role in defining what aspects of their disease need to be modified, the risks and benefits that shape their decisions, and in some cases even the design of trials. PatientsLikeMe is an online community for patients with life-changing conditions that is bringing the patient voice into the center of the pharmaceutical industry to improve outcomes.

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TRACK 6:
eCLINICAL TRIALS TECHNOLOGY

2:15 Addressing the Challenges of Implementing New Tools and Processes that Enable Transparency and Accountability in the Enrollment Planning Process

Munther Baara, Director, R&D Clinical Business Systems & Processes, Wyeth

We are executing on our global strategic vision to make measurable industry leading changes in the management of Trial Operations. We implemented a SaaS application that uses predictive analytics to help model and adjust plans on the fly and collaborate across global teams. It allowed us to plan, forecast, track, model, analyze, and adjust clinical trial enrollment. This project utilizes our operational data warehouse as a common database layer to serve (transmit) data from several source systems (multiple enrollment systems, EDC tools and CTMS application) to the planning tool in a near real-time basis. Governed by the information domain stewards and guided by 2 principles: 1) One version of the truth 2) Collect data as close as possible to the source and fix data issues where we collect them.

2:45 Featured Presentation

Presented by caBIG

The BIG Idea: Strategies to Achieve a Rapid-Learning Health System

(Joint Talk with Tracks 2, 3, 4, 6, and 7)

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

Considerable momentum has been building in government, academe and the commercial sector towards implementation of a "rapid-learning health system". In this approach to biomedicine, research and clinical care are seamlessly linked in a virtuous circle that enables the collection and analysis of information on clinical outcomes of large populations. This talk will outline the requisite components of such a system—including a mega-community called the BIG Health Consortium™ encompassing the various sectors of biomedicine and electronic interoperability that enables the liquidity of information—and will showcase this new model in action.

3:15 Refreshment Break, Poster and Exhibit Viewing

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SAE COLLECTION AND INTEGRATION

3:45 Optimizing Serious Adverse Event Collection via Technology

Adrian Hsing, Senior Director, Clinical Data Management, Gilead Sciences, Inc.

Wolfgang Summa, Ph.D., Executive Vice President Europe & Asia/Pacific, OmniComm Europe GmbH

Reconciliation of safety and clinical database is not just labor intensive but often becomes a rate limiting factor for clinical trials. We have developed a software module and the corresponding process to link EDC front end to a safety system.

4:15 Integration, Not Reconciliation, Boehringer Ingelheim's Plan to Integrate SAE Collection with EDC

Tricia Gregory, Senior Associate Director, Global BDM Process & Technology Improvement , Boehringer Ingelheim Pharmaceuticals, Inc.

Lesia Tontisakis, SAE Business Lead, Boehringer Ingelheim Pharmaceuticals, Inc.

We will describe the international project within BI to integrate our Drug Safety serious adverse event reporting with collection of trial data through our EDC system and the subsequent transfer of these data to our safety database. The project was started in late 2008 and is well on its way to the goal of having a pilot underway in early 2010. We will discuss the challenges faced and resolved, as well as those still outstanding. These challenges are both technical and process-based. Issues include consistent definitions of fields to be mapped, designing the 'perfect' data collection form, easy printing for sites, prioritized thesaurus coding and investigator approval. We will describe the high-level processes that have been defined by the project team to date.

4:45 Sponsored Presentation *(Opportunity Available)*

5:15 – 6:15 2010 Best of Show Awards in the Exhibit Hall

6:15 Exhibit Hall Closes

6:30 – 10:00 2010 Best Practices Awards Reception & Dinner

Sponsored by GenomeQuest, Tessella

THURSDAY, APRIL 22

8:00 am Registration and Morning Coffee

8:45 Event Chairperson's Opening Remarks

Sponsored by imprivata

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

Keynote Introduction: *Eric Blatte, Vice President of Sales, Commercial & Public Sector, Imprivata*

8:50 PLENARY KEYNOTE: There is No Magic, There is Only Awesome: Scientific Computing with Amazon Web Services

Deepak Singh, Ph.D., Business Development Manager, Amazon Web Services

Presentation delivered via a live, interactive videoconferencing platform.

9:30 KEYNOTE PANEL

The Future of Personal Genomics

A special plenary panel discussion featuring:

James Heywood, Co-founder and Chairman, PatientsLikeMe
Dan Vorhaus, J.D., M.A., Attorney, Robinson, Bradshaw & Hinson; Editor, Genomics Law Report
Dietrich Stephan, Ph.D., President & CEO, Ignite Institute
Kári Stefánsson, MD, Dr Med, Executive Chairman and President of Research, deCODE genetics
Kevin Davies, Ph.D., Editor-in-Chief, Bio-IT World

10:30 Coffee Break, Poster Competition, Vendor Theater Presentations and Exhibit Viewing

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R&D AND IT COLLABORATION TO IMPROVE CLIN OPS

10:55 Track Chairperson's Remarks

Craig H. Lipset, Director/Commercial Lead (Molecular Medicine) and eHealth Team Member, Pfizer, Inc.

11:00 Making Clinical Data Integration Work in a Heterogeneous Environment

John Walker, Associate Director of Clinical Informatics, Infinity Pharmaceuticals

Infinity Pharmaceuticals' clinical infrastructure has evolved over the past 5 years to accommodate trials of varying phase, indication and breadth. Execution of the trials involves a hybrid of internal and external resources leading the team to create an architecture that supports information sharing across organizations. The integrated architecture, comprised of the following systems: CTMS, Pharmacovigilance, EDC and a CDISC-compliant data warehouse, contains validated and commercial off the shelf components interspersed with not validated and custom software. Automated reporting and a progressive approach to data visualization and analysis have led to broad use of the platform throughout the company. This adoption has improved communication between groups and facilitated more efficient strategic and tactical decision-making.

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TRACK 6:
eCLINICAL TRIALS TECHNOLOGY

UTILIZATION OF ELECTRONIC MEDICAL RECORDS (EHR/EMR) FOR CLINICAL RESEARCH

11:30 Connecting Healthcare and Clinical Research

Catherine Celingant, Senior Director, Medical Informatics Operations & Innovative Technologies, Millennium: The Takeda Oncology Company

The term Electronic Healthcare Record (EHR) is commonly used to refer to a system which stores individual patient health and healthcare histories in an electronic format. EHR systems are thought to be beneficial in providing an instantly accessible, patient-centric view across medical practitioners, thereby improving the quality of medical care and reducing healthcare costs. The use of EHRs in healthcare institutions is currently on the rise, in many cases encouraged by government initiatives to accelerate adoption. A secondary benefit of such systems is the potential to access to unprecedented amounts of clinical data which can support and promote evidence based medicine and medical practices. This is viewed by government agencies, epidemiologists and the wider clinical research community as a quantum step forward in delivery of their respective needs.

12:00 pm A Primer: Opportunities and Challenges with EHR and EDC System Integration

Frances Nolan, VP, Quality Assurance, Medidata Solutions

It has long been a desire to effectively and efficiently leverage Electronic Health/Medical Record (EHR/EMR) systems in clinical research, most recently with a focus on integration with clinical Electronic Data Capture (EDC) systems. This presentation provides a "back to basics" foundation, outlining the opportunities associated with EHR/EDC integration, as well as a discussion of the various challenges and how some of these challenges are being addressed. Topics addressed include those related to regulatory requirements, privacy and security, standards (e.g., HL7 and CDISC CDASH), and dictionary usage (SNOMED, ICD-9/ICD-10 and MedDRA).

12:30 Luncheon in the Exhibit Hall

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2:00 Exhibit Hall Closes

ACHIEVING INTEROPERABILITY: BEST PRACTICES IN DATA COLLECTION AND ANALYSIS

1:55 Track Chairperson's Remarks

Laszlo Vasko, Director, Business Relationship Management, Global Drug Development IS, AstraZeneca

2:00 Interoperability of Analyses and Data within Clinical Trials from a Biotechnology Perspective

Lynn DiFinizio, Director, Statistical Programming and Operations, Biometrics, Biogen Idec

A summary of how one Biotech company supports interoperability/reusable data exchange using industry standards (CDISC), internal standards (Analysis Output), EHR (RDC technology), along with a strong IT foundation (Software Development Lifecycle & Validation best practices) to ensure efficiency, compliance and productivity in a Biotech environment.

2:30 Best Practices in Lab Data Collection and Analysis

Julia Zhang, Ph.D., Associate Director, Biomedical Data Sciences and Informatics, Genzyme

Interoperability is a key standard goal in data management. Genzyme has implemented the CDISC lab standard in the lab data collection and analysis. We have coordinated with central lab vendors, such as Covance and Quintiles, EDC vendors and CROs. We experienced many different situations in collaborating with in-house data management and different vendors and gained best practices from our experiences. We also explored technology in data validation tools.

3:00 Integrated Signal Detection Tools: An Innovative Suite of Tools Developed by and for Pharmacovigilance Physicians

Steven Bailey, M.D., Senior Director & Lead, Medical Pharmacovigilance, Vaccines and Technology, Wyeth

Robert Maroko, M.D., Medical Pharmacovigilance-Vaccines and Technology, Wyeth

A presentation of the development of new signal detection tools for use in pre-marketing and post-marketing environments. These tools have been developed by physicians with an IT background, used to build efficiencies within a safety/pharmacovigilance department. We will review the development and use of this unique set of tools for early detection of safety signals and how they both improve process and greatly reduce resource requirements. We will also discuss the role of users in developing the most useful and efficient signal detection tools.

3:30 Why an Interoperable Digital Identity and Signature Standard is Fundamental to Improved Efficiencies and Costs in Global eClinical Trials

Mollie Shields Uehling, CEO, Executive, SAFE-BioPharma Association

The research community is under enormous pressure to improve R&D productivity, reduce costs and cycle times, and to raise the quality of regulatory submissions. Moving to eClinical Trials holds the promise to deliver against these goals. One of the key challenges in going electronic is the need to link our many disparate healthcare IT islands with interoperable and standardized identities that are recognized by leading regulatory authorities and meet the requirements of many different legal jurisdictions. The proposed presentation will explain the challenge and present how the SAFE-BioPharma digital identity and signature standard (developed as a pan-biopharmaceutical industry initiative) will accelerate a new phase in drug development.

4:00 Conference Adjourns

TRACK 7:
eHEALTH SOLUTIONS

Accessing a patient's personalized health record and genetic profile at point-of-care or in a clinical setting can aid in early diagnosis of disease, guide treatment and minimize harmful side-effects. Informatics tools and IT infrastructure to support such efforts are being rapidly deployed in hospitals, medical centers and at point-of-care in both the US and other countries. This track will bring together CIO, CMIO's and other medical informatics experts, technology providers who support these efforts as well as those who provide online health information to the consumer to track personal health status and disease management. Personalized approaches to drug discovery, development and the use of pharmacogenomic data can reduce the time and cost of drug development and reduce the failure rate at clinical trial. Advances in informatics tools that support and integrate data from these efforts will also be featured in our program.

TUESDAY, APRIL 20

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INTEROPERABLE FRAMEWORKS FOR PERSONALIZED HEALTHCARE

10:50 Track Chairperson's Remarks
Eric Perakslis, Ph.D., Vice President, R&D Informatics, Johnson & Johnson Pharma R&D

11:00 Transformation of American Healthcare through Medical IT and Informatics
William F. Bria, M.D., CMIO, Shriners Hospitals for Children; President, AMDIS
America is now entering the "rapid growth phase" of applied medical informatics (AMI). The interest in a plethora of technologies is intense and catalyzed by a political and legislative agenda to more broadly introduce HIT seeking benefits in quality, safety and decreased cost of care. The Medical profession however has been slow to incorporate these technologies into clinical decision making at the point of care. With the perspective of 30 years of AMI in this country, the speaker will discuss the key lessons learned in closing the information gap in this "last mile" of American Medical practice and achieving truly "meaningful use".

11:30 E-Health from the Ground Up: The Building of the King Hussein Institute for Biotechnology and Cancer in Amman, Jordan
Eric Perakslis, Ph.D., VP, R&D Informatics, Johnson & Johnson Pharma R&D
The King Hussein Institute for Biotechnology and Cancer is a $350 MM effort to construct a new 260-bed hospital and biotechnology research center in Amman, Jordan. KHIBC will be a village of healing and scientific discovery and the first such center in the Arab world. To optimize the technology infrastructure of this green field opportunity, all technology from medical equipment through the IT infrastructure is being engineered by a single team of engineers, scientists and informatics experts.

12:00 pm eHealth: Personalized Medicine and Clinical Decision Support Integration
Sharon Marsh, Faculty of Pharmacy and Pharmaceutical Sciences, University of Alberta
Personalized medicine optimizes health care by incorporating pharmacogenomics-based tests into medication selection and dosing recommendations. Although validated and approved tests are available for targeted therapeutics, a major challenge is the ability to process and return information to the physician within a narrow time frame. Targeted therapeutics through EHR-based clinical decision support will provide the informatics pipeline to drive both the acceptance and adaptation of EHR systems by providing personalized information at point of care.

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

INTEROPERABLE FRAMEWORKS FOR PERSONALIZED HEALTHCARE (CONTINUED)

1:40 Chairperson's Remarks 5AM SOLUTIONS
Brent Gendleman, CEO, 5AM Solutions

1:45 The Evolution of IT Support for Personalized Medicine
Samuel J. Aronson, Executive Director, Information Technology, Harvard Medical School & Partners Healthcare Center for Genetics and Genomics
Continued advances in molecular diagnostics are creating a need for new types of clinical IT support for clinicians. This talk will describe infrastructure that has been built and is being continuously refined to meet that need. The interdependent needs of laboratories and treating clinicians will also be discussed.

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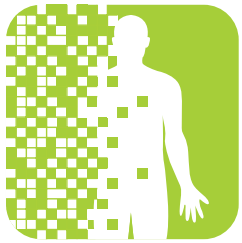
TRACK 7: eHEALTH SOLUTIONS



2:15 Leveraging Semantics for Effective and Accurate Sharing of Clinical Observations

Vipul Kashyap, Director, Applied Informatics, CIGNA

The imperative to control rising healthcare costs and yet achieve optimum outcomes suggests the need for holistic services to deliver optimum therapy and care for patients. Those services embrace biomedical research, clinical research and practice. Re-use of clinical data is also beneficial to healthcare providers, e.g., evaluating clinical care quality; payors, e.g., monitoring patient risk profile, and pharma, e.g., determining patient eligibility for clinical trials, monitoring adverse events during and after trials. We propose an extensible framework and architecture for sharing and exchange of clinical data. This is illustrated via a demonstration utilizing eligibility specifications from several clinical research protocols (using the CDISC-based standards) and (structured) patient data from a real world EHR (using HL7-based standards) to screen the EHR data for potential candidates.

2:45 Featured Presentation

Presented by caBIG

The BIG Idea: Strategies to Achieve a Rapid-Learning Health System

(Joint Talk with Tracks 2, 3, 4, 6, and 7)

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

Considerable momentum has been building in government, academe and the commercial sector towards implementation of a "rapid-learning health system". In this approach to biomedicine, research and clinical care are seamlessly linked in a virtuous circle that enables the collection and analysis of information on clinical outcomes of large populations. This talk will outline the requisite components of such a system—including a mega-community called the BIG Health Consortium™ encompassing the various sectors of biomedicine and electronic interoperability that enables the liquidity of information—and will showcase this new model in action.

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ENABLING SYSTEMS MEDICINE AT POC

Chairperson: *Andrew Gantt, Partner, Healthcare & Life Sciences Department, Latham & Watkins LLP*

3:45 Informatics Solutions to Enable Systems Medicine

Yuriy Gusev, Ph.D., Senior Bioinformatics Scientist, Lombardi Comprehensive Cancer Center, Georgetown University Medical Center

Research shows that only 50% of the data on an individual is used during a patient-physician encounter. What if we were able to increase the amount of useful data in this context? Our intent here is to utilize informatics tools and resources to integrate data across multiple clincial and "omics" platforms from research and standard of care studies to develop novel data analytic methods that will in the future could allow medical professionals to use them to stratify patients for care, for differential diagnosis purposes, to optimize therapy and monitor recurrence in cancer patients to enable Systems Medicine.

4:15 A Patient Entered Family Health History Tool to Initiate Guidelines for Prenatal Genetic Testing Using Clinical Decision Support (CDS)

Kevin Hughes, M.D., Co-Director; Surgical Director, Avon Comprehensive Breast Evaluation Center; Breast and Ovarian Cancer Genetics and Risk Assessment Program, Massachusetts General Hospital

We have developed a novel prenatal family history tool that performs risk assessment and provides point-of-care guidance to health-care providers and patients. This tool collects patient-entered data on pregnancy health and family history conditions relevant to prenatal care, in alignment with professional society recommendations. The clinician instantly receives a risk-assessment summary and suggested actions through Clinical Decision Support (CDS), including embedded educational materials to aid in patient management and communication.

4:45 New Presentation: E-Health: So Much Hype Yet So Few Results

Ralph A. Korpman, M.D., President & CEO, CentriHealth, Inc.; Professor, Loma Linda University School of Medicine

In 2009, the National Research Council published an extensive report on e-Health. Their conclusion: "…current efforts aimed at the nationwide deployment of health care IT will not be sufficient to achieve the vision of 21st century health care, and may even set back the cause if these efforts continue wholly without change from their present course." A continuing string of reports in respected media like Archives of Internal Medicine, The New York Times and The Wall Street Journal note again and again that digital records are not living up to their promise. Successes are anecdotal at best. This presentation pinpoints reasons for these failures, presents a new solution set, and reports on third-party studies documenting the new level of cost and quality success achievable using this approach, including implications for personalized medicine and health reform.

5:15 – 6:15 2010 Best of Show Awards in the Exhibit Hall

6:15 Exhibit Hall Closes

6:30 – 10:00 2010 Best Practices Awards Reception & Dinner

Sponsored by GenomeQuest, Tessella

THURSDAY, APRIL 22

8:00 am Registration and Morning Coffee

8:45 Event Chairperson's Opening Remarks

Sponsored by imprivata

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

Keynote Introduction: *Eric Blatte, Vice President of Sales, Commercial & Public Sector, Imprivata*

8:50 PLENARY KEYNOTE: There is No Magic, There is Only Awesome: Scientific Computing with Amazon Web Services

Deepak Singh, Ph.D., Business Development Manager, Amazon Web Services

Presentation delivered via a live, interactive videoconferencing platform.

9:30 KEYNOTE PANEL

The Future of Personal Genomics

A special plenary panel discussion featuring:

James Heywood, Co-founder and Chairman, PatientsLikeMe
Dan Vorhaus, J.D., M.A., Attorney, Robinson, Bradshaw & Hinson; Editor, Genomics Law Report
Dietrich Stephan, Ph.D., President & CEO, Ignite Institute
Kári Stefánsson, MD, Dr Med, Executive Chairman and President of Research, deCODE genetics
Kevin Davies, Ph.D., Editor-in-Chief, Bio-IT World

10:30 Coffee Break, Poster Competition, Vendor Theater Presentations and Exhibit Viewing

****Drop off your business card at the CHI Sales Re-Sign Booth for a chance to win 1 of 2 Prizes! (Nintendo® Wii™ System or Apple® - iPod touch®)*

10:55 Track Chairperson's Remarks

Tibor van Rooij, Director, Bioinformatics, Pharmacogenomics Centre, Genome Quebec

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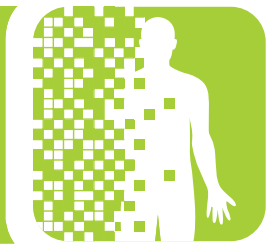
TRACK 7:
eHEALTH SOLUTIONS



11:00 Family Health Portrait - Illustrating How Simplicity & Standards Can Benefit Patients and Physicians

Gregory Downing, Ph.D., Program Director, Personalized Health Care Initiative, Office of the Secretary, Department of Health and Human Services

A recent survey found that 96 percent of Americans believe that knowing their family health history is important to their own health, yet only one-third have ever tried to collect their family's health history. Because family health history is such a powerful screening tool, the Surgeon General created a web-based system to help make it fun and easy for anyone to create a sophisticated portrait of their family's health. Although its interface is simple to comprehend, the "My Family Health Portrait" tool is backed by the HL7 family history model, making it interoperable with other systems, including health risk analysis tools and electronic health records. This tool converges three components of e-health solutions - of users becoming comfortable using the web to manage their health information, of systems exchanging information through a standards-based approach, and of IT supporting the integration of health-care providers, researchers, and patients. Our discussion will explore the tool and how it interoperates with a breast cancer risk analysis tool used by genetic counselors, a colorectal risk analysis web service, and Microsoft HealthVault.

11:30 Unlocking the Value of Electronic Medical Records

Victor Lobanov, Ph.D., Director, Informatics, Johnson & Johnson Pharmaceutical Research & Development LLC

Electronic databases of medical records contain a wealth of information critical to many areas of medical research. Through these databases, researchers can gain a better understanding of the short- and long-term impact of exposure to drugs and medical devices, identify populations at risk for adverse effects, estimate the prevalence and natural history of medical conditions, and assess drug utilization across different demographic groups. Using a combination of a relational data management strategy and a graphical user front-end, we have developed an approach that allows any medical researcher to explore this data.

12:00 pm Leveraging the Research Enterprise to Promote Personalized Medicine and Quality Precision Healthcare *Sponsored by* Microsoft

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

Discoveries that will make personalized medicine a reality depend on life science research to collect, validate, store, analyze and share information/data that can be utilized to identify and generate valuable therapies. In the complex healthcare ecosystem, there are many such parallel isolated webs of activity across the ecosystem - from scientific discovery, research, and development of new treatments through to healthcare delivery and subsequent monitoring. Quality personalized care (and subsequent ecosystem sustainability) is only achieved through unified collaboration and coordination among the contributing populations, ranging from scientists to patients and the physicians who take care of them.

However, effectively discovering valuable therapies and achieving such quality care requires overcoming hurdles such as data inaccessibility, information heterogeneity, extended analysis cycle times, torrential data volumes, siloed processes, and inability to interrogate the clinical population on demand. These capabilities are not only essential for identifying the personalized treatments that can provide immense value to patients, they are vital for enabling clinical research, development, and delivery to nimbly respond to changes within this dynamic ecosystem- promoting quality precision healthcare.

We will examine these challenges against the backdrop of an industry in transformation, where patients are taking a stronger participatory role. We will describe a scalable and customizable environment that enables dynamic and holistic analysis across the healthcare ecosystem from research to outcomes- supporting deeper, more knowledgeable insights for advancing personalized care.

12:30 Luncheon in the Exhibit Hall

****Drop off your business card at the CHI Sales Re-Sign Booth for a chance to win 1 of 2 Prizes! (Nintendo® Wii™ System or Apple® - iPod touch®) Winners will be announced at 1:45pm in the Exhibit Hall*

2:00 Exhibit Hall Closes

ACADEMIC MEDICAL CENTERS & PERSONALIZED MEDICINE DATA CHALLENGES

1:55 Track Chairperson's Remarks

Lynn H. Vogel, Ph.D., FHIMSS, FCHIME, Vice President and CIO, Associate Professor, Bioinformatics and Computational Biology, The University of Texas M.D. Anderson Cancer Center

2:00 Building an Interoperable Architecture for Personalized Medicine

Lynn H. Vogel, Ph.D., FHIMSS, FCHIME, Vice President and CIO, Associate Professor, Bioinformatics and Computational Biology, The University of Texas M.D. Anderson Cancer Center

In this presentation, Dr. Vogel will discuss M.D. Anderson's experience with developing an Electronic Medical Record (EMR) in-house on one of the most fully implemented Services Oriented Architecture (SOA) in the healthcare industry. M.D. Anderson's EMR vision covers not just data from a patient's clinical experience, but is intended to encompass as well data from scientific inquiries and biospecimens—all of which are derived from a patient's experience with M.D. Anderson. Dr. Vogel will also contrast the historical and currently prevailing views of software architecture with the promise of SOA, and draw on M.D. Anderson's experience with successfully implementing SOA to respond to their interoperability challenges. M.D. Anderson is using SOA to bridge the gap between clinical workflow and research, which is one of the most significant challenges facing e-health. This is of course one of the most challenging issues for personalized medicine—how to truly integrate the molecular work of the research scientists with the clinical work of the physician diagnosing and treating the patient.

2:30 Personalized Approaches to Drug Discovery, Development and Clinical Care

Wayne Ashton Rosenkrans, Ph.D., Distinguished Fellow, Massachusetts Institute of Technology

The current DC reprise about healthcare is "Pay for What Works." But in order to do so other questions need to be considered including: What works best (comparative effectiveness), for whom (personalized healthcare), under what circumstances (real world effectiveness)? This presentation will touch on the new world for drug development as part of a Learning Healthcare System.

3:00 Bringing Evidence and Analysis to and from Clinical Operation

Tibor van Rooij, Director, Bioinformatics, Pharmacogenomics Centre, Genome Quebec

Targeted therapeutics and their Clinical Decision Support delivery, enabling personalized medicine at Point of Care (PoC), will drive the acceptance and adaptation of Electronic Health Record (HER) systems. We developed a pharmacogenomic clinical informatics system that integrates with EHRs. BEACON, is a collection of web services with validated and standardized data formats using XML. This informatics pipeline bridges research, clinicians and patients. BEACON integrates pharmacogenomics-driven dosing algorithms into a range of EHRs thus providing clinical decision support at PoC.

3:30 Semantic Data Modeling for Personalized Clinical Research

Mark Wilkinson, Ph.D., Assistant Professor, Department of Medical Genetics, University of British Columbia; Principal Investigator, Bioinformatics, The Heart & Lung Institute, St. Paul's Hospital

In parallel with the evolution of personalized medicine - where the intervention is customized for the patient - we have been exploring frameworks that enhance the personalization of medical research - where the data and models are customized to the opinions and perspectives of the individual clinical researcher. CardioSHARE (Cardiovascular Semantic Heath And Research Environment) is our initial attempt to leverage the power of Semantic Web technologies to enable this kind of personalized view of clinical data. In CardioSHARE, lightweight local ontologies are layered over local and remote datasets to enable customized queries, where the expert knowledge and personal perspective of the researcher are embedded within the query itself.

4:00 Conference Adjourns

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Identify yourself as a Cambridge Healthtech Institute conference attendee to receive the discounted room rate. Reservations made after the cut-off date or after the group room block has been filled (whichever comes first) will be accepted on a space-and-rate-availability basis. Rooms are limited, so please book early.

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

If you're planning to attend Bio-IT World, consider coming to Boston a little early to run or see a marathon!
The Boston Marathon 2010 will be held on Monday, April 19 right before Bio-IT World. Visit www.bostonmarathon.org for more details.

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- *Bio-IT World* is the only life sciences conference that focuses on enabling technologies for predictive biology
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- The Best of Show offers exhibitors an exclusive opportunity to distinguish their new products from the competition. Judged by a joint team of *Bio-IT World* magazine editors and leading industry experts in the Exhibit Hall, this awards program will identify exceptional innovation in new product technologies used by life science professionals today. Deadline for entry is March 26th, 2010 so reserve your booth space today!
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The Best of Show Awards offer exhibitors an exclusive opportunity to distinguish their new products from the competition. Judged by a joint team of *Bio-IT World* magazine editors and leading industry experts, this awards program will indentify exceptional innovation in new product technologies used by life sciences professionals today. Judging and the announcement of winners is conducted live in the Exhibit Hall. To learn more about this program and submission deadlines, call Demetrios Loulloudes at 781-972-5445 or email dloulloudes@healthtech.com.

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LUNCHEON PRESENTATIONS

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

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

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

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Bio-IT World's Best Practices Awards Dinner (April 21, 2010)	❒ $105

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