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Bio-IT World
CONFERENCE & EXPO '16

Enabling Technology.
Leveraging Data.
Transforming Medicine.

APRIL 5 - 7, 2016 | SEAPORT WORLD TRADE CENTER | BOSTON, MA

Final Agenda

Plenary Keynote Speakers:

Catherine Brownstein, MPH, Ph.D.
Manager, Molecular Genomics Core Facility, Boston Children's Hospital


Bill Evans
Chief Marketing Officer, IBM WATSON HEALTH


Howard Jacob, Ph.D.
Executive Vice President for Medical Genomics and Chief Medical Genomics Officer, HudsonAlpha


Heidi L. Rehm, Ph.D., FACMG, *Chief Laboratory Director, Laboratory for Molecular Medicine, Partners Healthcare Personalized Medicine; Clinical Director, Broad Institute Clinical Research Sequencing Platform; Associate Professor of Pathology, Brigham & Women's Hospital and Harvard Medical School*


Yaron Turpaz, Ph.D., MBA
Chief Information Officer, Human Longevity, Inc.

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- Access All 13 Tracks for One Price
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- Hear 200+ Technology and Scientific Presentations
- Connect with Attendees Using CHI's Intro-Net
- Participate in the Poster Competition
- Choose from 16 Pre-Conference Workshops
- See the Winners of these 2016 Awards:
  - *Benjamin Franklin* • *Best of Show* • *Best Practices*
- View Novel Technologies and Solutions in the Expansive Exhibit Hall

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"The Bio-IT community is maturing rapidly, shifting from products to collaborative solutions. I'm looking forward to seeing this growth continue at the Bio-IT World Conference & Expo in April."

Allison Proffitt,
Editorial Director, Bio-IT World

CO-LOCATED EVENT

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Medical Informatics World Conference 2016

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Medical Informatics World kicks off the week of informatics programs, bringing together senior-level healthcare providers, payers, technology vendors, biomedical scientists, academic researchers, informaticists and national health organizations to discuss emerging trends and collaborations in health IT for improved outcomes in the healthcare ecosystem.

Special 20% Registration Discount Available
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#BioIT16

SCHEDULE-AT-A-GLANCE

TUESDAY, April 5, 2016

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

WEDNESDAY, April 6, 2016

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

THURSDAY, April 7, 2016

7:00 – 7:50am	Breakfast Presentation
8:00 – 10:00am	Plenary Keynote Session Panel
10:00am – 1:55pm	Exhibit Hall Open
10:00 – 10:30am	Coffee Break in the Exhibit Hall and Poster Competition Winners Announced
10:30am – 12:10pm	Tracks 1-13
12:20 – 1:20pm	Luncheon Presentations *(Sponsorship Opportunities Available)*
1:20 – 1:55pm	Dessert Refreshment Break in the Exhibit Hall with Poster Viewing
1:55 – 4:00pm	Tracks 1-13

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Plenary Keynote Presentations

TUESDAY, APRIL 5 | 4:00 – 5:00 PM

Keynote Introduction:
Ketan Paranjape, General Manager, Life Sciences, Intel Corporation

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Heidi L. Rehm, Ph.D., FACMG

Chief Laboratory Director, Laboratory for Molecular Medicine, Partners Healthcare Personalized Medicine; Clinical Director, Broad Institute Clinical Research Sequencing Platform; Associate Professor of Pathology, Brigham & Women's Hospital and Harvard Medical School

Heidi L. Rehm, Ph.D., FACMG is the Director of the Partners Laboratory for Molecular Medicine (LMM), the Clinical Director of the Broad Institute's Clinical Research Sequencing Platform and Associate Professor of Pathology at Brigham & Women's Hospital and Harvard Medical School. Both clinical labs focus on the rapid translation of new genetic discoveries into clinical tests and bringing novel technologies and software systems into molecular diagnostics to support the integration of genomics into clinical use. The LMM has been a leader in translational medicine, offering disease panel tests as well as whole genome and exome sequencing services for both clinical diagnostics and to support several genomic medicine research projects including the MedSeq and BabySeq projects.

WEDNESDAY, APRIL 6 | 8:00 – 9:45 AM

Keynote Introduction:
George Vacek, Ph.D., MBA, Global Director, Life Sciences, DDN

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Howard Jacob, Ph.D.

Executive Vice President for Medical Genomics and Chief Medical Genomics Officer, HudsonAlpha

Throughout the course of nearly two decades at the Medical College of Wisconsin, Howard Jacob, Ph.D., served as Founding Director of the Human and Molecular Genetics Center and Professor of Physiology, and was awarded the Warren P. Knowles Chair of Genetics. Previously, he was on the faculty at Massachusetts General Hospital and Harvard Medical School. Dr Jacob received his Ph.D. in Pharmacology from the University of Iowa, and he completed post-doctoral fellowships in functional genomics and molecular genetics/genomics at Harvard Medical School, Stanford University, and the Massachusetts Institute of Technology. Dr Jacob's 25 years of genetic sequencing experience bolsters HudsonAlpha's roster of expert researchers and supports the Institute's mission to bridge laboratory discoveries to medical improvements for patients. He brings specific expertise in using clinical genomics to discover undiagnosed disorders.

Benjamin Franklin Awards and Laureate Presentation

Best Practices Awards Program

THURSDAY, APRIL 7 | 8:00 – 10:00 AM

Keynote Introduction:
Jason Stowe, CEO, Cycle Computing

Sponsored by CYCLE COMPUTING

Panel: Big Data, Big Science, Smart Medicine

The life sciences industry continues to face challenges in integrating data from multiple 'omics sources and aligning it with clinical action. As data types and sources explode, big data and data engineering will be more important than ever in accelerating the discovery of useful new diagnostics and therapies. The companies and groups at the cutting edge of these challenges are using health records, patient portals, new data sources like NGS and activity trackers, and other technology innovations to turn big data into smart data leading to real time assistance in disease prevention, prognosis, diagnostics, and therapeutics.

Catherine Brownstein, MPH, Ph.D.

Manager, Molecular Genomics Core Facility, Boston Children's Hospital

Dr. Brownstein is the Manager of the Molecular Genomics Core Facility and a research associate in Genetics and Genomics at Boston Children's Hospital. An active member of the Manton Center for Orphan Disease Research with specialization in gene discovery, Dr. Brownstein has been instrumental in the elucidation of several new genes implicated in conditions such as intellectual disability, nemaline myopathy, psychosis, and hypophosphatemic rickets. Now a core member of Robert's Program in Sudden Unexpected Death in Pediatrics at Boston Children's Hospital, Dr. Brownstein applies her genomics expertise in the program's approach to SIDS as a set of undiagnosed diseases. She is also focused on advancing the fields of next generation sequencing and analysis, as evidenced in her management of the international CLARITY and CLARITY Undiagnosed competitions. Before coming to BCH and HMS, Dr. Brownstein created online patient communities for individuals with chronic or terminal diseases, and worked as a toxicologist for Massachusetts Department of Public Health.

Who are the hundreds of participating organizations that make up
The Bio-IT Community?
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Plenary Keynote Presentations

Bill Evans

Chief Marketing Officer, IBM WATSON HEALTH

Bill Evans is the Chief Marketing Officer for IBM Watson Health. As CMO, he has global responsibility for marketing strategy, communications, social media, demand generation, and events. He is working to help commercialize the healthcare industry offerings based on IBM Watson's cognitive technology. Prior to joining IBM, Mr. Evans was the Executive Vice President and Chief Digital Officer for Team Chemistry @ WPP, leading the consolidated digital marketing business for Johnson & Johnson. Mr. Evans was responsible for driving strategic innovations, ensuring creative excellence and leading the R&D of emerging technologies in order to protect and grow market share for a multi-billion dollar product portfolio. Previous to this, Mr Evans lead the digital practice for FleishmanHillard New York, working with brands to develop and manage digital and social business initiatives to increase both revenue and reputational indices. In addition to his daily responsibilities, Mr. Evans served Global Co-Chair for the agency's healthcare practice, working with colleagues and clients around the world. He was one of the primary strategists behind the agency's approach to social media, helping clients navigate the evolving world of communication, conversation, and community. Mr. Evans has been a frequent speaker on the future of digital and the innovative role social media and mobile can play in healthcare and has been a featured guest on Fox News and CNBC.

Yaron Turpaz, Ph.D., MBA

Chief Information Officer, Human Longevity, Inc.

Dr. Yaron Turpaz is a proven research and development IT leader in the biotech and pharma space with hands on experience using computational and informatics platforms for drug discovery and development applications. In his role as CIO at Human Longevity, Inc. (HLI), Dr Turpaz is responsible for building and growing the company's genomic and phenotypic database business, and leads all bioinformatics/informatics and software engineering efforts. Dr Turpaz is expanding informatics program at HLI's California facility, as well as building a computing and informatics program and facility in Singapore. Prior to joining HLI, he worked at AstraZeneca as Vice President, R&D IT; Eli Lilly Singapore Centre for Drug Discovery as Director of Integrative Computational Sciences, and Affymetrix, Inc. as Senior Manager, Bioinformatics and Algorithms Development. Dr Turpaz has BS in Biology from Tel Aviv University, a Ph.D. in Bioengineering from the University of Illinois and an MBA from the University of Chicago, Booth School of Business. He also held an adjunct assistant professor at the Centre for Quantitative Medicine of Duke-National University of Singapore, Graduate Medical School in Singapore.

Additional Speakers to be Announced

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Pre-Conference Workshops

MORNING WORKSHOPS: TUESDAY, APRIL 5, 2016 | 8:00 – 11:30 AM

W2: Intelligent Methods Optimization of Algorithms for NGS
Michele Busby, Ph.D., Computational Biologist, Broad Technology Labs, Broad Institute
Kaitlin Samocha, Research Scientist, Mark Daly Laboratory, Analytic and Translational Genetics Unit, Broad Institute
Dinanath Sulakhe, Engagement Manager and Solutions Architect, Computation Institute, University of Chicago and Argonne National Lab
Lu Zhang, Ph.D., Principal Bioinformatics Scientist, Seven Bridges Genomics

W3: Visualization for Biomedical Data Analysis: From the Basics to Applications
Nils Gehlenborg, Ph.D., Assistant Professor, Department of Biomedical Informatics, Harvard Medical School

W4: Data Management for Biologics: Registration and Beyond
Monica Wang, Ph.D., Principal Bioinformatics Architect, Takeda Oncology
Beth Basham, Ph.D., IT Director, Client Services, Biologics & Vaccines Discovery, Merck
Ralph Haffner, Local Area Head, Research Informatics, F. Hoffmann-La Roche AG
Peter Henstock, Ph.D., Senior Principal Scientist, Research Business Technologies, Pfizer
Sergio H. Rotstein, Ph.D., Director, Research Business Technology, Pfizer, Inc.
Ryan Luce, Ph.D., Program Manager, LabKey Software

W5: Security Considerations for Virtual Research
Michael H. Elliott, CEO, Atrium Research & Consulting LLC
Mohit Agnihotri, Associate Director, Informatics, Novartis Institutes for BioMedical Research
Art Morales, Ph.D., Vice President, Technology and Corporate Development, Beryllium
Ton van Daelen, ScienceCloud Product Director, Marketing, Dassault Systemes, BIOVIA
Hongmei Huang, Ph.D., Vice President, IT & Informatics, Assembly BioSciences

W6: Opportunities and Challenges of Mobile Health, Wearables, and Sensors for Pharma
Michelle Crouthamel, Project Manager, ID, NS, Digital PPU, Projects Clinical Platforms & Science, GlaxoSmithKline
Marc Foster, Co-Founder and COO, Transparency Life Sciences
Munther Baara, Senior Director, Development Business Technology, Pfizer
John Reites, Head, Digital Health Acceleration, Quintiles

W8: Creating a Best of Breed Informatics Environment for Your Organization
Gregg TeHennepe, IT Project Manager, The Jackson Laboratory
Susan McClatchy, M.S., Bioinformatician and Research Program Manager, Center for Genome Dynamics, The Jackson Laboratory

AFTERNOON WORKSHOPS: TUESDAY, APRIL 5, 2016 | 12:30 – 4:00 PM

W9: Growth Strategy: Leveraging Cloud Scalability to Enable Rapid Growth and Change
R. Mark Adams, Ph.D., Partner and Computational Biologist, GroupEP
Benny Ayalew, Solution Engineer Lead, Life Sciences, Google
Benjamin Breton, Senior Data Scientist, Good Start Genetics
Michael Keller, Ph.D., Senior Associate, Booz Allen Hamilton
Anthony R. Kerlavage, Ph.D., Chief, Cancer Informatics Branch, National Cancer Institute
Jason Stowe, CEO, Cycle Computing

W11: Determining Genome Variation and Clinical Utility
Catherine Brownstein, MPH, Ph.D., Instructor, Pediatrics, Harvard Medical School; Research Associate, Genetics and Genomics, Boston Children's Hospital; Manager, Molecular Genomics Core Facility
Heather Mason-Suares, Ph.D., FACMG, Associate Laboratory Director, Laboratory for Molecular Medicine, Partners HealthCare Personalized Medicine; Instructor, Pathology, Brigham and Women's Hospital
Liz Worthey, Ph.D., Faculty Investigator & Director, Software Development and Informatics, HudsonAlpha Institute for Biotechnology

W12: Data Science Driving Better Informed Decisions
James Cai, Head Data Science, Pharmaceutical Research and Early Development Informatics, Roche Innovation Center New York
Francesca Milletti, Principal Scientist, Data Science, Roche Innovation Center New York
Wei-Yi Cheng, Ph.D., Scientist, Roche Innovation Center New York, Roche TCRC, Inc.
Christian Blumenroehr, Ph.D., Information Scientist, Roche Innovation Center Basel, F. Hoffmann-La Roche
Philip C. Ross, Ph.D., Director, Data Sciences TR&D, BMS
Nils Weskamp, Principal Scientist, Computational Chemistry, Lead Discovery, Boehringer Ingelheim Pharma GmbH & Co KG
Anna Kohlmann, Ph.D., Associate Director, Discovery Informatics and Computational Chemistry, Research Technologies, ARIAD Pharmaceuticals, Inc.
John F. Conway, Global Director R&D Strategy and Solutions, LabAnswer

W14. Designing Storage Solutions for Life Sciences
Ari Berman, Ph.D., Vice President and General Manager of Consulting Services, BioTeam, Inc.
Aaron Gardner, Senior Scientific Consultant, BioTeam, Inc.

W15: Foundational Services for Bioinformatics in the AWS Cloud with Intel
Angel Pizarro, Scientific Computing, Amazon Web Services
Adam Kraut, Senior Scientific Consultant, BioTeam

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Awards Programs

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

Best Practices Awards - Call for Entries!

BEST PRACTICES AWARDS
Bio-IT World 2016

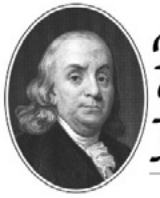
The 2016 Bio-IT World Best Practices competition has released its call for entries. Bio-IT World has held the Best Practices awards since 2003, highlighting outstanding examples of technology innovation in the life sciences, from basic R&D to translational medicine. We particularly encourage vendors to nominate entries from valued academic and/or industry partners. Winners will be selected by a peer review expert panel in early 2016. Bio-IT World will present the Awards on Wednesday, April 6 during the Plenary Keynote and Awards Program. Early bird deadline (no fee) for entry is December 11, 2015 and final deadline (fee) for entry is February 6, 2016. Full details including previous winners and entry forms are available at Bio-ITWorld.com/BestPractices.

Best of Show Awards

BEST OF SHOW
Bio-IT World

The Best of Show Awards offer exhibitors an opportunity to distinguish their products from the competition. Judged by a team of leading industry experts and Bio-IT World editors, this award identifies exceptional innovation in technologies used by life science professionals today. Judging and the announcement of winners is conducted live in the Exhibit Hall. Winners will be announced on Wednesday, April 6. The deadline for product submissions is Friday, February 19, 2016. To learn more about this program, contact Ryan Kirrane at 781-972-1354 or email rkirrane@healthtech.com.

2016 Benjamin Franklin Award



Benjamin Franklin Award

The Benjamin Franklin Award for Open Access in the Life Sciences is a humanitarian/bioethics award presented annually by the Bioinformatics Organization to an individual who has, in his or her practice, promoted free and open access to the materials and methods used in the life sciences. Nominations are now being accepted! The winner will be announced in the Amphitheater at 9:00am on Wednesday, April 6 during the Plenary Keynote and Awards Program. Full details including previous laureates and entry forms are available at www.bioinformatics.org/franklin.

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Track 1

Data & Storage Management

Infrastructure and Storage Capabilities and Solutions in the R&D Ecosystem

TUESDAY, APRIL 5

7:00 am Workshop Registration and Morning Coffee

8:00 – 11:30 Recommended Morning Pre-Conference Workshops*
Creating a Best of Breed Informatics Environment for Your Organization

12:30 – 4:00 pm Recommended Afternoon Pre-Conference Workshops*
DNA for Data Storage

** Separate registration required*

2:00 – 6:00 Main Conference Registration

4:00 PLENARY KEYNOTE SESSION
Please see page 3 for details.

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

WEDNESDAY, APRIL 6

7:00 am Registration Open and Morning Coffee

8:00 PLENARY KEYNOTE SESSION
Please see page 3 for details.

9:00 Benjamin Franklin Awards and Laureate Presentation

9:30 Best Practices Awards Program

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

GLOBAL ECOSYSTEM FOR CANCER RESEARCH AND TREATMENT:

TECHNOLOGIES, TOOLS, AND PLATFORMS TO BRING ADVANCES IN SCIENCE FROM BENCH TO BEDSIDE

10:50 Chairperson's Opening Remarks
Anil Srivastava, President, Open Health Systems Laboratory

11:00 PANEL DISCUSSION: IUCKA: Indo-US Cancer Knowledge Alliance
Moderator: Anil Srivastava, President, Open Health Systems Laboratory
Kenneth Buetow, Ph.D., Director, Computational Sciences and Informatics, Complex Adaptive Systems Initiative (CASI), Arizona State University
Rajendra Joshi, Ph.D., Associate Director and Head, Bioinformatics Group, Centre for Development of Advanced Computing, Pune University Campus
IUCKA: Indo-US Cancer Knowledge Alliance is being designed as an integrated biomedical informatics cyberinfrastructure for cancer treatment and research in India. It will be a true translational research platform from bench to bedside connecting cancer treatment and research centers across the country with access and connection to global centers of research, especially in the United States. The promoters of the IUCKA are Arizona State University, Open Health Systems Laboratory and Varian Medical Systems. IUCKA is being implemented as a PPP (public-private partnership) and is bringing together technology products, service providers and cancer treatment and research centers in an ecosystem to directly benefit cancer patients in India and contribute to global research collaboration, especially between cancer centers in India.

DATA & STORAGE MANAGEMENT SOLUTIONS

Sponsored by DDN STORAGE

12:00 pm Managing Data Across the Research Life-Cycle for Life Sciences
George Vacek, Global Director, Life Sciences, DDN
Dr. Vacek will deliver several in-depth case studies of leading life sciences organizations leveraging high performance & high scale data solutions for genomics, imaging & simulation workflows. Cases will focus on implemented solutions: capturing & effectively exploiting large scale data at speed, regulated & non-regulated stewardship considerations, transitioning from non-scaling architectures & bringing the benefits of high-end HPC technologies & techniques into smaller deployments & collaborative scenarios.

Sponsored by sgi

12:15 Data Management in Large Scale Sequencing and Analysis
Kirill Malkin, Director, Storage Engineering, SGI
Next Generation Sequencing and its accompanying analyses are driving exponential growth in sequence data that needs to be stored, analyzed, and made accessible for future interrogations. This session presents a converged storage-and-analytics infrastructure framework based on SGI's experience in enabling data-intensive supercomputing solutions – along with genomics customer case examples and best practices for simplifying the management of data sets that can contain billions of files/objects.

12:30 Session Break

Sponsored by intel

12:40 Luncheon Presentation I: Accelerating the Analysis of High-Throughput Sequencing
Ketan Paranjape, General Manager, Life Sciences, Health and Life Sciences, Intel
Panelists: Paolo Narvaez, Ph.D., Principal Engineer & Director, Personalized Care Platform, Intel Corporation
Adam Kiezun, Ph.D., Senior Group Leader, Computational Methods Development, Broad Institute of MIT and Harvard
Jeff Gentry, Principal Software Engineer, Broad Institute
Accelerating the analysis of high-throughput sequencing data enables all of us to push the boundaries of precision medicine. The BROAD's Genome Analysis Toolkit (GATK) is the industry standard software package for variant discovery and genotyping. In this luncheon, experts from the BROAD and

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Track 1

Data & Storage Management

Infrastructure and Storage Capabilities and Solutions in the R&D Ecosystem

Intel will discuss the exciting new capabilities that are coming to GATK, and the impact that this could have on the industry.

1:10 Luncheon Presentation II: High-Performance Server and Storage Solutions for Life Sciences

Sponsored by Silicon Mechanics

Dan Chow, COO & CTO, Silicon Mechanics

Hear from Silicon Mechanics COO/CTO, Daniel Chow, as he describes current challenges and trends that are impacting computational and storage needs for researchers.

1:40 Session Break

1:50 Chairperson's Remarks

Sanjay Joshi, CTO, EMC

1:55 High-Performance Computing Clusters and Storage Enabling Big Data Genomic Analyses Outcomes across Research and Clinical Domains: Implementations, Operations, and Lessons Learned

Jason Hughes, MBA, MS, Director, Enterprise Research Applications & High-Performance Computing, Penn Medicine Academic Computing Services, Perelman School of Medicine at the University of Pennsylvania

Storage and analysis of large datasets is a growing need for academic researchers, as is the analysis of genomic data in the pursuit of personalized medicine. In 2012, The Perelman School of Medicine at the University of Pennsylvania made a capital investment in a centrally supported HPC environment. Housing 2PB of disk storage, 1.8PB of archive storage, and over 4,500 computing cores, this HPC is available to faculty, staff, students, and clinicians. This presentation will review the three-year history of the HPC environment, the technical, administrative, and financial constructs within which these services are provided, lessons learned in the areas of data storage and management, and how HPC storage and compute capabilities are enabling the tri-part organizational mission of education, research, and clinical care.

2:25 Low Cost Data Management System for Large Scale Ion Sequencing Systems

Mohamed Abouelhoda, Ph.D., Head, Bioinformatics, Saudi Human Genome Project, Genetics Department, King Faisal Specialist Hospital and Research Center

Storage infrastructure is a major problem when running NGS based sequencing projects. Reducing storage requirements means cost and effort reduction. Our presentation will provide a solution to an urgent demand for genome sequencing projects, and it will be appealing for both project owners and IT specialists. We will also discuss best practices achieved in handling thousands of sequencing runs in the Saudi Genome Project.

2:55 How Web-Scale Storage is Enabling Faster, Efficient Medical Research Collaboration for More Effective Patient Treatments

Sponsored by cleversafe

Piers Nash, Ph.D., Director, Business Development and Outreach, University of Chicago

Learn how the University of Chicago's Center for Data Intensive Science (CDIS) accelerates medical discoveries by democratizing access to data for scientific research. Utilizing an object storage solution, CDIS centrally stores and manages vast amounts of genomic and clinical data at web-scale, allowing researchers to collaborate via shared access to harmonized data sets, speeding discovery and enabling precision medicine.

3:10 Life Science - Fast & Slow

Sponsored by EMC²

Patrick Combes, Principal Solution Architect, Life Science & HPC, EMC

The handling of data from Life Science workflows can be characterized as fast and slow. While no single storage or computing technology can address the entire continuum of fast-n-slow requirements, EMC has introduced several new products and made significant enhancements to existing lines in the past few years to cover as much as possible. We will highlight these new developments for HPC, converged infrastructure and research data management and illustrate how they can be applied to Life Science applications and workflows.

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

4:00 PANEL DISCUSSION: The IUPAC InChI Standard for Large Molecules

Steve Heller, Ph.D., Project Director, InChI Trust; Scientific Information Consultant (Chairperson/Moderator)

Evan Bolton, Ph.D., Lead Scientist, National Center for Biotechnology Information (NCBI), National Library of Medicine (NLM), and National Institutes of Health (NIH)

Keith T. Taylor, BSc, Ph.D., MRSC, Principal, Ladera Consultancy

Tyler Peryea, Informatics Scientist, National Center for Advancing Translational Sciences (NCATS)

Lawrence Callahan, Ph.D., Chemist, Substance Registration System, Office of Critical Path Programs, Food and Drug Administration (FDA)

This session will present the ongoing work of IUPAC and the US Government agencies involved in the development of a standard method for describing large molecules, often called biologics, to allow for easier linking of diverse sources of data and information about these molecules. The term biologics in regard to this work means chemically modified amino acid sequences, nucleic acid sequences, carbohydrates, lipids or any combination of these. These large molecules are a rapidly growing portion of the chemical substance descriptions and bioactivity data bring made available online by many diverse and valuable resources.

5:00 Scale, Speed, Smart — IBM Genomics Reference Architecture

Sponsored by IBM

Frank Lee, Ph.D., Global Healthcare Life Sciences Industry Leader, IBM

Dr. Frank Lee will share the IBM Genomics Reference Architecture as an open and innovative platform to address the explosive growth of data from genomics research, drug discovery and clinical application. With seamless integration of workload orchestration and data management, the architecture is designed to handle large amounts of data and job throughput, yet flexible enough to be deployed on-premise, in the cloud or as a hybrid. A demo will be shown for a genomics pipeline in operation from a hybrid cloud.

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

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Track 1

Data & Storage Management

Infrastructure and Storage Capabilities and Solutions in the R&D Ecosystem

with Poster Viewing

THURSDAY, APRIL 7

7:00 am Breakfast Presentation: Enabling Technology. Leveraging Data. Transforming Precision Medicine.

Sponsored by intel

Sanjay Joshi, CTO, Life Sciences, EMC

Angel Pizarro, Director, Scientific Computing, Amazon Web Services

Ari Berman, Ph.D., General Manager, Government Services, Principal Investigator, BioTeam, Inc.

Eric A. Stahlberg, Ph.D., Leidos Biomedical Research, Inc., Frederick National Laboratory for Cancer Research (FNLCR)

Through collaborations, research and innovation, Intel is supporting the advancement of processing, storage, networking, data security, sequencing efficiency, accelerated bioinformatics and advanced analytics—to push the boundaries of this new "precision medicine" and bring us closer than ever to truly making care personal. Listen to this panel discuss how technology and bioscience are coming together to accelerate precision medicine through on-premise and cloud based solutions.

8:00 PLENARY KEYNOTE SESSION PANEL
Please see page 3 for details.

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

HPC TRENDS IN THE TRENCHES 2016

10:30 Chairperson's Opening Remarks

Sanjay Joshi, CTO, EMC

10:40 FEATURED PRESENTATION: HPC Trends in the Trenches 2016

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

In one of the most popular presentations of the Expo, Chris delivers a candid assessment of the best, the worthwhile, and the most overhyped information technologies (IT) for life sciences. He'll cover what has changed (or not) in the past year around infrastructure, storage, computing, and networks. This presentation will help you understand IT to build and support data intensive science.

NEXT GENERATION SCALE-OUT STORAGE SOLUTIONS

11:40 Realize a Fiftyfold Increase in Sequencing by Combining Performance Scale-Out Storage with the Latest Next-Gen Sequencers

Sponsored by panasas

David Sallak, Vice President, Products & Solutions, Panasas

In this talk, you will learn how to easily harness and manage data by deploying scale-out storage that accelerates workflows and brings plug-and-play simplicity to data management. Panasas customer Garvan Institute of Medical Research accomplished a 50X increase in their sequencing capabilities after combining the Illumina HiSeq X Ten sequencer with Panasas ActiveStor performance scale-out NAS.

11:55 How Next Generation Scale-Out Storage Is Enabling the Next Frontier of Life Sciences Breakthroughs

Sponsored by Qumulo

Joel Groen, Product Manager, Qumulo

With major technology advances in genomic IT, data is being created at a faster rate than ever before – creating massive storage and data management challenges for Life Sciences and bioinformatics organizations that are tasked with managing hundreds of millions to trillions of files. Enter next-generation scale-out storage – which provides real-time answers about data footprints at incredible scale, abstracts away the underlying infrastructure, and achieves breakthrough performance using intelligent software and commodity hardware – all while balancing performance, capacity and cost

12:10 pm Session Break

12:20 Luncheon Presentation I: Object Storage: Enabling Genomic Sequencing at Petabyte Scale

Sponsored by SwiftStack

Joe Arnold, President and Chief Product Officer, Leadership, SwiftStack

The audience will learn the following from our presentation: 1) How incorporating multi-petabyte storage-as-a-service into research environments can be cost-efficient, scalable and manageable; 2) How to implement an open source object storage system that keeps up with data volume while improving data management and organization by using arbitrary tags and metadata; and 3) How chargebacks can determine storage user behavior.

12:50 Luncheon Presentation II: Searching through Petabytes of Data to Find What You Actually Want

Sponsored by Igneous

Kiran Bhageshpur, CEO, Igneous Systems

Just a decade ago, large data sets were still measured in the TB's and PB data sets were rare. In today's world, even a modest laboratory can generate petabytes of data that needs to be ingested, processed, curated and stored for decades. Yet, our ways of interacting with these large data sets remain mired in tools and techniques build for MB data sets. Surely there has to be a better way?

1:20 Dessert Refreshment Break in the Exhibit Hall with Poster Viewing

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Track 1

Data & Storage Management

Infrastructure and Storage Capabilities and Solutions in the R&D Ecosystem

CONVERGENCE OF PREDICTIVE ANALYTICS AND BIG DATA

1:55 Chairperson's Remarks
Eric A. Stahlberg, Ph.D., [Contractor], High-Performance Computing Strategy, Data Science and Information Technology Program, Leidos Biomedical Research, Inc., Frederick National Laboratory for Cancer Research (FNLCR)

2:00 PANEL DISCUSSION: Actionable Big Data Analytics
Moderator: Eric A. Stahlberg, Ph.D., Leidos Biomedical Research, Inc., Frederick National Laboratory for Cancer Research (FNLCR)
Kiran Bhageshpur, CEO, Igneous Systems, Inc.
David King, CEO, Exaptive
Timothy Danford, Ph.D., Field Engineer, Tamr, Inc.
Leading life sciences experts will discuss trends and best practice case studies of turning big data into smart data that can lead to real time assistance in organization decision making, disease prevention, prognosis, diagnostics, and therapeutics. Learn how and where these organizations have assembled and analyzed information from different data 'silos' and deployed solutions to make decisions. We'll discuss technology tools used to move data and information from retrospective reporting to real-time predictive analytics. Walk away hearing practical steps, solutions, and capabilities that you can implement within your own organization.

3:30 Future Convergence
Eric A. Stahlberg, Ph.D., Leidos Biomedical Research, Inc., Frederick National Laboratory for Cancer Research (FNLCR)

4:00 Conference Adjourns

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Track 2

Data Computing

Advances in Computing Applications for Big Data

TUESDAY, APRIL 5

7:00 am Workshop Registration and Morning Coffee

8:00 – 11:30 Recommended Morning Pre-Conference Workshops*
Creating a Best of Breed Informatics Environment for Your Organization

12:30 – 4:00 pm Recommended Afternoon Pre-Conference Workshops*
Data Science Driving Better Informed Decisions

** Separate registration required*

2:00 – 6:00 Main Conference Registration

4:00 PLENARY KEYNOTE SESSION
Please see page 3 for details.

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

WEDNESDAY, APRIL 6

7:00 am Registration Open and Morning Coffee

8:00 PLENARY KEYNOTE SESSION
Please see page 3 for details.

9:00 Benjamin Franklin Awards and Laureate Presentation

9:30 Best Practices Awards Program

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

DATA WORKFLOWS AND PIPELINES

10:50 Chairperson's Opening Remarks

11:00 Advancing Translational R&D - Clinical Image Management
David Witt, Imaging Biomarkers Informatics Lead, Bristol-Myers Squibb
Incorporating a clinical trial Medical Image Management System (MIMS) into the drug development platform requires the re-examination of existing workflows to maximize the qualitative and quantitative benefits realized with MIMS. This talk will present improved workflows and underlying technology challenges and opportunities with advancing translational R&D using high-quality clinical image management.

11:30 Intercorporate Delivery of NGS Analysis Pipelines in Software Containers
Satu Nahkuri, Ph.D., Data Scientist, Pharma Research and Early Development Informatics, Roche Innovation Center Basel
Learn how software containers can make NGS analysis toolchains more portable, maintainable, and reproducible. Notably, this novel method can support software deployment in cloud computing, high performance computing and local small-scale computing environments alike. Because of this, it offers smooth interoperability between collaborators as well as between different in-house setups such as development and production environments.

12:00 pm Pushing the Limits of Discovery with Internet2 - Cloud to Supercomputing in Life Sciences
Sponsored by INTERNET2
Dan Taylor, Director, Business Development, Network Services, Internet2
Advances in life sciences rely on both world class collaboration and an ecosystem of secure cloud services and supercomputing seamlessly connected by a high-performance network. Learn how organizations are leveraging commercial clouds such as AWS, private big data scientific research clouds, supercomputing resources such as NCSA and San Diego Supercomputing, and dynamic combinations of these tactics to advance life science research with Internet2.

12:15 Managing NGS Data: Smaller is Better!
Sponsored by GENEFORMICS
Rafael Feitelberg, CEO, Geneformics
The tremendous growth of NGS data is a blessing and a curse, leading to increasing pain in management and requiring escalating investments in infrastructure. We will review how organizations are reducing data volumes by up to 10X - on-premises and in the cloud - without any change to their workflow.

12:30 Session Break

12:40 Luncheon Presentation I: Genome Analysis Pipelines, Big Data Style
Sponsored by MAPR
Allen Day, Principal Data Scientist, MapR Technologies
Bioinformatics workflow requirements are well-matched to BigData tools' capabilities. However Spark, for example, is not commonly used because many bioinformatics tool authors assume a legacy computing environment will be used. Barriers are quickly coming down. We'll examine a few conventional bioinformatics analyses and show how they can be modernized to save time, money, and make new types of analysis possible.

1:10 Luncheon Presentation II: Cover Your Bases: 7 Ways Genomics Workflows Can Benefit From Multi-Tier Storage
Sponsored by Quantum
Claire Giordano, Senior Director, Emerging Storage Markets, Quantum
Dramatic declines in the cost and run times for genome sequencing are enabling bioinformaticians to do more, faster. But these advances come with a challenge—how to manage all of this valuable data? Quantum's Claire Giordano explores how multi-tier storage (including object storage) can help genomics researchers accelerate time to discovery, improve access for distributed teams, and cost-effectively keep sequenced genome data for decades.

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1:40 Session Break

CLOUD PLATFORMS TO SPEED RESEARCH GOALS AND MOVE DATA

1:50 Chairperson's Remarks
Chris Dwan, Acting Director, IT, Broad Institute

1:55 To the Cloud(s): Broad Institute's Journey Outside of Our Walls
Chris Dwan, Acting Director, IT, Broad Institute

2:25 Handling Cloud Project
Gurpreet Kanwar, Senior Project Manager, Information Management, NAV Canada

2:55 How Bluebee & Others Solve the File Exchange Problem for Bioinformatics
Sponsored by aspera an IBM company
Michelle Munson, President, CEO & Co-Founder, Aspera, an IBM Company
Hans Cobben, CEO, Bluebee
As new research techniques create terabytes of NGS data, the need to quickly, easily, and securely ingest and exchange large genome data files with the cloud's scale-up capacity becomes critical. Learn how Bluebee and other bioinformatics companies overcome this challenge by integrating or using Aspera FASP technologies and solutions to securely move large files at high-speed to and from multiple cloud and on-premise storage systems, regardless of where the data is located.

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

4:00 The Matchmaker Exchange: A Platform for Rare Disease Gene Discovery
Anthony Philippakis, M.D., Ph.D., Chief Data Officer, Broad Institute

4:30 Using Cloud Platforms for Consumer-Driven Integration of Research and Operations
Jonas Almeida, Ph.D., Professor & CTO, Department of Biomedical Informatics, Stony Brook University (SUNY)

5:00 Managing the Mayhem: Overcoming the Challenges of Long-Term Data Retention
Sponsored by HGST
David Hiatt, Marketing, Vertical Marketing, Health and Life Sciences, HGST
Data volumes continue to grow and retention periods lengthen—whether by need or by mandate—so researchers and IT leaders face increasingly difficult decisions about how to meet long-term retention requirements yet keep the storage budget in check. Learn practical methods for managing the mayhem and making sure that more research dollars go to research rather than to infrastructure.

5:30 – 6:30 Best of Show Awards Reception in the Exhibit Hall with Poster Viewing

THURSDAY, APRIL 7

7:00 am Registration and Morning Coffee

8:00 PLENARY KEYNOTE SESSION PANEL
Please see page 3 for details.

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

HPC TRENDS IN THE TRENCHES 2016

10:30 Chairperson's Opening Remarks

10:40 FEATURED PRESENTATION: HPC Trends in the Trenches 2016
Chris Dagdigian, Founding Partner & Director, Technology, BioTeam, Inc.
In one of the most popular presentations of the Expo, Chris delivers a candid assessment of the best, the worthwhile, and the most overhyped information technologies (IT) for life sciences. He'll cover what has changed (or not) in the past year around infrastructure, storage, computing, and networks. This presentation will help you understand IT to build and support data intensive science.

11:40 Realize a Fiftyfold Increase in Sequencing by Combining Performance Scale-Out Storage with the Latest Next-Gen Sequencers
Sponsored by panasas
David Sallak, Vice President, Products & Solutions, Panasas
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11:55 How Next Generation Scale-Out Storage Is Enabling the Next Frontier of Life Sciences Breakthroughs
Sponsored by Qumulo
Joel Groen, Product Manager, Qumulo
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12:10 pm Session Break

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Track 2

Data Computing

Advances in Computing Applications for Big Data

12:20 Luncheon Presentation I: Object Storage: Enabling Genomic Sequencing at Petabyte Scale

Sponsored by SwiftStack

Joe Arnold, President and Chief Product Officer, Leadership, SwiftStack

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Sponsored by Igneous

Kiran Bhageshpur, CEO, Igneous Systems

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1:20 Dessert Refreshment Break in the Exhibit Hall with Poster Viewing

CONVERGENCE OF PREDICTIVE ANALYTICS AND BIG DATA

1:55 Chairperson's Remarks

Eric A. Stahlberg, Ph.D., [Contractor], High-Performance Computing Strategy, Data Science and Information Technology Program, Leidos Biomedical Research, Inc., Frederick National Laboratory for Cancer Research (FNLCR)

2:00 PANEL DISCUSSION: Actionable Big Data Analytics

Moderator: Eric A. Stahlberg, Ph.D., Leidos Biomedical Research, Inc., Frederick National Laboratory for Cancer Research (FNLCR)
Kiran Bhageshpur, CEO, Igneous Systems, Inc.
David King, CEO, Exaptive
Timothy Danford, Ph.D., Field Engineer, Tamr, Inc.

Leading life sciences experts will discuss trends and best practice case studies of turning big data into smart data that can lead to real time assistance in organization decision making, disease prevention, prognosis, diagnostics, and therapeutics. Learn how and where these organizations have assembled and analyzed information from different data 'silos' and deployed solutions to make decisions. We'll discuss technology tools used to move data and information from retrospective reporting to real-time predictive analytics. Walk away hearing practical steps, solutions, and capabilities that you can implement within your own organization.

3:30 Future Convergence

Eric A. Stahlberg, Ph.D., Leidos Biomedical Research, Inc., Frederick National Laboratory for Cancer Research (FNLCR)

4:00 Conference Adjourns

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Track 3

Software Applications & Services

Tools that Best Utilize Data to Drive Scientific Decision Making

TUESDAY, APRIL 5

7:00 am Workshop Registration and Morning Coffee

8:00 – 11:30 Recommended Morning Pre-Conference Workshops*
Security Considerations for Virtual Research

12:30 – 4:00 pm Recommended Afternoon Pre-Conference Workshops*
Growth Strategy: Leveraging Cloud Scalability to Enable Rapid Growth and Change
** Separate registration required*

2:00 – 6:00 Main Conference Registration

4:00 PLENARY KEYNOTE SESSION
Please see page 3 for details.

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

WEDNESDAY, APRIL 6

7:00 am Registration Open and Morning Coffee

8:00 PLENARY KEYNOTE SESSION
Please see page 3 for details.

9:00 Benjamin Franklin Awards and Laureate Presentation

9:30 Best Practices Awards Program

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

DATA INTEGRATION & MANAGEMENT: MODELS, CAPABILITIES, APPLICATIONS, AND SCALABILITY

10:50 Chairperson's Opening Remarks
Jane Reed, Ph.D., Head of Life Science Strategy, Business Development, Linguamatics

11:00 Allotrope Foundation: Driving Metadata and Master Data Management through Improved Data Modeling with Semantic Technologies
Dana Vanderwall, Associate Director, Cheminformatics, Research Information Technology & Automation, Bristol-Myers Squibb; Vice Chair, Allotrope Board of Directors
We will briefly describe some of the current data integration and management challenges facing the industry and how the Allotrope Framework provides a semantic basis for improved metadata and master data management through the use of modularized semantic models that capture the most pertinent entities, attributes and relationships needed to capture the plethora of laboratory data.

11:30 An Overview of the RightFind XML for Mining Platform
Haralambos Marmanis, Ph.D., CTO & Vice President, Engineering & Product, Copyright Clearance Center
In the pharmaceutical and biomedical industries, easy access to the complete scientific corpus can become a catalyst for new discoveries in drug and treatment research. We have created a single platform that provides access to full-text XML articles from the most sought after international, peer-reviewed, scientific journals. We will present the current platform capabilities, talk about the problems it solves, and future opportunities.

12:00 pm Integration and Flexibility Supporting Advanced Biologics Processes
Sponsored by BIOVIA
Sean McGee, Product Marketing Manager, BIOVIA
The complex processes in Biologics require flexible tools that at the same time support integration and compliance. The Electronic Lab Notebook from BIOVIA, based on an open foundation allows streamlining and integrating the flow of information and tasks within and between teams. It works as an integration hub enhancing efficiency and collaboration while reducing compliance risks for Biologics processes throughout the biotherapeutics lifecycle.

12:15 Strategies for Interoperability Using Modern API's
Sponsored by CORE INFORMATICS
John Stalker, Product Manager, Core Informatics
R&D organizations need to analyze and manage data across informatics systems. Historically, this interoperability has required coding complex, one-off integrations. Well-architected modern API's can leverage a standardized platform to broker data exchange, mitigating the need for purpose-built code. This presentation will share strategies and examples of how modern API's can help you achieve these interoperability goals.

12:30 Session Break

12:40 Instant 3D Molecular Search for Everyone: FastROCS on the Web
Sponsored by OpenEye Scientific Software
Brian Cole, Toolkit Product Manager & Lead Technology Strategist, OpenEye Scientific Software
FastROCS won the BioIT World 2011 Best of Show for its paradigm-shifting performance improvements using GPUs. Adoption continues, but is still restricted to molecular modeling platforms used by full-time modelers. To reach a broader audience of chemists OpenEye broke free from traditional monolithic modeling applications and created an interface in the universal language of the web. The web-platform is the future direction of OpenEye and a perfect place to showcase OpenEye's other novel technology: Grapheme-TK.

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

1:40 Session Break

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Track 3

Software Applications & Services

Tools that Best Utilize Data to Drive Scientific Decision Making

DATA INTEGRATION & MANAGEMENT: MODELS, CAPABILITIES, APPLICATIONS, AND SCALABILITY

1:50 Chairperson's Remarks
Brian Bissett, Senior Member, Baltimore Section, Institute of Electrical and Electronic Engineers (IEEE)

1:55 Enabling Cross-Group Collaboration on Cell Lines via Arxspan's ArxLab
Bruce Kozuma, Systems Analyst & Project Manager, Broad Information Technology Services, The Broad Institute of MIT and Harvard
Gain insight into how the Broad solved a common and intransigent issue facing a variety of diverse organizations using cloud-based, current generation laboratory data management software in a manner that can be reapplied in a variety of situations. Learn how different departments within the Broad worked collaboratively with Arxspan to solve this issue in a manner horizontally, i.e., differently from either a bottom up or top down approach.

2:25 Regeneron Genetics Center's Use of the DNAnexus Annex in the Amazon Cloud for Large-Scale NGS Downstream Compute
Christopher Sprangel, Director, IT, Human Genetics, Genome Informatics, Regeneron Genetics Center
Nathan Wallace, Founder & CEO, Turbot
The Regeneron Genetics Center (RGC) has worked with DNAnexus to build out a secure but highly flexible high performance compute (HPC) environment in the AWS cloud. This compute environment, providing high scalability and security, is managed by a high-reliability DNAnexus system that provides layered, software-defined compute instances, with continual monitoring and patching of the systems, available in VPCs for general compute use.

2:55 Combining Life Science Applications with the Economical Benefits of a Cloud-Based Archive
Sponsored by caringo
Tony Barbagallo, VP, Product Marketing, Caringo
Advancements in research instrumentation such as gene sequencers, and mass spectrometers combined with increases in image resolution are leading to a tremendous amount of data. Often the resulting data is stored in silos, limiting reuse and collaboration. We will describe how you can consolidate all data on one public/private or hybrid cloud storage solution and provide secure access and search across the consolidated data set while still using your existing applications.

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

DATA INTEGRATION & MANAGEMENT: MODELS, CAPABILITIES, APPLICATIONS, AND SCALABILITY

4:00 Computerized Clinical Decision Support for Laboratory Services: The Brigham and Women's Hospital Experience
Milenko Tanasijevic, M.D., MBA, Vice Chair for Clinical Pathology, Department of Pathology & Director, Clinical Laboratories, Brigham and Women's Hospital and Dana Farber Cancer Institute; Associate Professor of Pathology, Harvard Medical School
The talk will focus on our experience with development and deployment of various computerized, physician order-entry driven interventions to improve utilization of laboratory tests. These include lab charge displays, reminders for redundant tests, computerized alerting protocols, messaging about appropriate frequency and timing of therapeutic drug monitoring levels. Their impact on lab utilization will be discussed along with plans for future interventions using our newly implemented EPIC / eCare hospital information system.

4:30 From Bathroom to Healthroom: How Magical Technology Will Revolutionize Health
Juhan Sonin, Director, Design, Mechanical Engineering, GoInvo, MIT
As design harnesses digital, materials and networking technologies, a very new health experience is just over the horizon. Proactive, lifestyle design. Tracking real-time health data. Non-invasive tools. Custom "just for you" treatments based on your actual genome. These are all real technologies, being used by ordinary people. From Bathroom to Healthroom introduces participants to the macro factors shaping these realities, along with an in-depth exploration of the various impacts of and opportunities for design.

5:00 How Biogen Doubled Biologics Manufacturing Yield through Advanced Predictive Analytics
Matt Griffiths, Senior Vice President and CIO, Biogen

5:30 – 6:30 Best of Show Awards Reception in the Exhibit Hall with Poster Viewing

THURSDAY, APRIL 7

7:00 am Registration and Morning Coffee

8:00 PLENARY KEYNOTE SESSION PANEL
Please see page 3 for details.

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

PRACTICES AND POLICIES TO PROTECT SENSITIVE DATA

10:30 Chairperson's Opening Remarks
Dinesh Vandayar, Vice President, Personalized Medicine, SAP SE

10:40 Standardized Security Systems: How They Protect Pharmaceutical Data from Breaches
Mollie Shields-Uehling, President, SAFE-BioPharma Association
Information security breaches are a problem. Globalization and digitization of drug development relies on the Web to share information, exposing patient data and scientific intellectual property to hacks. The session reviews standardized security systems, and their use allowing the secure free flow of information across firewalls among collaborating parties. It includes best practices used by stakeholders such as Merck, GSK and Pfizer.

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Track 3

Software Applications & Services

Tools that Best Utilize Data to Drive Scientific Decision Making

11:00 Possession is 9/10ths of the Law: Considerations and Evaluations for IT Security Policies

Brian Bissett, Senior Member, Baltimore Section, Institute of Electrical and Electronic Engineers (IEEE)

High-level IT security breaches have made the news numerous times over the past year. Despite the awareness of the risks security breaches pose to organizations, they are still occurring with alarming frequency across all enterprises in both the public and private sector. Is this to become the new norm or has it ushered in a catalyst for change?

11:20 Accessing and Utilizing Public Genomic Data: How Hard Can It Be?

Dianne Pacheco, Information Security Officer, The Jackson Laboratory

Gregg TeHennepe, IT Project Manager, The Jackson Laboratory

The world is awash in Big Data, including large public genomic data sets such as TCGA. Access to these data sets is cited as a high-priority need for research programs; however, the technical and administrative logistics can be daunting. In this talk we will cover the security policies and practices needed to satisfy the data use requirements associated with major public genomic data sets.

11:40 Innovating, Reimaging, and Digitally Transforming Personalized Medicine

Sponsored by SAP

David Delaney, Ph.D., CMO, SAP SE

With a flexible platform and advanced analytics, new digital solutions from SAP are uniquely positioned to help advance personalized medicine. The SAP Foundation for Health and applications such as SAP Health Engagement support deeper insights and connect data silos. Bring together your mission-critical structured, unstructured, public private, and experimental health data to provide better patient outcomes.

12:10 pm Session Break

12:20 Luncheon Presentation *(Sponsorship Opportunity Available)* **or Lunch on Your Own**

1:20 Dessert Refreshment Break in the Exhibit Hall with Poster Viewing

BIG DATA: SHARING VS. PRIVACY VS. SECURITY IN HEALTHCARE

1:55 Chairperson's Remarks

John M. Conley, J.D., Ph.D., William Rand Kenan, Jr. Professor of Law, University of North Carolina, Chapel Hill; Counsel, Robinson Bradshaw & Hinson

2:00 FEATURED PRESENTATION: precisionFDA

Taha A. Kass-Hout, M.D., MS, Chief Health Informatics Officer & Director, Office of Health Informatics, FDA

precisionFDA is an informatics cloud-based platform for ensuring the accuracy of Next-Generation Sequencing (NGS) tests by crowdsourcing reference material and data. A key part of President Obama's Precision Medicine Initiative, it serves as a collaborative research effort that will inform later regulatory pathways and decision making. During this talk, Dr. Taha Kass-Hout, FDA's Chief Health Informatics Officer, describes the platform and its successes since the December 2015 beta release.

2:30 FEATURED PRESENTATION: How the Plecosystem, Blockchain, and Federated Data Enclaves will Shape Genomics Innovation and Application: Emerging Initiatives from the Global Alliance for Genomics and Health

John E. Mattison, M.D., Chief Medical Information Officer, Assistant Medical Director, Southern California Medical Group, Kaiser Permanente; Co-Chair, eHealth Workgroup, Global Alliance for Genomics and Health GA4GH

How can we maximize genomic research for the good of all citizens without violating their privacy? We need powerful new approaches to ensure ethical research without unwarranted risk to citizens who consent to use of personal data. The Global Alliance for Genomics and Health includes worldwide institutions seeking consensus on policy frameworks supported by creative technical solutions to achieve these paired goals of higher value and lower risk. I discuss progress to date.

3:00 FEATURED PRESENTATION: Large-Scale Data Commons for Genomic and Clinical Data and the Changing Landscape for Sharing Research Data

Robert Grossman, Ph.D., Director, Center for Data Intensive Science (CDIS); Core Faculty, Institute for Genomics & Systems Biology and Computation Institute, Professor of Medicine, Section of Genetic Medicine, University of Chicago

Open commons containing large amounts of public biomedical data from the research community can, potentially, dramatically speed up medical research. We describe our experiences developing large-scale open source data commons for genomic and associated clinical data. We also discuss options for integrating and interoperating in-house genomic and clinical data with public data commons and private data partnerships.

3:30 PANEL DISCUSSION: How Will Data Sharing Innovations Fare in the Regulatory Environment?

Moderator: John M. Conley, J.D., Ph.D., William Rand Kenan, Jr. Professor of Law, University of North Carolina, Chapel Hill; Counsel, Robinson Bradshaw & Hinson

Panelists:

Robert Grossman, Ph.D., University of Chicago

Taha A. Kass-Hout, M.D., MS, FDA

John E. Mattison, M.D., Kaiser Permanente

Andrew K. Porter, Merck & Co.

Mollie Shields-Uehling, SAFE-BioPharma Association

The growth in patient healthcare and life sciences innovations can be attributed to technology enhancements like cloud computing, big data analytics and mobile applications, but may conflict with increasing regulatory compliance demands to ensure protection of healthcare life and quality as well as patient data privacy and security. This panel of esteemed technology solution providers and regulators debates real-world challenges and how regulation must also innovate at technology's pace.

4:00 Conference Adjourns

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Track 4

Cloud Computing

Applying Cloud for Next-Generation Computing

TUESDAY, APRIL 5

7:00 am Workshop Registration and Morning Coffee

8:00 – 11:30 Recommended Morning Pre-Conference Workshops*
Security Considerations for Virtual Research

12:30 – 4:00 pm Recommended Afternoon Pre-Conference Workshops*
Growth Strategy: Leveraging Cloud Scalability to Enable Rapid Growth and Change
** Separate registration required*

2:00 – 6:00 Main Conference Registration

4:00 PLENARY KEYNOTE SESSION
Please see page 3 for details.

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

WEDNESDAY, APRIL 6

7:00 am Registration Open and Morning Coffee

8:00 PLENARY KEYNOTE SESSION
Please see page 3 for details.

9:00 Benjamin Franklin Awards and Laureate Presentation

9:30 Best Practices Awards Program

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

ADOPTING CLOUD WITH VARIOUS DEPLOYMENT MODELS

10:50 Chairperson's Opening Remarks
David LaBrosse, Strategic Partner Manager, NetApp Healthcare

11:00 Building the Bionic Cloud
Michaela Iorga, Ph.D., Senior Security Technical Lead for Cloud Computing; Co-Chair, NIST Cloud Security Working Group; Co-Chair, NIST Cloud Forensic Science Working Group, National Institute of Standards and Technology
When coupling the continuously growing and changing landscape of advance persistent threats with the explosion of "pervasive computing" or "ambient intelligence" founded by the hyperconnectivity of "everyware", we reach a technical inflection point which calls for innovative solutions to support the further development of a strong, secure backbone of the Internet of Things (IoT) – a bionic cloud.

11:30 Adopting Public Cloud at Enterprise Scale: Public IaaS at AstraZeneca
Don Barber, Infrastructure Architect, Enterprise Computing, IT Infrastructure & Operations, AstraZeneca
Public cloud adoption at scale requires significant rethinking of enterprise systems, processes and culture. This talk outlines how AstraZeneca IT has made this journey to offer public cloud as an enterprise service by tackling challenges with provisioning, management, security and qualification. Subject material will range broadly from technical issues to policy challenges and workforce education needs, concluding with a few predictions about the future.

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

Sponsored by Google Cloud Platform

12:15 Bringing Data and Computing Together to Enable Research Innovation
Joe Corkery, M.D., Senior Product Manager, Google Cloud Platform
We will discuss how the vast data storage, sharing, and computing capabilities of Google Cloud Platform have enabled numerous researchers to bring together previously unwieldy data sets to gain novel insights. We will also explore how access to Google's cloud resources enables researchers to revisit traditional approaches to data analysis and pursue new methodologies that would otherwise be out-of-reach in a traditional environment.

12:30 Session Break

Sponsored by LabAnswer LABORATORY INFORMATICS

12:40 Luncheon Presentation I: Making Cloud R&D Electronic Laboratory Environments a Reality
John Conway, Global Director, Strategy and Technology, Research and Development, LabAnswer
The drivers behind moving to Cloud-based, enterprise class, scientific software applications are substantial, and the trend is rapidly gaining momentum. LabAnswer will showcase examples and discuss the practical considerations of deploying electronic laboratory environments (ELE) via the Cloud, including Electronic Laboratory Notebooks, LIMS, etc. Capabilities and functionality topics to be addressed include Data Governance, Entity Registration, Request/Sample/Inventory Management, and Data Aggregation & Analytics.

Sponsored by amazon web services

1:10 Luncheon Presentation II: Large-Scale Cancer Genomics in the AWS Cloud
Brian O'Connor, Ph.D., Managing Director, Cloud Technologies, Informatics and Bio-Computing, The Ontario Institute for Cancer Research
Angel Pizarro, MSE, Technical Business Development Manager, Scientific Computing, Amazon Web Services
ICGC recently made available the genomes of approximately 1,300 cancer donors as part of the AWS Public Data Sets program. In this presentation, learn how the Ontario Institute of Cancer Research leverages the cloud to process large-scale data sets like ICGC and uniformly analyze 900 TB of data in less than four months.

1:40 Session Break

1:50 Chairperson's Remarks
Tom Johnson, Senior Director & Product Manager, Pharma and Life Sciences Services, Exostar

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Track 4

Cloud Computing

Applying Cloud for Next-Generation Computing

1:55 Cloud Computing in a GxP Environment
Krista Woodley, Director, Digital Quality and Risk Management, Biogen
We discuss the regulatory expectations and associated challenges with moving to cloud-based solutions (SaaS, IaaS, PaaS). Discussion points include requirements for vendor oversight, validation and maintenance of cloud-based solutions.

2:25 Case Study: How Merck Is Leveraging Information Security to Enable & Accelerate Clinical Trials
Andrew K. Porter, Director, Enterprise Architecture, IT Planning & Innovation, Merck & Co.
Bringing data, applications and people together for clinical trials takes too long, costs too much and leaves security gaps that threaten intellectual property and regulatory compliance. Merck explains its cloud-based solution to close these gaps and mitigate risks by leveraging entitlements management and fine-grained provisioning to automate partner onboarding, connect required applications and data, assign permissions and control access by authenticating identities.

2:55 Why Would You NOT Use Public Clouds for Your Big Compute Workloads?
Sponsored by CYCLE COMPUTING
Jason Stowe, CEO, Cycle Computing
Up to now there's been resistance to leveraging the cloud for the compute and data intensive workloads that historically run on in-house HPC environments. But genomics, computational chemistry, and other data collection and analytics have outpaced internal capacity. The lure of zero queue times, unlimited amounts of processing, and the ability to directly fit jobs to budget/value instead to available capacity is proving impossible to resist. This talk will highlight the risks and rewards of doing science in the cloud.

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

APPLYING CLOUD FOR CANCER RESEARCH

4:00 Building Cloud-Enabled Cancer Genomics Workflows with Luigi and Docker
Jacob Feala, Ph.D., Principal Scientist, Bioinformatics, Caperna, an affiliate of Moderna Therapeutics
As bioinformatics scientists, we tend to write custom tools for managing our workflows, even when viable, open-source alternatives are available from the tech community. Our field has, however, begun to adopt Docker containers to stabilize compute environments. I introduce Luigi, a workflow system built by engineers at Spotify to manage long-running big data processing jobs with complex dependencies. Focusing on a case study of next-generation sequencing analysis in cancer genomics research, I show how Luigi can connect simple, containerized applications into complex bioinformatics pipelines that can be easily integrated with compute, storage, and data warehousing on the cloud.

4:30 The ISB Cancer Genomics Cloud
Sheila Reynolds, Ph.D., Senior Research Scientist, Ilya Shmulevich Laboratory, Institute for Systems Biology
The ISB-CGC is a cloud-based platform that will serve as a large-scale data repository for TCGA data, while also providing the computational infrastructure and interactive exploratory tools necessary to carry out cancer genomics research at unprecedented scales. The ISB-CGC will provide both interactive and programmatic access to the TCGA data, leveraging many aspects of Google Cloud Platform including BigQuery and Compute Engine.

5:00 GATK4 - The Next Generation of Broad Institute's Genomics Tools, on the Cloud
Adam Kiezun, Ph.D., Senior Group Leader, Computational Methods Development, Broad Institute of MIT and Harvard
The breathtaking pace of genomics growth requires tools and pipelines that can support cutting-edge analyses, at petabyte scales, with optimized speed and cost. With this in mind, we have launched GATK4, a complete reimagining of Broad's Genome Analysis Toolkit. GATK4 now supports both germline and somatic mutation analysis, CNV and SV detection, tumor heterogeneity analysis, and more. Designed with cloud infrastructure in mind, GATK4 is implemented with support for Apache Spark and is hundreds of times faster than previous generations of GATK.

5:30 – 6:30 Best of Show Awards Reception in the Exhibit Hall with Poster Viewing

THURSDAY, APRIL 7

7:00 am Registration and Morning Coffee

8:00 PLENARY KEYNOTE SESSION PANEL
Please see page 3 for details.

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

APPLYING CLOUD FOR LARGE-SCALE GENOMIC PROJECTS

10:30 Chairperson's Opening Remarks
Ben Cotton, Director, Customer Satisfaction, Cycle Computing

10:40 Splicing-Centric Analysis of RNA-Seq Data Using the SpliceCore Platform
Martin Akerman, Ph.D., CTO & Co-Founder, Envisagenics, Inc.; Cold Spring Harbor Laboratory
Over 15% of disease mutations can cause structural errors in mRNA through Alternative Splicing (AS). SpliceCore is a cloud-based platform for AS discovery, analysis and interpretation using RNA-seq data. SpliceCore assists the increasing demand of data analysis and innovation for RNA therapeutics. I demonstrate SpliceCore in a breast cancer study case, including implementation and experimental validation in collaboration with Cold Spring Harbor Laboratory.

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Track 4

Cloud Computing

Applying Cloud for Next-Generation Computing

11:10 A Cloud Computing Infrastructure for BLAST
Thomas L. Madden, Ph.D., Staff Scientist, National Center for Biotechnology Information, National Library of Medicine, National Institutes of Health
The BLAST Cloud platform allows a user to perform a large number of sequence similarity searches. The platform supports queries through a REST style API, a webpage and command-line searches. There is minimal setup as a FUSE client downloads the latest database. We discuss the project design and performance as well as the use of this project in an existing workflow.

11:40 Turning Biology into an Information Technology: Moving Experimental Biology into The Cloud
Max Hodak, Founder & CEO, Transcriptic, Inc.
Despite rapid advances in the science, the practice of molecular and cell biology looks similar today to 20 years ago. Transcriptic allows scientists to use a remote, software-defined infrastructure for complex workflows without upfront capital costs. This advance makes the lab itself another part of your data workflow, and lifts the focus from the bench to the analytics and science.

12:10 pm Session Break

12:20 Luncheon Presentation *(Sponsorship Opportunity Available)* **or Lunch on Your Own**

1:20 Dessert Refreshment Break in the Exhibit Hall with Poster Viewing

BIG DATA: SHARING VS. PRIVACY VS. SECURITY IN HEALTHCARE

1:55 Chairperson's Remarks
John M. Conley, J.D., Ph.D., William Rand Kenan, Jr. Professor of Law, University of North Carolina, Chapel Hill; Counsel, Robinson Bradshaw & Hinson

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Taha A. Kass-Hout, M.D., MS, Chief Health Informatics Officer & Director, Office of Health Informatics, FDA
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John E. Mattison, M.D., Chief Medical Information Officer, Assistant Medical Director, Southern California Medical Group, Kaiser Permanente; Co-Chair, eHealth Workgroup, Global Alliance for Genomics and Health GA4GH
How can we maximize genomic research for the good of all citizens without violating their privacy? We need powerful new approaches to ensure ethical research without unwarranted risk to citizens who consent to use of personal data. The Global Alliance for Genomics and Health includes worldwide institutions seeking consensus on policy frameworks supported by creative technical solutions to achieve these paired goals of higher value and lower risk. I discuss progress to date.

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Robert Grossman, Ph.D., Director, Center for Data Intensive Science (CDIS); Core Faculty, Institute for Genomics & Systems Biology and Computation Institute, Professor of Medicine, Section of Genetic Medicine, University of Chicago
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Panelists:
Robert Grossman, Ph.D., University of Chicago
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Track 5

Bioinformatics

Computational Resources and Tools to Turn Big Data into Smart Data

TUESDAY, APRIL 5

7:00 am Workshop Registration and Morning Coffee

8:00 – 11:30 Recommended Morning Pre-Conference Workshops*
Visualization for Biomedical Data Analysis: From the Basics to Applications

12:30 – 4:00 pm Recommended Afternoon Pre-Conference Workshops*
iConquerMS™: A Patient-Centered Research Model
** Separate registration required*

2:00 – 6:00 Main Conference Registration

4:00 PLENARY KEYNOTE SESSION
Please see page 3 for details.

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

WEDNESDAY, APRIL 6

7:00 am Registration Open and Morning Coffee

8:00 PLENARY KEYNOTE SESSION
Please see page 3 for details.

9:00 Benjamin Franklin Awards and Laureate Presentation

9:30 Best Practices Awards Program

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

DATA MANAGEMENT, MODELING AND VALUE COMPARISON

10:50 Chairperson's Opening Remarks
John Quinn, Ph.D., Application Scientist, FlowJo, LLC

11:00 canvasXpress: A Highly Interactive JavaScript Library for Analytic Visualization of Genomics (and Other High Dimensional) Data
Isaac Neuhaus, Ph.D., Senior Principal Scientist, Bristol-Myers Squibb
This talk will describe how this package integrates with our R environment.

11:30 eTRIKS and tranSMART in IMI's PreDiCT-TB: Data Management, Modeling and Comparison
Francisco Bonachela Capdevila, Ph.D., Postdoc Data Coordinator, Translational Informatics and External Innovation, Janssen Pharmaceutica
PreDiCT-TB is an IMI-funded project which takes a comprehensive model-based approach to fill the gaps in the current drug development pathway in tuberculosis. Preclinical information is propagated into the clinical stage in order to optimize drug selection at the clinical phase. In this context, we have developed a tranSMART-based solution that extracts PK-PD modeling data from studies at any *in vitro*, *in vivo* or clinical stage of the drug development chain.

12:00 pm Fusing Systems Biology & Predictive Analytics for Multi `Omic Data: Demo of the PATH Platform for Knowledge Generation
Sponsored by Precision for Medicine
Scott Marshall, Ph.D., Managing Director, Biomarker and IVD Analytics, Precision for Medicine
The future of healthcare will be transformed by flexible frameworks designed to discover complex signals in rich datasets through the merger of predictive genomic analytics and systems biology that are designed to incorporate information about molecular and cellular systems across multi `omic data. PATH™ a secure, scalable, cloud-based solution for predictive genomic analytics serves as a knowledge generation platform for translational and clinical research.

12:30 Session Break

12:40 Luncheon Presentation I: Medical Evidence Is Becoming the Currency of Healthcare Transformation
Sponsored by IBM
Mark Sexton, Principal Offering Manager, Epidemiology Method
This session will share experiences applying IBM Watson Real World Evidence solutions to help researchers explore huge volumes of unstructured and structured content to discover insights and information and produce medical evidence. Examples include identifying unmet medical needs; demonstrating product value and differentiation for pharmaceuticals and medical devices; improving drug comparative effective studies; and competitive intelligence.

1:10 Luncheon Presentation II: When Every Piece Matters: Mobilizing Informational Resources for Rare Diseases
Sponsored by Elsevier R&D Solutions
Anton Yuryev, Ph.D., Consultant, R&D Solutions, Elsevier
Disease-centric knowledgebases remain a challenge as information is scattered across multiple resources. Elsevier collaborates with Findacure charity to create a portal for patients, researchers, and doctors to help finding up-to-date information and assist in new treatment discovery. We describe our integrative approach to construct a knowledgebase for congenital hyperinsulinism containing disease mechanisms, targets, drugs, key opinion leaders and institutions.

1:40 Session Break

NOVEL BIOINFORMATICS AND DATA ANALYSIS APPROACHES

1:50 Chairperson's Remarks
Michael Liebman, Ph.D., Managing Director, IPQ Analytics, LLC

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Track 5

Bioinformatics

Computational Resources and Tools to Turn Big Data into Smart Data

1:55 From Phenotype to Genotype: Using TranSMART for Managing Human Genetics Data
Andrew Hill, Science and Technology Lead, Research Business Technology, Pfizer
Genotype/phenotype analysis informs target identification, validation, mechanistic understanding, and precision medicine. Genetic variants and associated phenotype datasets are large, complex, and difficult to manage and access. The bioinformatics community needs to share information about both challenges and solutions. In this presentation we'll describe our experience with using TranSMART as a repository for human genotype-phenotype data.

2:25 Case Study: Cloud-based High- Performance Platforms to Unblock and Speed Genome Analysis
Kurt Florus, CTO, Bluebee
Reducing cost and complexity of genetic analysis in a rapidly growing number of genome studies is challenging. Learn from our recent key projects how cutting-edge innovations in hardware acceleration and distributed computing are affecting cloud-based genomics platforms, and how leveraging HPC techniques enable researchers to ask even more ambitious research questions, and allow clinicians to take full advantage of these powerful NGS diagnostic tools.

2:55 Increasing the Competitiveness of Pharma Companies: Real Time Search and Analytics Across Structured & Unstructured Data
Sponsored by SINEQUA
Xavier Pornain, WW Vice President, Sales and Alliances, Sales, Sinequa
This presentation highlights how Sinequa's platform helps leading pharma companies in the following areas: 1) Speed up submission of New Drug Applications to reduce costs for new drugs development; 2) Drive innovation, accelerate research and shorten Drug Time-to-Market; 3) Foster cooperation in R&D while respecting information governance and security; and 4) Optimize clinical trials and catalyze drug repositioning.

3:10 From Out that Shadow: Diagnosis, Discovery and Data Integration in Single-Cell Phenomics
Sponsored by FLOWJO, LLC
Michael Stadnisky, Ph.D., CEO, FlowJo, LLC
The standardization, throughput, and content of single cell assays has brought flow cytometry and digital PCR into the mainstream. However, data analysis has remained in the shadows, relying on expert supervision and manual analysis, and rarely integrated into the life science data ecosystem. We show that an intuitive analysis platform can democratize diagnosis and discovery in single cell assays and significantly accelerate time to insight.

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

4:00 Selected Poster Presentation: A Computational Approach to Identify Antibody Functional Paratopes for Synthetic Antibody Library Design
Hung-Pin Peng, Ph.D., Postdoctoral Fellow, Genomics Research Center, Academia Sinica

4:30 From GWAS and Whole Genomes to Personalized Therapeutics: Non-Coding Variants for New Drugs
Leonard Lipovich, Ph.D., Associate Professor, Center for Molecular Medicine and Genetics, Wayne State University
Although two-thirds of human genes do not encode proteins, studies of significant human disease-associated genetic variants from exomes, Genome-Wide Association Studies, and whole-genome sequencing continue to emphasize protein-coding genes. However, coding genes are often far, and separated by recombination breakpoints from, these significant variants. Here, we identify candidate disease causative non-coding variants for wetlab validation and eventual therapeutic targeting. A list of co-authors appears on the Bio-IT Conference website alongside this abstract.

5:00 Selected Poster Presentation: Right-Size Your TCO: Advanced Cost Optimization Techniques for Secure Genomics in the Amazon Cloud
Andrey Kislyuk, Ph.D., Research Assistant, Georgia Institute of Technology

5:30 – 6:30 Best of Show Awards Reception in the Exhibit Hall with Poster Viewing

THURSDAY, APRIL 7

7:00 am Registration and Morning Coffee

8:00 PLENARY KEYNOTE SESSION PANEL
Please see page 3 for details.

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

PATENT LAW AND MODELING RISKS/OPPORTUNITIES

10:30 Chairperson's Opening Remarks
Mike Stadnisky, Ph.D., CEO, FlowJo, LLC

10:40 Dramatic Changes in US Patent Law: The Implications for Bioinformatics
John Conley, J.D., Ph.D., Professor, Law, University of North Carolina
Not too long ago, patents on software and software-based analytical methods--in medicine, finance, and business generally--were commonplace and concern about their effects was profound. Now, after a series of Supreme Court cases, those patents are facing legal extinction. This presentation will explain the recent developments in patent law and their legal, practical, and economic implications for the bioinformatics industry.

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Track 5

Bioinformatics

Computational Resources and Tools to Turn Big Data into Smart Data

11:10 Building a Platform for Modeling Risk and Opportunities in Drug Development
Michael Liebman, Ph.D., Managing Director, IPQ Analytics, LLC
Sabrina Molinaro, Ph.D., Institute for Clinical Physiology, National Research Council, Italy

11:40 Capturing BIA-10-2474 and Related FAAH Inhibitor Data in the IUPHAR/BPS Guide to PHARMACOLOGY
Christopher Southan, Ph.D., Database Curator, IUPHAR/BPS Guide to PHARMACOLGY, University of Edinburgh

12:10 pm Session Break

12:20 Luncheon Presentation *(Sponsorship Opportunity Available)* **or Lunch on Your Own**

1:20 Dessert Refreshment Break in the Exhibit Hall with Poster Viewing

MOLECULAR BIOTECHNOLOGY AND BIOINFORMATICS: INFORMATICS TOOL AND THERAPEUTIC APPLICATIONS

1:55 Chairperson's Remarks
William Loging, Ph.D., Associate Professor of Genomics & Head, Production Bioinformatics, Genetics and Genomics Sciences, Icahn School of Medicine at Mount Sinai

2:00 Bioinformatics Pipeline for Detection of Fusions and Gene Expression in Clinical Oncology Samples using RNA-Seq
Keith Callenberg, Ph.D., Lead Bioinformatics Scientist, Molecular & Genomic Pathology, University of Pittsburgh Medical Center

2:30 Talk Title to be Announced
Andreas Matern, VP, Partnerships and Innovation, Executive Management, GeneDx

3:00 Molecular Impacts of Immune Modulating Drugs on Cancer Patients
William Loging, Ph.D., Associate Professor of Genomics & Head, Production Bioinformatics, Genetics and Genomics Sciences, Icahn School of Medicine at Mount Sinai

The area of Immuno-Oncology provides a novel strategy for cancer treatment by utilizing the patient's Immune system to combat tumor growth. We investigated the impact of specific immune modulating drugs on patients with diagnosed tumors in order to understand the molecular changes that take place at the pathway level. These data are correlated to phenotypic effect and provide insights into the mechanism of immune system directed therapies for cancer.

3:30 Biosimilar Structural Comparability Assessment by NMR: From Small Proteins to Monoclonal Antibodies
Bostjan Japelj, Ph.D., Senior Scientist, Protein Biophysics and Bioinformatics, Sandoz Biopharmaceuticals

This talk will discuss 1) the insight on how to use NMR as a method to evaluate high order similarity between biosimilar and reference product on the market; 2) methods to evaluate degree of similarity between two NMR spectra of proteins shown by examples from three case studies; and 3) an update on the current state of the art NMR spectroscopy in biosimilar drug product formulations and associated challenges.

4:00 Conference Adjourns

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Track 6

Next-Gen Sequencing Informatics

Advances in Large-Scale Computing

TUESDAY, APRIL 5

7:00 am Workshop Registration and Morning Coffee

8:00 – 11:30 Recommended Morning Pre-Conference Workshops*
Intelligent Methods Optimization of Algorithms of NGS

12:30 – 4:00 pm Recommended Afternoon Pre-Conference Workshops*
Determining Genome Variation and Clinical Utility

** Separate registration required*

2:00 – 6:00 Main Conference Registration

4:00 PLENARY KEYNOTE SESSION
Please see page 3 for details.

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

WEDNESDAY, APRIL 6

7:00 am Registration Open and Morning Coffee

8:00 PLENARY KEYNOTE SESSION
Please see page 3 for details.

9:00 Benjamin Franklin Awards and Laureate Presentation

9:30 Best Practices Awards Program

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

BEST PRACTICES OF PERSONAL GENOME ASSEMBLY AND INFORMATION MANAGEMENT SYSTEMS

10:50 Chairperson's Opening Remarks
Hans Cobben, CEO, Bluebee

11:00 Time to Build Personal Genome
Wenming Xiao, Ph.D., Staff Fellow, Division of Bioinformatics and Biostatistics, National Center for Toxicological Research, FDA

This presentation will discuss the importance of establishing the best practice of personal genome assembly and quality matrices and to provide guidance for usage of personal genome in clinical application by investigating the impact of various the next-generation sequencing (NGS) parameters, such as coverage, read length, and methods on assembly quality.

11:30 An Innovative and Globally Distributed Genome Management System
Thomas Thies, Senior Scientist, Data/Information Architecture and Terminology, pREDi, Roche

The huge amount of genomic data which needs to be analyzed timely by a globally distributed scientific workforce cannot move around the globe. Instead the analysis pipes are brought to the data. This talk will introduce you to a solution that follows this new paradigm. In addition it will explain how we are leveraging existing HPC environments including governance models which fuel the innovative capacity of our computational scientists.

Sponsored by IBM

12:00 pm An Integrated High Performance Analytics Solution for Genomics and Translational Research
Kathy Tzeng, WW Technical Lead, Healthcare and Life Science Solutions, IBM Systems, IBM
Janis Landry-Lane, WW Program Director, Healthcare and Life Science Solutions, IBM Systems, IBM

The rapid advances in sequencing technology are driving the use of genomics information in various domains. Processing raw data from a sequencer and translating it into insights in a timely fashion requires a high performance, scalable analytics solution to integrate genomics information with other data sources. IBM's approach of building integrated solutions with our customers and partners will be highlighted.

12:30 Session Break

Sponsored by illumina

12:40 Luncheon Presentation I: Not Just Noise: Transforming Big Data into Smart Data
Brady Davis, Senior Director, Informatics, Illumina, Inc.

When it comes down to it, big data is only a big deal when you can attach context and meaning to it. Smart data -- that is the right data at the right time to the right person -- can help professionals enhance and inform care decisions. That's the prize; and while everyone's got their eyes on it, not everyone knows how to get their hands on it. This session will focus on how Illumina is working to provide solutions that look at data at every stage, from collection and protection to collaboration, storage and analysis.

Sponsored by CRAY

1:10 Luncheon Presentation II: The Edge of Analytics Insight
Matt Gianni, Functional Solution Architect, Cray Inc
Ted Slater, M.A., M.S., Global Head of Healthcare & Life Sciences, Cray Inc.

Learn how to power your life science pipelines — from deep learning to clinical genomics — using the latest advances in analytics. Step up performance, enable the rigor your workloads require, and flex with the evolving needs of your business. Learn what software strategies scale best with Cray's novel, advanced system — including interconnects, advanced memory stacks, graph engines, storage and cluster management.

1:40 Session Break

LARGE SCALE COMPUTING

1:50 Chairperson's Remarks
Shanrong Zhao, Ph.D, Director, Pfizer Worldwide Research & Development

1:55 QuickRNASeq Lifts Large-scale RNA-seq Data Analyses to the Next Level of Automation and Interactive Visualization

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Track 6

Next-Gen Sequencing Informatics

Advances in Large-Scale Computing

Shanrong Zhao, Ph.D, Director, Pfizer Worldwide Research & Development

RNA sequencing is being increasingly used, in part driven by the decreasing cost of sequencing. Nevertheless, the analysis of the massive amounts of data generated by large-scale RNA-seq remains a challenge. By combing the best open source tools developed for RNA-seq data analyses and the most advanced web 2.0 technologies, we have implemented QuickRNASeq (http://quickrnaseq.sourceforge.net), a pipeline for large-scale RNA-seq data analyses and visualization. The high degree of automation and interactivity in QuickRNASeq leads to a substantial reduction in the time and effort, and QuickRNASeq advances primary RNA-seq data analyses to the next level of automation, and is mature for public release and adoption.

2:25 High-Throughput NGS Sequencing Using Ion Proton in a Clinical Genetic Testing Lab

Yirong Wang, Associate Director, Production Informatics, Department of Genetics and Genomic Sciences, Icahn School of Medicine at Mount Sinai

Clustered Ion Protons provide a highly scalable framework for high throughput sequencing in any genetic testing labs or core sequencing facilities while keeping the cost manageable. Highly customized LIMS and efficient data analysis pipeline also play critical roles in quality control and report generation and delivery. In an initial pilot study, we are able to sequence and process 6000 samples for a large panel (500+ genes) screening under 8 weeks.

2:55 Shifting a Pure Academic HPC Environment to a Mixed Protected and Free Environment – on the Same Platform

Sponsored by DDN STORAGE

Vanessa Borcherding, Director, Scientific Computing Unit, Weill Cornell Medicine, Department, Physiology and Biophysics, Weill Cornell Medical College

Completely open research computing platforms make sense. They're less expensive to design, build, and maintain, while giving unfettered access to data helps the collaborative process. However, increased collaborations with commercial entities and increased use of "deidentified" patient data are putting pressure on HPC operations to make security options seamless but without sacrificing performance and price points to which users are accustomed

3:10 Genomic Analysis on a Loosely Coupled AWS Platform with Highly Distributed NGS Data Analytics at a Massive Scale

Sponsored by bina TECHNOLOGIES

Tristan Lubinski, Associate Scientist, NGS Informatics, AstraZeneca

The global NGS team at AstraZeneca implements a robust, flexible and consumable platform to perform genomic analysis at scale. The Bina solution was tested by processing tens of thousands of TCGA exomes with modern algorithms against latest reference genome (hg38), in turn demonstrating that the driver mutational landscape of the TCGA can be redefined when comparing against public domain data.

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

LARGE SCALE COMPUTING

4:00 Lessons Learned Analyzing Thousands of Samples for Clinical Use Cases Using Amazon Web Services

Ravi Madduri, Fellow, Computation Institute, University of Chicago; Project Manager, Math and Computer Science Division, Argonne National Lab

Globus Genomics is a cloud-based, large scale genomics analysis service that is used by research consortiums, healthcare providers for analyzing 1000s of raw genomics datasets. In order to deliver results of the analyses on the tight deadlines, we created cost-aware resource scheduling on AWS resources and reusable recipes for setting up appropriate security controls required for compliance. In this talk, we will present some of the use cases and success stories from our work.

4:30 Federated EHR Network for Patient Cohort Discovery

Bhanu Bahl, Director of Informatics, Harvard Catalyst

Patient Cohort discovery, across multiple healthcare institutions is a challenge. The Shared Health Research Information Network ('SHRINE'), a Harvard Catalyst's open source web-based query tool helps overcome the barriers arising due to variability in the source electronic health record (EHR) systems and returns aggregate numbers of patients across all sites with user-defined characteristics, currently demographics, diagnoses, medications, and selected lab values.

5:00 Selected Poster Presentation: Integrating Data, Tools, and Infrastructure for Efficient Collaboration and Management in Large-scale Biomedicine

Sven Nahnsen, Ph.D., Head, Quantitative Biology Center (QBiC), University of Tuebingen

High-throughput biology in the medical context aims at developing predictive models for disease development and therapy outcome. OMICS technologies and especially next-generation sequencing are becoming increasingly popular for the acquisition of adequate system-wide data. Such experiments need to involve stringent modelling of experiments and bioinformatics workflows to reach comprehensive metadata annotation and to enable automated processing and analyses. We present the latest developments towards the integrative analysis of large and complex high-throughput data; these include the integration of data and project management with state-of-the-art bioinformatics pipelines, as well as a production-scale hard- and software stake. Our integrated technology builds on Liferay as a portlet container, on workflow engines and finally on openBIS for data management application. The infrastructure is embedded in a multi-center environment and allows for distributed data acquisition and management. The modular nature of our software architecture allows for rapid extension of the functionality, such as novel pipelines are visualisation tools for NGS data.

5:30 – 6:30 Best of Show Awards Reception in the Exhibit Hall with Poster Viewing

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Track 6

Next-Gen Sequencing Informatics

Advances in Large-Scale Computing

THURSDAY, APRIL 7

7:00 am Registration and Morning Coffee

8:00 PLENARY KEYNOTE SESSION PANEL
Please see page 3 for details.

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

NGS AND INFORMATICS TO ADVANCE CANCER THERAPIES

10:30 Chairperson's Opening Remarks
Brandi Davis Dusenbury, Senior Scientist, Seven Bridges

10:40 Application of Targeted NGS Sequencing in Personalized Clinical Cancer Therapies
Qichao Zhu, Ph.D., Associate Professor, Genetics & Genomics Sciences, Icahn School of Medicine at Mount Sinai
Our current clinical cancer genome research project is focused on the three key components, sequence analysis for patient genetic profiling, biomarker (genetic variation) collection for cancer precision medicine, and the data processing and integration platform application for clinical report. The goal of the project is developing a comprehensive platform that can totally support precision medicine approach in cancer treatment.

11:10 Integration of Whole Genome and RNA Sequencing to Inform Clinical Treatment of Cancer
Michael Zody, Ph.D., Research Director, Computational Biology, New York Genome Center

11:40 Building National-Scale Genomics Projects with Collaborative, Portable, Reproducible Analysis
Sponsored by SevenBridges
Deniz Kural, CEO, Seven Bridges
The number of large genomics projects worldwide is rapidly growing. Such projects involve analysis of hundreds of thousands of whole genomes to accelerate discovery in basic and clinical research. National-scale genomics projects make intensive demands on computation and storage, and test the limits of existing infrastructure. They present severe challenges that require novel approaches to overcome.

12:10 pm Session Break

12:20 Luncheon Presentation *(Sponsorship Opportunity Available)*
or Lunch on Your Own

1:20 Dessert Refreshment Break in the Exhibit Hall with Poster Viewing

NGS AND INFORMATICS TO ADVANCE PRECISION CARE

1:55 Chairperson's Remarks
Yuval Itan, Ph.D., MRes, Postdoctoral Associate, Human Genetics of Infectious Diseases, The Rockefeller University

2:00 Talk Title to be Announced
Gunaretnam (Guna) Rajagopal, Ph.D., Vice President & Global Head, Computational Sciences, Discovery Sciences, Janssen Research & Development, A Johnson & Johnson Company

2:30 A Clinical Genetics Diagnostic System Incorporating Next-Gen Sequencing and Informatics to Advance Pediatric Precision Care
Marcia Nizzari, MS, CIO, Claritas Genomics
Claritas Genomics serves children affected with complex genetic disorders by providing timely and accurate results, resolving families' long search for answers. We developed a unique "orthogonal sequencing" approach that simultaneously sequences exomes on both the Illumina NextSeq and the Life Technologies Ion Proton instruments. This talk will cover both the lab approach and the bioinformatics analysis pipelines, key components of Claritas' enterprise architecture for pediatric precision care.

3:00 Software for Interpretation of Next-Gen Sequencing Data in a Clinical Setting
Neil Miller, Director, Informatics, Center for Pediatric Genomic Medicine, Children's Mercy, Kansas City
The Center for Pediatric Genomic Medicine at Children's Mercy, Kansas City has developed novel software applications which are specifically designed to enable non-expert clinicians and researchers to make use of targeted NGS in the diagnosis and management of rare disease. Learn about an end to end solution for interpretation of NextGen Sequence data which is used extensively in a children's hospital.

3:30 Finding a Needle in a Haystack: New Approaches to Identify Disease-Causing Mutations in Patients' Next Generation Sequencing Data
Yuval Itan, Ph.D., MRes, Postdoctoral Associate, Human Genetics of Infectious Diseases, The Rockefeller University

4:00 Conference Adjourns

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Track 7

Clinical Research & Translational Informatics

Transforming Biological Data to Clinical Development

TUESDAY, APRIL 5

7:00 am Workshop Registration and Morning Coffee

8:00 – 11:30 Recommended Morning Pre-Conference Workshops*
Opportunities and Challenges of Mobile Health, Wearables, and Sensors for Pharma

12:30 – 4:00 pm Recommended Afternoon Pre-Conference Workshops*
iConquerMS™: A Patient-Centered Research Model

** Separate registration required*

2:00 – 6:00 Main Conference Registration

4:00 PLENARY KEYNOTE SESSION
Please see page 3 for details.

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

WEDNESDAY, APRIL 6

7:00 am Registration Open and Morning Coffee

8:00 PLENARY KEYNOTE SESSION
Please see page 3 for details.

9:00 Benjamin Franklin Awards and Laureate Presentation

9:30 Best Practices Awards Program

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

BUILDING FRAMEWORKS, USING NEW TOOLS & INTEGRATING SYSTEMS TO IMPROVE THE RESEARCH PIPELINES

10:50 Chairperson's Opening Remarks
Jason Johnson, Ph.D., Executive Vice President and Head of R&D, PatientsLikeMe

11:00 Digital Biomarker Development at Roche pRED - From Sporadic Assessments to Continuous Monitoring of Parkinson's Disease in a Clinical Trial
Alain Nanzer, Ph.D., Global Head Safety & Development Workflows, Pharma Research and Early Development Informatics, Roche Innovation Center Basel
Automated and high frequency measures of disease progression are hard to come by. Traditional physician-led tests are only done periodically, missing the fluctuations of disease activity that strongly affect patient's quality of life. They also lack the objectivity that is crucial when developing medicines. Roche Pharma Research & Early Development (pRED) has developed a smartphone-based monitoring system for those with Parkinson's disease that complements the traditional physician-led assessments with automated tests that continuously measure their symptom fluctuations.

11:30 Establishing, Improving and Sustaining Primary and Secondary Clinical Exploratory Research Pipelines
Jay Bergeron, Director, Translational and Bioinformatics, Pfizer
Vendor-based (e.g. Oracle's TRC) and open source (e.g. tranSMART) solutions that manage exploratory clinical research data are available. However, establishing sustainable operational processes to support information flow from regulated to exploratory environments poses serious challenges to translational research. This talk will review the process elements that have been put in place at Pfizer to support an emerging exploratory data commons as well as the efforts undertaken to improve methods to prepare clinical exploratory data for access and analysis.

12:00 pm New Informatics for New Science: From Data Acquisition to Biomarker Validation
Sponsored by PerkinElmer For the Better
Jens Hoefkens, Director, Strategic Marketing, PerkinElmer
Here we present PerkinElmer Signals – a cloud-based data management platform that has been designed with flexible and scalable data models to provide the scalability and agility required to support modern life science research. To illustrate the versatility of the platform, we look at examples in areas as varied as Translational Medicine and High Content Screening.

12:15 More Than Code: True Interoperability Realized in Translational Medicine
Sponsored by Signet Accel True interoperability realized in healthcare.
Philip Payne, Ph.D., FACMI, Co-Founder, Signet Accel LLC
Does the promise of interoperability match the reality? Is the triple mandate of improving care, increasing safety and security, and lowering costs possible? Meet Avec™, a proven, working platform for data integration and sharing in arguably the most complex healthcare and research environment in history, that connects your information management systems, genomic and biospecimen data, clinical trial data, and EMRs.

12:30 Session Break

12:40 Luncheon Presentation I: The Intersection of Translational Informatics with Precision Medicine
Sponsored by illumina
John Shon, Vice President, Data Science and Bioinformatics, Illumina, Inc.
The $1,000 genome has unlocked many possibilities toward improved healthcare that are closely linked to the creation of rich patient cohorts. Once data inconsistencies are addressed and coupled to big data analytics, one can uncover patterns for patient response that could ultimately be clinically validated. John will describe a patient-centric data model/big data platform for clinical and/or therapeutic area researchers that is used across disease classification to uncover potential patient stratification models.

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Track 7

Clinical Research & Translational Informatics

Transforming Biological Data to Clinical Development

1:10 Luncheon Presentation II: Accelerating Insights in Translational Research: Self-Service Analytics and Visualizations at Amgen

Sponsored by ConvergeHEALTH by Deloitte.

George Seegan, Ph.D., Research & Development Informatics, Amgen
David Hardison, Ph.D., Vice President, Health Sciences, ConvergeHEALTH by Deloitte

Translational researchers often have a clear direction about research hypotheses, but the high cost of resources and lack of timeliness means only the high priority questions are even addressed. Amgen decided to tackle this problem by taking a cloud-based platform approach to build an information integration factory that delivers relevant data on demand to researchers through easy to use, extensible analytics, and visualization portal. Hear about the platform architecture and user examples.

1:40 Session Break

1:50 Chairperson's Remarks

Sastry Chilukuri, Partner, Pharmaceuticals & Medical Products, McKinsey & Company
Kees van Bochove, MSc, CEO, The Hyve

1:55 A Flexible Framework to Systematically Integrate and Report Clinical and Translational Data

John Lin, Manager, Software Engineering, Systems Engineering, Five Prime Therapeutics

Here we present a technology framework designed to systematically process and integrate clinical, safety, and translational data from multiple sources into a centralized data repository. The system encompasses automated data processing and transformation services, a flexible but immutable database schema to capture attribute-rich data, and interactive reporting for exploratory analysis and decision making. Case studies will be presented on how safety, PK, biomarker, and other clinical data from disparate sources and formats are unified globally to feed into dynamic visualizations.

2:25 In Pursuit of Precision Medicine

Brian Wells, Associate Vice President, Health Technology and Academic Computing, Information Systems, Penn Medicine

This presentation will focus on the information technology requirements related to achieving the goals of precision medicine. From next-gen sequencing to CTMS and EMR integration, Mr. Wells will describe the accomplishments, challenges and plans that lie ahead.

2:55 The Benefits of Metadata Towards Successful Translational Research

Sponsored by DEXSTR

Erwan David, Chief Technical Officer and Co-Founder, DEXSTR

Managing metadata is becoming as critical as the data itself. Hear how Inquiro, an unstructured data repository that leverages scientific metadata, will help scientists to store, access and share valuable data while facilitating curation and promoting data re-use in a translational approach.

3:10 The Information Management Platform of the Future

Sponsored by MarkLogic

James Morris, Information Architect, Smartlogic

Forward-looking life sciences companies are driving business value by integrating disparate data silos into a unified knowledge platform for a single view and using semantic technologies to harmonize and link the data. Join Smartlogic and MarkLogic to learn how their customers are leveraging MarkLogic's NoSQL database platform and Smartlogic's semantic technologies to construct the information management platform of the future.

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

NEW DIGITAL TECHNOLOGIES FOR CLINICAL TRIALS

4:00 From Bedside to Bench: Leveraging Biomarker and Clinical Trial Data to Inform Early Assets in the Pipeline

Som Bandyopadhyay, Ph.D., Translational Bioinformatics, Department of Genetically Defined Diseases and Genomics, Bristol-Myers Squibb

Baseline biomarker data and associated clinical trial data can be very informative in understanding disease pathophysiology and can help identify potential patient populations who may be responsive to other drugs in the development pipeline for that indication. To this end, at BMS, we are leveraging biomarker and clinical data from large clinical trials to help prioritize the development of multiple drugs in the pipeline for a given indication; help identify multiple indications for a given drug or identify new indications for an existing drug.

4:30 Disrupting Clinical Trials through Patient Engagement

Kamal Abbassi, BS, MS, Information Manager & Project Manager, Early Development Workflows, pRED Informatics, Roche Innovation Center NYC
Margaret Chan, Team Leader, Operations, Roche Innovation Ctr New York

Learn how to improve the clinical trial experience for patients through the use of digital technologies. Hear how to improve recruitment, engagement and retention with direct patient involvement. Discuss how to empower patients to make informed decisions.

5:00 De-Risking Drug R&D through Informatics, Genomics and Clinical Information

Sponsored by GeneDx

Andreas Matern, VP, Partnerships and Innovation, Executive Management, GeneDx

Stratifying populations for clinical trials is very complicated, even with the advent of Big Data. Understanding the genetic basis of a target, genotype-phenotype correlation, and patient selection remains challenging. This talk will highlight our expertise and informatics to help biopharmaceutical companies understand genomic data and identify patients with genetic diseases.

5:30 – 6:30 Best of Show Awards Reception in the Exhibit Hall with Poster Viewing

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Track 7

Clinical Research & Translational Informatics

Transforming Biological Data to Clinical Development

THURSDAY, APRIL 7

7:00 am Registration and Morning Coffee

8:00 PLENARY KEYNOTE SESSION PANEL
Please see page 3 for details.

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

TRANSLATIONAL INFORMATICS

10:30 Chairperson's Opening Remarks

10:40 Transforming Use of Real World Data Analytics
Minnie Chou, Director, Information Systems, Amgen
Real world data (RWD) analytics is a key enabler for bringing effective and safe medicines to patients faster and cheaper. It can improve study designs, reduce trial enrollment times, facilitate fast-track filing strategies, shorten response time to health authority queries, and support value proposition of medicines. This presentation will discuss our approach and learnings unlocking the power of real world data assets.

11:10 Virtual Systems Pharmacology – The Next Generation of a TR&D Modeling and Simulation Environment
Marko Miladinov, Informatics Lead, Bristol-Myers Squibb
The internally developed Virtual Systems Pharmacology (ViSP) platform was implemented at BMS as a dynamic, highly scalable, model agnostic and therapeutic area agnostic application. The system seamlessly integrates the modelling tool of choice by the user, a web-based application, command line utilities, a database back-end and automatically scaling HPC environment built in the BMS Research Cloud environment that can be used to configure, manage and execute large-scale simulations for multiple models (of any sort) by multiple users.

11:40 The New World: Improving Patient Lives through Clinical Analytics and Real World Evidence
Sastry Chilukuri, Partner, Pharmaceuticals & Medical Products, McKinsey & Company
Jonathan Usuka, Knowledge Expert, Pharmaceuticals & Medical Products, McKinsey & Company
Unprecedented access to RWE is unlocking new insights into treatment, conditions & precision medicine, with implications for shifting value in the pharmaceutical development ecosystem. An understanding of how a patient will respond to therapy is complex & requires large investments in trials, often leading to failure & frustration. But there are clues to predict & show therapeutic benefit hidden in piles of medical claims data. Where will the data take us? How can it be used to create value & possibly to replace pharma R&D?

11:55 Global Specimen Solutions - Technology Facilitating Unlocking the Future of Medicine™
Sponsored by GLOBAL SPECIMEN SOLUTIONS Unlocking the Future of Medicine™
Peter Tearle, Head, IT Architecture, Global Specimen Solutions, Inc.

12:10 pm Session Break

12:20 Luncheon Presentation I: Why is Data Integration So Hard?
Sponsored by THOMSON REUTERS
Tim Miller, VP, Integrated Applications, Thomson Reuters
Innovation is the life blood of the pharmaceutical industry and innovation runs on data. The Life Sciences industry is blessed with some of the best data resources – commercial and public databases, literature and ontologies. The Big Data revolution has given us a plethora of information and astounding tools for working with data, yet, the most common single issue faced by researchers is the problem of data integration.

12:50 Luncheon Presentation II *(Sponsorship Opportunity Available)*
or Lunch on Your Own

1:20 Dessert Refreshment Break in the Exhibit Hall with Poster Viewing

DATA VISUALIZATION FOR CLINICAL AND TRANSLATIONAL DATA

1:55 Chairperson's Remarks
Nirmal Keshava, Ph.D., Senior Principal Informatics Scientist, Research & Development Information, AstraZeneca PLC

2:00 Delivering Standardized Clinical and Pre-Clinical Data to Investigators in Guided Visualization Using Spotfire 6.5
Baisong Huang, Principal Statistical Analyst, NIBR Informatics, Novartis Institutes for BioMedical Research
As visualization tools evolve and become widely accepted in investigating and monitoring drug safety and efficacy, rapid access to standardized, interpretable data views is becoming essential. We will present some examples how we standardized and aggregated data in both translational and clinical settings and provided guided analysis to visualize the data in real time.

2:30 Deriving Knowledge from Real-World Evidence Using Large-Scale Analytics
Nirmal Keshava, Ph.D., Senior Principal Informatics Scientist, Research & Development Information, AstraZeneca PLC
In this talk, I will discuss the effort to develop large-scale analytics to derive knowledge and value from real-world evidence. This will be done in the context of using clinical data in real-world evidence databases to answer critical questions that can arise in both the clinical and pre-clinical problem spaces. I will focus on defining how the business problem is accurately translated into a mathematical problem and how that problem is addressed by data from real-world evidence databases.

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Track 7

Clinical Research & Translational Informatics

Transforming Biological Data to Clinical Development

3:00 Instrumenting the Healthcare Enterprise for Discovery Research

Shawn Murphy, M.D., Ph.D., Director, Research Computing and Informatics, Partners Healthcare; Associate Professor, Neurology, Harvard Medical School; Associate Director, Laboratory of Computer Science, Massachusetts General Hospital

The Healthcare Enterprise produces enormous amounts of data during clinical care that could potentially be used for human research. However, the quality of the data is very raw, and privacy concerns are paramount. Deriving knowledge from the data requires a combination of searching the data visually for hypotheses, computing derived patient attributes with well understood accuracies, and obfuscating data when necessary to preserve patient privacy.

3:30 Visualizing Variability in Electronic Health Records: The Variability Explorer Tool (VET)

Hossein Estiri, Ph.D., Senior Fellow, Institute of Translational Health Sciences, University of Washington

This presentation describes application of visual analytics in development of the Variability Explorer Tool (VET), which is designed to detect and explore variability in Electronic Health Records (EHR) data. Existing variability in EHR data limits their utility for healthcare decision-making and research. VET provides a suit of open-source statistical solutions to detect and explore variability across time and between units of analysis in EHR data.

4:00 Conference Adjourns

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Cambridge Healthtech Institute

Track 8

Data Visualization & Exploration Tools

Genomics, Drug Discovery, and Clinical Development

TUESDAY, APRIL 5

7:00 am Workshop Registration and Morning Coffee

8:00 – 11:30 Recommended Morning Pre-Conference Workshops*
Integrative Visualization Strategies for Large-Scale Biological Data

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

** Separate registration required*

2:00 – 6:00 Main Conference Registration

4:00 PLENARY KEYNOTE SESSION
Please see page 3 for details.

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

WEDNESDAY, APRIL 6

7:00 am Registration Open and Morning Coffee

8:00 PLENARY KEYNOTE SESSION
Please see page 3 for details.

9:00 Benjamin Franklin Awards and Laureate Presentation

9:30 Best Practices Awards Program

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

DATA VISUALIZATION FOR GENOMIC DATA AND DRUG DISCOVERY

10:50 Chairperson's Opening Remarks
Tom Johnstone, Managing Partner, Health & Life Sciences, Knowledgent

11:00 Approaches for the Integration of Visual and Computational Analysis of Biomedical Data
Nils Gehlenborg, Assistant Professor, Department of Biomedical Informatics, Harvard Medical School

The integration of computational and statistical approaches with visualization tools is becoming crucial as biomedical data sets are rapidly growing in size. Finding efficient solutions that address the interplay between data management, algorithmic and visual analysis tools is challenging. I will discuss some of these challenges and demonstrate how we are addressing them in our Refinery Platform project (http://www.refinery-platform.org).

11:30 FireBrowse: Mining the Firehose of TCGA Genomic Data
Michael Noble, Assistant Director for Data Science, Cancer Genome Analysis, Broad Institute

We introduce FireBrowse, a companion portal to the Broad Institute GDAC Firehose analysis pipeline. Developed for The Cancer Genome Atlas, and backed by a powerful compute infrastructure, programming interface, online reports and modern graphical tools, FireBrowse provides a simple yet capable means of visually and programmatically exploring one of the most comprehensive and deeply characterized open cancer datasets in the world.

12:00 pm Bringing Modeling to the Masses: LiveDesign, a Platform for Collaborative Drug Discovery
Sponsored by SCHRÖDINGER.
Sol Reisberg, Director, Business Development for Enterprise Informatics, Schrödinger

While the scientific power of computational chemistry has dramatically increased over the last several years, usage of computational methods in industry remains limited because of difficulties associated with software usage. Here, we present LiveDesign, a tool designed to allow collaborative design of small-molecule compounds, and rapidly prioritize designed ideas based on computational feedback. The thin client provides users with extreme ease-of-use, while the cloud-hosted server is highly scalable.

12:30 Session Break

12:40 Luncheon Presentation I *(Sponsorship Opportunity Available)*
or Lunch on Your Own

1:10 Luncheon Presentation II: If 80% of Your R&D Was Externalized, Could Your Current Informatics Infrastructure Support it?
Scott Weiss, Ph.D., Senior Director, Product Management & Product Strategy, IDBS

Externalization has fundamentally changed the way R&D teams plan work, share information and secure IP assets in a dynamic environment of ever changing partners. This presentation will review IDBS' E-WorkBook Connect a new, Cloud-based Informatics Solution, designed specifically to provide an easy to use, secure environment for B2B collaboration.With Connect, business users can quickly set up new projects, invite teams, capture and review content and securely publish data, document content back to the corporate systems.

1:40 Session Break

1:50 Chairperson's Remarks
Nils Gehlenborg, Assistant Professor, Department of Biomedical Informatics, Harvard Medical School

1:55 IOBIO: Interactive, Visually-Driven, Real-Time Analysis of Genomic Big Data
Chase Miller, Director of Research and Science, University of Utah, Eccles Department of Genetics, USTAR Center for Genetic Discovery, University of Utah School of Medicine

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Data Visualization & Exploration Tools

Genomics, Drug Discovery, and Clinical Development

IOBIO is a web-based system for big genomic data, which uses visualization coupled with real-time analysis to better understand complex and opaque data. We have developed several IOBIO web apps including quality control analysis of genomic alignment and variant data, interrogation of potential disease causing variants, and species identification and classification of raw sequencing data.

2:25 Big Mechanism Visualization: Interactive Analysis Techniques for Understanding Biological Pathway Networks

Angus Forbes, Assistant Professor, Computer Science, University of Illinois at Chicago

Understanding causality in biological pathways remains an active area of research for systems biologists, cancer researchers, and drug designers. This talk discusses recent explorations of interactive techniques that enable visual analysis tasks related to representing and analyzing causality in pathway networks, including identifying feedback loops and simulating the downstream effects of perturbing networks by "knocking out" proteins or protein complexes.

2:55 Innovation through Information: Enabling Proactive Healthcare Outcomes

Sponsored by Knowledgent

Chris Blotto, Managing Partner, Knowledgent

Today, methods to collect information about health and disease state are more advanced than ever. Modern day devices such as wearables and tablets, allow us to capture real world data that's now being combined with data sets such as cross-study clinical outcomes data, genetic biomarkers and compound/biologic target data to perform advanced analytics that are truly game changing. These methods are reducing the time it takes to execute analytic research projects from months, to days or hours. This discussion will focus on introducing the audience to architectures, technologies and models that have proven successful in this capacity.

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

TOOLS FOR EXPLORING AND VISUALIZING IMAGING DATA

4:00 Automating Image-Based High Content Screening

Fethallah Benmansour, Ph.D., Senior Imaging Specialist, Pharma Research & Early Development Informatics (pREDi), Roche Innovation Center Basel

Our integrated solution allows for automated data processing, on-the-fly interactive data mining and data visualization. By linking the data points to the images in a dynamically adjustable fashion, the solution allows for efficient QCing of the high content screening processes (including image analysis). It simplifies the study summary reports providing more confidence on the scientific findings.

4:30 BugID: An Intelligent Recognition System for Storage Pest Fragments Contaminating Food Products

Joshua Z. Xu, Ph.D., Senior Computer Scientist, Division of Bioinformatics and Biostatistics, National Center for Toxicological Research, U.S. Food and Drug Administration

Species identification of food contaminating insect fragments is critical to FDA's risk analysis and decision making during safety inspection of FDA-regulated food products. Combining image analysis and machine intelligence techniques, BugID will increase the reliability and throughput of food inspection by providing fast, consistent, and accurate insect identification results.

5:00 Enable Cancer Immunotherapy via Integrative Tissue Analytics

Franziska Mech, Ph.D., Data Scientist, Pharma Research and Early Development, pRED Informatics, Roche Innovation Center Penzberg

Establishing automated tissue imaging as high-throughput tool for understanding tissue context in the era of cancer immunotherapy. Integrating the obtained imaging data with other data sources such as clinical and genomic information and making it available for data scientists and biomarker experts via tailored interactive visualization tools.

5:30 – 6:30 Best of Show Awards Reception in the Exhibit Hall with Poster Viewing

THURSDAY, APRIL 7

7:00 am Registration and Morning Coffee

8:00 PLENARY KEYNOTE SESSION PANEL

Please see page 3 for details.

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

VISUALIZING ELECTRONIC HEALTH RECORDS FOR CLINICIANS

10:30 Chairperson's Opening Remarks

Tom Johnstone, Managing Partner, Health & Life Sciences, Knowledgent

10:40 A Real-Time Data-Driven Visualization within the Electronic Health Record

Randi Foraker, Ph.D., M.A., Assistant Professor, Epidemiology, College of Public Health, The Ohio State University

Health visualizations at the point-of-care can help bring electronic health record data to life for the patient and the provider. Automated tools that provide such visualizations can enhance patient-provider communication and shared decision-making, and make the healthcare encounter more efficient.

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Track 8

Data Visualization & Exploration Tools

Genomics, Drug Discovery, and Clinical Development

11:00 Information Visualization for Cognitively Guided Chronic Disease Risk Assessment and Personalized Interventions

Rema Padman, Professor of Management, Science & Healthcare Informatics, The H. John Heinz III College, Carnegie Mellon University

This presentation describes a novel methodology and a prototype software tool for quantitatively summarizing and visually displaying contextualized information on many relevant risk factors across many patients, which is particularly appropriate for chronic disease risk assessment. Using statistical dimensionality reduction methods combined with a novel data visualization approach, the tool provides two-dimensional visualizations and binary classification of chronic disease risk.

11:20 Visualizing Big Data and The Future of Cancer Care

Andrew K. Stewart, MA, Chief, Oncology Data, CancerLinQ

CancerLinQ is an clinical quality of care initiative of the American Society of Clinical Oncology. Data visualization for practicing oncologists is a cornerstone of the project. This presentation will illustrate approaches to visualizing quality of care performance metrics, longitudinal patient time-lines, and facilitating ad-hoc data interrogation by clinical users.

11:40 Raising the Bar for Central Medical Review

Sponsored by COVANCE SOLUTIONS MADE REAL

Victor Lobanov, Ph.D., Executive Director, Data Sciences, Covance Inc.

Periodic review of clinical data is critical for the patient safety and data quality. Covance's Medical Review is aligned with the FDA guidance for a greater role of central monitoring and provides timely, integrated views of all relevant clinical data along with the unique, interactive capabilities to detect outliers and trends, create and analyze cohorts, execute review workflows, annotate clinical data, and communicate observations.

12:10 pm Session Break

12:20 Luncheon Presentation *(Sponsorship Opportunity Available)* **or Lunch on Your Own**

1:20 Dessert Refreshment Break in the Exhibit Hall with Poster Viewing

DATA VISUALIZATION FOR CLINICAL AND TRANSLATIONAL DATA

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4:00 Conference Adjourns

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Track 9

Pharmaceutical R&D Informatics

Collaboration, Data Science and Biologics

TUESDAY, APRIL 5

7:00 am Workshop Registration and Morning Coffee

8:00 – 11:30 Recommended Morning Pre-Conference Workshops*
Data Management for Biologics: Registration and Beyond

12:30 – 4:00 pm Recommended Afternoon Pre-Conference Workshops*
Data Science Driving Better Informed Decisions

** Separate registration required*

2:00 – 6:00 Main Conference Registration

4:00 PLENARY KEYNOTE SESSION
Please see page 3 for details.

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

WEDNESDAY, APRIL 6

7:00 am Registration Open and Morning Coffee

8:00 PLENARY KEYNOTE SESSION
Please see page 3 for details.

9:00 Benjamin Franklin Awards and Laureate Presentation

9:30 Best Practices Awards Program

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

STRATEGY & ANALYTICS

10:50 Chairperson's Opening Remarks
Yuriy Gankin, Ph.D., Chief Life Sciences Officer; Vice President, Life Sciences, EPAM Systems, Inc.

11:00 Leverage the Wealth of Internal and External Information to Drive Collaboration and Project-Centricity into Your Research Informatics Platform for Drug Discovery and Development; A Strategic Imperative
James Connelly Ph.D., Global Head, Research Data Management, Sanofi U.S.
Drug Discovery Research organizations have a strategic imperative to fully leverage internal data and external data to drive efficiency and therapeutic innovation. Pilot studies with IBM Watson for toxicology and drug-repurposing along with the use of "Big Data" integration technologies with cloud-based SAR data platforms for collaboration will illustrate this opportunity.

11:30 Making Scientific Data 100x Easier to Use: Transforming Pharmaceutical R&D with Scalable Approaches to Data Stewardship and Data Integration
Carol Rohl, Ph.D., Executive Director, Scientific Information Management, Merck & Co., Inc.
The majority of resources in most scientific informatics projects are dedicated to accessing, understanding, curating, and integrating the input data assets. Declining R&D productivity and expanding data volume and variety are driving dramatic demand increases for analytics. To address the data challenges at scale we are combining stewardship capabilities that leverage crowdsourcing to enrich context and a platform solution to manage data variety, building on the Big Data technology stack as key components of an ecosystem of agile fit for purpose datasets and informatics solutions.

Sponsored by dotmatics

12:00 pm Informatics Solutions to Address the Changing Research Paradigms
Robert Brown, Ph.D., Vice President, Global Informatics, Dotmatics Ltd
Conducting research projects across multiple organizations presents a number of challenges which must be overcome for them to be successful. Using case studies from industry and academia, this talk will discuss how dedicated hosted informatics systems designed to support collaborative small molecule and biologics research can help enhance the success of these projects.

Sponsored by ACD/Labs

12:15 Integration of Rich, Connected Analytical Information Across Corporate Informatics Landscapes and the Impact on Innovation
Andrew Anderson, Vice President, Global Informatics, Advanced Chemistry Development, Inc
A variety of informatics tools are utilized to facilitate lab-to-lab, or scientist-to-scientist collaboration. However, these tools often require "abstraction" of certain data types – especially data resulting from analytical experiments conducted to characterize materials. This case study aims to provide a overview of how forward-looking organizations are enriching their collaboration interfaces with rich, standardized, live data "assemblies."

12:30 Session Break

Sponsored by COVANCE SOLUTIONS MADE REAL

12:40 Luncheon Presentation I: Raising the Bar for Central Medical Review
Victor Lobanov, Ph.D., Executive Director, Data Sciences, Covance Inc.
Periodic review of clinical data is critical for the patient safety and data quality. Covance's Medical Review is aligned with the FDA guidance for a greater role of central monitoring and provides timely, integrated views of all relevant clinical data along with the unique, interactive capabilities to detect outliers and trends, create and analyze cohorts, execute review workflows, annotate clinical data, and communicate observations.

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1:10 Luncheon Presenation II: Talk Title to be Announced
Scott Weiss, Ph.D., Senior Director, Product Management & Product Strategy, IDBS

1:40 Session Break

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Track 9

Pharmaceutical R&D Informatics

Collaboration, Data Science and Biologics

INNOVATION IN TEXT MINING & COMPUTATIONAL DESIGN

1:50 Chairperson's Remarks
Peter Covitz, Senior Director, Information Strategy & Analytics, Pfizer Worldwide Research and Development

1:55 Improving Decisions with Richer Data: Text Mining and Text Search
James Gill, Ph.D., Director, Research Analytics, Bristol-Myers Squibb
Recently there has been much ado about the amount of untapped data trapped in unstructured formats and the challenges extracting that data. Our group has been focusing on provisioning search and analysis of unstructured content for a number of years in domains such as patent analysis and literature searching. We will dive into examples our ongoing efforts and the tools and approaches we use to make text data more accessible and valuable to R&D scientists.

2:25 Of Soft Drinks and Software: A Framework to Sustain Innovation in Computational Molecular Design
Enoch Huang, Ph.D., Executive Director, Computational Sciences, Pfizer R&D
One of the challenges in sustaining innovation in computational molecular design is the need to harness and deliver promising solutions irrespective of their source, without creating new software applications or re-write existing ones. In this talk, I will provide an overview of Pfizer's molecular design infrastructure and the paradoxical solution that we've used to address this classic dilemma. I will also provide examples of specific computational methods and algorithms enabled by this approach, and describe our recent foray into cloud computing.

2:55 How Smart Data Transforms Life Science R&D
Sponsored by CAMBRIDGE SEMANTICS
Jim LaPointe, Managing Director, Pharma & Life Sciences, Cambridge Semantics
Learn how Smart Data solutions are transforming the R&D landscape through better Competitive Intelligence, Site Intelligence & Selection, Clinical Trial Data Integration & Discovery, Scientific Data Integration & Collaboration, PharmacoVigilence & Safety Surveillance, and Real-World Evidence Driven Clinical Trial Design. Cambridge Semantics is putting Big Data analytics into the hands of R&D teams for immediate data insights and business value.

3:10 Taking Scientific Collaboration in the Cloud to the Next Level
Sponsored by BIOVIA
Ton van Daelen, ScienceCloud Product Director, Marketing, Dassault Systemes, BIOVIA
Externalized collaborative research projects require integration and analysis of compound and bioactivity data from multiple sources. ScienceCloud supports secure data sharing in a "Cloud" and facilitates pipelining of data to/from internal data systems. In addition, ScienceCloud is now also used by small and medium research organizations to serve as their primary compute infrastructure, drastically lowering TCO while increasing nimbleness.

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

CLINICAL & TRANSLATIONAL INFORMATICS/IT

4:00 Impacting Clinical Research with Data Analytics
James Cai, Head Data Science, Pharmaceutical Research and Early Development Informatics, Roche Innovation Center New York
Data come in all shapes, sizes, and colors in today's clinical research and development. Whether single-protein biomarker data or high dimensional sequencing data, structured or unstructured, numeric or in pixels, we need to understand them and manage them effectively. In this presentation, I will describe several new challenges facing clinical research teams, and how Data Science has been critical in addressing them. I will provide examples of how data visualization, machine learning, and image analysis all contribute to uncovering new insights that impacted scientific or business decisions.

4:20 From Genome Exploration to Clinical Implementation: The Challenge of Translational Pharmacogenomic Informatics
Peter Covitz, Senior Director, Information Strategy & Analytics, Pfizer Worldwide Research and Development
In the realm of discovery science, tools and infrastructure evolve rapidly, keeping pace with the availability of ever-larger data sets and increasingly scalable industrial cloud computing. In the realm of regulated clinical drug trials, however, informatics infrastructure and tooling is – by necessity - far more stable. This presentation will discuss the challenges that arise when these two very different environments intersect, and will describe strategies for addressing the impedance mismatch.

4:40 Building an Operational Data Repository for Exploratory Biomarkers
Al Wang, Associate Director, Exploratory Clinical & Translational Research IT, Bristol-Myers Squibb
Data integration continues to be a significant impediment to translational research and development. In particular, the ability to flexibly combine diverse biomarker data with relevant patient-level information to produce analysis-ready data sets is a challenge that has not been fully solved by existing tools and approaches. This talk will describe the use cases around biomarker data in drug research & development, as well as an ongoing project to implement a platform that assists in these use cases.

5:00 Accelerating Discovery with Data Integration
Sponsored by Elsevier R&D Solutions
Frederik van den Broek, Ph.D., Consultant, R&D Solutions, Elsevier
Deriving insights for R&D decision-making from data requires capabilities and processes to navigate the deluge of data. This talk will present use cases that show once data is correctly aggregated, normalized and integrated, it allows for an integrated view across multiple disparate data sets, such as scientific literature, patents as well as internal databases from in-house researchers and their external collaborators.

5:30 – 6:30 Best of Show Awards Reception in the Exhibit Hall with Poster Viewing

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THURSDAY, APRIL 7

7:00 am Registration and Morning Coffee

8:00 PLENARY KEYNOTE SESSION PANEL
Please see page 3 for details.

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

TRANSLATIONAL INFORMATICS

10:30 Chairperson's Opening Remarks
Sastry Chilukuri, Partner, Pharmaceuticals & Medical Products, McKinsey & Company

10:40 Transforming Use of Real World Data Analytics
Minnie Chou, Director, Research & Development Informatics, Amgen, Inc.
Real world data (RWD) analytics is a key enabler for bringing effective and safe medicines to patients faster and cheaper. It can improve study designs, reduce trail enrollment times, facilitate fast-track filing strategies, shorten response time to health authority queries, and support value proposition of medicines. This presentation will discuss our approach and learnings unlocking the power of real world data assets.

11:10 Virtual Systems Pharmacology – The Next Generation of a TR&D Modeling and Simulation Environment
Marko Miladinov, Informatics Lead, Bristol-Myers Squibb
The internally developed Virtual Systems Pharmacology (ViSP) platform was implemented at BMS as a dynamic, highly scalable, model agnostic and therapeutic area agnostic application. The system seamlessly integrates the modelling tool of choice by the user, a web-based application, command line utilities, a database back-end and automatically scaling HPC environment built in the BMS Research Cloud environment that can be used to configure, manage and execute large-scale simulations for multiple models (of any sort) by multiple users.

11:40 The New World: Improving Patient Lives through Clinical Analytics and Real World Evidence
Sastry Chilukuri, Partner, Pharmaceuticals & Medical Products, McKinsey & Company
Jonathan Usuka, Knowledge Expert, Pharmaceuticals & Medical Products, McKinsey & Company
Unprecedented access to RWE is unlocking new insights into treatment, conditions & precision medicine, with implications for shifting value in the pharmaceutical development ecosystem. An understanding of how a patient will respond to therapy is complex & requires large investments in trials, often leading to failure & frustration. But there are clues to predict & show therapeutic benefit hidden in piles of medical claims data. Where will the data take us? How can it be used to create value & possibly to replace pharma R&D?

11:55 Global Specimen Solutions - Technology Facilitating Unlocking the Future of Medicine™
Sponsored by
Peter Tearle, Head, IT Architecture, Global Specimen Solutions, Inc.

12:10 pm Session Break

12:20 Luncheon Presentation I: Why is Data Integration So Hard?
Sponsored by
Tim Miller, VP, Integrated Applications, Thomson Reuters
Innovation is the life blood of the pharmaceutical industry and innovation runs on data. The Life Sciences industry is blessed with some of the best data resources – commercial and public databases, literature and ontologies. The Big Data revolution has given us a plethora of information and astounding tools for working with data, yet, the most common single issue faced by researchers is the problem of data integration.

12:50 Luncheon Presentation II (Sponsorship Opportunity Available) or Lunch on Your Own

1:20 Dessert Refreshment Break in the Exhibit Hall with Poster Viewing

INFORMATICS TOOLS IN DRUG DISCOVERY & DRUG REPURPOSING

1:55 Chairperson's Remarks
Farida Kopti, Ph.D., Director, Chemistry, Pharmacology, HTS Informatics & IT, Merck & Co., Inc.

2:00 Harnessing Edge Informatics to Accelerate Collaboration in BioPharma
Tom Plasterer, Ph.D., US Cross-Science Director, Research & Development Information, AstraZeneca
Using both technical and social solutions together knowledge can be shared and leveraged across the drug development process. This is accomplished by making data assets discoverable, accessible, self-described, reusable and annotatable. The Open PHACTS project pioneered this approach and has provided a number of the technical and social solutions to enable Edge Informatics. A number of pre-competitive consortia and some content providers have also embraced this approach, facilitating networks of collaborators within and outside a given organization.

2:30 A Platform Strategy for Research
Farida Kopti, Ph.D., Director, Chemistry/Pharmacology/HTS Informatics & IT, Merck & Co., Inc.
Merck is designing an open, cloud-based, integrated research data capture, management, and analytics platform to drive operational efficiency, improved user experience, scientific collaboration (internal and external) and accelerated decision-making. The objective is to enhance reusability of data and scientific informatics capabilities by standardizing data capture and management, and

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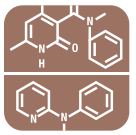

Track 9

Pharmaceutical R&D Informatics

Collaboration, Data Science and Biologics

creating an application ecosystem that enables rapidly advancing science, while reducing the total cost of operations.

3:00 Integrative, Automated Assessment of Human Genetic Evidence to Enable Decision Making for Drug Target Identification and Validation

Janna Hutz, Ph.D., Director, Head of Human Biology & Data Science, Andover Product Creation Innovation System, Eisai, Inc.

Accessing and interpreting human genetic associations with complex traits is often a manual, labor intensive process. Eisai has established bioinformatic systems for capturing and integrating human genetic data from a variety of study types (GWAS, sequencing, familial, candidate gene, etc.). Automated integration of genetic associations with functional data enables the delivery of summary reports and calibrated numeric scores to biologists and geneticists alike, who are using this information to drive portfolio-level decision-making on selection of targets, biomarkers, and indications.

3:30 Managing Controlled Substances and Other Liability Flags

Roman Affentranger, Head, Small Molecule Discovery Workflows, Roche

Following up on the pre-work done by the Pistoia Alliance, we implemented a comprehensive solution managing our extensive set of liability flags for compounds including e.g. narcotic substances.

4:00 Conference Adjourns

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Track 10

Clinical Genomics

Determining Genomic Variation's Contribution to Disease

TUESDAY, APRIL 5

7:00 am Workshop Registration and Morning Coffee

8:00 – 11:30 Recommended Morning Pre-Conference Workshops*
Intelligent Methods Optimization of Algorithms for NGS

12:30 – 4:00 pm Recommended Afternoon Pre-Conference Workshops*
Determining Genome Variation and Clinical Utility
DNA for Data Storage

** Separate registration required*

2:00 – 6:00 Main Conference Registration

4:00 PLENARY KEYNOTE SESSION
Please see page 3 for details.

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

WEDNESDAY, APRIL 6

7:00 am Registration Open and Morning Coffee

8:00 PLENARY KEYNOTE SESSION
Please see page 3 for details.

9:00 Benjamin Franklin Awards and Laureate Presentation

9:30 Best Practices Awards Program

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

IT IS ADVANCING GENOMICS IN CLINICAL CARE

10:50 Chairperson's Opening Remarks
David Heckerman, Ph.D., Distinguished Scientist, Microsoft Research, Microsoft

11:00 FEATURED PRESENTATION: Precision Medicine
Tim Harris, Ph.D., D.Sc., Venture Partner, SV Life Sciences
Before long, whole-genome sequencing will become routine and patients will have this information as part of their electronic medical record. The problem is how to associate changes in the genome with particular clinical phenotypes. This problem is starting to be tackled using information from GWAS. Examples of how this can help to find new drugs to treat patients with will be provided.

11:30 FEATURED PRESENTATION: The Potential for IT to Enhance and Broaden the Use of Genetics in Clinical Care
Samuel (Sandy) Aronson, Executive Director, IT, Partners HealthCare Center for Personalized Genetic Medicine
Information technology can improve the effectiveness of genetic testing in clinical care, but such support is lacking in many environments. Efforts to address this issue will be discussed.

12:00 pm FEATURED PRESENTATION: Next-Generation Health Exploration and Analytics in Precision Healthcare
Yaron Turpaz, Ph.D., MBA, Chief Information Officer, Human Longevity, Inc.
Scott Skellenger, MBA, Vice President, Health Nucleus IT and Informatics, Human Longevity, Inc.
Human Longevity, Inc. (HLI) has built a cloud-based multifaceted genomic and phenotype knowledge management and application ecosystem that includes the HLI Knowledgebase™, the HLI Health Nucleus™ client and clinician portals and the Health Nucleus™ Avatar Application. The HLI Knowledgebase™ currently includes over 10,000 integrated health records and the infrastructure to store, query and visualize genomic, metabolomic, microbiome and high-quality phenotype data in scientifically meaningful ways. As a key source to the Knowledgebase™, the Health Nucleus™ suite of modalities and applications provides the broadest set of phenotype and medical data available, while the Integrated Avatar application puts the client in the center of their integrated genomic and phenotype results in a novel and engaging way new to the health exploration market. Together, these applications represent a state-of-the-art technology continuum supporting the comprehensive assembly and utility of the deepest and broadest genomics and phenotypic knowledge management solution available. This talk includes a brief introduction followed by an application demonstration of both the HLI Knowledgebase™ and the Health Nucleus™ Avatar Application.

12:30 Session Break

12:40 Luncheon Presentation I: Discovering Novel Structures in Large Cancer Data Sets from Both FMI and TCGA with SciDB
Sponsored by paradigm4 answer harder questions
Eric Neumann, Ph.D., Vice President, Knowledge Discovery and Technology Innovations, Foundation Medicine, Inc.
Zachary Pitluk, Ph.D., Vice President, Life Sciences, Business Development, Paradigm4, Inc.
FMI has the largest genomics knowledge base of real-world clinical profiles. With such large data sets comes great analytic power. The SciDB platform enables FMI to integrate and align FMI proprietary data with TCGA data to enable deep analyses and comparisons for many different cancers. The combined results offer deeper insights into both tumor mechanisms and therapeutic responses of these cancers in patients.

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

1:40 Session Break

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Track 10

Clinical Genomics

Determining Genomic Variation's Contribution to Disease

MINING DATABASES FOR GENOTYPE/ PHENOTYPE CORRELATIONS

1:50 Chairperson's Remarks

John E. Mattison, M.D., Chief Medical Information Officer, Assistant Medical Director, Southern California Medical Group, Kaiser Permanente; Co-Chair, eHealth Workgroup, Global Alliance for Genomics and Health GA4GH

1:55 Update of the Department of Veterans Affairs Precision Oncology (POP) Program

Louis Fiore, M.D., MPH, Executive Director, MAVERIC, Research, Veterans Affairs Boston Healthcare System

This presentation reviews the progress made to date on the VA Precision Oncology Program. The review includes progress on the informatics infrastructure and clinical success of the clinical trial matching, patient engagement, clinical prediction engine and sharing of genomic data components.

2:25 Connecting Rare Disease Patient Databases with the Matchmaker Exchange API

Orion Buske, Research Scientist, Department of Computer Science, University of Toronto; Genetics and Genome Biology Program, Hospital for Sick Children

Over 350 million people are affected by rare diseases, but many remain unsolved due to the challenge of finding additional families with the same disease. Using structured phenotype and genotype data, we are able to discover similar patients within patient databases such as PhenomeCentral. The Matchmaker Exchange API then enables patient matchmaking between such organizations, lowering the barrier for clinicians to finding similar patients.

2:55 An Ensemble Approach with Machine Learning to Detect Cancer Variants

Sponsored by bina TECHNOLOGIES

Li Tai Fang, Senior Scientist, Bioinformatics, Research & Development, Bina Technologies

Accurately detecting somatic mutations in cancer is a challenging task due to tumor heterogeneity and sample contamination. To address this problem, Bina has developed SomaticSeq, a somatic mutation detection pipeline that integrates multiple cutting edge tools and machine learning. It has recently placed No. 1 and No. 2 in INDEL and SNV, respectively, during the last stage of the ICGC-TCGA DREAM Somatic Mutation Calling Challenge

3:10 Beyond the Cancer Genome - Computational Enablement of Holistic, Evidence-Driven Patient Care in Clinical Oncology

Sponsored by MOLECULAR HEALTH

Laura Housman, MPH, MBA, SVP of Corporate Development, Corporate Development, Molecular Health, Inc.

In oncology, the molecular characterization of tumor genes as part of patient care is now synonymous with the concept of precision medicine. In this talk, I describe a computational platform that enables holistic clinical interpretation of multiple clinico-molecular parameters.

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

GENOMIC DATA SECURITY AND PRIVACY

4:00 The Next Phase for Healthcare Privacy and Security - Information Governance

Katherine Downing, Director, Practice Excellence, American Health Information Management Association

Security and privacy are of huge importance in business as our organizations continue to be the target of attack. Taking a holistic approach using Information Governance is the next generation for privacy and security. Information Governance is an organization-wide framework for managing information throughout its lifecycle and for supporting the organization's strategy, operations, regulatory, legal, risk, and environmental requirements.

4:30 Securing Personal Genomic Data: The Potential of the Blockchain

Richard Shute, Ph.D., Consultant, Curlew Research

More people are having their genomes sequenced and letting sequencing companies use their data for research. What if people want to take back control of their own data? How would they confidently and securely manage their most highly personalized information? Blockchain technology (the global ledger behind Bitcoin) could be the answer to securely protecting genomic information and managing transactions associated with personal genomic data.

5:00 FEATURED PRESENTATION: The Role of Cybersecurity Leadership in This New World

Mansur Hasib, D.Sc., CISSP, PMP, CPHIMS, Cybersecurity Professor and Author, University System of Maryland

The world has changed. Technology drives the mission of the bio-IT world today. Yet this world has been the subject of some of the most sensational data breaches and even ransomware. What are we doing wrong? Technology certainly does not appear to be the answer. Yet, organizations appear prepared to dump money on the problem. In a highly interactive session, Dr. Hasib shares his views and analysis on the importance of people, leadership, and culture in cybersecurity.

5:30 – 6:30 Best of Show Awards Reception in the Exhibit Hall with Poster Viewing

THURSDAY, APRIL 7

7:00 am Registration and Morning Coffee

8:00 PLENARY KEYNOTE SESSION PANEL

Please see page 3 for details.

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Track 10

Clinical Genomics

Determining Genomic Variation's Contribution to Disease

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

PREDICTING PATHOGENICITY OF VARIANTS

10:30 Chairperson's Opening Remarks
Zachary Pitluk, Ph.D., Vice President, Life Sciences, Business Development, Paradigm4, Inc.

10:40 Predicting Variants Likely to Cause Glanzmann Thrombasthenia
Yupu Liang, Ph.D., Director, Bioinformatics Program, Center for Clinical and Translational Science, Rockefeller University
As genetic testing becomes increasingly popular, patients and physicians are faced with tough questions: Does a particular genetic variation translate into a predisposition to an illness, or is it simply a benign rearrangement? This talk describes our experience on evaluating clinical impact of novel mutations on Integrin aggregation receptor from NGS data.

11:10 When Exomes Fail: Whole-Genome and Transcriptome Sequencing for Rare Disease Diagnosis
Monkol Lek, Ph.D., Senior Research Fellow, Analytic and Translational Genetics Unit, Massachusetts General Hospital
The current diagnosis rate from exome sequencing in our cohort of over 1,200 muscle disease samples is approximately 30-40%. This presentation focuses on how whole-genome sequencing and RNA sequencing can be applied to identify pathogenic variants.

11:40 Genomic Variants in Context and at Scale - Integrative Approaches to Predict Pathogenicity and Stratify Patient Cohorts
Janusz Dutkowski, Ph.D., Founder and CEO, Data4Cure, Inc.
Improved understanding of individual genomic variants may be possible if we study them at a systems level rather than in isolation. New integrative methods allow us to analyze many genomes together in the context of molecular networks and pathways to detect aberrations clustering in key cellular machinery. We use these approaches to develop multiscale maps of disease biology that span individual variants, genes, pathways and processes, and inform the identification of disease subtypes and biomarkers, as well as characterization of individual variants.

12:10 pm Session Break

12:20 Luncheon Presentation *(Sponsorship Opportunity Available)* **or Lunch on Your Own**

1:20 Dessert Refreshment Break in the Exhibit Hall with Poster Viewing

SHARING DATA AND VALIDATING CLINICAL UTILITY

1:55 Chairperson's Remarks
Samantha A. Schrier Vergano, M.D., FAAP, FACMG, Division Director, Medical Genetics and Metabolism, Children's Hospital of The King's Daughters

2:00 What If Your Biology Holds the Key that Protects Others from Disease? Changing the Discourse around Sharing Health Data
Jason Bobe, Associate Professor, Director, Sharing Lab, Icahn Institute for Genomics and Multiscale Biology, Mount Sinai School of Medicine; Executive Director, PersonalGenomes.org
The protection of personal health and medical data has been recognized as an important goal for decades. The societal value of sharing data is immense, but to date paid much less attention. Designing a biomedical research enterprise that provides individuals access to their own data and improved options for sharing is paramount for addressing critical social concerns like better health, new therapies and disease prevention strategies.

2:30 Community-Driven Approaches to Support Variant Interpretation
Steven Harrison, Ph.D., Variant Scientist, Laboratory for Molecular Medicine, Partners HealthCare Personalized Medicine; Harvard Medical School
Improving our knowledge of genomic variation requires a massive effort in data sharing. Community-driven groups are working to incorporate shared data into variant assessment processes by guiding gene and disease specifications to the ACMG Interpreting Sequence Variant Guidelines, developing variant curation applications, aggregating shared data to inform the community of discrepancies and concordance in variant interpretations, and developing resources to facilitate data sharing.

3:00 Military Health Care Dilemmas and Genetic Discrimination: A Cautionary Tale of One Family's Experience with Whole-Exome Sequencing
Samantha A. Schrier Vergano, M.D., FAAP, FACMG, Division Director, Medical Genetics and Metabolism, Children's Hospital of The King's Daughters
Whole-exome sequencing (WES) has increased our ability to analyze large parts of the human genome, bringing with it complicated ethical considerations. Secondary findings, results that convey genetic risk in asymptomatic individuals outside the initial indication for testing, can have significant social or legal implications. We discuss these issues in the experience with a family with careers in the U.S military, potentially jeopardizing their employment and privacy.

3:30 Development and Validation of an SNP Panel for Sample Identity Quality Control for Use in a High-Throughput Clinical Genetics Laboratory
Thomas B. Freeman, Senior Data Scientist, Genetics and Genomic Sciences, Icahn School of Medicine at Mount Sinai
In clinical genetic testing, it is absolutely imperative that each patient receives the proper test results. We describe the development, implementation and validation of a sample identity SNP panel run in parallel with the DNA-Seq pipeline for sample identity verification. This workflow is integrated with LIMS and data analysis pipeline to provided automated sample identity quality control.

4:00 Conference Adjourns

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Track 11

Open Source Innovations

Integrated Informatics Solutions to Optimize Collaborative Biomedical Research

TUESDAY, APRIL 5

7:00 am Workshop Registration and Morning Coffee

8:00 – 11:30 Recommended Morning Pre-Conference Workshops*
Security Considerations for Virtual Research

12:30 – 4:00 pm Recommended Afternoon Pre-Conference Workshops*
iConquerMS™: A Patient-Centered Research Model

** Separate registration required*

2:00 – 6:00 Main Conference Registration

4:00 PLENARY KEYNOTE SESSION
Please see page 3 for details.

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

WEDNESDAY, APRIL 6

7:00 am Registration Open and Morning Coffee

8:00 PLENARY KEYNOTE SESSION
Please see page 3 for details.

9:00 Benjamin Franklin Awards and Laureate Presentation

9:30 Best Practices Awards Program

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

GLOBAL ECOSYSTEM FOR CANCER RESEARCH AND TREATMENT:
TECHNOLOGIES, TOOLS, AND PLATFORMS TO BRING ADVANCES IN SCIENCE FROM BENCH TO BEDSIDE

10:50 Chairperson's Opening Remarks
Anil Srivastava, President, Open Health Systems Laboratory

11:00 PANEL DISCUSSION: IUCKA: Indo-US Cancer Knowledge Alliance
Moderator: Anil Srivastava, President, Open Health Systems Laboratory
Kenneth Buetow, Ph.D., Director of Computational Sciences and Informatics, Complex Adaptive Systems Initiative (CASI), Arizona State University
Rajendra Joshi, Ph.D., Associate Director and Head, Bioinformatics Group, Centre for Development of Advanced Computing, Pune University Campus
IUCKA: Indo-US Cancer Knowledge Alliance is being designed as an integrated biomedical informatics cyberinfrastructure for cancer treatment and research in India. It will be a true translational research platform from bench to bedside connecting cancer treatment and research centers across the country with access and connection to global centers of research, especially in the United States. The promoters of the IUCKA are Arizona State University, Open Health Systems Laboratory and Varian Medical Systems. IUCKA is being implemented as a PPP (public private partnership) and is bringing together technology products and service providers and cancer treatment and research centers in an ecosystem to directly benefit cancer patients in India and contribute to global research collaboration, especially between cancer centers in India.

12:00 pm Managing Data Across the Research Life-Cycle for Life Sciences
Sponsored by DDN STORAGE
George Vacek, Global Director, Life Sciences, DDN
Dr. Vacek will deliver several in-depth case studies of leading life sciences organizations leveraging high performance & high scale data solutions for genomics, imaging & simulation workflows. Cases will focus on implemented solutions: capturing & effectively exploiting large scale data at speed, regulated & non-regulated stewardship considerations, transitioning from non-scaling architectures & bringing the benefits of high-end HPC technologies & techniques into smaller deployments & collaborative scenarios.

COMPUTATIONAL AND COLLABORATIVE SOLUTIONS

12:15 Data Management in Large Scale Sequencing and Analysis
Sponsored by sgi
Kirill Malkin, Director, Storage Engineering, SGI
Next Generation Sequencing and its accompanying analyses are driving exponential growth in sequence data that needs to be stored, analyzed, and made accessible for future interrogations. This session presents a converged storage-and-analytics infrastructure framework based on SGI's experience in enabling data-intensive supercomputing solutions – along with genomics customer case examples and best practices for simplifying the management of data sets that can contain billions of files/objects.

12:30 Session Break

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Track 11

Open Source Innovations

Integrated Informatics Solutions to Optimize Collaborative Biomedical Research

12:40 Luncheon Presentation I: Accelerating the Analysis of High-Throughput Sequencing

Sponsored by intel

Ketan Paranjape, General Manager, Life Sciences, Health and Life Sciences, Intel

Panelists: Paolo Narvaez, Ph.D., Principal Engineer & Director, Personalized Care Platform, Intel Corporation

Adam Kiezun, Ph.D., Senior Group Leader, Computational Methods Development, Broad Institute of MIT and Harvard

Jeff Gentry, Principal Software Engineer, Broad Institute

Accelerating the analysis of high-throughput sequencing data enables all of us to push the boundaries of precision medicine. The BROAD's Genome Analysis Toolkit (GATK) is the industry standard software package for variant discovery and genotyping. In this luncheon, experts from the BROAD and Intel will discuss the exciting new capabilities that are coming to GATK, and the impact that this could have on the industry.

1:10 Luncheon Presentation II: High-Performance Server and Storage Solutions for Life Sciences

Sponsored by SILICON MECHANICS SERVERS • STORAGE • HPC

Dan Chow, COO & CTO, Silicon Mechanics

Hear from Silicon Mechanics COO/CTO, Daniel Chow, as he describes current challenges and trends that are impacting computational and storage needs for researchers.

1:40 Session Break

DATA & STORAGE MANAGEMENT SOLUTIONS

1:50 Chairperson's Remarks

1:55 MSSNG – An Open Science Approach to Facilitate Discovery in Autism

Mathew Pletcher, Vice President & Head, Genomic Discovery, Autism Speaks

Autism Speaks has undertaken an effort, entitled MSSNG, in collaboration with Google and The Hospital for Sick Children to generate whole genome sequence from at least 10,000 individuals from families with autism. This genomic data has be made available along with associated clinical and phenotypic data through multiple interfaces under the principles of open science. MSSNG operates under the principle that best was to ensure the delivery of new discoveries and tools to the autism community is to share this valuable resource as broadly as possible and with as few restrictions as possible.

2:25 An Open Embedded Live Image-Analysis Prototyping Platform

Patrick Oberthuer, Research Associate, Chair, Bioprocess Engineering, Technische Universität Dresden

This talk will discuss the idea of open embedded low-cost hardware platforms like the RaspberryPi and widely used open Image-Analysis Platform ImageJ. This will be completed with live imaging devices. This will fulfill the dream of easily prototyping any All-In-One image-analysis System.

2:55 The Case for Adaptive, Hierarchical Metadata

Sponsored by EMC²

Stephen Worth, Director, Engineering, EMC

Groups maintaining data repositories at the petabyte-scale are discovering that cataloguing associated metadata is necessary to properly access and analyze data. To be successful they depend on researchers and data curators to provide the user-defined metadata. EMC recently contributed MetaInx to aid researchers with metadata management under iRODS. We will be demonstrating the principles of operation for MetaInx and discuss how adaptive, hierarchical metadata can be applied to research curation.

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

4:00 No ELN is an Island

Paul Whitehead, pRED Informatics Center Head, Roche

Research at Roche has an extended bench concept that utilizes external scientists to contribute to internal projects. Externalization requires, inter alia, reduced costs and shortened project life cycles to justify its continued use. Externalized projects should be monitored, directed and recorded using suitable planning, electronic laboratory notebook and collaboration tools, and together with automated data exchange, be done quickly and with high quality. The evaluation, selection, implementation and integration of the cloud-based Dotmatics ELN for Roche Research will be presented.

4:30 Between Open and Closed Antimalarial Drug Discovery: Comparing Data Connectivity Gaps and Disclosure Speed

Christopher Southan, Ph.D., Database, Curator, IUPHAR/BPS Guide to PHARMACOLGY, University of Edinburgh

Antimalarial research is the poster child for Open Source Drug Discovery (OSDD). However, many leads compounds still have their origins in Traditional Closed Drug Discovery (TCDD) and uncertainty remains as to the differences. To provide an assessment, this work examined 32 recent antimalarial structures in terms of their PubChem connectivity.

5:00 Selected Poster Presentation: Embracing Ambiguity: Representation of Macromolecules Using the Enhanced Standard HELM 2.0

Markus Weisser, Ph.D., Managing Director, quattro research GmbH

5:30 – 6:30 Best of Show Awards Reception in the Exhibit Hall with Poster Viewing

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Track 11

Open Source Innovations

Integrated Informatics Solutions to Optimize Collaborative Biomedical Research

THURSDAY, APRIL 7

7:00 am Registration and Morning Coffee

8:00 PLENARY KEYNOTE SESSION PANEL
Please see page 3 for details.

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

COLLABORATION PROJECTS IN DIGITAL HEALTH AND LIFE SCIENCES R&D INFORMATICS

10:30 Chairperson's Opening Remarks
Narges Bani Asadi, Founder and CEO Bina Technologies Inc., Roche Sequencing

10:40 Selected Poster Presentation: Nephele: A Cloud-Based Scientific Computing Platform for Improved Efficiency, Standardization, and Collaboration in Microbiome Data Analysis
Ian Misner, Ph.D., Computational Genomics Specialist and Contractor, Bioinformatics and Computational Biosciences Branch (BCBB), NIH/NIAD/OD/OSMO/OCICB

11:10 Tackling Life Sciences R&D Informatics Challenges through Cross-Industry Pre-Competitive Collaboration Projects at The Pistoia Alliance
Carmen Nitsche, Executive Director, Business Development North America, Pistoia Alliance

Market pressures are driving the Life Sciences industry to embrace pre-competitive collaboration in some aspects of their R&D processes. We will examine several areas that lend themselves to such efforts and review ongoing projects that address common challenges.

11:40 Selected Poster Presentation: Projections Meta Filesystem - Novel Approach for Distributed Data Access and Annotation
Anton Bragin, Ph.D., Systems Architect, Bioinformatics Institute

Nowadays bioinformatics data may exist in different forms such as text and binary files, SQL and NoSQL database records, data objects behind common application programming interfaces (BioMart, GA4GH Genomics API), or APIs specific to data owner (NCBI E-utilities) or data-module vendor (ThermoFisher Torrent SuiteT Software API, Illuimina BaseSpace API). Typical bioinformatics project requires simultaneous access to data splitted between multiple data locations and forms each having special logical data organization. To make one data source talk to another or enable data consumption by some software tool the researcher should translate data requests by directly converting data (e.g., by dumping database records to flat files) or by implementing some data integration logic via scripting which is slow, error-prone and often requires extra local storage. To conquer the problems described we developed Projections meta filesystem aimed to provide uniform file-based access to heterogeneous resources and decouple logical resource representation from physical data storage. Projections system uses universal format for description of logical structure of data and metadata (including data object linking) stored in prototype files and set of resource-specific drivers that project actual data objects from some local or remote resource on local FUSE-mounted filesystem. That enables uniform view of remote data storage content or its part with data transfer upon request. Another point of Projections system is that metadata is first-class citizen enabling versatile metadata descriptions exceeding traditional tags and key-value properties and providing flexible search capabilities. Typical Projections usage scenarios include: Providing file access to non-file objects such as NCBI web resources or ThermoFisher Torrent SuiteT Software data and their metadata. Using metadata for search and ability to annotate data objects with searchable custom metadata. Data analysis upon request. Projection provide logical representation of resource including its metadata that can be searched and analyzed, while data transfer is typically suspended until the data in actually needed (different cashing policies may be applied). Exchange of data resource representations and selected data objects by the mean of prototype files, which are small text files that can be easily edited and transferred. Projections is open-source software based on Filesystem in Userspace (FUSE) and can be used on any modern Linux machine. Currently the system is equipped with drivers for making data projections from NCBI SRA, Genbank, Amazon S3, local filesystem, ThermoFisher Torrent SuiteT, Illumina MiSeq/HiSeq Control Software and can be readily expanded. We hope that Projections meta filesystem will promote data consolidation and make data access, exchange and usage patterns more uniform, metadata-driven and reliable.

12:10 pm Session Break

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12:20 Luncheon Presentation I: Innovation through Collaboration: Cultural and Technological Advancements Empowered in the Pediatric Research Arena
Adam Resnick, Director, Children's Brain Tumor Tissue Consortium Division, Neurosurgery Children's Hospital, Philadelphia

The Children's Hospital of Philadelphia has partnered with academic institutions, clinical trial consortia and industry partners to build a new pediatric biospecimen and informatics platform that defines an open-access data discovery ecosystem. These new open-source tools and workflows support "big-data" innovation and define an alternative, sustainable model for collaborative data-driven discovery, in which researchers "compete" to share, connect, and integrate data on behalf of patients.

12:50 Luncheon Presentation II *(Sponsorship Opportunity Available)*

1:20 Dessert Refreshment Break in the Exhibit Hall with Poster Viewing

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Track 11

Open Source Innovations

Integrated Informatics Solutions to Optimize Collaborative Biomedical Research

SHARING DATA AND VALIDATING CLINICAL UTILITY

1:55 Chairperson's Remarks

Samantha A. Schrier Vergano, M.D., FAAP, FACMG, Division Director, Medical Genetics and Metabolism, Children's Hospital of the King's Daughters

2:00 What If Your Biology Holds the Key that Protects Others from Disease? Changing the Discourse around Sharing Health Data

Jason Bobe, Associate Professor, Director, Sharing Lab, Icahn Institute for Genomics and Multiscale Biology, Mount Sinai School of Medicine; Executive Director, PersonalGenomes.org

The protection of personal health and medical data has been recognized as an important goal for decades. The societal value of sharing data is immense, but to date paid much less attention. Designing a biomedical research enterprise that provides individuals access to their own data and improved options for sharing is paramount for addressing critical social concerns like better health, new therapies and disease prevention strategies.

2:30 Community-Driven Approaches to Support Variant Interpretation

Steven Harrison, Ph.D., Variant Scientist, Laboratory for Molecular Medicine, Partners HealthCare Personalized Medicine; Harvard Medical School

Improving our knowledge of genomic variation requires a massive effort in data sharing. Community-driven groups are working to incorporate shared data into variant assessment processes by guiding gene and disease specifications to the ACMG Interpreting Sequence Variant Guidelines, developing variant curation applications, aggregating shared data to inform the community of discrepancies and concordance in variant interpretations, and developing resources to facilitate data sharing.

3:00 Military Health Care Dilemmas and Genetic Discrimination: A Cautionary Tale of One Family's Experience with Whole-Exome Sequencing

Samantha A. Schrier Vergano, M.D., FAAP, FACMG, Division Director, Medical Genetics and Metabolism, Children's Hospital of the King's Daughters

Whole-exome sequencing (WES) has increased our ability to analyze large parts of the human genome, bringing with it complicated ethical considerations. Secondary findings, results that convey genetic risk in asymptomatic individuals outside the initial indication for testing, can have significant social or legal implications. We discuss these issues in the experience with a family with careers in the U.S military, potentially jeopardizing their employment and privacy.

3:30 Development and Validation of an SNP Panel for Sample Identity Quality Control for Use in a High-Throughput Clinical Genetics Laboratory

Thomas B. Freeman, Senior Data Scientist, Genetics and Genomic Sciences, Icahn School of Medicine at Mount Sinai

In clinical genetic testing, it is absolutely imperative that each patient receives the proper test results. We describe the development, implementation and validation of a sample identity SNP panel run in parallel with the DNA-Seq pipeline for sample identity verification. This workflow is integrated with LIMS and data analysis pipeline to provided automated sample identity quality control.

4:00 Conference Adjourns

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Track 12

Cancer Informatics

Applying Computational Biology to Cancer Research & Care

TUESDAY, APRIL 5

7:00 am Workshop Registration and Morning Coffee

2:00 – 6:00 Main Conference Registration

4:00 PLENARY KEYNOTE SESSION
Please see page 3 for details.

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

WEDNESDAY, APRIL 6

7:00 am Registration Open and Morning Coffee

8:00 PLENARY KEYNOTE SESSION
Please see page 3 for details.

9:00 Benjamin Franklin Awards and Laureate Presentation

9:30 Best Practices Awards Program

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

GLOBAL ECOSYSTEM FOR CANCER RESEARCH AND TREATMENT:

TECHNOLOGIES, TOOLS, AND PLATFORMS TO BRING ADVANCES IN SCIENCE FROM BENCH TO BEDSIDE

10:50 Chairperson's Opening Remarks
Anil Srivastava, President, Open Health Systems Laboratory

11:00 PANEL DISCUSSION: IUCKA: Indo-US Cancer Knowledge Alliance
Moderator: Anil Srivastava, President, Open Health Systems Laboratory
Kenneth Buetow, Ph.D., Director of Computational Sciences and Informatics, Complex Adaptive Systems Initiative (CASI), Arizona State University
Rajendra Joshi, Ph.D., Associate Director and Head, Bioinformatics Group, Centre for Development of Advanced Computing, Pune University Campus
IUCKA: Indo-US Cancer Knowledge Alliance is being designed as an integrated biomedical informatics cyberinfrastructure for cancer treatment and research in India. It will be a true translational research platform from bench to bedside connecting cancer treatment and research centers across the country with access and connection to global centers of research, especially in the United States. The promoters of the IUCKA are Arizona State University, Open Health Systems Laboratory and Varian Medical Systems. IUCKA is being implemented as a PPP (public private partnership) and is bringing together technology products and service providers and cancer treatment and research centers in an ecosystem to directly benefit cancer patients in India and contribute to global research collaboration, especially between cancer centers in India.

Sponsored by DDN STORAGE

12:00 pm Managing Data Across the Research Life-Cycle for Life Sciences
George Vacek, Global Director, Life Sciences, DDN
Dr. Vacek will deliver several in-depth case studies of leading life sciences organizations leveraging high performance & high scale data solutions for genomics, imaging & simulation workflows. Cases will focus on implemented solutions: capturing & effectively exploiting large scale data at speed, regulated & non-regulated stewardship considerations, transitioning from non-scaling architectures & bringing the benefits of high-end HPC technologies & techniques into smaller deployments & collaborative scenarios.

COMPUTATIONAL AND STORAGE SOLUTIONS FOR RESEARCHERS

Sponsored by sgi

12:15 Data Management in Large Scale Sequencing and Analysis
Kirill Malkin, Director, Storage Engineering, SGI
Next Generation Sequencing and its accompanying analyses are driving exponential growth in sequence data that needs to be stored, analyzed, and made accessible for future interrogations. This session presents a converged storage-and-analytics infrastructure framework based on SGI's experience in enabling data-intensive supercomputing solutions – along with genomics customer case examples and best practices for simplifying the management of data sets that can contain billions of files/objects.

12:30 Session Break

Sponsored by intel

12:40 Luncheon Presentation I: Accelerating the Analysis of High-Throughput Sequencing
Ketan Paranjape, General Manager, Life Sciences, Health and Life Sciences, Intel
Panelists: Paolo Narvaez, Ph.D., Principal Engineer & Director, Personalized Care Platform, Intel Corporation
Adam Kiezun, Ph.D., Senior Group Leader, Computational Methods Development, Broad Institute of MIT and Harvard
Jeff Gentry, Principal Software Engineer, Broad Institute
Accelerating the analysis of high-throughput sequencing data enables all of us to push the boundaries of precision medicine. The BROAD's Genome Analysis Toolkit (GATK) is the industry standard software package for variant discovery and genotyping. In this luncheon, experts from the BROAD and Intel will discuss the exciting new capabilities that are coming to GATK, and the impact that this could have on the industry.

Sponsored by SILICON MECHANICS SERVERS • STORAGE • HPC

1:10 Luncheon Presentation II: High-Performance Server and Storage Solutions for Life Sciences
Dan Chow, COO & CTO, Silicon Mechanics
Hear from Silicon Mechanics COO/CTO, Daniel Chow, as he describes current challenges and trends that are impacting computational and storage needs for researchers.

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1:40 Session Break

MINING DATABASES FOR GENOTYPE/ PHENOTYPE CORRELATIONS

1:50 Chairperson's Remarks
John E. Mattison, M.D., Chief Medical Information Officer, Assistant Medical Director, Southern California Medical Group, Kaiser Permanente; Co-Chair, eHealth Workgroup, Global Alliance for Genomics and Health GA4GH

1:55 Update of the Department of Veterans Affairs Precision Oncology (POP) Program
Louis Fiore, M.D., MPH, Executive Director, MAVERIC, Research, Veterans Affairs Boston Healthcare System
This presentation reviews the progress made to date on the VA Precision Oncology Program. The review includes progress on the informatics infrastructure and clinical success of the clinical trial matching, patient engagement, clinical prediction engine and sharing of genomic data components.

2:25 Connecting Rare Disease Patient Databases with the Matchmaker Exchange API
Orion Buske, Research Scientist, Department of Computer Science, University of Toronto; Genetics and Genome Biology Program, Hospital for Sick Children
Over 350 million people are affected by rare diseases, but many remain unsolved due to the challenge of finding additional families with the same disease. Using structured phenotype and genotype data, we are able to discover similar patients within patient databases such as PhenomeCentral. The Matchmaker Exchange API then enables patient matchmaking between such organizations, lowering the barrier for clinicians to finding similar patients.

2:55 An Ensemble Approach with Machine Learning to Detect Cancer Variants
Sponsored by bina TECHNOLOGIES
Li Tai Fang, Senior Scientist, Bioinformatics, Research & Development, Bina Technologies
Accurately detecting somatic mutations in cancer is a challenging task due to tumor heterogeneity and sample contamination. To address this problem, Bina has developed SomaticSeq, a somatic mutation detection pipeline that integrates multiple cutting edge tools and machine learning. It has recently placed No. 1 and No. 2 in INDEL and SNV, respectively, during the last stage of the ICGC-TCGA DREAM Somatic Mutation Calling Challenge.

3:10 Beyond the Cancer Genome - Computational Enablement of Holistic, Evidence-Driven Patient Care in Clinical Oncology
Sponsored by MOLECULAR HEALTH
Laura Housman, MPH, MBA, SVP of Corporate Development, Corporate Development, Molecular Health, Inc.
In oncology, the molecular characterization of tumor genes as part of patient care is now synonymous with the concept of precision medicine. In this talk, I describe a computational platform that enables holistic clinical interpretation of multiple clinico-molecular parameters.

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

APPLYING CLOUD FOR CANCER RESEARCH

4:00 Building Cloud-Enabled Cancer Genomics Workflows with Luigi and Docker
Jacob Feala, Ph.D., Principal Scientist, Bioinformatics, Caperna, an affiliate of Moderna Therapeutics
As bioinformatics scientists, we tend to write custom tools for managing our workflows, even when viable, open-source alternatives are available from the tech community. Our field has, however, begun to adopt Docker containers to stabilize compute environments. I introduce Luigi, a workflow system built by engineers at Spotify to manage long-running big data processing jobs with complex dependencies. Focusing on a case study of next-generation sequencing analysis in cancer genomics research, I show how Luigi can connect simple, containerized applications into complex bioinformatics pipelines that can be easily integrated with compute, storage, and data warehousing on the cloud.

4:30 The ISB Cancer Genomics Cloud
Sheila Reynolds, Ph.D., Senior Research Scientist, Ilya Shmulevich Laboratory, Institute for Systems Biology
The ISB-CGC is a cloud-based platform that will serve as a large-scale data repository for TCGA data, while also providing the computational infrastructure and interactive exploratory tools necessary to carry out cancer genomics research at unprecedented scales. The ISB-CGC will provide both interactive and programmatic access to the TCGA data, leveraging many aspects of Google Cloud Platform including BigQuery and Compute Engine.

5:00 GATK4 - The Next Generation of Broad Institute's Genomics Tools, on the Cloud
Adam Kiezun, Ph.D., Senior Group Leader, Computational Methods Development, Broad Institute of MIT and Harvard
The breathtaking pace of genomics growth requires tools and pipelines that can support cutting-edge analyses, at petabyte scales, with optimized speed and cost. With this in mind, we have launched GATK4, a complete reimagining of Broad's Genome Analysis Toolkit. GATK4 now supports both germline and somatic mutation analysis, CNV and SV detection, tumor heterogeneity analysis, and more. Designed with cloud infrastructure in mind, GATK4 is implemented with support for Apache Spark and is hundreds of times faster than previous generations of GATK.

5:30 – 6:30 Best of Show Awards Reception in the Exhibit Hall with Poster Viewing

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Track 12

Cancer Informatics

Applying Computational Biology to Cancer Research & Care

THURSDAY, APRIL 7

7:00 am Registration and Morning Coffee

8:00 PLENARY KEYNOTE SESSION PANEL
Please see page 3 for details.

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

NGS AND INFORMATICS TO ADVANCE CANCER THERAPIES

10:30 Chairperson's Opening Remarks
Brandi Davis Dusenbury, Senior Scientist, Seven Bridges

10:40 Application of Targeted NGS Sequencing in Personalized Clinical Cancer Therapies
Qichao Zhu, Ph.D., Associate Professor, Genetics & Genomics Sciences, Icahn School of Medicine at Mount Sinai
Our current clinical cancer genome research project is focused on the three key components, sequence analysis for patient genetic profiling, biomarker (genetic variation) collection for cancer precision medicine, and the data processing and integration platform application for clinical report. The goal of the project is developing a comprehensive platform that can totally support precision medicine approach in cancer treatment.

11:10 Integration of Whole Genome and RNA Sequencing to Inform Clinical Treatment of Cancer
Michael Zody, Ph.D., Research Director, Computational Biology, New York Genome Center

11:40 Building National-Scale Genomics Projects with Collaborative, Portable, Reproducible Analysis
Sponsored by SevenBridges
Deniz Kural, CEO, Seven Bridges
The number of large genomics projects worldwide is rapidly growing. Such projects involve analysis of hundreds of thousands of whole genomes to accelerate discovery in basic and clinical research. National-scale genomics projects make intensive demands on computation and storage, and test the limits of existing infrastructure. They present severe challenges that require novel approaches to overcome.12:10 pm Session Break

12:20 Luncheon Presentation *(Sponsorship Opportunity Available)* **or Lunch on Your Own**

1:20 Dessert Refreshment Break in the Exhibit Hall with Poster Viewing

MOLECULAR BIOTECHNOLOGY AND BIOINFORMATICS: INFORMATICS TOOL AND THERAPEUTIC APPLICATIONS

1:55 Chairperson's Remarks
William Loging, Ph.D., Associate Professor of Genomics & Head, Production Bioinformatics, Genetics and Genomics Sciences, Icahn School of Medicine at Mount Sinai

2:00 Bioinformatics Pipeline for Detection of Fusions and Gene Expression in Clinical Oncology Samples using RNA-Seq
Keith Callenberg, Ph.D., Lead Bioinformatics Scientist, Molecular & Genomic Pathology, University of Pittsburgh

2:30 Talk Title to be Announced
Andreas Matern, VP, Partnerships and Innovation, Executive Management, GeneDx

3:00 Molecular Impacts of Immune Modulating Drugs on Cancer Patients
William Loging, Ph.D., Associate Professor of Genomics & Head, Production Bioinformatics, Genetics and Genomics Sciences, Icahn School of Medicine at Mount Sinai
The area of Immuno-Oncology provides a novel strategy for cancer treatment by utilizing the patient's Immune system to combat tumor growth. We investigated the impact of specific immune modulating drugs on patients with diagnosed tumors in order to understand the molecular changes that take place at the pathway level. These data are correlated to phenotypic effect and provide insights into the mechanism of immune system directed therapies for cancer.

3:30 Biosimilar Structural Comparability Assessment by NMR: From Small Proteins to Monoclonal Antibodies
Bostjan Japelj, Ph.D., Senior Scientist, Protein Biophysics and Bioinformatics, Sandoz Biopharmaceuticals
This talk will discuss 1) the insight on how to use NMR as a method to evaluate high order similarity between biosimilar and reference product on the market; 2) methods to evaluate degree of similarity between two NMR spectra of proteins shown by examples from three case studies; and 3) an update on the current state of the art NMR spectroscopy in biosimilar drug product formulations and associated challenges.

4:00 Conference Adjourns

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Track 13

Data Security

Meeting the Challenge in the Big Data-Centric World

TUESDAY, APRIL 5

7:00 am Workshop Registration and Morning Coffee

8:00 – 11:30 Recommended Morning Pre-Conference Workshops*
Security Considerations for Virtual Research

12:30 – 4:00 pm Recommended Afternoon Pre-Conference Workshops*
Growth Strategy: Leveraging Cloud Scalability to Enable Rapid Growth and Change

** Separate registration required*

2:00 – 6:00 Main Conference Registration

4:00 PLENARY KEYNOTE SESSION
Please see page 3 for details.

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

WEDNESDAY, APRIL 6

7:00 am Registration Open and Morning Coffee

8:00 PLENARY KEYNOTE SESSION
Please see page 3 for details.

9:00 Benjamin Franklin Awards and Laureate Presentation

9:30 Best Practices Awards Program

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

BUILDING A SECURE CLOUD

10:50 Chairperson's Opening Remarks
David LaBrosse, Strategic Partner Manager, NetApp Healthcare

11:00 Building the Bionic Cloud
Michaela Iorga, Ph.D., Senior Security Technical Lead for Cloud Computing; Co-Chair, NIST Cloud Security Working Group; Co-Chair, NIST Cloud Forensic Science Working Group, National Institute of Standards and Technology

When coupling the continuously growing and changing landscape of advance persistent threats with the explosion of "pervasive computing" or "ambient intelligence" founded by the hyperconnectivity of "everyware", we reach a technical inflection point which calls for innovative solutions to support the further development of a strong, secure backbone of the Internet of Things (IoT) – a bionic cloud.

11:30 Adopting Public Cloud at Enterprise Scale: Public IaaS at AstraZeneca
Don Barber, Infrastructure Architect, Enterprise Computing, IT Infrastructure & Operations, AstraZeneca

Public cloud adoption at scale requires significant rethinking of enterprise systems, processes and culture. This talk outlines how AstraZeneca IT has made this journey to offer public cloud as an enterprise service by tackling challenges with provisioning, management, security and qualification. Subject material will range broadly from technical issues to policy challenges and workforce education needs, concluding with a few predictions about the future.

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

Sponsored by Google Cloud Platform

12:15 Bringing Data and Computing Together to Enable Research Innovation
Joe Corkery, M.D., Senior Product Manager, Google Cloud Platform

We will discuss how the vast data storage, sharing, and computing capabilities of Google Cloud Platform have enabled numerous researchers to bring together previously unwieldy data sets to gain novel insights. We will also explore how access to Google's cloud resources enables researchers to revisit traditional approaches to data analysis and pursue new methodologies that would otherwise be out-of-reach in a traditional environment.

12:30 Session Break

Sponsored by LabAnswer LABORATORY INFORMATICS

12:40 Luncheon Presentation I: Making Cloud R&D Electronic Laboratory Environments a Reality
John Conway, Global Director, Strategy and Technology, Research and Development, LabAnswer

The drivers behind moving to Cloud-based, enterprise class, scientific software applications are substantial, and the trend is rapidly gaining momentum. LabAnswer will showcase examples and discuss the practical considerations of deploying electronic laboratory environments (ELE) via the Cloud, including Electronic Laboratory Notebooks, LIMS, etc. Capabilities and functionality topics to be addressed include Data Governance, Entity Registration, Request/Sample/Inventory Management, and Data Aggregation & Analytics.

Sponsored by amazon web services

1:10 Luncheon Presentation II to be Announced

1:40 Session Break

1:50 Chairperson's Remarks
Tom Johnson, Senior Director & Product Manager, Pharma and Life Sciences Services, Exostar

1:55 Cloud Computing in a GxP Environment
Krista Woodley, Director, Digital Quality and Risk Management, Biogen

We discuss the regulatory expectations and associated challenges with moving to cloud-based solutions (SaaS, IaaS, PaaS). Discussion points include requirements for vendor oversight, validation and maintenance of cloud-based solutions.

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2:25 Case Study: How Merck Is Leveraging Information Security to Enable & Accelerate Clinical Trials

Andrew K. Porter, Director, Enterprise Architecture, IT Planning & Innovation, Merck & Co.

Bringing data, applications and people together for clinical trials takes too long, costs too much and leaves security gaps that threaten intellectual property and regulatory compliance. Merck explains its cloud-based solution to close these gaps and mitigate risks by leveraging entitlements management and fine-grained provisioning to automate partner onboarding, connect required applications and data, assign permissions and control access by authenticating identities.

2:55 Why Would You NOT Use Public Clouds for Your Big Compute Workloads?

Sponsored by CYCLE COMPUTING

Jason Stowe, CEO, Cycle Computing

Up to now there's been resistance to leveraging the cloud for the compute and data intensive workloads that historically run on in-house HPC environments. But genomics, computational chemistry, and other data collection and analytics have outpaced internal capacity. The lure of zero queue times, unlimited amounts of processing, and the ability to directly fit jobs to budget/value instead to available capacity is proving impossible to resist. This talk will highlight the risks and rewards of doing science in the cloud.

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

GENOMIC DATA SECURITY AND PRIVACY

4:00 The Next Phase for Healthcare Privacy and Security - Information Governance

Katherine Downing, Director, Practice Excellence, American Health Information Management Association

Security and privacy are of huge importance in business as our organizations continue to be the target of attack. Taking a holistic approach using Information Governance is the next generation for privacy and security. Information Governance is an organization-wide framework for managing information throughout its lifecycle and for supporting the organization's strategy, operations, regulatory, legal, risk, and environmental requirements.

4:30 Securing Personal Genomic Data: The Potential of the Blockchain

Richard Shute, Ph.D., Consultant, Curlew Research

More people are having their genomes sequenced and letting sequencing companies use their data for research. What if people want to take back control of their own data? How would they confidently and securely manage their most highly personalized information? Blockchain technology (the global ledger behind Bitcoin) could be the answer to securely protecting genomic information and managing transactions associated with personal genomic data.

5:00 FEATURED PRESENTATION: The Role of Cybersecurity Leadership in This New World

Mansur Hasib, D.Sc., CISSP, PMP, CPHIMS, Cybersecurity Professor and Author, University System of Maryland

The world has changed. Technology drives the mission of the bio-IT world today. Yet this world has been the subject of some of the most sensational data breaches and even ransomware. What are we doing wrong? Technology certainly does not appear to be the answer. Yet, organizations appear prepared to dump money on the problem. In a highly interactive session, Dr. Hasib shares his views and analysis on the importance of people, leadership, and culture in cybersecurity.

5:30 – 6:30 Best of Show Awards Reception in the Exhibit Hall with Poster Viewing

THURSDAY, APRIL 7

7:00 am Registration and Morning Coffee

8:00 PLENARY KEYNOTE SESSION PANEL

Please see page 3 for details.

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

PRACTICES AND POLICIES TO PROTECT SENSITIVE DATA

10:30 Chairperson's Opening Remarks

Dinesh Vandayar, Vice President, Personalized Medicine, SAP SE

10:40 Standardized Security Systems: How They Protect Pharmaceutical Data from Breaches

Mollie Shields-Uehling, President, SAFE-BioPharma Association

Information security breaches are a problem. Globalization and digitization of drug development relies on the Web to share information, exposing patient data and scientific intellectual property to hacks. The session reviews standardized security systems, and their use allowing the secure free flow of information across firewalls among collaborating parties. It includes best practices used by stakeholders such as Merck, GSK and Pfizer.

11:00 Possession is 9/10ths of the Law; Considerations and Evaluations for IT Security Policies

Brian Bissett, Senior Member, Baltimore Section, Institute of Electrical and Electronic Engineers (IEEE)

High-level IT security breaches have made the news numerous times over the past year. Despite the awareness of the risks security breaches pose to organizations, they are still occurring with alarming frequency across all enterprises in both the public and private sector. Is this to become the new norm or has it ushered in a catalyst for change?

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Track 13

Data Security

Meeting the Challenge in the Big Data-Centric World

11:20 Accessing and Utilizing Public Genomic Data: How Hard Can It Be?
Dianne Pacheco, Information Security Officer, The Jackson Laboratory
Gregg TeHennepe, IT Project Manager, The Jackson Laboratory
The world is awash in Big Data, including large public genomic data sets such as TCGA. Access to these data sets is cited as a high-priority need for research programs; however, the technical and administrative logistics can be daunting. In this talk we will cover the security policies and practices needed to satisfy the data use requirements associated with major public genomic data sets.

11:40 Innovating, Reimaging, and Digitally Transforming Personalized Medicine
Sponsored by SAP
David Delaney, Ph.D., CMO, SAP SE
With a flexible platform and advanced analytics, new digital solutions from SAP are uniquely positioned to help advance personalized medicine. The SAP Foundation for Health and applications such as SAP Health Engagement support deeper insights and connect data silos. Bring together your mission-critical structured, unstructured, public private, and experimental health data to provide better patient outcomes.

12:10 pm Session Break

12:20 Luncheon Presentation *(Sponsorship Opportunity Available)* **or Lunch on Your Own**

1:20 Dessert Refreshment Break in the Exhibit Hall with Poster Viewing

BIG DATA: SHARING VS. PRIVACY VS. SECURITY IN HEALTHCARE

1:55 Chairperson's Remarks
John M. Conley, J.D., Ph.D., William Rand Kenan, Jr. Professor of Law, University of North Carolina, Chapel Hill; Counsel, Robinson Bradshaw & Hinson

2:00 FEATURED PRESENTATION: precisionFDA
Taha A. Kass-Hout, M.D., MS, Chief Health Informatics Officer & Director, Office of Health Informatics, FDA
precisionFDA is an informatics cloud-based platform for ensuring the accuracy of Next-Generation Sequencing (NGS) tests by crowdsourcing reference material and data. A key part of President Obama's Precision Medicine Initiative, it serves as a collaborative research effort that will inform later regulatory pathways and decision making. During this talk, Dr. Taha Kass-Hout, FDA's Chief Health Informatics Officer, describes the platform and its successes since the December 2015 beta release.

2:30 FEATURED PRESENTATION: How the Plecosystem, Blockchain, and Federated Data Enclaves will Shape Genomics Innovation and Application: Emerging Initiatives from the Global Alliance for Genomics and Health
John E. Mattison, M.D., Chief Medical Information Officer, Assistant Medical Director, Southern California Medical Group, Kaiser Permanente; Co-Chair, eHealth Workgroup, Global Alliance for Genomics and Health GA4GH
How can we maximize genomic research for the good of all citizens without violating their privacy? We need powerful new approaches to ensure ethical research without unwarranted risk to citizens who consent to use of personal data. The Global Alliance for Genomics and Health includes worldwide institutions seeking consensus on policy frameworks supported by creative technical solutions to achieve these paired goals of higher value and lower risk. I discuss progress to date.

3:00 FEATURED PRESENTATION: Large-Scale Data Commons for Genomic and Clinical Data and the Changing Landscape for Sharing Research Data
Robert Grossman, Ph.D., Director, Center for Data Intensive Science (CDIS); Core Faculty, Institute for Genomics & Systems Biology and Computation Institute, Professor of Medicine, Section of Genetic Medicine, University of Chicago
Open commons containing large amounts of public biomedical data from the research community can potentially dramatically speed up medical research. We describe our experiences developing large-scale open source data commons for genomic and associated clinical data. We also discuss options for integrating and interoperating in-house genomic and clinical data with public data commons and private data partnerships.

3:30 PANEL DISCUSSION: How Will Data Sharing Innovations Fare in the Regulatory Environment?
Moderator: John M. Conley, J.D., Ph.D., William Rand Kenan, Jr. Professor of Law, University of North Carolina, Chapel Hill; Counsel, Robinson Bradshaw & Hinson
Panelists:
Robert Grossman, Ph.D., University of Chicago
Taha A. Kass-Hout, M.D., MS, FDA
John E. Mattison, M.D., Kaiser Permanente
Andrew K. Porter, Merck & Co.
Mollie Shields-Uehling, SAFE-BioPharma Association
The growth in patient healthcare and life sciences innovations can be attributed to technology enhancements like cloud computing, big data analytics and mobile applications, but may conflict with increasing regulatory compliance demands to ensure protection of healthcare life and quality as well as patient data privacy and security. This panel of esteemed technology solution providers and regulators debates real-world challenges and how regulation must also innovate at technology's pace.

4:00 Conference Adjourns

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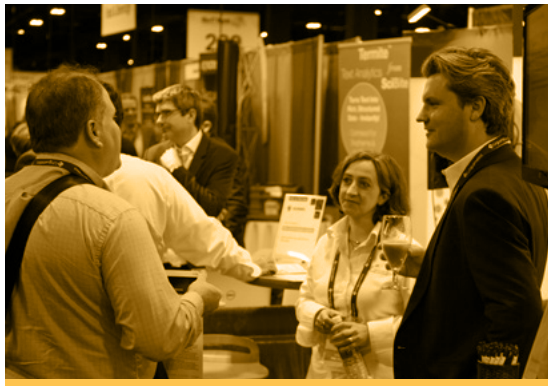

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