P4 Medicine

Catalyzing the transformation of medicine from its current reactive mode to a proactive mode that is predictive, preventive, personalized and participatory.
ISB FACULTY

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On behalf of the Institute for Systems Biology and our co-hosts The Gladstone Institutes, The Ohio State University, and the P4 Medicine Institute, welcome to our 10th annual international symposium.

This year's event, Systems Biology and P4 Medicine will showcase how systems approaches have already been transformational in laying the foundation for P4 Medicine, and will have even more impact in the future in accelerating innovation in ways that will revolutionize healthcare.

We are moving toward a new era of medicine where we will quantify wellness and demystify disease. This will enable a dramatic shift in the health care system to a proactive mode. It will enable the creation of a virtual cloud of billions of data points around each individual, which will require the development of analytic tools to translate this enormous data cloud into accurate predictions about health and disease.

Over the next decade, P4 Medicine will enable us to focus on health & wellness, and consider the consumer as the central figure in care. We will predict early or even prevent disease and provide consumer-oriented services that advance well being, more effectively promoting healthy lifestyle changes. We will demystify the complexities of disease through stratification, which will lead to better diagnoses and targeted therapies.

P4 Medicine is emerging out of the new capabilities provided by a fundamental transformation of the science of biology. Within the last few years biology has increasingly become an information-based discipline focused on systems approaches to a holistic understanding of complex biological systems. These systems approaches are based on the application of information technology to increasingly comprehensive sets of molecular, cellular, and phenotypic data.

It is an exciting time in biology and medicine and we look forward to your participation and insights throughout the symposium.

Sincerely,

Lee Hood

Nitin Baliga, PhD
Institute for Systems Biology
Professor
DAY 1 SCHEDULE: SUNDAY, MAY 15

11:30 AM  REGISTRATION

SYMPOSIUM OPENING

12:45 PM  WELCOMING REMARKS
Leroy Hood, MD, PhD
Co-founder and President, Institute for Systems Biology

1:05 PM  OPENING KEYNOTE ADDRESS
George Poste, PhD
The Evolution of Personalized Medicine: Opportunities and Challenges

SESSION 1: PERSONALIZED MEDICINE

Session Chair:
R. Sanders Williams, MD
The Gladstone Institutes

1:50 PM  Ralph Snyderman, MD
Personalized Medicine: From Theory to Practice

2:15 PM  Anne Wojcicki

2:40 PM  Break 20 Minutes

3:00 PM  Nicole Urban, PhD
Identification, Validation and Application of Biomarkers for Epithelial Ovarian Cancer

3:25 PM  Clay Marsh, MD
Realizing the Potential of P4 / Systems Medicine

3:50 PM  Session 1 Panel Discussion

4:15 PM  Break 20 Minutes
SESSION 2: PERSONALIZED GENOME
Sponsored by OVP Venture Partners

Session Chair:
George Church, PhD .......................................................... p.28
Harvard Medical School

4:35 PM  Panel Discussion: Current Sequencing Systems
Mark P. Stevenson .............................................................. p.8
Clifford A. Reid, PhD ............................................................ p.8
David Bentley, PhD, FMedSci .................................................. p.8

5:20 PM  Break 20 Minutes

5:40 PM  Panel Discussion: Future Sequencing Systems
Barrett Bready, MD .............................................................. p.8
Eric Schadt, PhD ................................................................. p.20

6:25 PM  Session 2 Closed

7:00 PM  Reception and Poster Session
DAY 2 SCHEDULE: MONDAY, MAY 16

9:00 AM  Continental Breakfast

SESSION 3: SYSTEMS APPROACH TO DISEASE

Session Chair:
Leroy Hood, MD, PhD
Co-founder and President, Institute for Systems Biology

9:50 AM  Aimée Dudley, PhD  From Sake to Chocolate: Systems Genetics in Yeast  p.18

10:15 AM  Eric Schadt, PhD  A Multi-Scale Biology Approach to Understanding and Treating Human Disease  p.20

10:40 AM  Break 20 Minutes

11:00 AM  Joseph Nadeau, PhD  From Peas to Disease  p.22

11:25 AM  Session 3 Panel Discussion

11:50 AM  Break 20 Minutes

SESSION 4: ETHICS, POLICY AND ECONOMICS

Session Chair:
Mauricio A. Flores, JD
Managing Director, The P4 Medicine Institute

12:10 PM  Session 4 Panel Discussion
Nancy Andrews, MD, PhD  p.9
R. Sanders Williams, MD  p.9
Steve Gabbe, MD  p.9

12:55 PM  Lunch Break 60 Minutes
SESSION 5: TECHNOLOGY

Session Chair:
Rob Moritz, PhD
Associate Professor and Director of Proteomics, Institute for Systems Biology

1:55 PM  Gary Siuzdak, PhD ........................................... p.24
Mass Spectrometry-Based Metabolomics as a Unique Biochemical Approach for Therapeutic Discovery

2:20 PM  Jim Heath, PhD ........................................... p.26
Approaches for Dramatically Reducing the Cost of Clinical In Vitro Protein Diagnostic Measurements, with Applications to Melanoma and GBM Cancer Patients

2:45 PM  Break 20 Minutes

3:05 PM  George Church, PhD ........................................... p.28
Technologies for Collecting and Integrating Genome, Environment and Trait Data

3:30 PM  Session 5 Panel Discussion

3:55 PM  Break 20 Minutes

4:15 PM  CLOSING KEYNOTE ADDRESS
Huntington Willard, PhD ........................................... p.30
The Rising Tide of Personalized Medicine: Learning to Swim, Riding the Wave and Avoiding the Undertow

5:00 PM  CLOSING REMARKS
Dr. George Poste is Chief Scientist, Complex Adaptive Systems Initiative (CASI) and Del E. Webb Professor of Health Innovation at Arizona State University (ASU). He assumed this post in 2009. From 2003 to 2009 he directed and built the Biodesign Institute at ASU. In addition to his academic post he serves on the Board of Directors of Monsanto, Exelixis, Caris Life Sciences and the Scientific Advisory Board of Synthetic Genomics. From 1992 to 1999 he was Chief Science and Technology Officer and President, R&D of SmithKline Beecham (SB). During his tenure at SB he was associated with the successful registration of 31 drug, vaccine and diagnostic products. In 2004 he was named as ‘R&D Scientist of the Year’ by R&D Magazine, in 2006 he received the Einstein award from the Global Business Leadership Council and in 2009 received the Scrip Lifetime Achievement award voted by the leadership of the global pharmaceutical industry.

Dr. Poste has published over 350 research papers and edited 14 books on pharmaceutical technologies and oncology. He has received honorary degrees in science, law and medicine for his research contributions and was honored in 1999 by HM Queen Elizabeth II as a Commander of the British Empire for his contributions to international security.

Dr. Poste is a Fellow of the UK Royal Society, the Royal College of Pathologists and the UK Academy of Medicine, a Distinguished Fellow at the Hoover Institution, Stanford University, a member of the Council for Foreign Relations and the US Institute of Medicine Forum on Microbial Threats. He also serves on several US government panels related to biosecurity and national competitiveness.
The Evolution of Personalized Medicine: Opportunities and Challenges

Rapid progress in systems biology and molecular analytical platforms offers the promise of major gains in the detection, treatment and prevention of diseases and for targeting therapeutic interventions to match the molecular and pharmacogenetic profiles of individual patients (personalized medicine).

Molecular diagnostics, next-generation imaging and miniaturized on body: in-body sensors will assume increasing importance in the healthcare value chain as powerful technology platforms for precision diagnosis, selection of optimum treatment, treatment compliance and remote monitoring of individual health status. These emerging diagnostic, imaging and health monitoring platforms will generate data on an unprecedented scale. Academia, industry, regulators and healthcare systems are ill-prepared for the technical, financial, organizational and cultural implications of large scale computing initiatives in healthcare.

Agility in forging new alliances between the hitherto separate sectors of (bio) pharmaceuticals, diagnostics, devices, computing, telecommunications and consumer social media networks will radically reshape the future healthcare landscape and the competitive environment.

Technical innovation has been, and will remain, fundamental to progress in healthcare. However, the anticipated acceleration of new discoveries will also generate complex economic, social and ethical questions regarding the ‘value’ of innovation, how much new technology society can afford and how priorities for the allocation of expensive healthcare resources are set.
SESSION 2 PANEL DISCUSSION: Current Sequencing Systems

Mark P. Stevenson
Life Technologies Corporation

From December 2007 to November 2008, Mr. Stevenson served as President and Chief Operating Officer of Applied Biosystems, which merged with Invitrogen Corporation in November 2008 to form Life Technologies. He joined Applied Biosystems in Europe in 1998, and held roles of increasing responsibility in Europe and Japan. He moved to the U.S. in 2004 to establish Applied Biosystems’ Applied Markets Division and in 2006 was named President of the Molecular and Cellular Biology Division.

Mr. Stevenson has more than 20 years of sales, marketing, and international executive management experience and received his bachelor’s degree in chemistry from the University of Reading, UK, and an M.B.A. from Henley Management School, UK. He serves on the board of trustees of the Keck Graduate Institute.

Clifford A. Reid, PhD
Complete Genomics, Inc.

Dr. Clifford A. Reid is co-founder of Complete Genomics, Inc. (NASDAQ: GNOM) and has served as President, Chief Executive Officer and Chairman since July 2005. From March 2003 to September 2005, Dr. Reid was Vice President of Collaborative Solutions at Open Text Corporation, a software company. In 1995, Dr. Reid co-founded Eloquent, Inc., a digital video communications company, and served as its Chief Executive Officer until 1999 and as its Chairman until 2003, when it was acquired by Open Text. In 1988, Dr. Reid co-founded Verity, Inc., an enterprise text search engine company, and served as its Vice President of Engineering from 1988 to 1992 and as its Executive Vice President from 1992 to 1993. Dr. Reid received a BS in Physics from the Massachusetts Institute of Technology, an MBA from Harvard University and a PhD in Management Science and Engineering from Stanford University.

David Bentley, PhD, FMedSci
Illumina, Inc.

Dr. David Bentley is Vice President and Chief Scientist at Illumina, Inc., developing new DNA sequencing technology for fast, accurate sequencing of complex genomes. His research interests include the study of human sequence variation and its impact on health and disease.

David was previously the Head of Human Genetics and a founder Member of the Board of Management at the Wellcome Trust Sanger Institute. He played a leading role in the Human Genome Project, The SNP Consortium, the International HapMap Project and initiation of the Wellcome Trust Case-Control Consortium multi-disease Genome-Wide Association Study.

David graduated with a Master of Arts in Natural Sciences from Cambridge and a PhD from Oxford. During his career, he has been Senior Lecturer at London University and has published over 150 articles in peer-reviewed journals.

SESSION 2 PANEL DISCUSSION: Future Sequencing Systems

Barrett Bready, MD
NABsys, Inc.

Dr. Bready has served as CEO of NABsys since 2005. He led the acquisition of GeneSpectrum as well as the execution of the licensing deal with Brown University. Since joining NABsys, Barrett has been named one of the top “30 under 30” in New England by Mass High Tech: The Journal of New England Technology and one of “25 movers and shakers” in the state of Rhode Island by the magazine Rhode Island Monthly.

Barrett teaches “Biotechnology Management” at Brown University where he holds the position of Adjunct Assistant Professor of Biotechnology. Dr. Bready received his M.D. from Brown Medical School and his Sc.B. in Physics from Brown University, both as part of Brown’s eight-year Program in Liberal Medical Education. He co-chairs BioGroup, Rhode Island’s biotechnology industry organization. Dr. Bready serves on the Board of Directors of the Brown Medical Alumni Association and is a Trustee of the Providence Preservation Society and WaterFire.

Eric Schadt, PhD
Pacific Biosciences; Sage Bionetworks

Eric Schadt is an expert in genomics and functional genomics. He is the Chief Scientific Officer of Pacific Biosciences, a company that is developing technologies to produce accurate, complete genome sequences. He is also the Chief Science Officer at Sage Bionetworks, a company that is developing data analysis and discovery tools to accelerate the understanding of human biology and disease. Eric has made significant contributions to the Human Genome Project and is a leader in the development of technologies for whole genome sequencing.
SESSION 4 PANEL DISCUSSION: Ethics, Policy and Economics

Nancy Andrews, MD, PhD
Duke University

Dr. Nancy Andrews has been Vice Chancellor for Academic Affairs and Dean of the Duke University School of Medicine since October 2007. She is also a Professor of Pediatrics and Pharmacology & Cancer Biology.

Dr. Andrews received her BS and MS degrees in Molecular Biophysics and Biochemistry from Yale University. As a student in the Harvard-MIT MD-PhD Program she earned her PhD with Nobel laureate David Baltimore at MIT along with her MD from Harvard Medical School. She completed her residency and fellowship in Pediatrics and Hematology/Oncology at Children’s Hospital Boston and the Dana-Farber Cancer Institute.

Dr. Andrews spent her entire professional career at Harvard before she moved to Duke. She was the George Richards Minot Professor of Pediatrics, Senior Associate in Medicine at Children’s Hospital, and a Distinguished Physician of the Dana-Farber Cancer Institute. Dr. Andrews was director of the Harvard-MIT MD-PhD Program from 1999 to 2003 and dean for Basic Sciences and Graduate Studies at Harvard Medical School from 2003 to 2007. Dr. Andrews was also an investigator of the Howard Hughes Medical Institute for 13 years.

R. Sanders Williams, MD
The Gladstone Institutes

Dr. R. Sanders Williams was educated and received postdoctoral training in public and international affairs, internal medicine, cardiology, biochemistry and molecular biology at Princeton University, Duke University, Harvard University (Massachusetts General Hospital), Oxford University and the Cold Spring Harbor Laboratory. Dr. Williams served on the faculty of Duke University and of the University of Texas Southwestern Medical Center before assuming the role of Dean of the School of Medicine at Duke in 2001. He was promoted to Senior Vice Chancellor in 2007, and took on the leadership of Duke University’s Office of Global Strategy in 2008. In 2010 he became President of Gladstone.

Dr. Williams has served as president of professional societies, on editorial boards of leading academic journals such as Science, and on the Director’s Advisory Committee of the National Institutes of Health and the Board of External Advisors to the National Heart, Lung and Blood Institute.

Dr. Williams is a fellow of the American Association for the Advancement of Science, and an elected member of the Institute of Medicine of the National Academy of Sciences, Alpha Omega Alpha, the American Society for Clinical Investigation, and the Association of American Physicians.

Steve Gabbe, MD
The Ohio State University

Dr. Steven Gabbe is the Senior Vice President for Health Sciences for The Ohio State University and Chief Executive Officer of The Ohio State University Medical Center. Dr. Gabbe has led the Medical Center to its first ranking on the U.S. News & World Report “Best Hospitals” Honor Roll of the nation’s top 21 hospitals, recertification as a Magnet Hospital for nursing excellence, honors as a Best Place to Work in central Ohio for the third consecutive year, growth in biomedical research funding to more than $205 million per year, and University Board of Trustees approval of ProjectONE, the largest construction project in University history.

Dr. Gabbe earned his undergraduate degree magna cum laude from Princeton University and his medical degree with Alpha Omega Alpha honors from Cornell University Medical College. He was a medical intern at New York Hospital, a research fellow in Reproductive Medicine at Boston Hospital for Women and a research fellow in Biological Chemistry at Harvard Medical School before completing his residency in obstetrics and gynecology at Boston Hospital for Women and a clinical fellowship in obstetrics and gynecology at Harvard Medical School.
Dr. Snyderman served as Chancellor for Health Affairs and Dean of the School of Medicine from 1989 to July 2004 and led the transition of the medical center into an internationally recognized leader of academic medicine. He oversaw the development of the Duke University Health System, one of the most successful integrated academic health systems in the country, and served as its first President and CEO. Dr. Snyderman has played a leading role in the conception and development of Prospective Care, a novel approach to personalized health and an evolving model of national health care delivery. He was among the first to envision and articulate the need to move the current focus of health care from treatment of disease events to personalized, predictive, preventative and participatory care. His approach, termed Prospective Care, embraces strategic health planning rather than reactive responses to late stage chronic disease.

In 2004, Dr. Snyderman founded, and now Chairs, Proventys, Inc., a company at the forefront of transforming health care into a personalized and preventative approach through the development of unique risk assessment and clinical decision support tools.
Personalized Medicine: From Theory to Practice

The introduction of science into the practice of medicine a century ago transformed the practice and led to a profound understanding of the mechanisms of disease. The scientific approach, following reductionist principles, delivered spectacular achievements in treating disease, but it has not been effective in preventing chronic illnesses which account for almost 75% of health care expenditures in the United States. Fortunately, recent breakthroughs in the sciences of genomics, proteomics, metabolomics and bioinformatics make it possible to again transform health care to address the problems of chronic diseases. The current focus on intervention for events of late-stage chronic disease is due, in part, to the lack of effective prevention, early intervention or personalized therapies. Emerging technologies and medical know-how are enabling prospective approaches to health which can mitigate these problems. Personalized, predictive and preventative care with meaningful patient engagement medicine; i.e., Prospective Health Care, is a new approach that uses individualized health risk assessment, personalized health planning and disease tracking tools to direct the best means of health promotion and disease prevention. If disease occurs, early intervention and therapy are personalized to meet the needs of the individual. To realize the potential of this new model of care, tools are needed to allow accurate personalized health risk assessment and disease tracking. Such tools will likely employ clinical information and biomarkers to create multivariate risk models and tools for identifying risk, tracking pathogenesis, predicting disease events and informing therapy. Providers and patients will be able to develop personalized strategies for health promotion, disease avoidance and therapeutic planning. To be successful, prospective care will require new approaches to medical reimbursement, training of a knowledgeable provider work force and creation of an organization structure capable of delivering and sustaining this rational approach to care. Importantly, prospective health care will turn the focus of medicine from fixing what’s broken to preventing disease and when needed, using personalized approaches to fix them.
Ms. Wojcicki brings to 23andMe a ten year background in healthcare investing, focused primarily on biotechnology companies. She left the investing world with the hope that she could have a positive impact on research and medicine through 23andMe. From her vantage point, Ms. Wojcicki saw a need for creating a way to generate more information - especially more personalized information - so that commercial and academic researchers could better understand and develop new drugs and diagnostics. By encouraging individuals to access and learn about their own genetic information, 23andMe will create a common, standardized resource that has the potential to accelerate drug discovery and bring personalized medicine to the public. (Plus, getting access to her own genetic information and understanding it has always been one of her ambitions.) Ms. Wojcicki graduated from Yale University with a BS in biology.
Consumers, Genomes and Research. The Power of Numbers for the Future of Personalized Medicine

Anne Wojcicki, President and Co-Founder of 23andMe, a personal genetics company, will discuss 23andMe’s online research model and the potential of dynamic databases to make discoveries faster, for less money and in doing so help usher in personalized medicine.

23andMe, Inc. (www.23andme.com) is a privately-held personal genetics company founded in 2006 by Anne Wojcicki and Linda Avey. Our aim is to help individuals understand their own genetic information through the latest advances in DNA analysis and web-based interactive tools. 23andMe customers provide a saliva sample to a Clinical Laboratory Improvement Amendments (CLIA)-certified laboratory to be run on a 23andMe-customized Illumina chip. Once the DNA has been analyzed, we provide scientifically accurate, high-quality information about their genetic code in a format that is easy to understand and use. Our hope is that the reports that we provide will help people gain deeper insight into their ancestry, inherited traits, disease risk, carrier status and drug response. We believe this information provides intriguing insights into an individual’s genetics, with the goal of expanding the collective knowledge base by enabling active participation in research.

In addition to the consumer product component of 23andMe, we also have a strong research focus. One of our core missions is to accelerate the pace of human genetics and disease research. Our website and 23andWe community pages enable a new kind of online research that gives individuals the opportunity to actively participate in research that directly affects their lives. Earlier this year, members of the 23andMe research team published our first manuscript in which we replicate many genetic associations for common traits as well as report on novel findings (http://www.plosgenetics.org/article/info:doi/10.1371/journal.pgen.1000993).
Dr. Nicole Urban is Associate Head of the Molecular Diagnostics Program in the Public Health Sciences Division at the Fred Hutchinson Cancer Research Center (FHCRC) and Research Professor of Health Services in the School of Public Health at the University of Washington (UW). She serves as Co-Program Head of the Women’s Cancer Research Program of the FHCRC/UW Cancer Consortium. Dr. Urban has played a leadership role nationally and locally in ovarian cancer biomarker research, including ovarian cancer screening trials.

Dr. Urban was formally trained in Biostatistics and Health Services Administration at the Harvard School of Public Health. She has extensive experience with outcomes research in cancer screening. For the past 20 years Dr. Urban has studied ways to improve the use, performance and efficacy of breast and ovarian cancer screening tools and is particularly interested in the discovery, development and validation of novel markers detectable in serum for use in cancer risk assessment and screening. She is best known for her identification and evaluation of candidate serum markers for ovarian cancer, including HE4 and Mesothelin, and for her analysis of the cost-effectiveness of screening for ovarian cancer.
Identification, Validation and Application of Biomarkers for Epithelial Ovarian Cancer

Epithelial ovarian cancer (EOC) is a significant cause of mortality in women due largely to the high proportion of cases that present at a late stage, when survival is poor. Early detection is a promising strategy but low prevalence of EOC makes high specificity necessary to achieve adequate positive predictive value (PPV). Recent reports suggest that serum markers may play a more important role in screening than thought previously. We identified and evaluated novel markers for their potential contribution to a multimodal screening strategy.

Using proximate samples from 112 women with EOC and 699 matched controls from the Prostate, Lung, Colon and Ovary (PLCO) trial we evaluated six serum markers for their potential to contribute to an ovarian cancer screening strategy. Using a subset of these samples from 88 cases of EOC and 517 matched controls for which transvaginal ultrasound (TVU) results were available, we compared alternative second-line screening tests in a strategy that employs an FDA-approved CA125 assay as a first-line screen.

We found that all six markers gave significant signal in cases identified by CA125. HE4 gave the highest signal, and was the only marker that gave significant signal in cases missed by CA125. We found that HE4 confirmed significantly more of the CA125-positive cases than did TVU at the same specificity. Holding constant the overall screening strategy’s specificity at 99.6%, we found that use of both HE4 and TVU in the second-line screen performed better than TVU alone.

CA125 and HE4 both outperform imaging in detecting ovarian cancer in asymptomatic postmenopausal women. When 2 of the 3 screening tests are positive, the screen can be considered positive and surgery may be warranted. This strategy is currently being evaluated in the Novel Markers Trial, an National Cancer Institute funded Phase I multi-site screening trial that is open in Seattle.
Dr. Clay Marsh, MD is Executive Director of the Center for Personalized Health Care and Vice Dean and Senior Associate Vice President for Research at the College of Medicine at the Ohio State University (OSU). He is also Professor of Internal Medicine in the Division of Pulmonary, Allergy, Critical Care and Sleep Medicine, Department of Internal Medicine and is board certified in Pulmonary and Critical Care Medicine. Dr. Marsh is the current director of the Center for Critical Care and Respiratory Medicine, one of six signature programs at OSU Medical Center, where he has implemented systems approaches to adherence to evidence-based guidelines to improve care delivery.

Dr. Marsh is focused at understanding deep biology underlying human health and disease and has a 17 year history of consecutive funding from National Institutes of Health (NIH) and regularly serves on NIH study sections. Dr. Marsh leads the efforts in Personalized Health Care at the Ohio State University, where he and the senior leadership are leading the effort in transforming health care delivery by creating pilot programs in wellness and chronic disease testing disruptive solutions that result in lower cost and higher quality/outcomes. Under his direction, OSU is a partner in the Coriell Institute’s Personalized Medicine Collaborative and led OSU’s efforts in partnering with the Institute for Systems Biology to form the P4 Medicine Institute.
Realizing the Potential of P4 / Systems Medicine

Health care today is reactive, expensive and variable and is in need of value innovation (lower cost and higher quality). We have partnered with the Institute for Systems Biology to form the P4 Medicine Institute, focused at realizing the potential of P4/Systems Medicine. As a large academic health care system, we have constructed a new rubric for health care delivery that has four pillars:

2. Stratifying patients into smaller, more precise groups through biomarker discovery.
3. Constructing computational and environmental approaches to the complexity of human health, disease and health care delivery.
4. Engaging participants through network activation (social, behavioral, environmental, games).

The ultimate goal of this program is to provide each person a health care experience and strategic plan that facilitates wellness, a multi-dimensional state (genetic/molecular, environmental, behavioral and physical) and brings the right solutions to the right person at the right time.
Aimée Dudley, PhD  
Institute for Systems Biology  
MONDAY | SESSION 3 | 9:50 AM

Dr. Aimée Dudley is an assistant professor at the Institute for Systems Biology (ISB). She is also an affiliate faculty member of the Department of Genome Sciences at the University of Washington and a faculty member of the University of Washington’s Molecular and Cellular Biology Graduate Program. Dr. Dudley’s formal training is in biology. She studied biochemistry and molecular biology as an undergraduate at the University of Massachusetts at Amherst, and earned her PhD in genetics at Harvard Medical School. Her graduate work in Dr. Fred Winston’s laboratory used yeast genetics, molecular biology, and biochemistry to decipher mechanisms by which transcription factors regulate gene expression. As a postdoctoral fellow in Dr. George Church’s laboratory at Harvard Medical School, she transitioned into the field of systems biology and gained experience in technology development and computational biology. As a member of the Church laboratory, she collaboratively developed experimental and computational methods to probe the structure of genetic networks using high-throughput analysis of gene function and regulation. Dudley’s lab at the ISB uses systems level approaches to understand gene function and regulation.
From Sake to Chocolate: Systems Genetics in Yeast

Among the most fundamental problems in biology is the relationship between an individual’s DNA sequence (genotype) and the ensuing observable characteristics (phenotype). This relationship is further complicated by the fact that many genes interact with each other and with the environment through complex interdependencies. Because many common diseases (such as asthma, diabetes, heart disease and cancer) result from the effects of multiple genes on several traits, understanding genetic interaction with respect to multiple phenotypes is of increasing relevance to the study of human health. Systems genetics uses large-scale, high-throughput methods to decipher the network of gene functions and interactions in an organism. This network, in which genes interact with each other and the environment, provides the framework through which biological information is transmitted, integrated and ultimately used by the downstream networks of proteins, RNAs and small molecules. I will present examples of how systems level approaches can be used to dissect complex quantitative traits in the yeast Saccharomyces cerevisiae.
Dr. Schadt joined Pacific Biosciences as Chief Scientific Officer in June 2009 to oversee the scientific strategy for the company, including creating the vision for next-generation sequencing applications of the company’s technology. Dr. Schadt is also a founding member of Sage Bionetworks, an open access genomics initiative designed to build and support databases and an accessible platform for creating innovative, dynamic models of disease.

Dr. Schadt’s current efforts were motivated by the genomics and systems biology research he carried out at Merck to elucidate common human diseases and drug response using novel integrative genomics approaches based on genetic and molecular profiling data. He also holds an affiliate professor position in the Departments of Medical Genetics and Biostatistics at the University of Washington in Seattle, and he was recently appointed as Fellow to the Institute of Systems and Synthetic Biology, Imperial College London. Dr. Schadt received his BS in applied mathematics/computer science from California Polytechnic State University, his MA in pure mathematics from University of California, Davis and his PhD in bio-mathematics from University of California, Los Angeles.
A Multi-Scale Biology Approach to Understanding and Treating Human Disease

Common human diseases and drug response are complex traits that involve entire networks of changes at the molecular level driven by genetic and environmental perturbations. Changes at the molecular level can induce changes in biochemical processes or broader molecular networks that affect cell behavior, and changes in cell behavior can affect normal tissue or whole organ function, eventually leading to pathophysiological states at the organism level that we associate with disease. While the vast majority of previous efforts to elucidate disease and drug response traits have focused on single dimensions of the system, achieving a more comprehensive view of common human diseases requires examining living systems in multiple dimensions and at multiple scales.

Studies focused on identifying changes in DNA that correlate with changes in disease or drug response traits, changes in gene expression that correlate with disease or drug response traits, or changes in other molecular traits (e.g., metabolite, methylation status, protein phosphorylation status and so on) that correlate with disease or drug response are fairly routine and have met with great success in many cases. However, to further our understanding of the complex network of molecular and cellular changes that impact disease risk, disease progression, severity and drug response, we can more formally integrate these different data dimensions. Here I present an approach for integrating a diversity of molecular and clinical trait data to uncover models that predict complex system behavior. By integrating diverse types of data on a large scale I demonstrate that some forms of common human diseases are most likely the result of perturbations to specific gene networks that in turn causes changes in the states of other gene networks both within and between tissues that drive biological processes associated with disease. These models elucidate not only primary drivers of disease and drug response, but they provide a context within which to interpret biological function, beyond what could be achieved by looking at one dimension alone. That some forms of common human diseases are the result of complex interactions among networks has significant implications for drug discovery: designing drugs or drug combinations to impact entire network states rather than designing drugs that target specific disease associated genes.
Dr. Joseph Nadeau is formerly James H. Jewel Professor and Chair of Genetics Department at Case Western Reserve University School of Medicine. Dr. Nadeau was a founding member of the International Mammalian Genome Society and a founding editor of Mammalian Genome and of Systems Biology and Medicine. He was founder and director of the Mouse Genome Informatics Project and founder of the Mouse Gene Expression Database Project. He has served on review panels and advisory groups at the National Institutes of Health, the National Science Foundation and the Human Genome Database, and has consulted for several biotech and major pharmaceutical companies. His research interests include cancer, metabolic disease and development, with an emphasis on mouse models, genetic, genomic, computational, bioinformatics, and systems studies. Dr. Nadeau has won several awards for his work and is an Elected Fellow of the American Association for the Advancement of Science.
From Peas to Disease

To understand human biology and to manage heritable diseases, a complete picture of the genetic basis for phenotypic variation and disease risk is needed. Unexpectedly however, most of these genetic variants, even for highly heritable traits, continue to elude discovery for poorly understood reasons. The genetics community is actively exploring the usual explanations for ‘missing heritability’. But given the extraordinary work that has already been done and the exceptional magnitude of the problem, it seems likely that unconventional genetic properties are involved.

We made two surprising discoveries that may dramatically change our understanding of the genetic basis for phenotypic variation and disease risk, and that may also explain much of ‘missing heritability’. The first property involves fractal genetics, where a very large number of often closely linked genetic variants act in a remarkably strong, non-additive and context-dependent manner to control phenotypic variation, suggesting that networks of gene interactions are more important than the constant action of individual variants. The second property involves transgenerational genetic effects, where genetic variants acting in one generation affect phenotypes in subsequent generations. Because these transgenerational effects are common, strong and persistent across multiple generations, they rival the action of genetic variants that are inherited in the conventional manner. The search is ongoing to identify the molecular basis for this non-DNA inheritance. Together these discoveries in model organisms shed light on genetic phenomena that impact human biology but that are difficult to extremely detect directly in human populations. In particular, inheritance of traits and diseases without the corresponding genetic variants could revolutionize our understanding of inheritance.
Dr. Gary Siuzdak is Director of the Scripps Center for Metabolomics and Professor of Chemistry and Molecular Biology at The Scripps Research Institute in La Jolla, California. He is also Faculty Guest at Lawrence Berkeley National Laboratory and served as Vice President of the American Society for Mass Spectrometry. His research includes developing novel approaches to metabolomics, the development of nanostructure platform for mass spectrometry imaging, novel approaches to virus characterization and inhibition, and mass-based inhibitor-enzyme screening. Dr. Siuzdak has over 170 peer-reviewed publications and two books, the latest being The Expanding Role of Mass Spectrometry in Biotechnology, 2nd Edition 2006.
Mass Spectrometry-Based Metabolomics as a Unique Biochemical Approach for Therapeutic Discovery

Quantitative global analysis of endogenous metabolites from cells, tissues, fluids or whole organisms - metabolomics, is becoming an integral part of functional genomics efforts as well as a tool for understanding fundamental biochemistry. Where the genome and proteome represent upstream biochemical events, the metabolites correlate with the most downstream biochemistry and therefore most closely represent the phenotype. This has been proven by the broad success of metabolite analysis in clinical diagnostics. The experimental aim in our studies is to obtain a comprehensive quantitative view of the metabolome to expand our understanding of what pathways are altered in specific diseases. We have developed multiple novel mass spectrometry platforms for metabolomics including both solution-based approaches and surface-based mass spectrometry, such as nanostructure-initiator mass spectrometry (NIMS) for tissue imaging, to address this problem. These platforms will be presented in the context of its application to discovering new disease therapies/pathways for chronic pain and multiple sclerosis.
Dr. James R. Heath received his BS in Chemistry from Baylor University in 1984 and his MS and PhD in Chemical Physics in 1988 from Rice University. He was a Miller Research postdoctoral Fellow UC Berkeley, then joined the IBM Watson Labs as Research Staff Member in 1991. He was appointed Assistant Professor at University of California, Los Angeles in 1994, and promoted to Professor in 1997. Dr. Heath founded the California NanoSystems Institute in 2000 and served as its Director until moving to the California Institute of Technology. Dr. Heath has worked in a number of areas, including nanomaterials, molecular electronics and quantum phase transitions. More recently he has turned his efforts to addressing translational and fundamental research problems in oncology. Dr. Heath has been a recipient of several awards, including the Spiers Medal from the Royal Society, a Public Service Commendation from California Governor Gray Davis, the Sackler Prize in the Physical Sciences and the Irvin Weinstein Prize and Lectureship from the American Association of Cancer Researchers. He has founded or co-founded several companies including NanoSys, Momentum Biosciences and Integrated Diagnostics. He serves as director of the National Cancer Institute funded NSB Cancer Center.
Approaches for Dramatically Reducing the Cost of Clinical In Vitro Protein Diagnostic Measurements, with Applications to Melanoma and GBM Cancer Patients

Even as we close in upon the $1000 genome, the cost of a clinical assay for a single protein biomarker ($50 - $100) has not changed much over the past few decades. Part of this stagnation arises from the fact that the clinical standard for a quantitative protein biomarker assay is the sandwich Enzyme-linked immunosorbent assay (ELISA). The associated antibodies are not only expensive, but, in addition, antibody-based assays present unique challenges in terms of multiplexing. In this talk, I will discuss two distinct approaches that are designed to lower the cost of protein-based in vitro diagnostics. The first approach is to simply miniaturize all aspects of such measurements — thereby permitting a large number of protein biomarkers to be assayed from very small sample sizes — including, for example, over 20 proteins assayed from single cells, with thousands of single cells analyzed in parallel. This approach yields benefits in terms of increased information content, reduced assay times and reduced reagent costs, and it has translated well into clinical studies. However, the cost bottleneck remains the antibodies. I will thus briefly discuss a protein capture agent alternative to antibodies, called protein-catalyzed capture agents, or PCC Agents. PCC Agents are exact chemical entities of molecular weight 4-5 kDa (roughly 30-40-fold less than IgGs), but share many similarities with monoclonal antibodies in key areas such as epitope targeting and high selectivity.
George Church, PhD
Harvard Medical School

MONDAY | SESSION 5 | 3:05 PM

Dr. George Church is Professor of Genetics at Harvard Medical School and Director of the Center for Computational Genetics. With degrees from Duke University in Chemistry and Zoology, he co-authored research on 3D-software & RNA structure with Sung-Hou Kim. His PhD from Harvard in Biochemistry & Molecular Biology with Wally Gilbert included the first direct genomic sequencing method in 1984; initiating the Human Genome Project then as a Research Scientist at newly-formed Biogen Inc. and a Monsanto Life Sciences Research Fellow at UCSF with Gail Martin. He invented the broadly-applied concepts of molecular multiplexing and tags, homologous recombination methods and array DNA synthesizers. Technology transfer of automated sequencing & software to Genome Therapeutics Corp. resulted in the first commercial genome sequence (the human pathogen, H. pylori, 1994). This multiplex solid-phase sequencing evolved into polonies, ABI-SOLiD, open-source Polonator.org and Personal Genomes.org. He has served in advisory roles for 12 journals, including five granting agencies and 24 biotech companies (e.g., 23andme & recently founding Codon Devices, Knome and LS9). Current research focuses on integrating biosystems-modeling with Personal Genomics & synthetic biology.
Technologies for Collecting and Integrating Genome, Environment and Trait Data

The human genome draft completed in 2004 (at eight-fold coverage) was a milestone, but at $3 billion it was not applicable to routine research or diagnostics. Expensive “common variant” association studies also generally failed to produce highly predictive and actionable diagnostics. Since 2004, we have pushed the cost of sequencing down by over a million-fold to $2K cost ($7K price) per 40-fold genome today. This also enables time-series studies of epigenomic and immunogenomic responses to cancers, microbes, allergens, vaccines, etc. Sharing saliva, skin, blood and stem cells and associated genome, environment and trait (GET) data greatly enables commercial and academic research, open-source software and data for interpreting whole and partial genome sequences as well as community tools for diverse phenomics. As the utility of cells, genes and traits increases, insights come from highly integrative approaches – evaluating individuals in cohorts holistically and computationally, often from outside the clinical specialty of the study, e.g. computer scientists, systems biologists or educational communities. Progress has been made by consenting volunteers with the understanding of open-access (including tests of comprehension of the consenting materials). Technologies for analysis of single-chromosome haplotypes and single-cell epigenomics include dilution libraries and in situ sequencing.
Dr. Huntington F. Willard has served as the founding Director of the Institute for Genome Sciences & Policy at Duke University and Duke University Medical Center since January 2003. He is also the Nanaline H. Duke Professor of Genome Sciences at Duke University, a position held jointly in the Department of Molecular Genetics & Microbiology and the Department of Biology.

Dr. Willard is a respected leader in the fields of genetics and genome biology, known both for his research accomplishments and for his commitment to integrating research and education at all levels. A graduate of Harvard College, he received his PhD from Yale University and carried out postdoctoral training at Johns Hopkins Medical Center. Prior to coming to Duke University, he held faculty positions at the University of Toronto, Stanford University, and Case Western Reserve University and was Chairman of the Department of Genetics at Case Western Reserve University from 1992 to 2001. He has served on the editorial boards of numerous scientific journals, most recently as co-founder and Executive Editor of Human Molecular Genetics for 14 years. Dr. Willard is the author or co-author of over 350 scientific publications. He is co-author of Genetics in Medicine, a widely used textbook, now in its seventh edition, and co-editor of Genomic and Personalized Medicine, a new two-volume reference text published in 2008. In addition, he is co-author of a forthcoming book on scientific and societal aspects of the Genome Revolution and is an author of numerous editorial and opinion pieces for the general public on the topics of biomedical research, education, genetics and the impact of the Genome Revolution on society.

A Fellow of both the American Association for the Advancement of Science and the American Academy of Arts and Sciences, Dr. Willard was awarded the 2009 William Allan Award by the American Society of Human Genetics for ‘substantial and far-reaching scientific contributions’. His scholarly interests include genetics and epigenetics; genome and chromosome biology; and the genome sciences and their broad implications for biology, medicine and society. He has received teaching awards from both Case Western Reserve University and Duke University and was appointed an HHMI Professor by the Howard Hughes Medical Institute in 2006 for his program to integrate undergraduate education and open-ended research opportunities in both the School of Arts & Sciences and the Pratt School of Engineering.

Huntington F. Willard, PhD
Duke University
Nanaline H. Duke Professor of Genome Sciences
Director, Duke Institute for Genome Sciences & Policy

MONDAY | CLOSING KEYNOTE | 4:15 PM
The Rising Tide of Personalized Medicine: Learning to Swim, Riding the Wave and Avoiding the Undertow

In the age of systems biology and personalized medicine, the transition from a traditional view of biology to a digital and genome-inspired one has been exhilarating, but fraught with difficult challenges and transitions for individuals and institutions. Here, I will explore some of these challenges in the context of a university model that needs to carry out its three missions of education, research and public service in real time. This experience has been marked by lessons, both good and bad, at various stages along the pipeline from basic research to clinical medicine. One of the greatest challenges – successfully met in individual cases, but not (yet) across the full spectrum of research and education – is the effective integration of digital and quantitative approaches to data analysis and handling with the more traditional and analog-driven view of biology and medicine. There would appear to be both individual and institutional costs to ignoring or failing to respond to these challenges, despite evident and significant advantages to those who successfully adapt to this sea change in the life sciences, both conceptually and operationally.
ABOUT ISB

The Institute for Systems Biology (ISB) was established to address the greatest challenge of 21st-century science — understanding biological complexity.

ISB is catalyzing fundamental paradigm changes in how the life sciences and medicine are practiced globally.

Researchers at ISB are generating results that can be applied to some of society’s most perplexing problems in medicine, global health and the environment. They are creating productive strategic partnerships with universities, companies and governments around the world, which are essential to attacking these challenges in a trans-disciplinary manner.

Since its founding in 2000, ISB has been a pioneering source of the new knowledge, innovative technologies and computational tools essential to deliver what ISB President Leroy Hood conceptualized and termed P4 Medicine, i.e., medicine that is predictive, preventive, personalized and participatory.

An independent, non-profit organization poised between academia and industry, ISB is deeply committed to discovering knowledge and translating its benefits to society. ISB commercializes its discoveries; advances science education; helps society better understand the impacts of science and technology; and creates exciting new organizations that facilitate these transfers.
ISB’S NEW STATE-OF-THE-ART FACILITY

ISB moved into its new facility in South Lake Union just a few weeks ago. This move is providing the Institute with exciting new opportunities for growth and expansion in science, technology, computation / mathematics, transformative strategic partnerships, and knowledge transfer to society.

ISB has a long-standing tradition of sharing its discoveries in computation, technologies, and related areas of systems biology research and resources with others. The Institute has moved to the South Lake Union neighborhood, in part because it is the hub of Seattle’s rich biotechnology community, with more than 20 life sciences research institutions, and biotech and technology companies within a few blocks. Many of these institutions will provide exciting new opportunities for collaboration to further ISB’s research agenda — from Amazon’s cloud computing to PATH’s diagnostic technologies efforts in global health.

The new facility provides ISB the opportunity to further increase the depth and breadth of its scientific capabilities and will enable the accommodation of additional faculty, researchers, and laboratory space. This effort began with the recruitment of Joe Nadeau as Director of Research and Academic Affairs, and ISB continues to enhance new skills to its existing cross-disciplinary group of scientists. Recruitment of two additional faculty members and their labs is underway, which will increase ISB’s expertise in cell biology, single cell analysis, theoretical studies, computational biology, environmental systems biology, and systems medicine.
THE POWER OF PARTNERSHIPS

In 2008, ISB launched a new program called Strategic Partnerships to foster innovation and collaborative discovery that includes a broad cross section of the world’s best talent and expertise.

Led by David Galas, a pioneer in computational biology, who joined ISB in 2008 to serve as the Senior Vice President for Strategic Partnerships and Professor, the team leads ISB’s business development efforts and is playing an increasingly important role at the intersection between science and business.

The group has opened doors to a wide range of relationships, including an historic partnership agreement with the Grand Duchy of Luxembourg, providing $100 million in funding for ISB to engage in innovative science initiatives in P4 Medicine that will accelerate translation of new knowledge into novel diagnostic, therapeutic and prevention strategies.

A REVOLUTIONARY PARTNERSHIP: LUXEMBOURG AND ISB

Signed in December of 2008, this unprecedented model leverages funding from outside of the United States to support science and training at ISB. It is multi-faceted, involving most of the science and clinical institutions in Luxembourg and a newly created biobank in the country. The scope of this five-year agreement includes:

- An ambitious scientific research program underway in Seattle
- Working with the newly established Luxembourg Centre for Systems Biomedicine
- Catalyzing economic development activities
  A new company — Integrated Diagnostics, Inc. was launched in Seattle in 2009, with funding from US and UK venture capital firms and a fund from Luxembourg
- Education and training of Luxembourg scientists in the emerging discipline of systems biology

This nascent relationship has already yielded significant scientific advances with the publication of more than 30 scientific papers, including the recent Science paper that integrated genetics and genomics for the first time through the analysis of the complete genome sequences of an entire family. The new methods and approaches to medical genetics made possible by the groundbreaking partnership between ISB and Luxembourg are now being developed into a rapidly growing new facet of human genetics and genomics, termed systems genetics leading the understanding of human disease.
TRANSLATING DISCOVERIES

Systems science at ISB is accelerating discovery in all aspects of human health and it will have enormous impact in P4 Medicine — both in the developed and the developing world.

ACCELERATOR CORPORATION

Accelerator Corporation is a vehicle for disciplined and efficient investment in and management of emerging biotechnology opportunities. It was launched in 2003 by the Institute for Systems Biology, Alexandria Real Estate Equities, Inc and prominent players in the biotech venture community. Located in Seattle, Accelerator has reviewed more than 750 business plans since 2003, selecting only the most compelling investments from this deep pool of promising opportunities.

Accelerator identifies, evaluates, finances, and manages ground-breaking emerging opportunities in systems biology and related fields. Amgen Ventures, ARCH Venture Partners, OVP Venture Partners, PPD, Inc., WRF Capital, and ISB provide investment capital, state-of-the-art facilities, world-class scientific and technical expertise and support, and experienced start-up management.

Accelerator’s seven portfolio companies and graduates are focused on a wide range of promising discoveries such as improved biotherapeutics, vaccines, and biomarkers, which are being applied to cancer, infectious diseases, auto-immune disease, inflammation and other major human health problems.

ISB SPIN OFFs

ISB’s faculty members have launched four other companies:

Cytopeia developed and marketed advanced flow cytometry cell sorting instruments. It was acquired by BD in 2008 for more than $50 Million (no venture funding sought).

Integrated Diagnostics is developing diagnostics and measurement technologies capable of monitoring hundreds of biomarkers simultaneously, for earlier detection and more accurate management of complex disease.

Macrogenics discovers, develops and delivers novel biologics for the treatment of autoimmune disorders, cancer and infectious diseases.

NanoString is developing a complete solution for detecting and counting large sets of target molecules in biological samples.

Accelerator Corporation and ISB Spin Offs
- Raised $377 Million in venture funding since 2003
- Employ 328 employees at 10 companies in Seattle and Rockville, MD
ISB has pioneered a vision for science education that supports the true needs of today’s K-12 students while preparing them for their future. Through the work of ISB’s Center for Inquiry Science (CIS), many ISB scientists, and partner school districts throughout Washington State, the Institute has awakened and nurtured an enthusiasm for science learning. Through its systemic approach to science education, CIS is working with teachers and district administrators to assure that all students receive high quality science education.

In an effort to help prepare students for participating effectively in a culture that includes P4 Medicine, CIS has embarked on some exciting K-12 projects:

- **Identifying Student Needs**
  With funding from Agilent and Caltech’s Nanosystems Biology Center grant, CIS is partnering with P4MI to develop a set of infomercial videos that will be completed this Spring. These videos will target teachers, students, parents, researchers, clinicians, etc. in a call to action for ideas about what students need to be doing in school in preparation for a world that includes P4 Medicine. The videos will encourage people to participate in an online market research survey: systemsbiology.org/P4Med_K12. The outcomes of the survey will inform P4 Medicine related curriculum for both traditional K-12 classrooms, as well as emerging biomedical related academies/schools.

- **Curriculum Development**
  CIS and the Ozinsky lab at ISB have submitted a proposal to the National Institute for Allergy and Infectious Diseases to develop P4 Medicine curriculum related to predictive biology for personalized health. In addition to scientists and educators, CIS has recruited three curriculum companies to the project; all having expressed interest in publishing the K-12 science, health, and/or Career Technology Education (CTE) developed.

- **Bioscience Academy Development**
  Several of ISB’s partner school districts are developing biomedical-type “academies” for their high school students and they all have asked the Center for Inquiry Science and the Institute at large to participate in these ventures.

Since the Center for Inquiry Science was launched a decade ago, research of select CIS programs now show that such targeted and purposed professional development impact student learning. Students whose teachers have participated in such CIS programs have made statistically significant gains in science achievement (as measured by the state’s assessment, the WASL and MSP) — ahead of the state average. Further, student achievement in schools with the highest levels of poverty show the greatest gains with steady trends towards closing the achievement gap, exceeding a statewide comparison group.
The P4 Medicine Institute was co-founded in 2010 by the Institute for Systems Biology and The Ohio State University to help catalyze the transformation of medicine from a reactive mode to a system that is predictive, preventive, personalized and participatory.

P4MI’s goal is to drive innovative approaches to disease prevention and maintenance of health and wellness by applying systems biology to medicine and care delivery. P4MI will recruit clinical centers, scientific research institutions and appropriate industrial partners to collaborate in a network of integrated demonstration projects in the United States and throughout the world. It will also engage other healthcare stakeholders and thought leaders to accelerate the emergence of a P4 Medicine healthcare system that delivers more effective clinical care at lower cost.

ISB AND OHIO STATE UNIVERSITY MEDICAL CENTER

ISB and Ohio State University’s Medical Center have launched two P4 Medicine demonstration projects, one to establish metrics for wellness and another to apply P4 strategies to deal with heart failure. The projects will provide patients with a range of services that go beyond traditional genomic or “personalized” medicine by integrating many levels of hierarchical biological information — DNA, RNA, proteins, metabolites, networks, cells and tissues — to ultimately create predictive and actionable models for care delivery based on individual patient needs and utilizing novel forms of patient participation.

The projects will deploy cutting-edge clinical assays developed by ISB to generate the P4 cloud of personalized health data using genomic, proteomic and cellular analyses. These types of assays, and the enormous volume of personalized health data they generate, are the core technological basis for P4 Medicine.
P4 MEDICINE WILL HAVE SIGNIFICANT SOCIETAL IMPACT:

• It will digitalize medicine — providing the tools to manage each individual’s billions of data points and create actionable diagnoses from one molecule, one gene, one genome, or one tissue.

• It will foster a transformation of one of the biggest engines of economic growth — the health care industry.

• It will create opportunities for the emergence of many new companies — some in a new medical sector that doesn’t even exist today.

• Over time, P4 Medicine will reverse the skyrocketing costs of healthcare.