

Opportunities to Enhance Translation from Discovery to Health

Geoffrey S Ginsburg MD PhD

Professor of Medicine and Biomedical Engineering

The Duke Center for Applied Genomics
& Precision Medicine

Precisionmedicine.duke.edu



Global Genomic
Medicine Collaborative



International Cohorts Summit

Duke MEDx
Medx.duke.edu

Large Cohort Studies: The Goals Are the Same; The Tools Have Evolved

- Discovery: to explain the etiology of diseases, to understand health and health-to-disease transitions, to better define gene-environment interactions
- Translation: to provide the basis for
 - Novel risk models of disease
 - Clinical prevention and control measures for populations at risk
 - Biomarkers
 - Diagnostics
 - Therapeutics
 - Public health measures and practices
- Delivery – implementation and use of findings
 - Clinicians, public health practitioners
 - Public and policy makers awareness
 - Industry applications

“Factors of Risk”

Annals of Internal Medicine

Established in 1927 by the American College of Physicians

Factors of Risk in the Development of Coronary Heart Disease—Six-Year Follow-up Experience

Kannel WB et al.

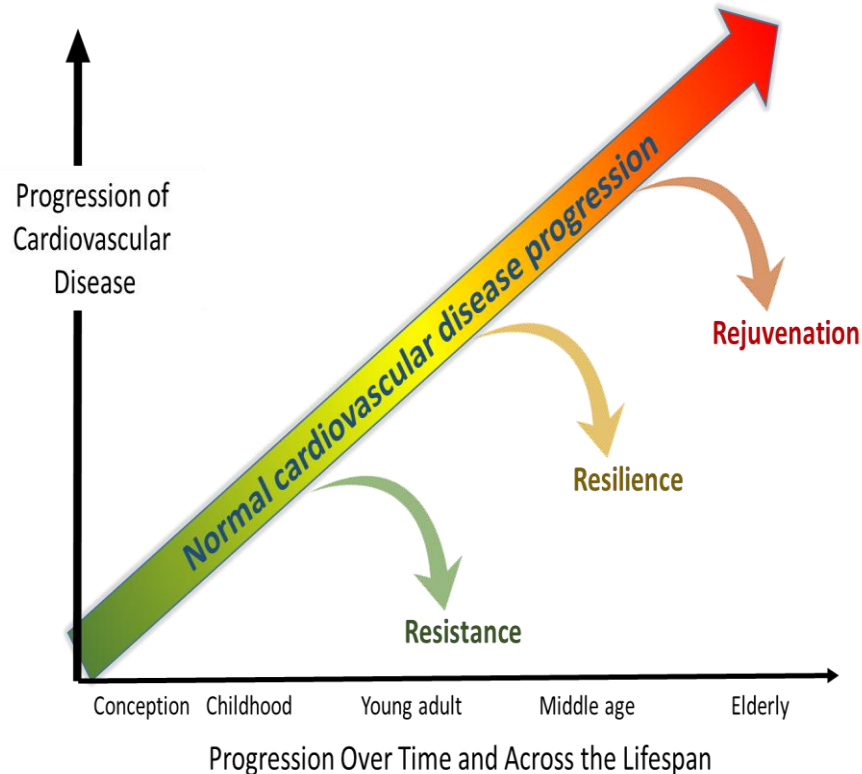
November 1961

- High blood pressure
- Increased cholesterol
- Smoking
- Diabetes
- Family history
- Male

Source: Kannel WB et al. *Ann Intern Med* 1961;55:33–50.

“Factors of Resilience”

Can we identify ‘health protection’ factors (vs risk factors) that preserve or restore health at multiple levels and their mechanisms of benefit



- **Resistance:** Protection from adverse stressors, including risk factors and environment
- *Examples of scientific inquiry: novel risk models, “disease resistance factors”*
- **Resilience:** Subclinical evidence of disease but without progression to overt disease over time.
- *Examples of scientific inquiry: regression of disease*
- **Rejuvenation:** Expediently restoring health in those with established, symptomatic disease, including regeneration and recovery.
- *Examples of scientific inquiry: medication reduction, rapid uneventful recovery from surgery*

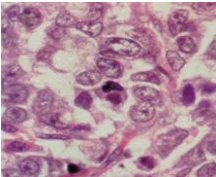
Analysis of 589,306 genomes identifies individuals resilient to severe Mendelian childhood diseases

Rong Chen^{1,2,12}, Lisong Shi^{1,2,12}, Jörg Hakenberg^{1,2}, Brian Naughton^{3,11}, Pamela Sklar^{1,2,4}, Jianguo Zhang⁵, Hanlin Zhou⁵, Lifeng Tian⁶, Om Prakash⁷, Mathieu Lemire⁸, Patrick Sleiman⁶, Wei-yi Cheng^{1,2}, Wanting Chen⁵, Hardik Shah^{1,2}, Yulan Shen⁵, Menachem Fromer^{1,2,4}, Larsson Omberg⁹, Matthew A Deardorff⁶, Elaine Zackai⁶, Jason R Bobe^{1,2}, Elissa Levin^{1,2}, Thomas J Hudson⁸, Leif Groop⁷, Jun Wang¹⁰, Hakon Hakonarson⁶, Anne Wojcicki³, George A Diaz^{1,2}, Lisa Edelmann^{1,2}, Eric E Schadt^{1,2} & Stephen H Friend^{1,2,9}

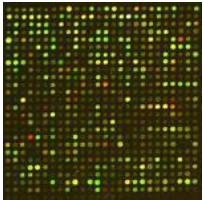
Transitions over 50 Years

Biology

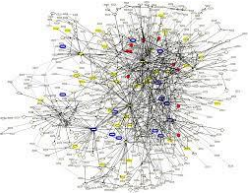
Observational
Science



Genomic (Digital)
Science



Systems Science



Medicine

Yesterday

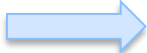
Today

Tomorrow

Symptom
Based

Population
Pattern
Based

Individual
Algorithm
Based



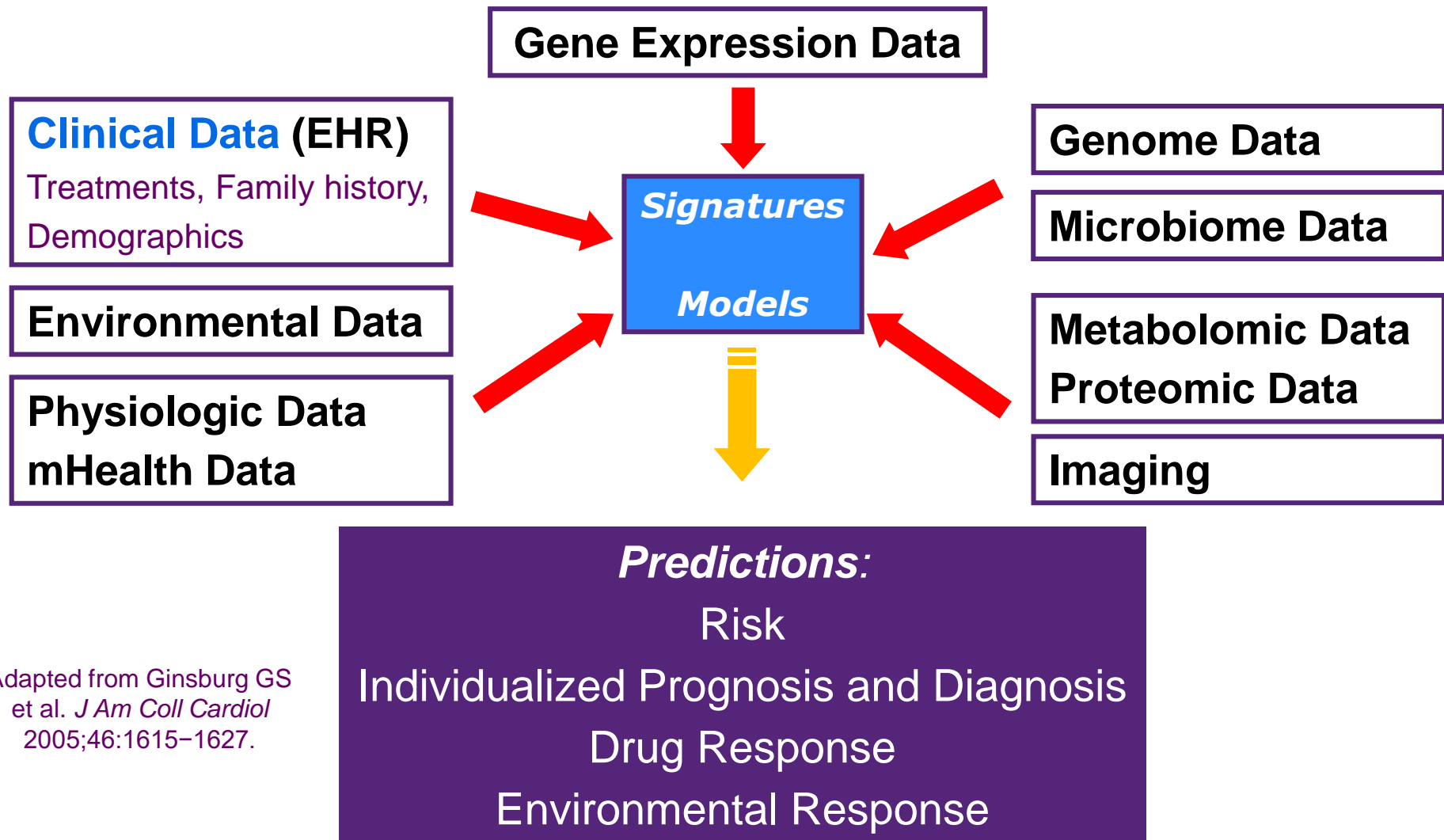
Intuitive
Medicine

Evidence-
based
Medicine

Precision
Medicine

*“People with this history and lab values also had...
... and responded to this treatment”*

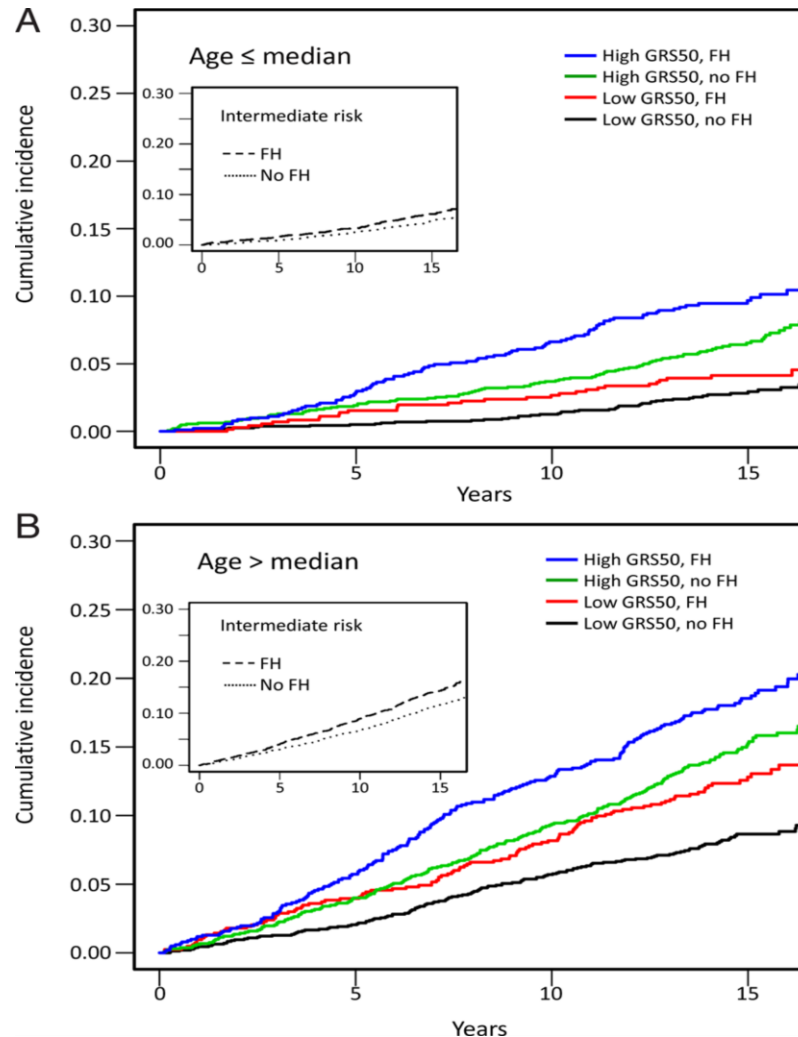
Diverse Data Enables Novel Predictive Models of Health and Disease



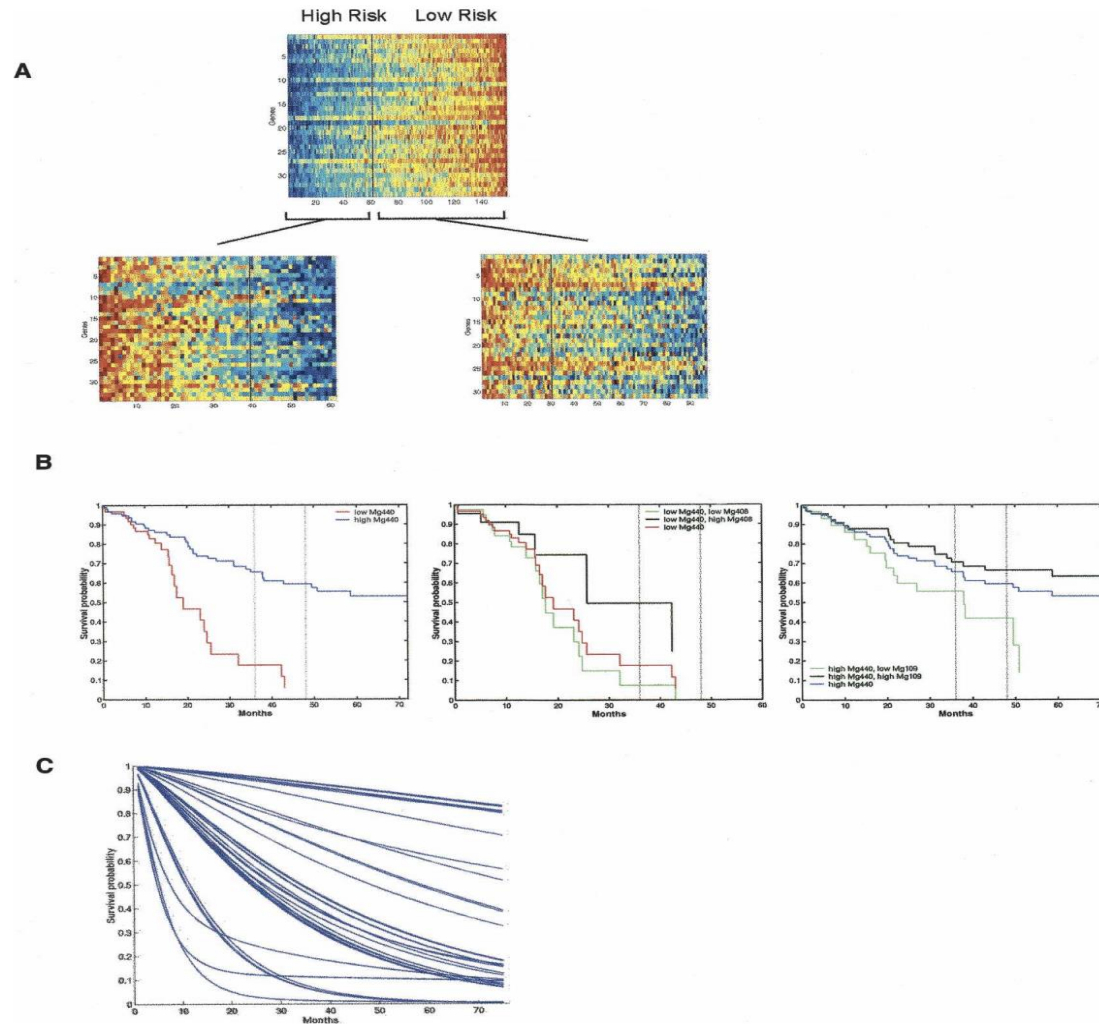
Adapted from Ginsburg GS
et al. *J Am Coll Cardiol*
2005;46:1615-1627.

Can We Do Better Than Clinical Models?

Risk prediction by genetic risk scores for coronary heart disease is independent of self-reported family history



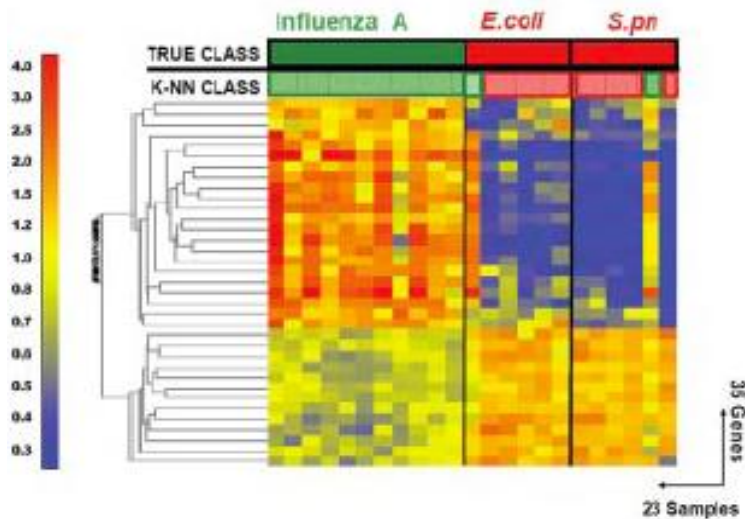
Can Genomic Analyses Refine Prognosis? (Breast Cancer)



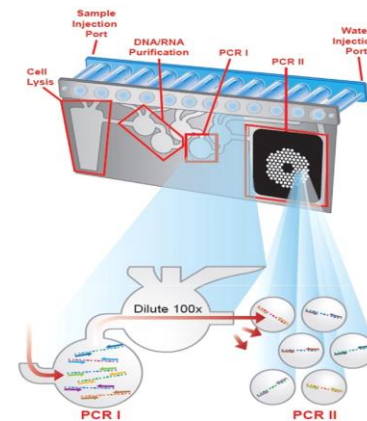
Can Genomics Analyses Provide Better Diagnostics? (Viral vs Bacterial Respiratory Infection)

Viral vs Bacterial Infection

< 60 min to result



The FilmArray Pouch



BIO FIRE[®]
A BIOMÉRIEUX COMPANY

ARLG
Antibacterial Resistance Leadership Group

Zaas et al, Cell Host and Microbe, 2009
Woods et al PLoS ONE 2013
Ramilo et al Blood 2007
Tsalik et al Sci Trans Med 2016

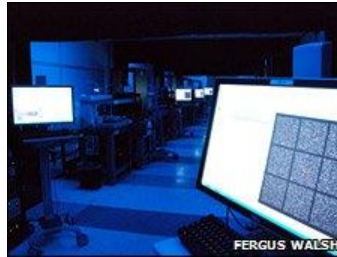
Genome Sequencing: *Affordable* Discovery and Clinical Application



HGP
2001
(13 years)
\$2.7B



Jim Watson
2007
\$1M



Complete Genomics
2009
\$4,400

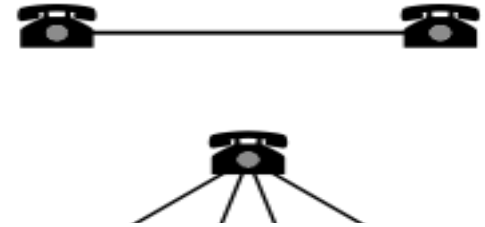
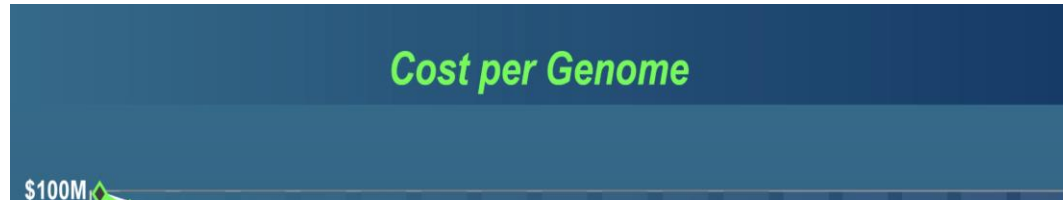


Ion Torrent
2012
\$1,000 (1 day)



Various Vendors
2018
< \$1000
> 50 Genomes/d

Moore's Law and Metcalf's Law – Convergence and Opportunity

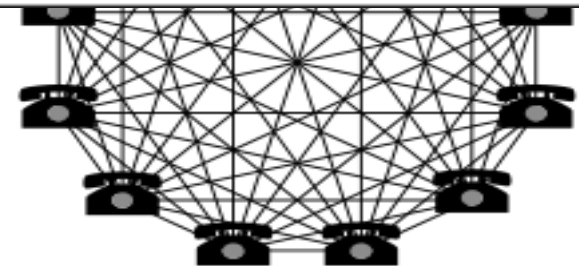
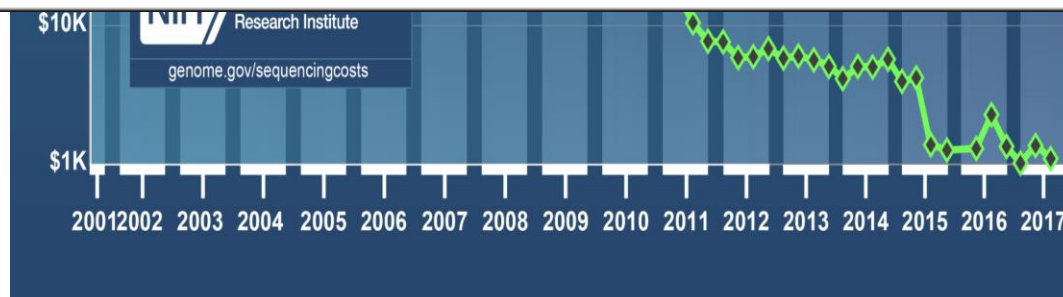


OPEN ACCESS Freely available online

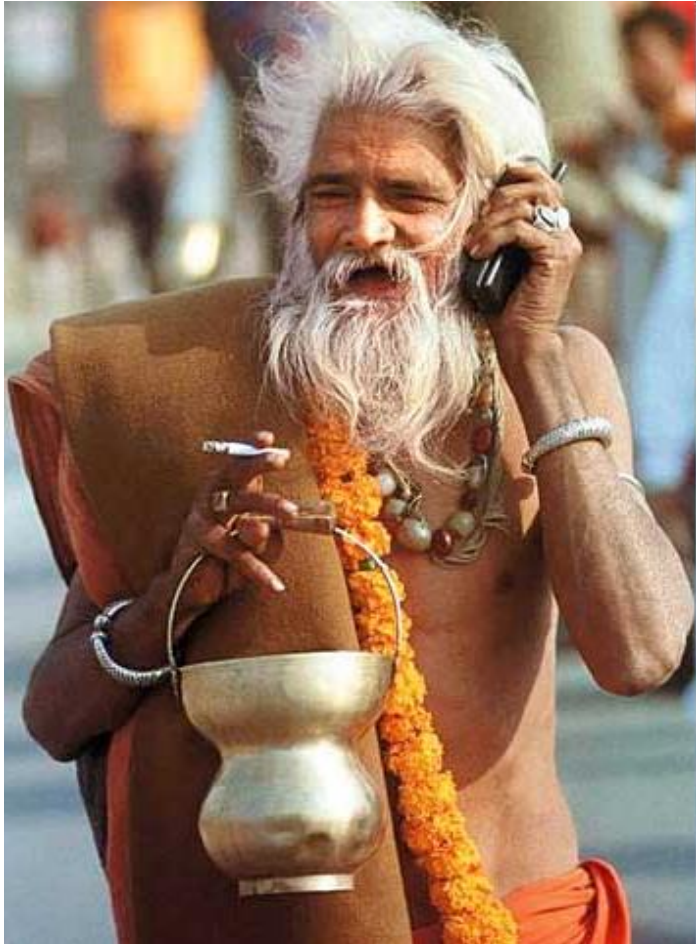
Efficient Replication of over 180 Genetic Associations with **Self-Reported Medical Data**

Joyce Y. Tung^{1*}, Chuong B. Do¹, David A. Hinds¹, Amy K. Kiefer¹, J. Michael Macpherson¹, Arnab B. Chowdry¹, Uta Francke^{1,2}, Brian T. Naughton¹, Joanna L. Mountain¹, Anne Wojcicki¹, Nicholas Eriksson¹

¹ 23andMe, Inc., Mountain View, California, United States of America, ² Department of Genetics, Stanford University, Stanford, California, United States of America



The Phone Has Changed Everything !



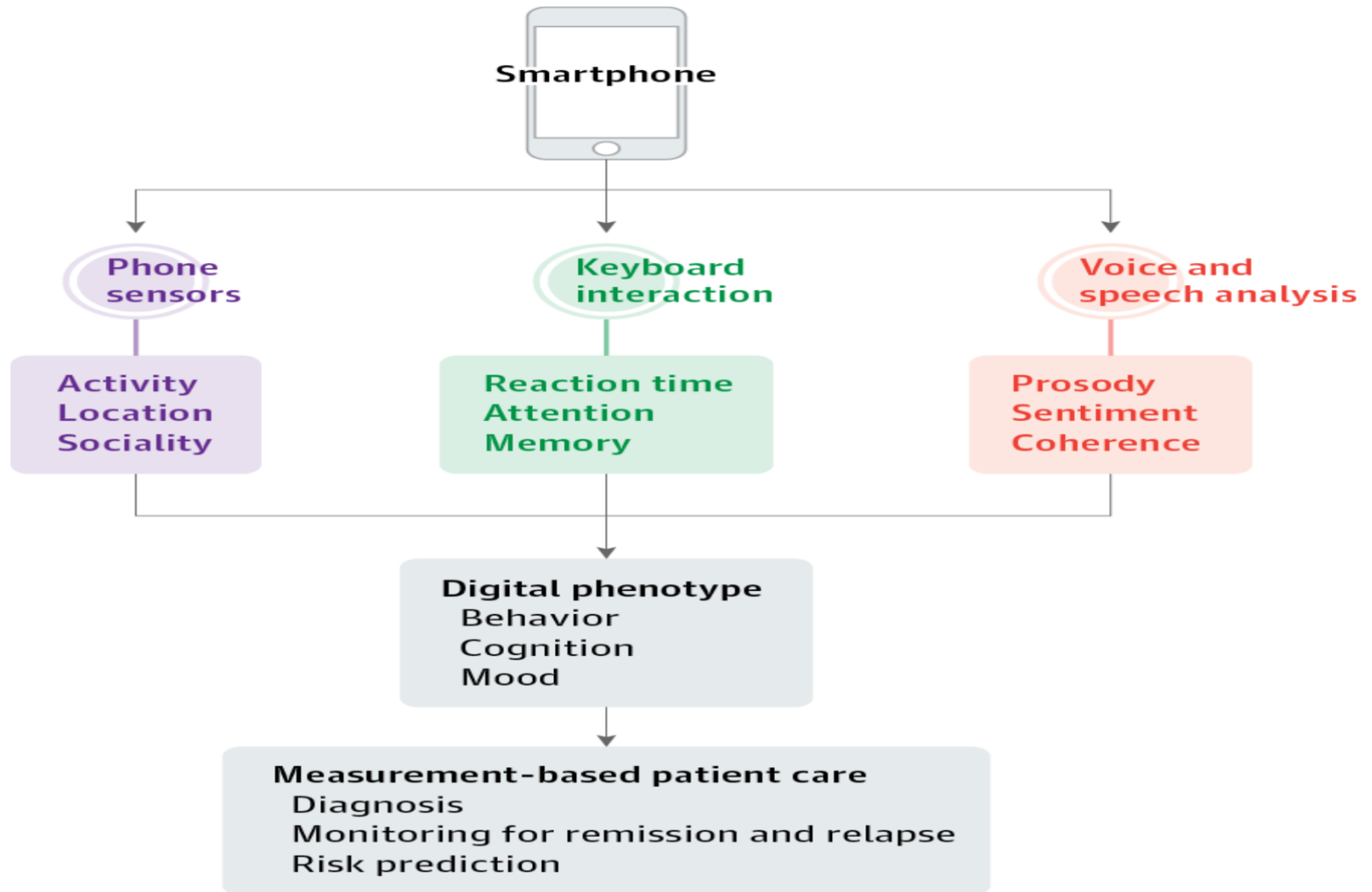
Source: W3C.org

- > 7 billion cell phone accounts
- > 80% of all people have one
- Health information
- Text messages
 - Cardiac health
 - HIV/AIDS
 - Diabetes
- **Data on Activity, Sleep, Nutrition**



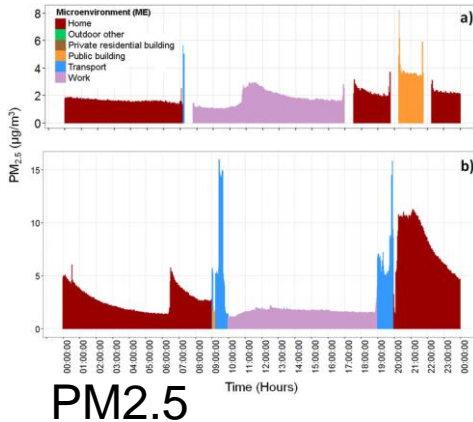
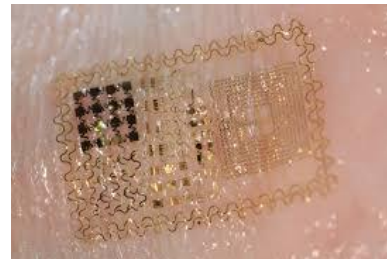
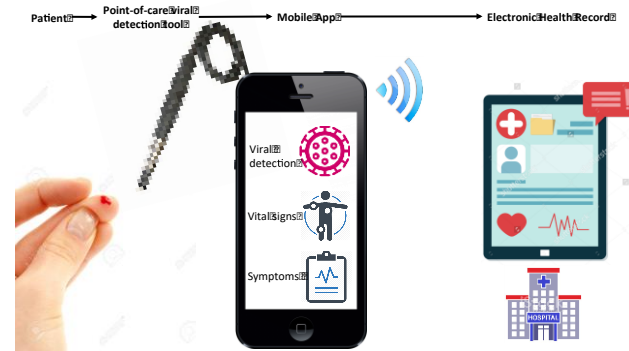
Feder, 2010, *Health Affairs*

Phone Enabled Digital Phenotyping: A New Science of Behavior



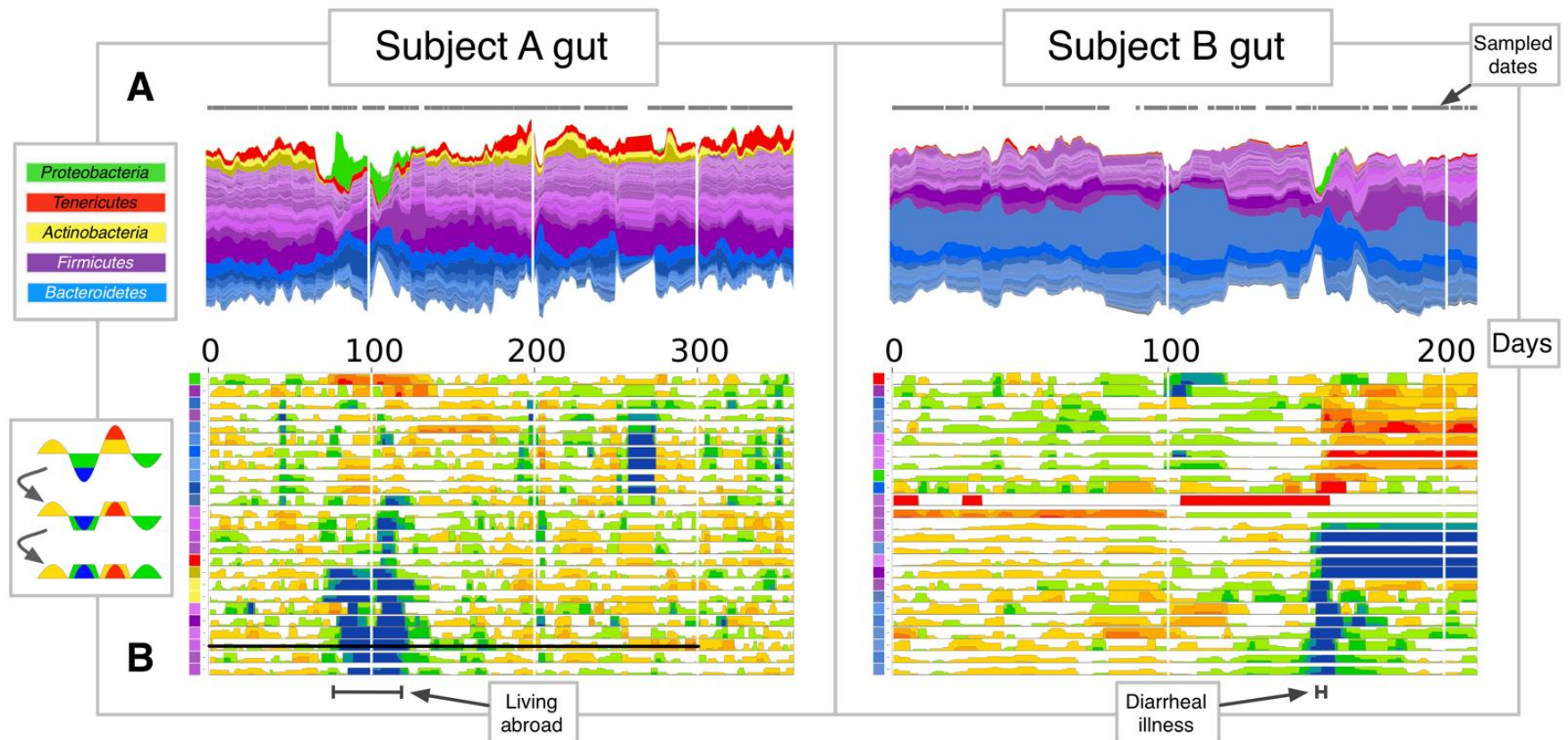
Decentralization of Research (and Medicine)

- Point-of-care devices
- Environmental sensors
- Health Monitors
- Wearable tattoos



Personal Microbiome Profiling

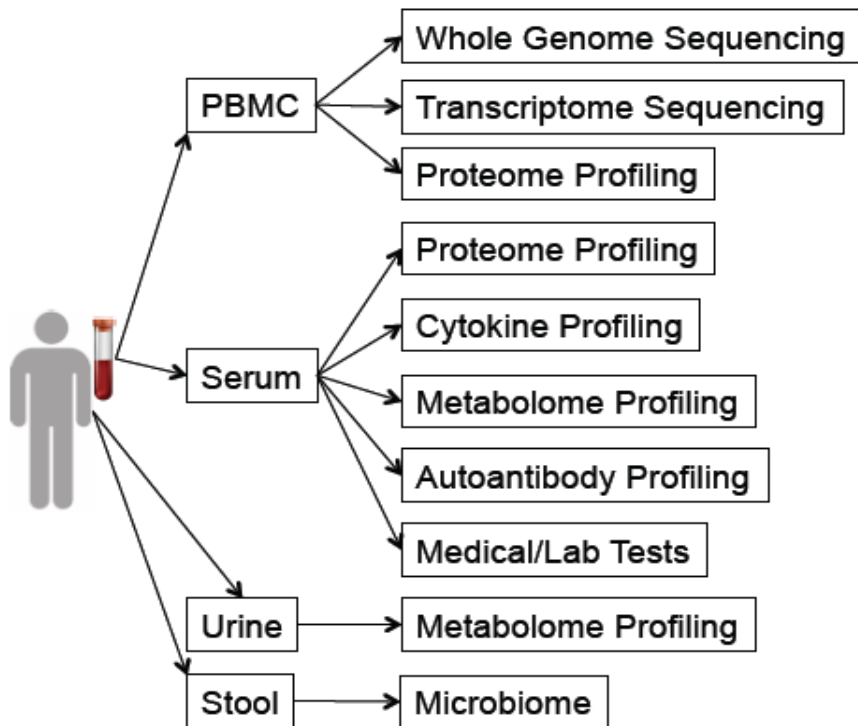
Dynamic Changes in Gut Flora (N=2)



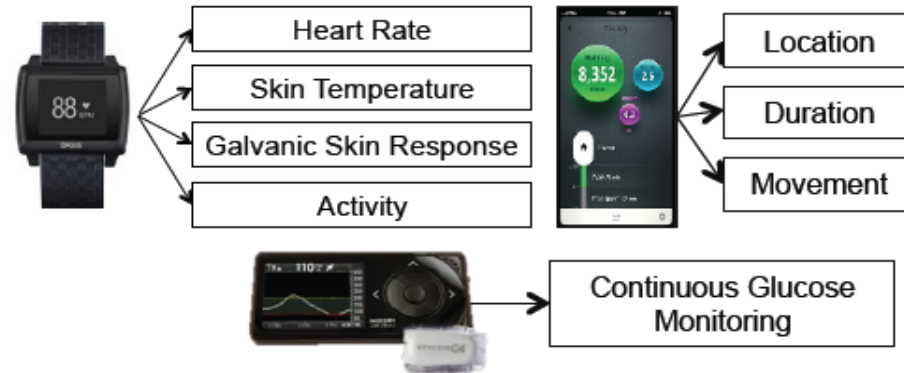
David et al, Genome Biology 2014

Multiscale biomedical data integration

Multi-omics



Wearable Devices



Electronic Health Records

Lipid Panel (7)
 Comprehensive Metabolic Panel (17)
 Complete Blood Count (19)
 Urinalysis (15)
 Electrolyte Panel (5)

Demographics
 Vital signs
 Lab orders
 Medication orders

 Up to 1017 Unique Clinical Lab Features

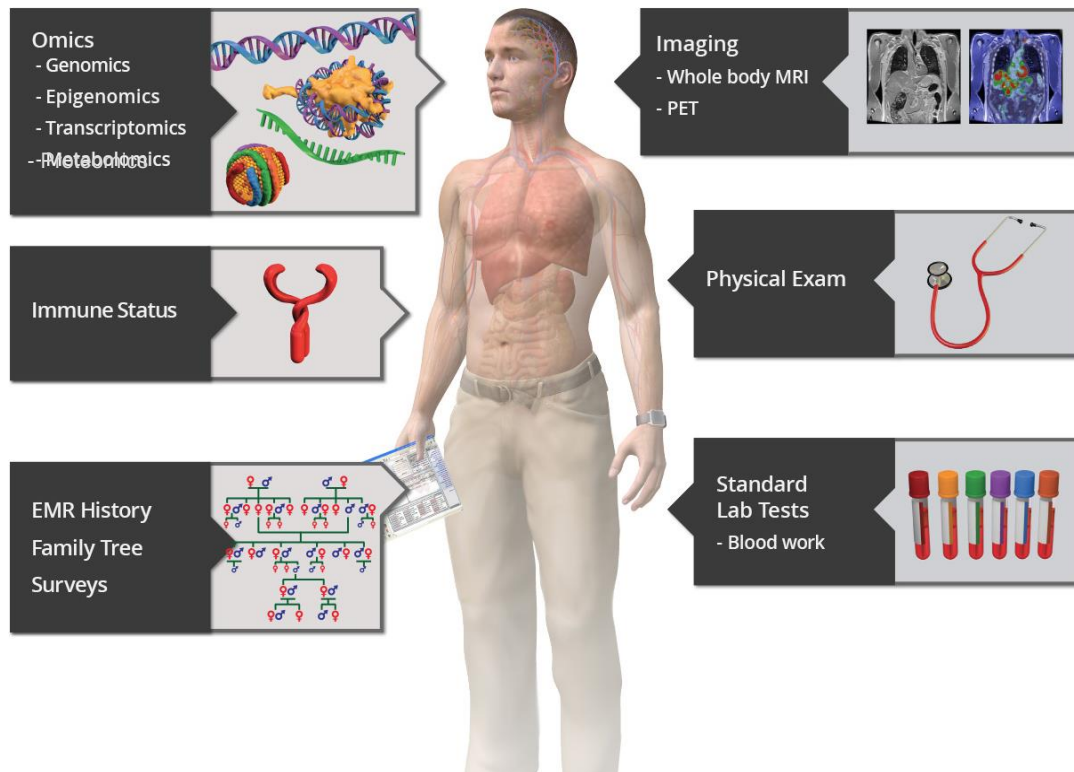
RESEARCH ARTICLE

Digital Health: Tracking Physiomes and Activity Using Wearable Biosensors Reveals Useful Health-Related Information

PLoS ONE, 2017

Xiao Li^{1*}, Jessilyn Dunn^{1,2*}, Denis Salins^{1*}, Gao Zhou¹, Wenyu Zhou¹, Sophia Miryam Schüssler-Florenza Rose^{3,4}, Dalia Perelman⁵, Elizabeth Colbert³, Ryan Runge¹, Shannon Rego³, Ria Sonecha¹, Somalee Datta¹, Tracey McLaughlin⁵, Michael P. Snyder^{1*}

Project Baseline: Human Health and Transition to Disease



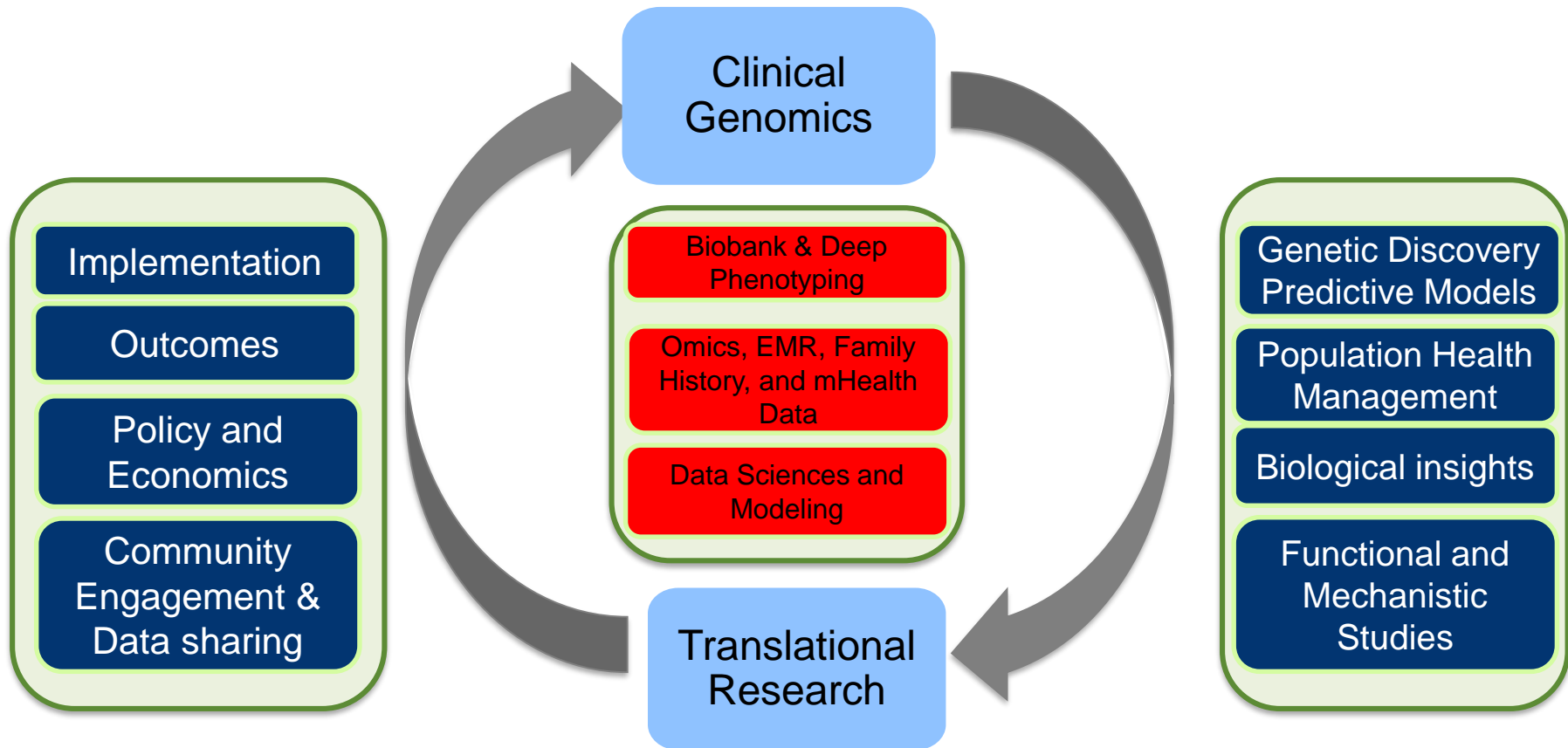
- Develop a **set of scalable and standardized tools** for acquiring, organizing, and analyzing clinical, molecular, imaging, sensor, behavioral, self-reported, psychological, environmental, health records, and other health-related data
- **Evaluate** approved and investigational **wearable and passive sensors**
- **Create a dataset** encompassing a wide spectrum of phenotypic measures
- **Identify biomarkers** of disease-related transitions, including those related to cardiovascular disease and cancer



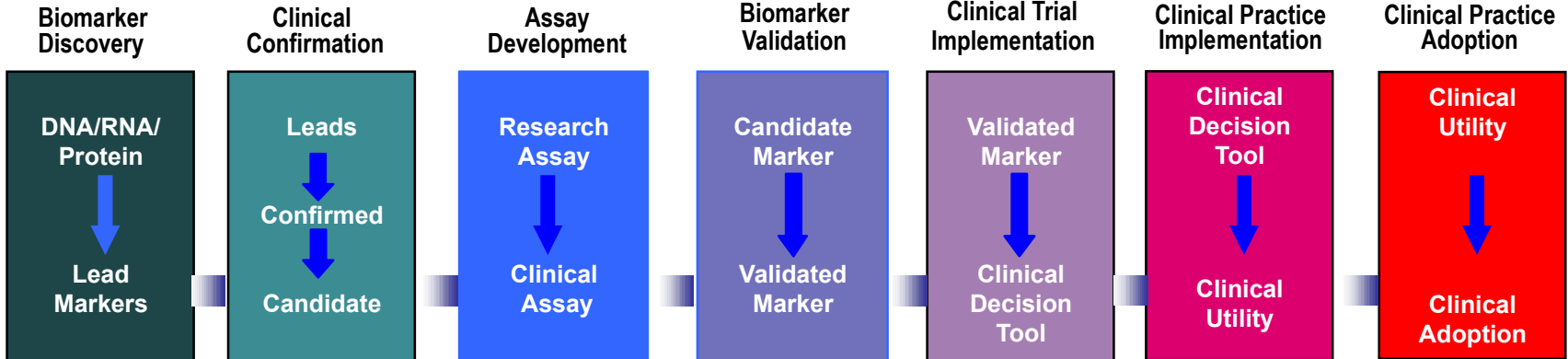
Deriving Drug Discovery Value from Large Scale Genetic Bioresources: A US National Academies Workshop

- Large scale population cohorts with genetic and phenotypic data are rich sources of potential drug targets
- Phenotypes are critical - Self reported phenotypes are powerful
- For participants – Trust is paramount
 - Return of results is valued
- Data sharing and the power of collaborative frameworks will accelerate the field
- Computational solutions will be disruptive

Large Scale Bioresources: Cycles of Genomics and Precision Medicine Research and Clinical Applications



The 'Translational Continuum' for Biomarkers And Molecular Tests



We are here

“Vision Without Implementation is Hallucination” (Thomas Edison)

Weitzel et al. *BMC Medical Genomics* (2016) 9:1
DOI 10.1186/s12920-015-0162-5

BMC Medical Genomics

RESEARCH ARTICLE

Open Access

The IGNITE network: a model for genomic medicine implementation and research



Kristin Wiisanen Weitzel¹, Madeline Alexander², Barbara A. Bernhardt³, Neil Calman⁴, David J. Carey⁵, Larisa H. Cavallari¹, Julie R. Field⁶, Diane Hauser⁴, Heather A. Junkins⁷, Phillip A. Levin⁸, Kenneth Levy⁹, Ebony B. Madden⁷, Teri A. Manolio⁷, Jacqueline Odgis⁷, Lori A. Orlando^{10,19}, Reed Pyeritz³, R. Ryanne Wu^{10,19}, Alan R. Shuldiner^{11,12}, Erwin P. Bottinger¹³, Joshua C. Denny^{14,15}, Paul R. Dexter⁹, David A. Flockhart⁹, Carol R. Horowitz¹⁶, Julie A. Johnson¹, Stephen E. Kimmel^{2,17}, Mia A. Levy¹⁸, Toni I. Pollin¹¹, Geoffrey S. Ginsburg^{19*} and on behalf of the IGNITE Network

- **Expand and link** existing genomic medicine efforts
- Develop **implementation** methods, in diverse settings and populations
- Contribute to **evidence** base regarding outcomes of incorporating genomic information into clinical care
- **Disseminate best practices** for genomic medicine implementation, diffusion, and sustainability

www.ignite-genomics.org



Envisioning How Large Cohorts Might Enable Translational Research

- **Integration of personal, clinical, biological information**
 - Develop models for individual and population health
 - Prediction of health to disease transitions
 - Research in resistance, resilience, and rejuvenation
- **Provide researchers and healthcare systems with continuously updated estimates of individual risk and health behaviors of neighborhoods and populations**
 - Enable directed education, prevention and treatment programs
- **Use a more profound understanding of health and disease to inform development of new therapeutics and diagnostics**
 - Early disease detection
 - Bio-surveillance for public health impact
 - Drug Discovery
- **Provide and apply these data to our participants and our communities**