Dreaming of Tenure and IPO's While patient's suffer

October 9th 2013-ZURICH

Stephen H Friend MD PhD
President
Sage Bionetworks
Seattle WA (Non-Profit)





"Completely Automated Public Turing test to tell Computers and Humans Apart"

THE PLATFORM

You are Here: Home / The Platform

The Ushahidi Platform was built for information collection, visualization and interactive mapping. Below are some of the countries and projects that are using it:



How does that possibly work?

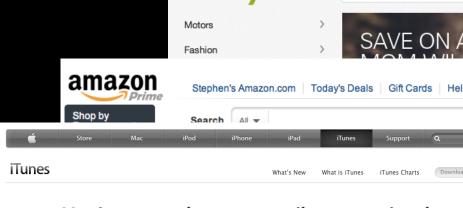
Why not engage in understanding of diseases?



Twentieth Century
Digital Media/internet

Helped people consume

A trillion hours/year of participatory value up for grabs



You've never been so easily entertained.







Twenty-First Century
Digital Media/internet

Helping people participate



A trillion hours/year of participatory value up for grabs



COGNITIVE SURPLUS

(Clay Shirky)





MODERN DIGITAL TOOLS

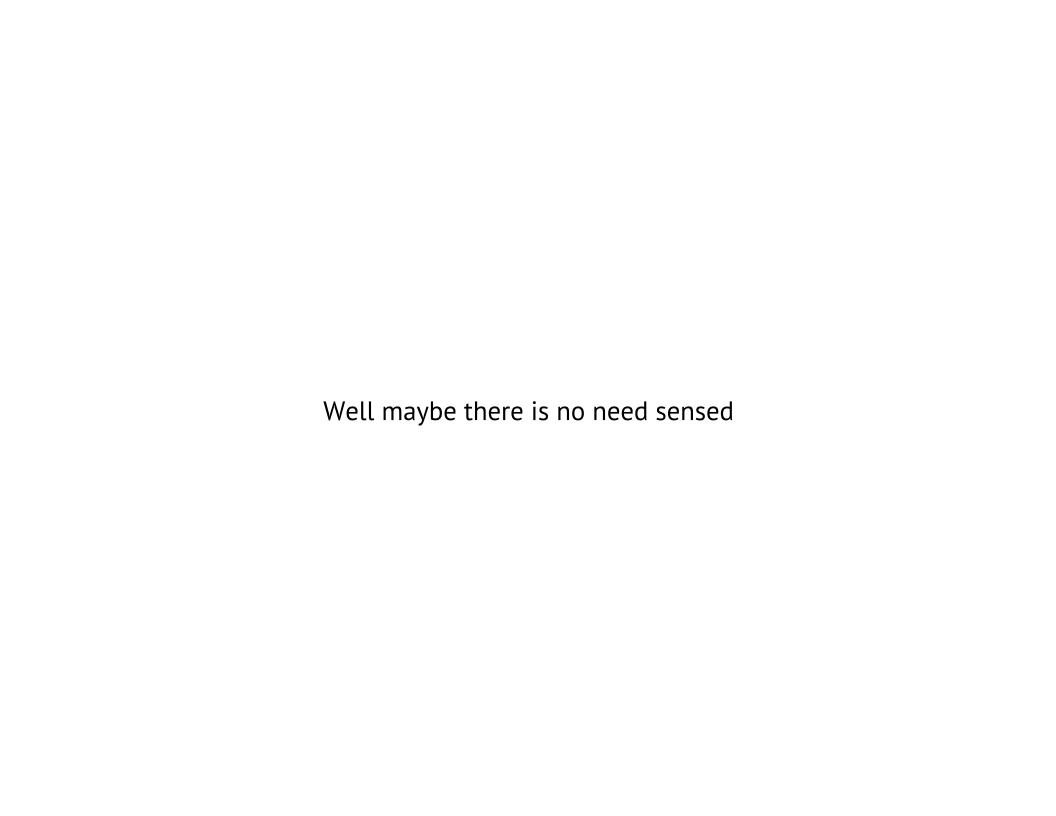


COGNITIVE SURPLUS

A trillion hours/year Of participatory value Up for grabs Twenty-First Century
Digital Media/internet

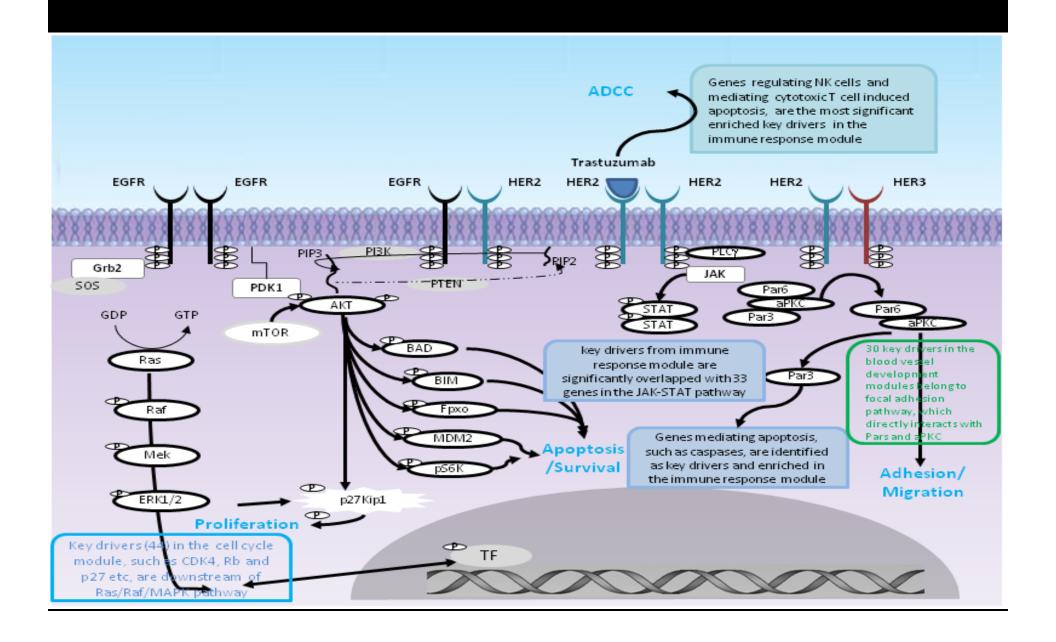
Helping people participate

So why can't we engage that power to help gain better understanding of health and disease?





Reality: Overlapping Pathways

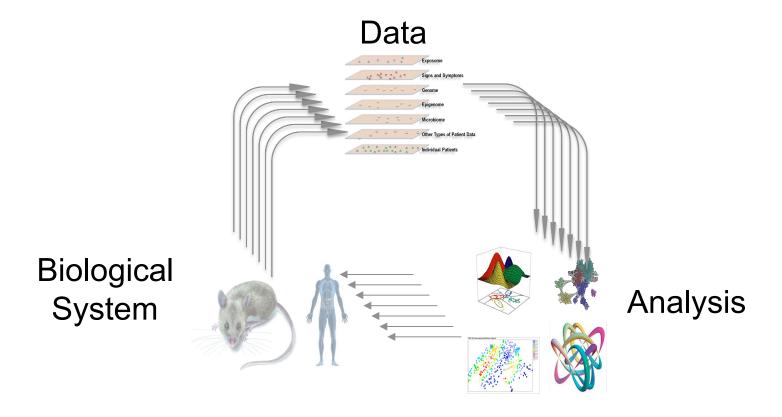






Existing Iterative Approaches To Generating Analyzing and Supporting New Models

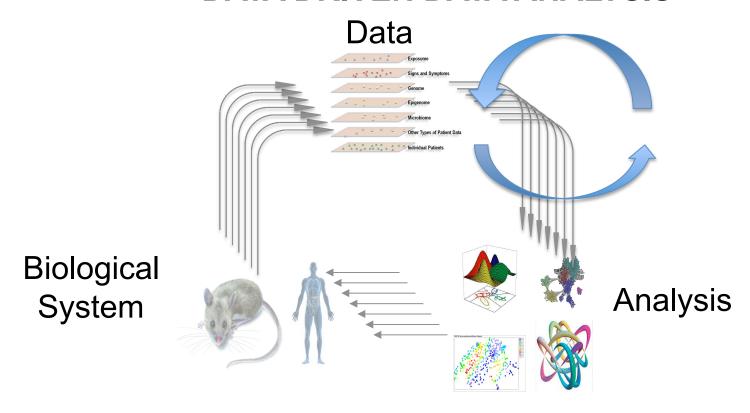
"HYPOTHESIS DRIVEN DATA ANALYSIS"



The automatic linkage between the data generators, analyzers, and validators from the time of hypothesis driven medical research

Beyond Iterative Approaches Generating Analyzing and Supporting New Models

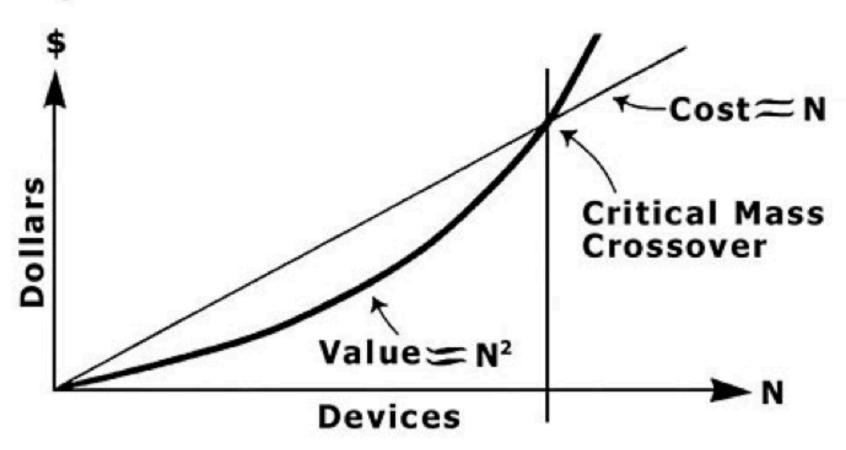
"DATA DRIVEN DATA ANALYSIS"



Potential benefit of uncoupling the automatic linkage between the data generators, analyzers, and validators

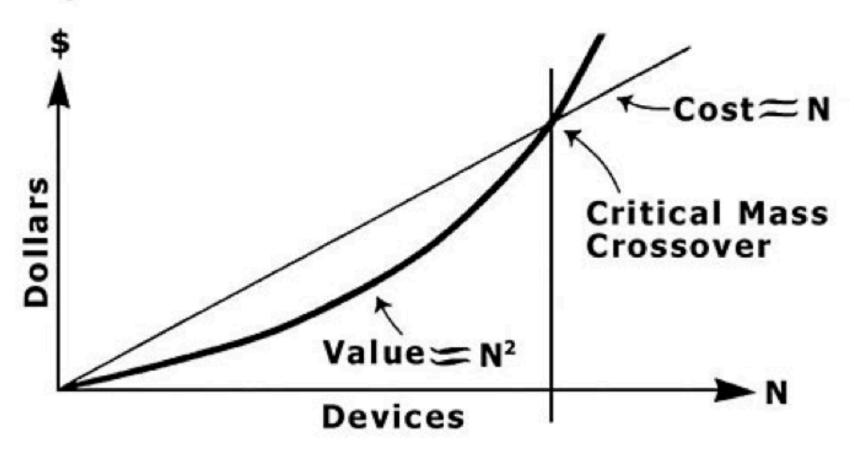
Metcalfe's Law

The Systemic Value of Compatibly Communicating Devices Grows as the Square of Their Number:



Remarkably stalled in Biomedicine where "communication devices" are primarily articles

The Systemic Value of Compatibly Communicating Devices Grows as the Square of Their Number:



COMMENTARY

Metcalfe's law and the biology information commons

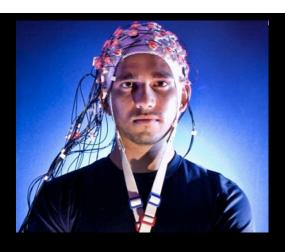
Stephen H Friend & Thea C Norman

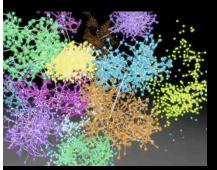
Open collaboration on biomedical discoveries requires a fundamental shift in the traditional roles and rewards for both investigators and participants in research.

"Following the light of the sun, we left the Old World." –Christopher Columbus

doctor's diagnosis is based on abnormal threshold measurements, such as broken bones or hemoglobin A1C scores, and provided withimplicate targets and biochemical pathways. Not surprisingly, drug development statistics confirm what we might expect from such a











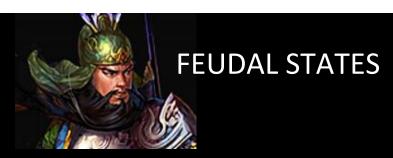
STATE OF THE TECHNOLOGY

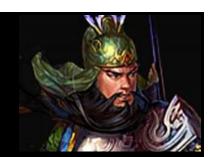
STATE OF THE INSTITUTIONS

DISCONTINUITY

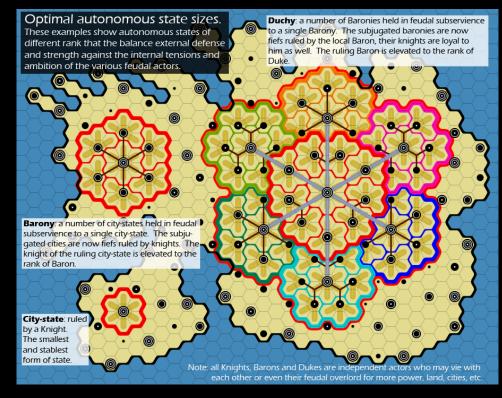


TENURE



















We focus on a world where **biomedical research** is about to fundamentally change. We think it will be often conducted in an **open, collaborative** way where **teams of teams** far beyond the **current guilds of experts** will contribute to making better, faster, relevant discoveries

NEWS

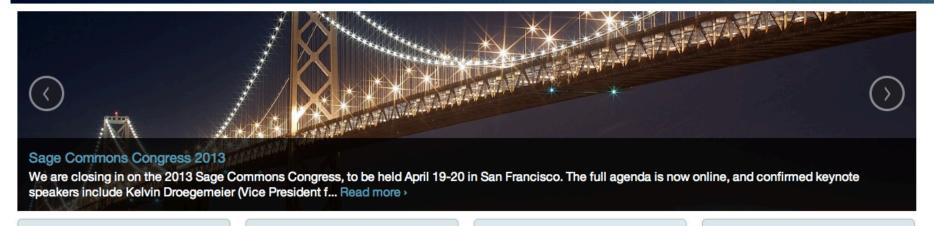
PLATFORMS AND SERVICES

RESEARCH

WORKING WITH US

Search

Redefining. Challenging. Predicting.



Philosophy

Ph

About us

Us

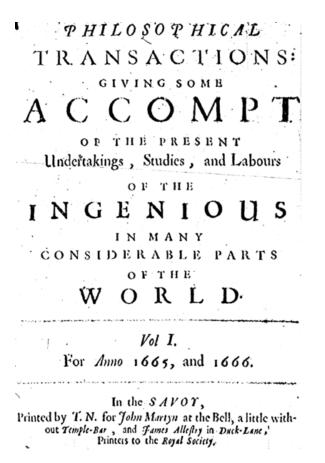
Platforms and Services

Research

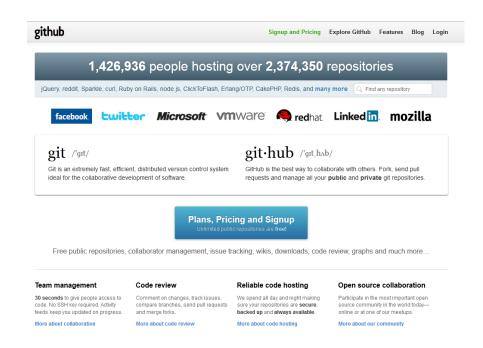
Re

TECHNOLOGY PLATFORM

two approaches to building common scientific knowledge



Text summary of the completed project Assembled after the fact

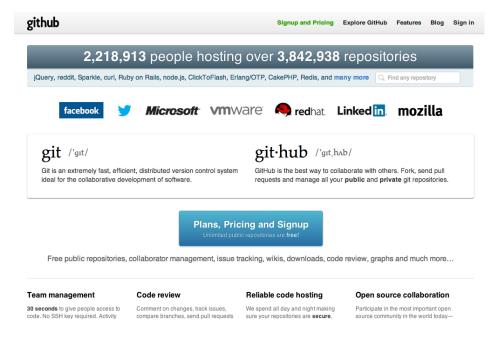


Every code change versioned
Every issue tracked
Every project the starting point for new work
All evolving and accessible in real time
Social Coding

Synapse is GitHub for Biomedical Data



- Data and code versioned
- Analysis history captured in real time
- Work anywhere, and share the results with anyone
- Social/Interactive Science



- · Every code change versioned
- Every issue tracked
- Every project the starting point for new work
- Social/Interactive Coding



Search Forum Register Login

What is Synapse?

- A private a or public workspace that allows you to aggregate, describe, and share your research.
- A tool to improve reproducibility of data intensive science, recording progress as you work with tools such as R and Python.
- A set of living research projects enabling contribution to large-scale collaborative solutions to scientific problems.
- Read more about Synapse

How to Use Synapse

- Getting Started Guide A quick start guide to using Synapse
- Synapse User Guide Using Synapse via the Web and programmatic clients
- Support Forums

 Help, frequently asked questions and support topics
- Contact Us Other questions about Synapse?

Get Started

Synapse is free to use as a Beta service.

Login

Register for a Synapse Account

DREAM8 Challenges



Adam Margolin

Download Edit Share Se Add . Tools .

Home » TCGA Pancancer Freeze » Glioblastoma multiforme » GBM.annotated.whitelist....

GBM.annotated.whitelist.maf (syn1331200)

Sharing: @ Public

Data use conditions: Open (info)

Added by: Kyle Ellrott on: Sat Sep 15 02:25:52 GMT-400 2012 Modified by: Kyle Ellrott on: Thu Nov 01 16:12:30 GMT-400 2012

Description

Please add a description by dicking the "Edit" button.

Provenance

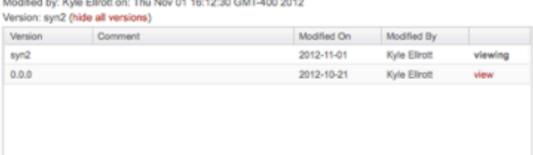
Everything *

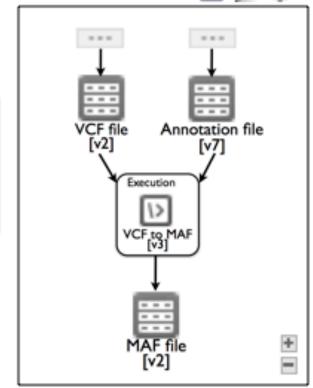






Search



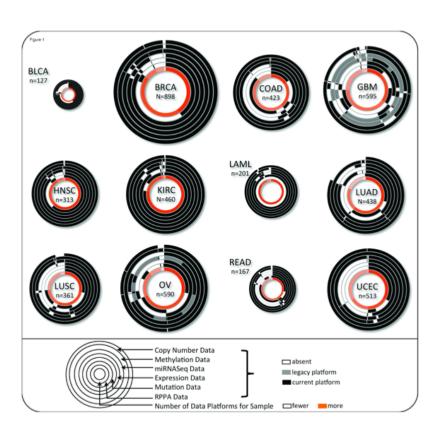


Synapse contributions to analyzing Cancers

The Cancer Genome Atlas

TCGA Pan-Cancer project

- Analysis of: 12 Tumor types, 6 molecular profiling platforms
- Performed by: 150 researchers from 30 institutions.





"Synapse is a compute platform for transparent, reproducible, and modular collaborative research."

Omberg, et al. Enabling collaborative and transparent analysis of 12 tumor types in the cancer genome atlas. S, Nature Genetics (published Oct 2013)

Colorectal Cancer Sub-classification Consortium











































University of Pittsburgh





CommonMind Consortium

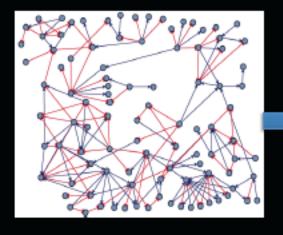
Disease Models for Neuropsychiatric Disease

Structure of a Challenge

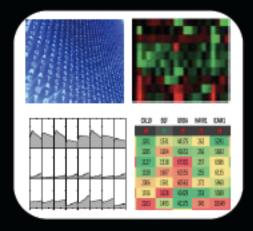
Crowdsourcing



Predictions



Data



Measurements

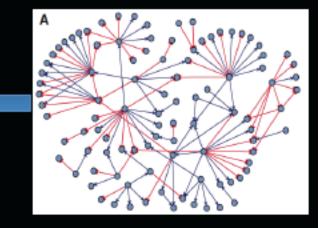


Unbiased Evaluation

Acceleration of Research

Collaboration

Ground Truth



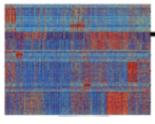
Contributors to the Sage / DREAM breast cancer prognosis challenge

Training data

Model development and submission to central database

All model predictions evaluated Scientific recognition base in held-out dataset based on pre-defined criteria

on model performance





Anne-Lise Borresen-Dale Lars Ottestad Hans Kristian Moen Vollan Vessela N. Kristensen Hege G. Russnes Daehoon Park Veronica O. Vang Jorg Tost



Carlos Caldas Oscar Rueda Christina Curtis



Samuel Aparicio



Google

Joseph Hellerstein

Tyler Pirtle

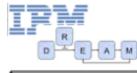
Lamia Youseff

The Sage/DREAM breast cancer challenge consortium



Synapse

Stephen Friend Adam Margolin Erich Huang Thea Norman Brig Mecham Ben Sauerwine In Sock Jang Michael Kellen Lara Mangravite Matthew Furia Brian Bot Justin Guinney Nicole A. Deflaux Bruce Hoff Xavier Schildwachter



Gustavo Stolovitzky Erhan Bilal



Erich Schadt Gauray Pandey Andrea Califano Mariano Alvarez Yishai Shimoni Trev Ideker Janusz Dutkowski Benjamin Logsdon



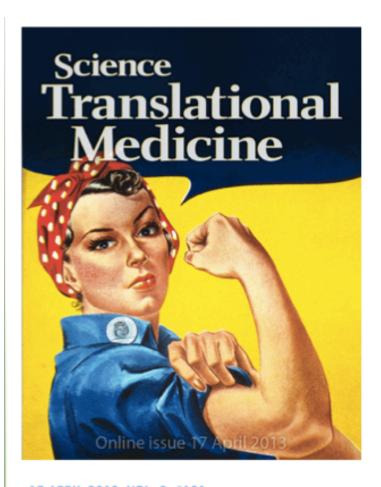
Kelly LaMarco Katrina Kelner

AVONFoundation for Women

Marc Hurlbert



Dinah Singer Dan Gallahan



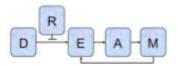
17 APRIL 2013, VOL. 5, #181

COVER STORY | RESEARCH ARTICLE AND REPORT

DREAMing of Biomedicine's Future

An Open Challenge yields fresh insights (Margolin et al.), a new progno model for breast cancer (Cheng et al.), and a modern approach to peer review (Editor's Summary).





CROWDSOURCING

Systematic Analysis of Challenge-Driven Improvements in Molecular Prognostic Models for Breast Cancer

Adam A. Margolin, 1xt Erhan Bilal, 2t Erich Huang, 1,3,4t Thea C. Norman, 1 Lars Ottestad, 5 Brigham H. Mecham, 1,6 Ben Sauerwine, Michael R. Kellen, Lara M. Mangravite, 1 Matthew D. Furia, 1.8 Hans Kristian Moen Vollan, 5,9,10,11 Oscar M. Rueda, 11 Justin Guinney, 1 Nicole A. Deflaux, Bruce Hoff, Xavier Schildwachter, Hege G. Russnes, 9,10,12 Daehoon Park, 13 Veronica O. Vang, 9,10 Tyler Pirtle, 7 Lamia Youseff, 7 Craig Citro, 7 Christina Curtis, 14 Vessela N. Kristensen, 9,10,15 Joseph Hellerstein, 7 Stephen H. Friend, 1* Gustavo Stolovitzky, 2 Samuel Aparicio, 16,17,18† Carlos Caldas, 11,19,20† Anne-Lise Børresen-Dale 9,10†



RESEARCH ARTICLE

COMPUTATIONAL MODELING

Development of a Prognostic Model for Breast Cancer Survival in an Open Challenge Environment

Wei-Yi Cheng, Tai-Hsien Ou Yang, Dimitris Anastassiou*



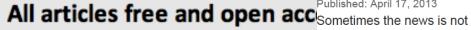
Breast Cancer: 'Geek Sandbox' Holds Clues to Survival

Download Complimentary Source PDF
By Charlene Laino, Senior Writer, Gupta Guide

Published: April 17, 2013

as important as how the researchers arrived at it.







Feb 2013



Sage-DREAM Challenges

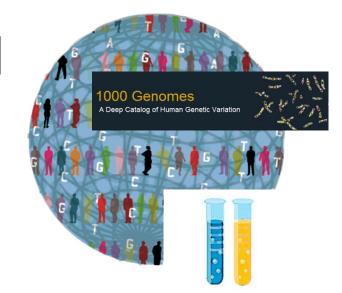


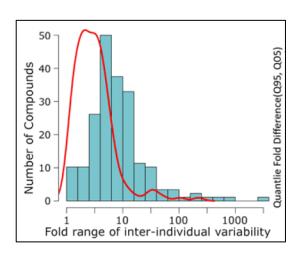
DREAM 8.0 NIEHS/NCATS/UNC DREAM Toxicogenetics Challenge

NIEHS-NCATS-UNC DREAM Toxicogenetics Challenge

Predict cytotoxic response to environmental compounds across a genetically diverse human population with the goal of

Enhancing our capacity to predict what individuals or groups are most sensitive to chemical exposures.











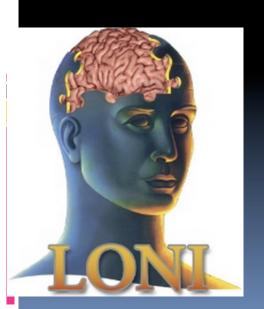
DREAM 8.5











alzheimer's PS association

the compassion to care, the leadership to conquer



Open Source Data – ADNI

Imaging
Clinical
Multiple Cognitive Testing
Whole Genome Sequencing

SAB- Co-Leads
Robert Green (Harvard)
Peter St. George-Hyslop (U Toronto)

Launch Fall 2013 Ending 2014

Prime Question: What model best predicts AD cognitive scores recording in ADNI using all Available imaging, genomic, biomarker data including any outside data sets

It is essential that we develop a global framework that unites government and business in a coordinated effort to increase innovation through real-time data sharing so that we may discover a means of treatment and prevention for Alzheimer's and dementia."

- George Vradenburg CEO Initiave/ Chairman USAgainstAlzheimer's

DREAM 8.5 RHEUMATOID ARTHRITIS RESPONDER CHALLENGE







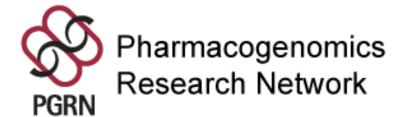








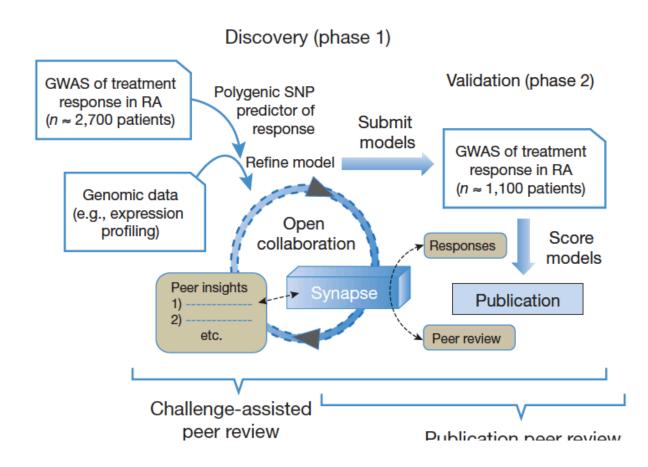




Crowdsourcing genetic prediction of clinical utility in the Rheumatoid Arthritis Responder Challenge

To the Editor:

The ability to translate large-scale genetics and genomics data into biological knowledge has not kept pace with our ability to generate these data sets. As a consequence, a major bottleneck in biomedical research has become access to data within a computational workspace that allows for robust, collaborative analyses. One innovative solution is to bring together scientific data, code, tools and disease models into an open commons or workspace, for example, the Synapse platform of Sage Bionetworks¹. This environment allows for real-time sharing of large genomic data sets, continuous peer review and rapid learning within a system constructed to provide data access in a manner aligned with the informed consent provided by patients and research participants.



Robert Plenge (Harvard Medical School) Lara Mangravite (Sage Bionetworks) Gustavo Stolovitszy (DREAM) Thea Norman (Sage Bionetworks)

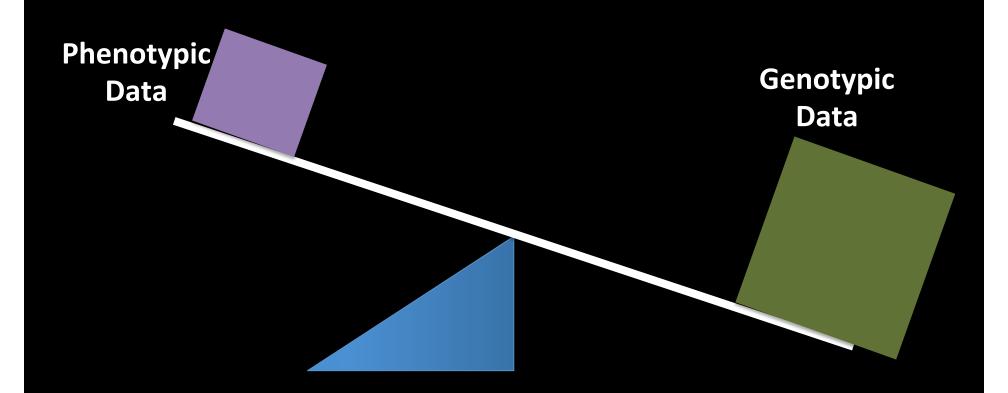
Jeff Greenberg (CORRONA) Anne Barton (UK, Manchester) Peter Gregersen (New York) Eli Stahl (Mt. Sinai, New York)

Marieke Coenen (Netherlands)
Lars Klareskog (Sweden)

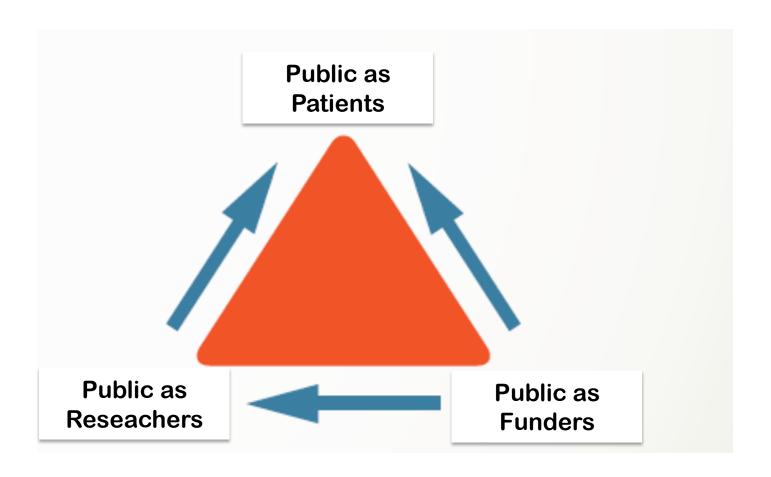
Limited Options As A Citizen



Asymmetry of Data: The public can help with this

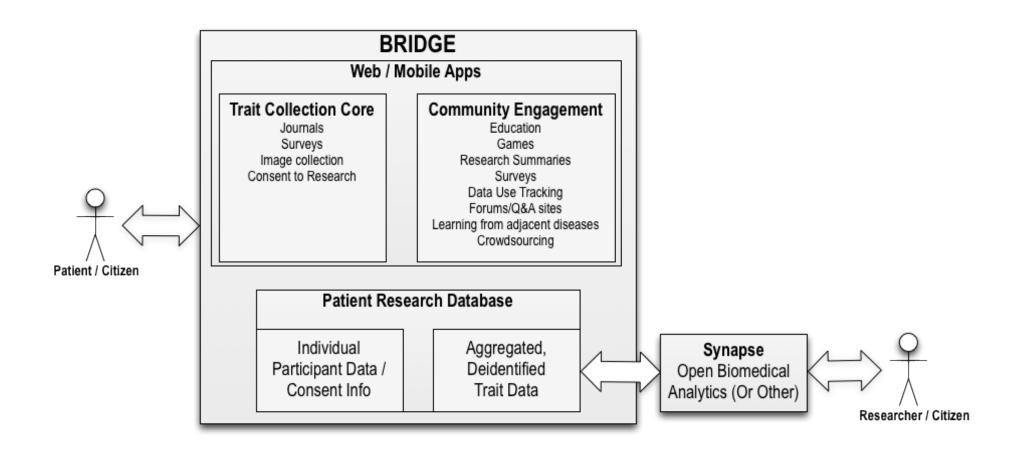


DEMOCRATIZATION OF BIOMEDICAL RESEARCH



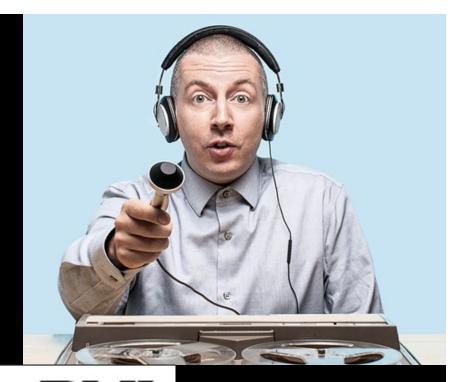
BRIDGE

BRIDGE CONCEPTUAL ARCHITECTURE



Diabetes Breast-Cancer Chronic-Fatigue-Syndrome Rare-Genetic-Disorders anconi-Anemia Fragile-X Melanoma

Parkinsons





Home Vision FAQ Request feedback Team

Whether you are healthy or living with Parkinson's, help provide the voice information needed to build a system to screen for and monitor the symptoms of this debilitating disease. All you need to do: make a low-cost, anonymous, three-minute phone call.

USA 1-857-284-8035

Brazil 11 3957-0683

Mexico 55-41703631

3K UK 01865 521168

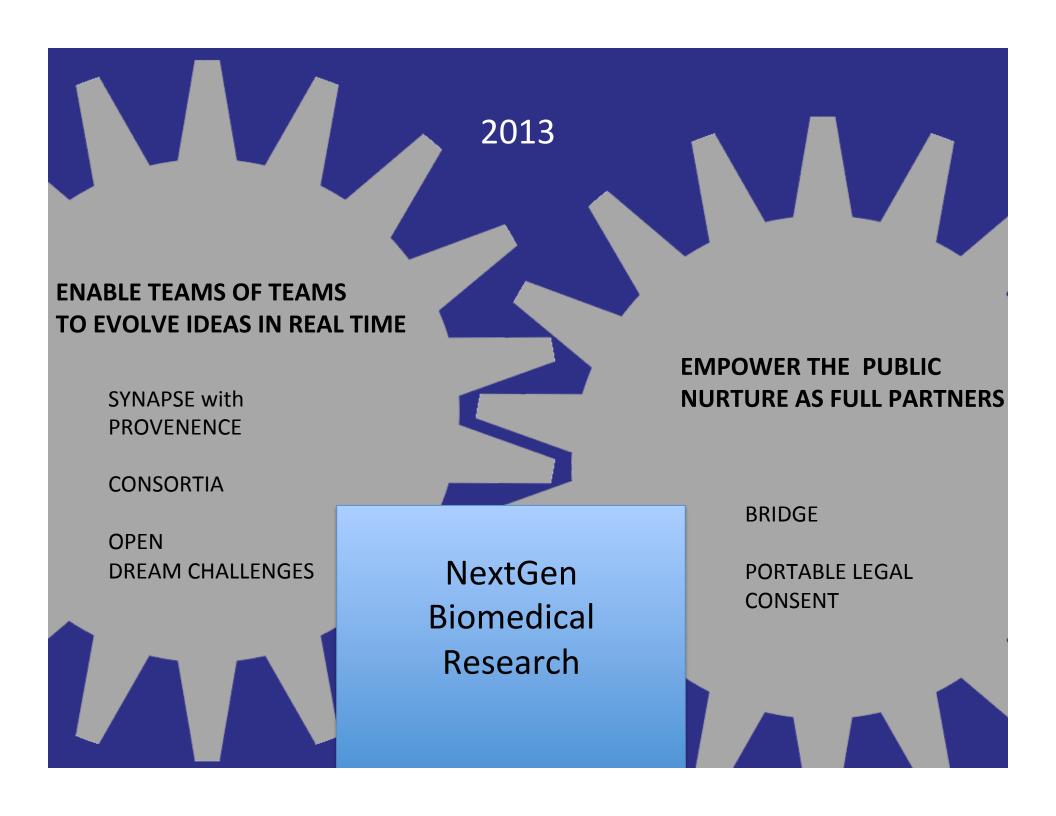
Spain 91 123 4793

Argentina 11.5252.8741

l+I Canada 1-647-931-5776

iSommeil





The Potential for a Distributed Network of Experts and Non-Experts working in a Generative Rapid Learning Space as an Alternative to Current Biomedical Research

Building a next generation model of biomedical research

NextGen Biomedical Research

Navigating between states of wellness **Normal State Disease State**

To avoid mismatch between State of the Institutions and States of the Technology
To avoid siloed problem solving by those gaming the system for tenure
To bring in citizens with their insights, data and funding
We need to fundamentally change the current guilds of experts approaches