adding personal data to pharmaceutical data: leverage from the commons

@wilbanks

3/31/14

Sage BIONETWORKS

ABOUT US NEWS PLATFORMS AND SERVICES RESEARCH WORKING WITH US

Converting Anecdotes Into Signals

Stephen Friend at TED 2014

Sage Bionetworks CEO spoke from the main stage yesterday at TED 2014 in Vancouver. He announced the R and Mt Sinai that is looking for healthy individu... Read more ›

Philosophy

Ph

Our Work

Wk

Platforms and Services

Ps

every age has its own lever.

ours is cheap data.


3G
9:42 AM
Messages
Tuesday
9
Calendar
Photos
Camera
YouTube
Stocks
280
Maps
73°
Weather
Voice Memos
Notes
Clock
Calculator
Settings
iTunes
App Store
Compass
Phone
Mail
Safari
iPod

cheap data changes how we justify our opinions.

$$OPS = AB(H + BB + HBP) + TB(AB + BB + SF + HBP) / AB(AB + BB + SF + HBP)$$

cheap data is
changing our politics.

(TS//SI//NF) PRISM Collection Details

Current Providers

- Microsoft (Hotmail, etc.)
- Google
- Yahoo!
- Facebook
- PalTalk
- YouTube
- Skype
- AOL
- Apple

What Will You Receive in Collection (Surveillance and Stored Comms)?
It varies by provider. In general:

- E-mail
- Chat – video, voice
- Videos
- Photos
- Stored data
- VoIP
- File transfers
- Video Conferencing
- Notifications of target activity – logins, etc.
- Online Social Networking details
- **Special Requests**

Complete list and details on PRISM web page:
Go PRISMFAA

cheap data is going to change our health.

1. research data v. cheap consumer data

My Home
Inbox (5)

My Health
Disease Risk
Carrier Status
Drug Response
Traits
Health Labs

My Ancestry
Maternal Line
Paternal Line
Relative Finder
Ancestry Painting
Global Similarity
Ancestry Labs

Sharing & Community
Compare Genes
Family Inheritance
23andMe Community

disease risk

Share my health results with family and friends

Show results for John Wilbanks

See new and recently updated reports »

23andWe Discoveries were made possible by 23andMe members who took surveys.

Elevated Risk

Name	Confidence	Your Risk	Avg. Risk	Compared to Average
Prostate Cancer ♂	★★★★	31.9%	17.8%	1.79x
Psoriasis	★★★★	22.4%	11.4%	1.98x
Alzheimer's Disease	★★★★	14.2%	7.2%	1.98x
Ankylosing Spondylitis	★★★			
Asthma	★★★			
Bipolar Disorder: Preliminary Research	★★★			
Chronic Lymphocytic Leukemia	★★★			
Follicular Lymphoma	★★★			
High Blood Pressure (Hypertension)	★★★			

UNITED STATES
DEPARTMENT OF VETERANS AFFAIRS

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BLUE BUTTON

- Blue Button Home
- Getting Started
- License the Blue Button®
- Blue Button Partners
- Resources
- VA Homepage
- Site Search

Need to Know: Update for Blue Button Partners

The rollout of the upgraded Blue Button on September 29 and October 9 means enhancements for our Veterans who download their health care data from VA's electronic health records. For our industry partners it means enhancements and improvements for their supporting software's functionality.

Based on Veteran user feedback, the minor enhancements in this rollout will make the output more readable and user friendly. There is also a new set of data for 'VA Immunizations,' enhancements to the online user interface and improved data from the Military Service Information (MSI) section. We have provided these instructions on our Resources page along with updated sample files.

One Million Blue Button Users - Veterans Talk to Markle

My healthevet
Manage Your VA Health Care Online

Blue Button Partners

Industry is building applications to help Veterans use the Blue Button to better manage their health or find employment. See which companies have committed to supporting the Blue Button Initiative on our list of Blue Button partners.

If your organization has created an application for Blue Button and would like to be added to this list, email us at VABlueButton@va.gov.

DISCLAIMER: VA does not endorse these products or companies.

Science EXCHANGE

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Search services...

The Scientific Services Marketplace

The easiest way to get experiments conducted by researchers in top core facilities and institutions.

Search All Services

RNA microarray	$107.50 per Sample
DNA Sequencing	$2.50 per Sample
Real Time qPCR	$3.50 per Sample
Mass Spectrometry	$10.00 per Sample
Immunohistochemistry	$10.00 per Sample
Bioinformatics	$50.00 per Hour

Featured RNA microarray Providers

Science Exchange has 63 verified RNA microarray providers including the following featured providers.

Virginia Bioinformatics Institute

Virginia Polytechnic Institute and State University | Blacksburg, VA, United States

The Core Laboratory Facility (CLF) at VBI functions as a multi-user resource dedicated to the development and application of various high-throughput technologies to aid in the discovery of biological macromolecules.

$284.00 USD per Sample

REQUEST ESTIMA

VirginiaTech Invent the Future

Duke UNIVERSITY

NORTHWESTERN UNIVERSITY

UCLA

BOSTON UNIVERSITY

https://www.scienceexchange.com

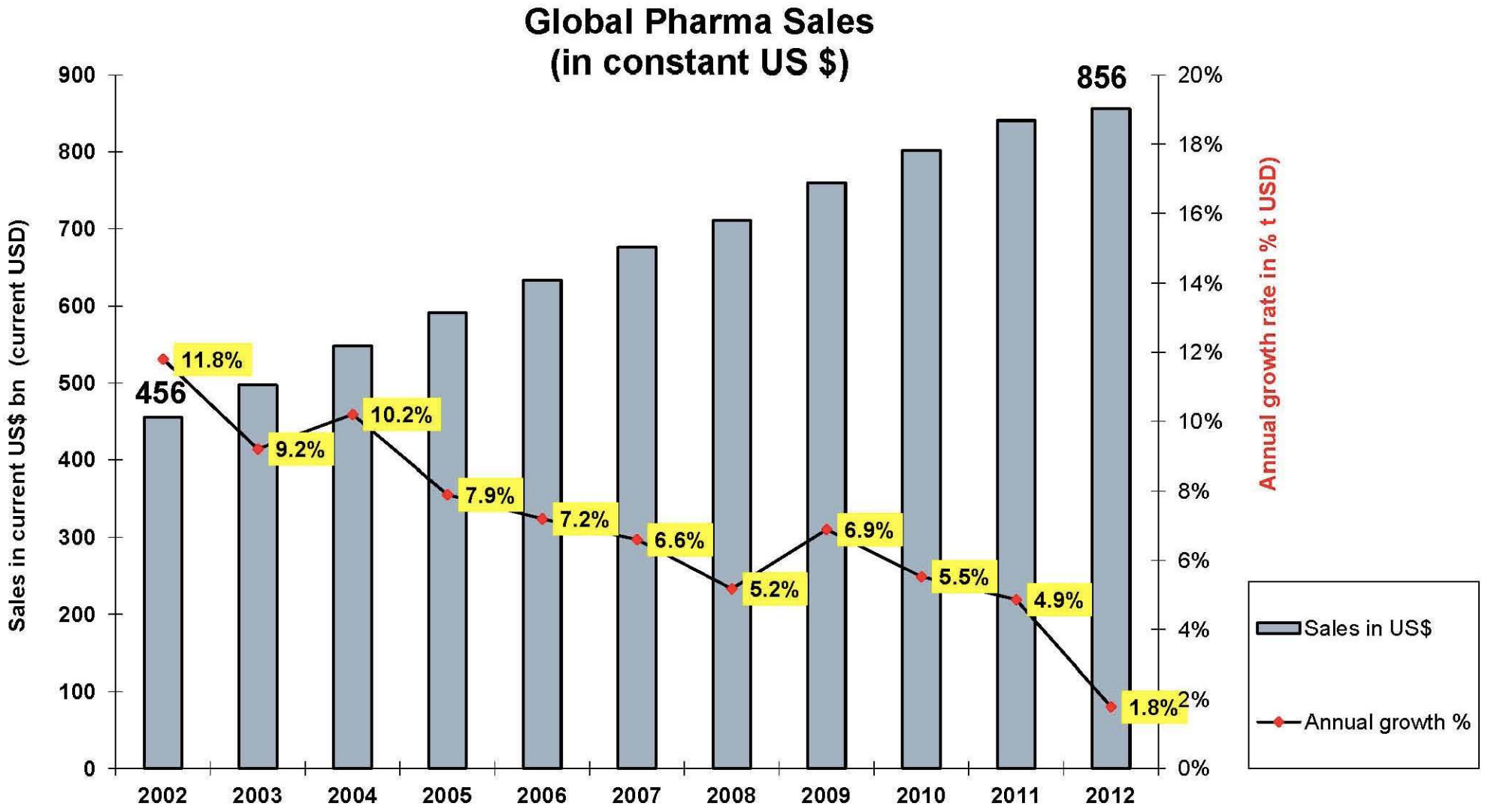
View all providers for this experiment →

Request estimates from all providers →


No Service
3:24 PM
AliveECG
00:04
bpm
68

2.
increasing tensions.

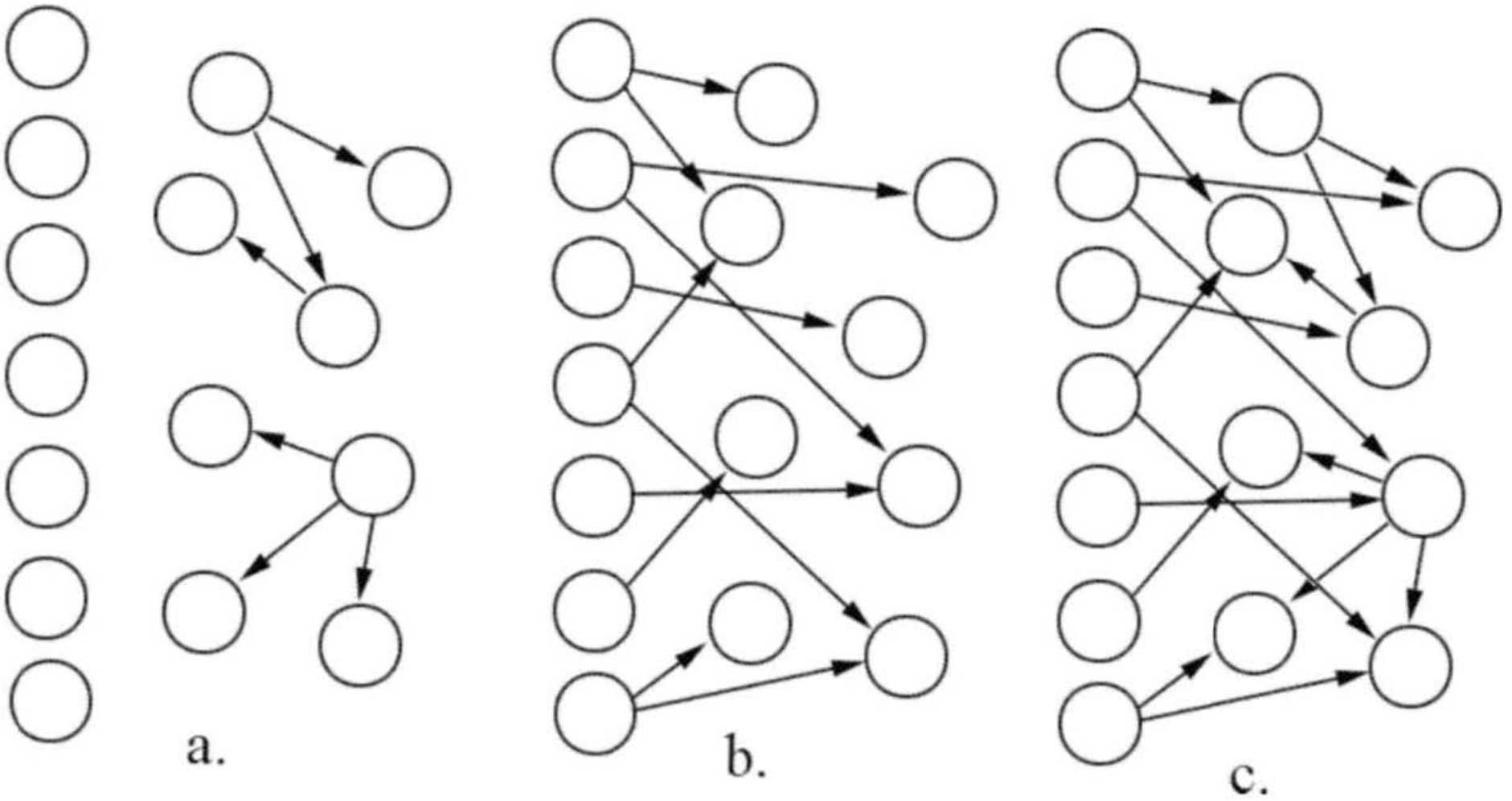
Global Sales in 2012: US$ 856 billion (in constant USD)
Growth is slowing



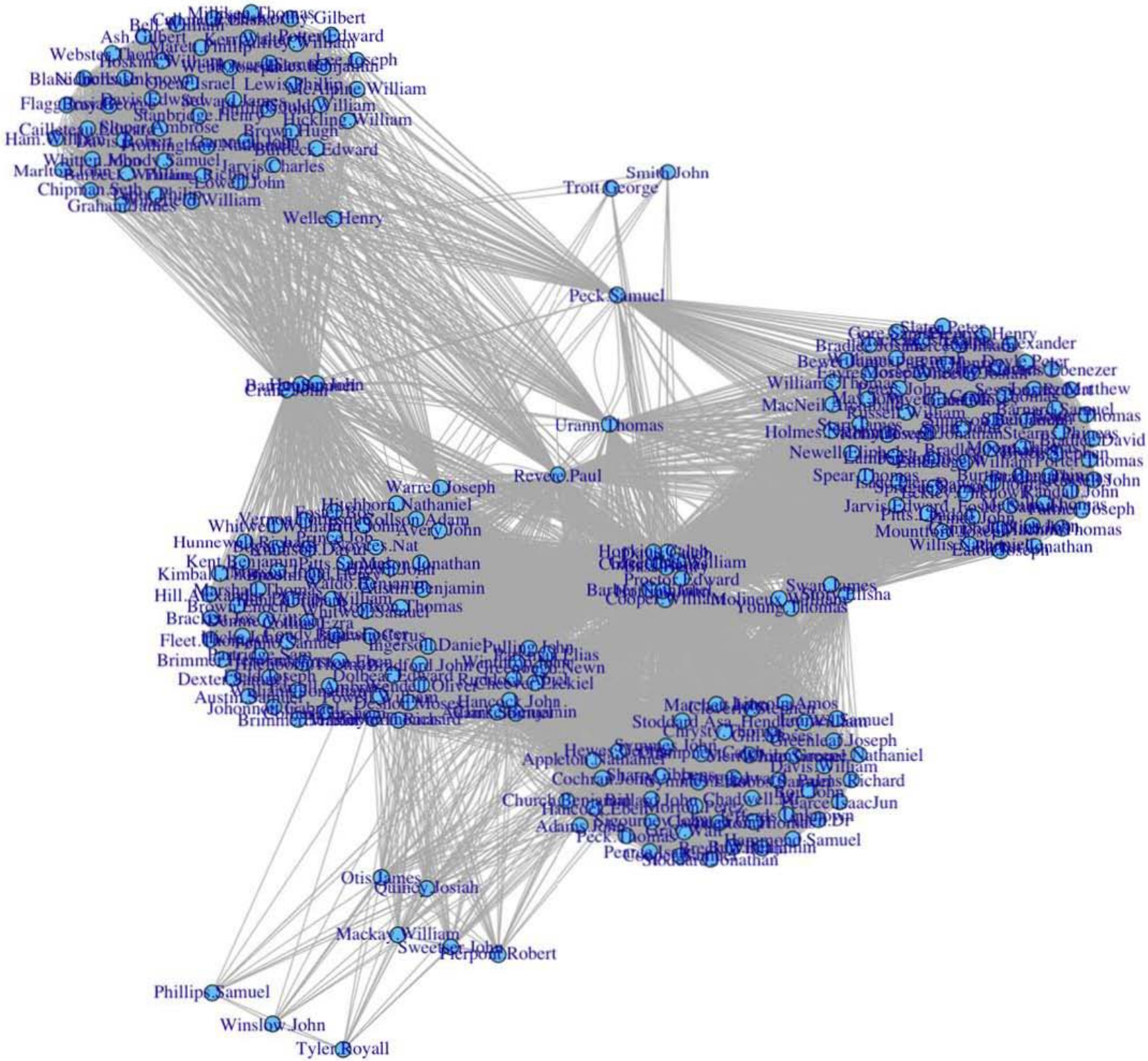
PHARMEXPAND

Source: Reconstructed from IMS Health.
May 2013 + history IMS April 2008

not just economic, but social tensions.


a.
b.
c.

tension between anonymity and utility.


Smith John
Trott George
Welles Henry
Peck Samuel
Urann Thomas
Revere Paul
Warren Joseph
Otis James
Quincy Josiah
Mackay William
Sweetser John
Pierpont Robert
Phillips Samuel
Winslow John
Tyler Royall

tension between
expectation and reuse.

JAMA Internal Medicine
Formerly Archives of Internal Medicine

Original Investigation | August 19, 2013

Public Preferences About Secondary Uses of Electronic Health Information ONLINE FIRST

David Grande, MD, MPA[1,2]; Nandita Mitra, PhD[3]; Anand Shah, MD, MSHP[4]; Fei Wan, MS[3]; David A. Asch, MD, MBA[1,2,5]

[+] Author Affiliations

JAMA Intern Med. Published online August 19, 2013. doi:10.1001/jamainternmed.2013.9166

tension between aggregate value and individual value.

How Much Are You Worth?

When you visit certain Web sites on the Internet, ad requests are sent to advertisers. They compete for a chance to serve ads to you. The bid prices they submitted to auctions are generally based on your information that advertisers possess, for example a profile inferred from your Web history, and your browsing context. The prices reflect how they evaluate your profile. We capture these prices to give you a quantification of your value from advertisers' perspective.

Results: We do not have any data associated with you. If you use Firefox or Chrome, please install the plugin and enable cookies. Note that our plugin does NOT work with Ad blocker extensions such as AdBlockPlus or any addons of these types. If you use Ad blockers, and still want to know how advertisers estimate your private data, you have three options:

- Deactivate Ab blockers, browse the Internet as usual, and reactivate your Ad blockers whenever enough prices are collected (i.e. our plugin starts showing you your average price and the number of prices is larger than 20-40). This could take a couple of days or just one day, depending on your browsing habits.
- Deactivate your Ad blockers, click on some (10 to 15, with e.g. several refreshes) of the links example from this list, and reactivate your Ad blockers later once you are done. This option is faster, but might somehow affect the results.
- For Firefox create a new Firefox profile and browse the Web as usual with our plugin installed. Of course do not use Ad Blockers. For Chrome, create a new browser user profile: see here or alternatively check this tutorial.

We show below some general highlights, if you do not use Firefox or Chrome, or do not wish to install the plugin.

The average price paid for user's private data (items in Web browsing history) for our users is:

$0.000564

if it can be sold, it will be sold at the lowest possible price.

tension between technology rate of change and policy rate of change.

our regulatory environment

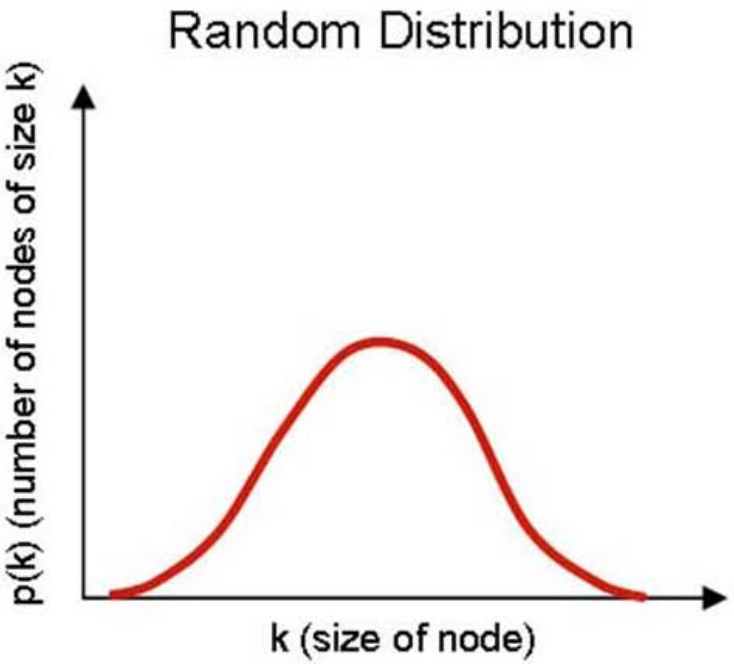

23andMe

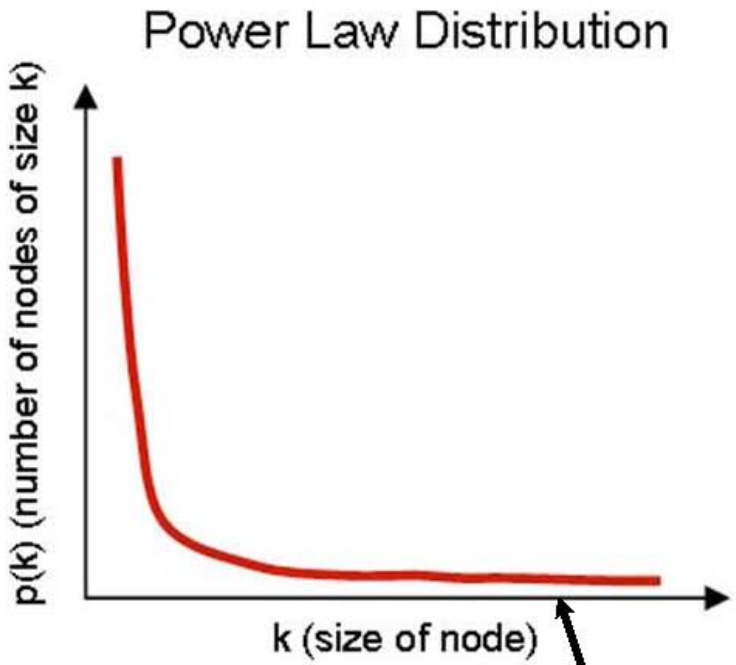
that’s the setup.

3.

we need freedoms, not just free stuff, for data to change health for the better.

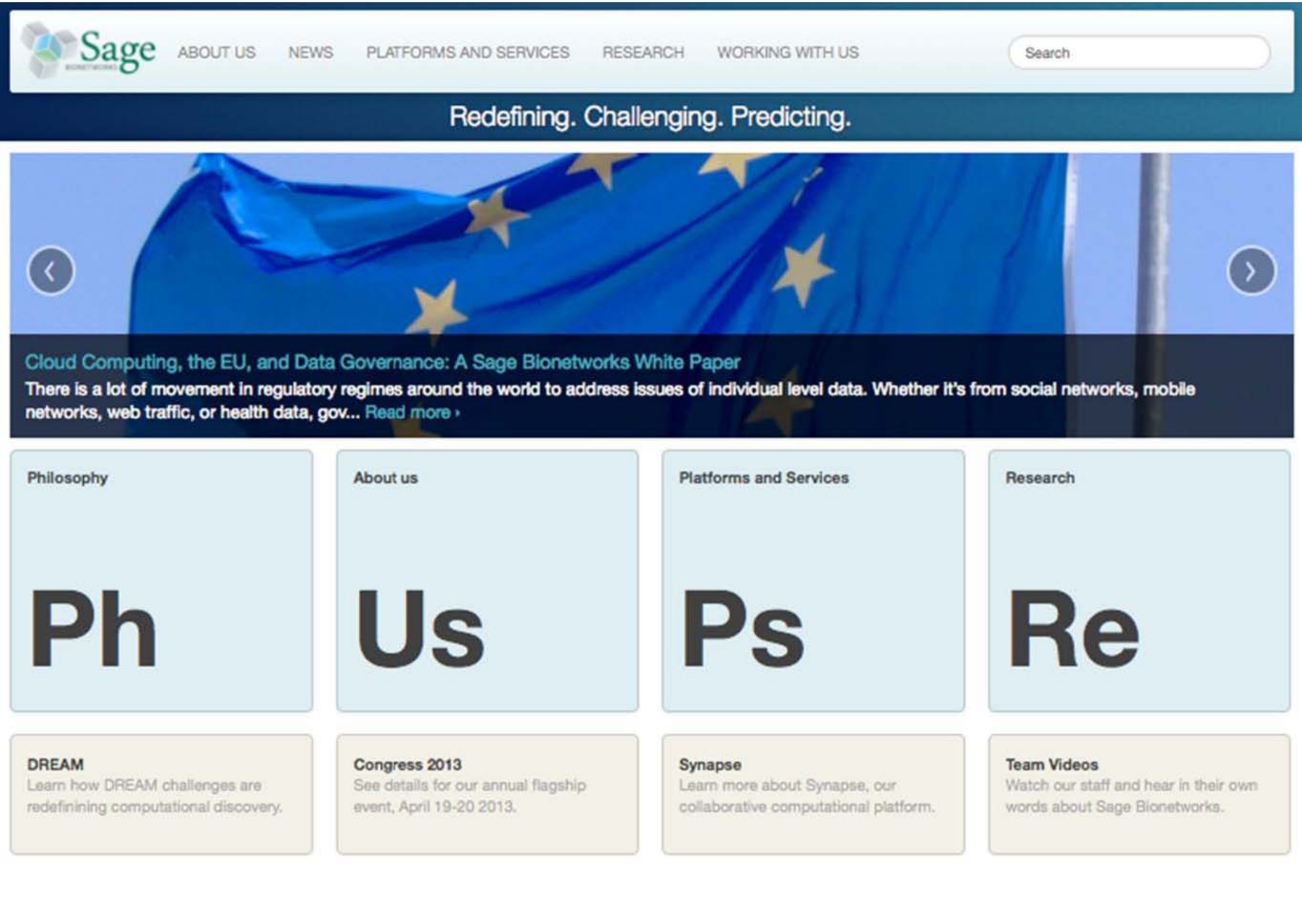
freedoms granted to
small but coherent
groups can create
asymmetrically valuable
resources.





small group sharing

proven to work in:
software
content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Redefining. Challenging. Predicting.
Cloud Computing, the EU, and Data Governance: A Sage Bionetworks White Paper
There is a lot of movement in regulatory regimes around the world to address issues of individual level data. Whether it's from social networks, mobile networks, web traffic, or health data, gov... Read more ›
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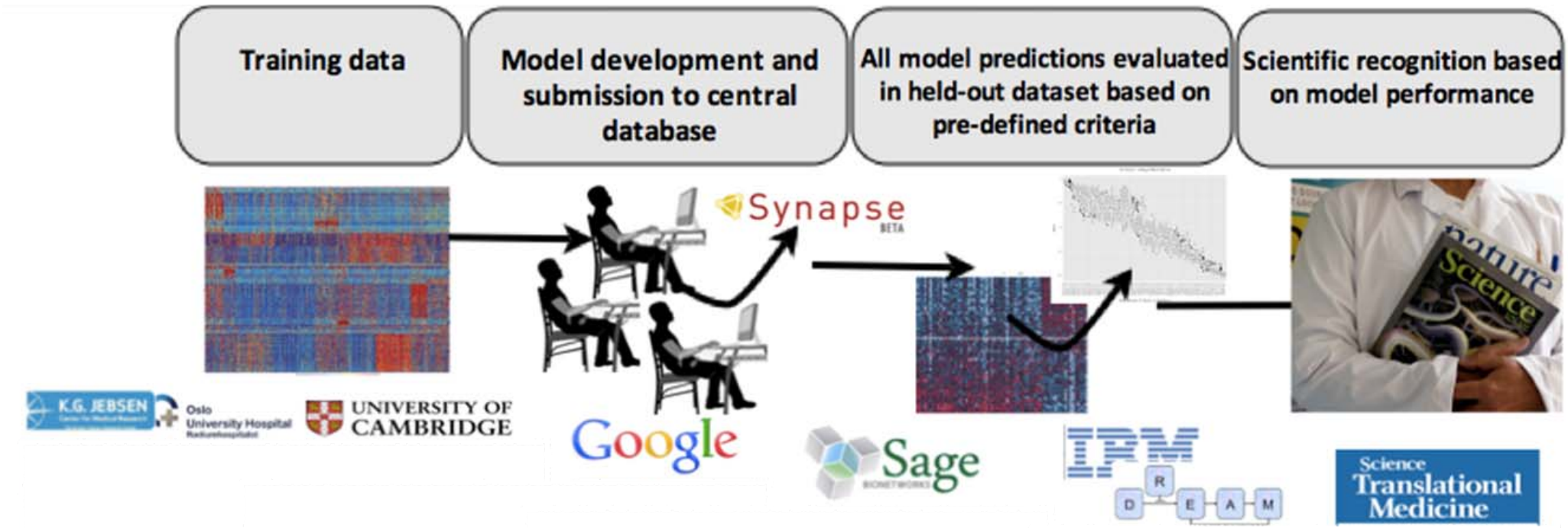
DREAM
Learn how DREAM challenges are redefinining computational discovery.
Congress 2013
See details for our annual flagship event, April 19-20 2013.
Synapse
Learn more about Synapse, our collaborative computational platform.
Team Videos
Watch our staff and hear in their own words about Sage Bionetworks.

let’s try a small but coherent group to share data and see if it works in breast cancer.



code sharing a prerequisite.

accuracy of model jumped three orders of magnitude in nine days.

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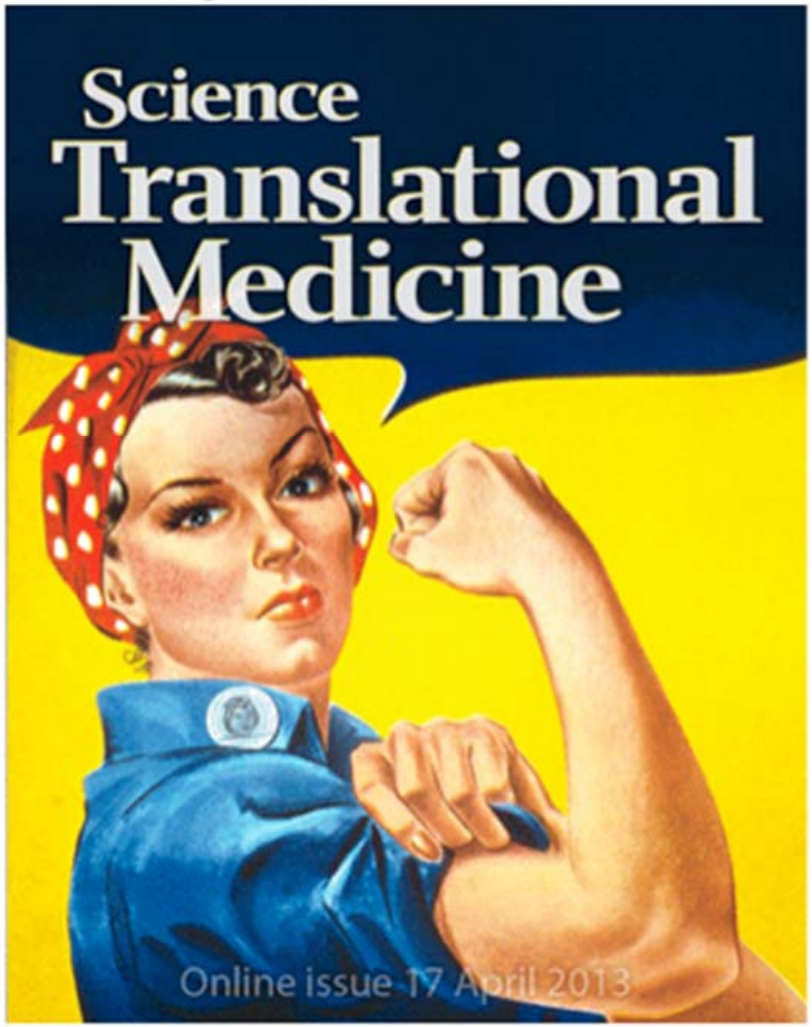


76% accurate.

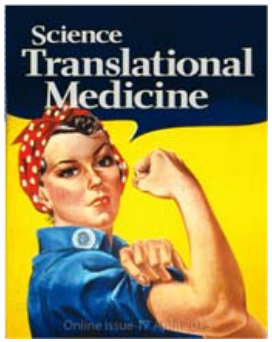
ONLINE COVER "Doin' It for Themselves"—and Future Generations. A U.S. cultural icon, Rosie the Riveter represents millions of American women who entered the workforce during World War II. Rosies worked in factories of all kinds, including some that manufactured munitions and other supplies needed

PLOS | COMPUTATIONAL BIOLOGY

21 february 2013

Biomolecular Events in Cancer Revealed by Attractor Metagenes

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



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 and Dimitris Anastassiou*

17 april 2013

Cornell University Library

arXiv.org

Multi-cancer molecular signatures and their interrelationships

Wei-Yi Cheng[1], Tai-Hsien Ou Yang[1], Hui Shen[2], Peter W. Laird[2], Dimitris Anastassiou[1] and the Cancer Genome Atlas Research Network

ongoing...

Multi-cancer molecular signatures and their interrelationships

Wei-Yi Cheng[1], Tai-Hsien Ou Yang[1], Hui Shen[2], Peter W. Laird[2], Dimitris Anastassiou[1] and the Cancer Genome Atlas Research Network

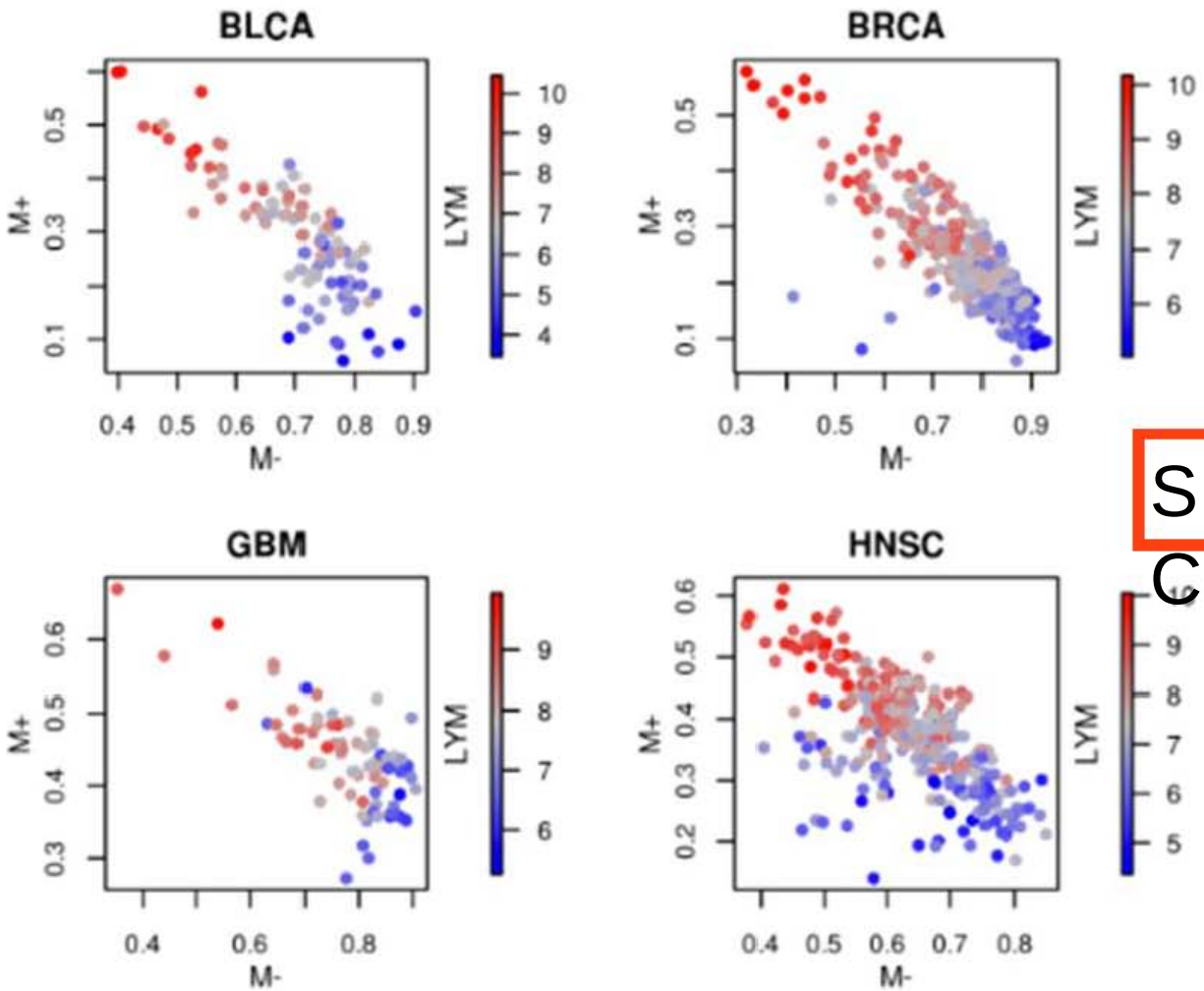
"Multi-cancer molecular signatures and their interrelationships"

AUTHORS: Wei-Yi Cheng, Tai-Hsien Ou Yang, Dimitris Anastassiou

ABSTRACT

Several molecular signatures, called attractor metagenes, present in multiple cancer types were recently identified and proved prog
survival. These signatures were found using an iterative data mining algorithm converging to the core of gene coexpressio
identification of additional multi-cancer molecular signatures resulting from analysis of data sets from twelve cancer types, i
methylation and protein signatures and an angiogenesis-related signature.

We had previously found7 all three LYM, M+ and M- signatures from their association with the expression of *miR-142*. We have now conf
in the pancan12 data sets, and we found that *miR-150* and *miR-155* are also strongly associated with the LYM signature. We had also pre
LYM signature as an attractor metagene3, and used it in the winning model of the Sage Bionetworks Breast Cancer Prognosis Challeng
strongly associated with improved prognosis in ER-negative breast cancers, and this fact also provides an explanation for the relati
compared with other types of high-grade breast cancers.



SHOW ME THE CODE!

Figure 2: Scatter plots connecting the LYM, M+ and M- meta-features in 12 cancer types. Each dot represents a cancer sample. The horizontal a
methylation values of the two methylation signatures, M- and M+, while the value of the expression of the LYM metagene is color-coded.

weiyi_gisl 4 months ago figure 2

0 contributors

file | 55 lines (44 sloc) | 1.527 kb

Edit Raw Blame

```
createFigure2 <- function(meta.pancan, x, y, z){

        fileName <- paste("scatter.", x, "x", y, "x", z, ".png", sep="")

        png(fileName, width=7.3, height=8, units="in", res=300, pointsize=12)
        par(mar = c(4,4,2,5),       #plot margin
          mfrow = c(4, 3),
          oma=c(0, 0, 0, 0),
          mgp=c(2, 1, 0)
          )

        # find the features
        temp <- meta.pancan[[1]]
        idxx <- NULL
        idxy <- NULL
        idxz <- NULL
        for(d in names(temp)){
                if(x %in% rownames(temp[[d]])) idxx <- d
                if(y %in% rownames(temp[[d]])) idxy <- d
```

let’s try a small but coherent group to share data and see if it works in “big science”.

The Cancer Genome Atlas Data Portal

Understanding genomics to improve cancer care

Home

TCGA Data Portal Overview

We provide 3 ways to download data: The Cancer Genome Atlas (TCGA) Data Portal provides a platform for researchers to search, download, and analyze data sets generated by TCGA. It contains clinical information, genomic characterization data, and high-throughput sequencing analysis of the tumor genomes.

The TCGA Data Portal does not host lower levels of sequence data. NCI's Cancer Genomics Hub (CGHub) is the new secure repository for storing, cataloging, and accessing BAM files and metadata for sequencing data. New users must still apply for authorized access through NCBI's Database of Genotypes and Phenotypes (dbGaP).

Download Data

Choose from three ways to download data

Available Cancer Types	# Cases Shipped by BCR	# Cases with Data*	Date Last Updated (mm/dd/yy)
Acute Myeloid Leukemia [LAML]	200	200	07/16/13
Adrenocortical carcinoma [ACC]	80	80	07/22/13

Announcements

06/13/2013 - DCC Software Released

The software release scheduled for today is complete and the TCGA Data Portal has been returned to normal operation. As part of this release, a new version of the TCGA Archive Validator has been provided and we strongly suggest that data submitting centers download and use this new version. The TCGA Archive Validator can be found on the TCGA Wiki here.

A complete list of the items addressed in this release can be found on the TCGA Wiki here and for those with JIRA access the tickets covered in this release can be found on the wiki here.

If you have any questions or concerns about this release, contact tcga-dcc-binf-l@list.nih.gov.

05/21/2013 - DCC Software Released

THE CANCER GENOME ATLAS

TCGA Pan-Cancer Consortium

Analysis of: 12 Tumor types, 6 molecular profiling platforms

Focus series of: 4 papers in *Nature Genetics*, with 14 more to follow in other *NPG* journals

Enabling transparent and collaborative computational analysis of 12 tumor types within The Cancer Genome Atlas

Larsson Omberg[1,6], Kyle Ellrott[2,6], Yuan Yuan[3,4], Cyriac Kandoth[5], Chris Wong[2], Stephen H Friend[1], Josh Stuart[2], Han Liang[3,4] & Adam A Margolin[1]

The Cancer Genome Atlas Pan-Cancer Analysis Working Group collaborated through Synapse, a software platform, to share and evolve data, results and methodologies to perform integrative analysis of molecular profiling data from 12 tumor types. The group's work serves as a pilot case study that provides (i) a template for future large collaborative studies; (ii) a system to support collaborative projects; and (iii) a public resource of highly curated data, results and automated systems for the evaluation of community-developed models.

Omberg, et al. *Nature Genetics*

68

core projects

1070

datasets

172

3

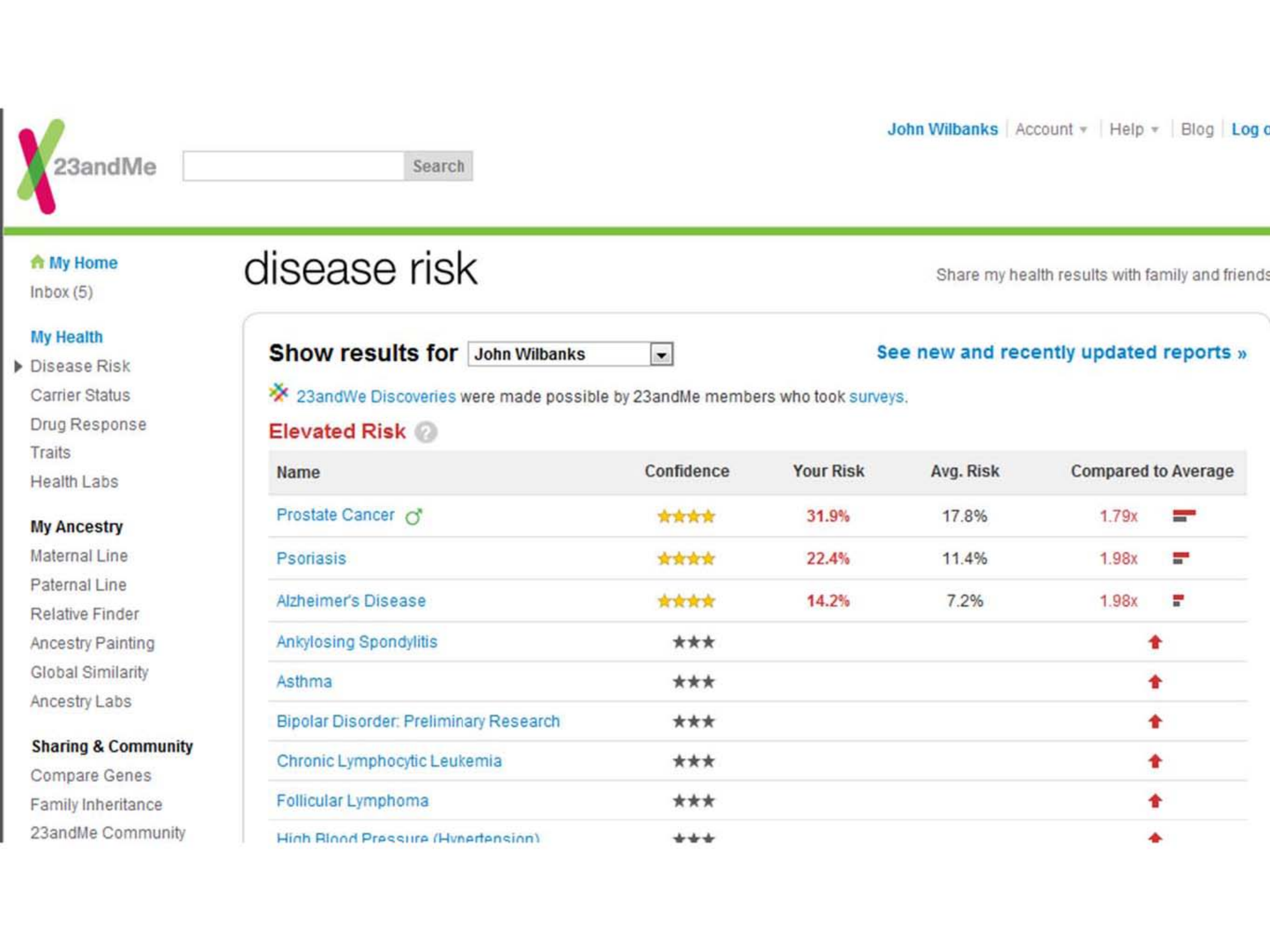
results

1

8

paper in press

let’s try a small but coherent group to share data and see if it works in health.


23andMe
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John Wilbanks | Account | Help | Blog | Log o
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Inbox (5)
My Health
Disease Risk
Carrier Status
Drug Response
Traits
Health Labs
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disease risk
Share my health results with family and friends
Show results for John Wilbanks
See new and recently updated reports »
23andWe Discoveries were made possible by 23andMe members who took surveys.
Elevated Risk
Name
Confidence
Your Risk
Avg. Risk
Compared to Average
Prostate Cancer
Psoriasis
Alzheimer's Disease
Ankylosing Spondylitis
Asthma
Bipolar Disorder: Preliminary Research
Chronic Lymphocytic Leukemia
Follicular Lymphoma
High Blood Pressure (Hypertension)

Table 1. Total Prostate-Specific Antigen for White Males

Men <40 years	<2 ng/mL	<2 µg/L (SI units)
Men 40–50 years	2–2.8 ng/mL	2–2.8 µg/L
Men 51–60 years	2.9–3.8 ng/mL	2.9–3.8 µg/L
Men 61–70 years	4–5.3 ng/mL	4–5.3 µg/L
Men >70 years	5.6–7.2 ng/mL	5.6–7.2 µg/L

Reprinted with permission from Prostate-specific antigen (PSA). Available at: http://www.webmd.com/hw/mens_conditions/hw5522.asp. Accessed August 13, 2006.[7]

JNCI JOURNAL OF THE NATIONAL CANCER INSTITUTE

Overdiagnosis Due to Prostate-Specific Antigen Screening: Lessons From U.S. Prostate Cancer Incidence Trends

Ruth Etzioni, David F. Penson, Julie M. Legler, Dante di Tommaso, Rob Boer, Peter H. Gann and Eric J. Feuer

+ Author Affiliations

Correspondence to: Ruth Etzioni, Ph.D., Program in Biostatistics, Fred Hutchinson Cancer Research Center, 1100 Fairview Ave. North, MP-665, Seattle, WA 98109-1024 (e-mail: retzioni@fhcrc.org).

Received November 19, 2001.
Revision received April 25, 2002.
Accepted May 15, 2002.

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Table of Contents

This Article

JNCI J Natl Cancer Inst (2002) 94 (13): 981-990.
doi: 10.1093/jnci/94.13.981

Abstract *Free*
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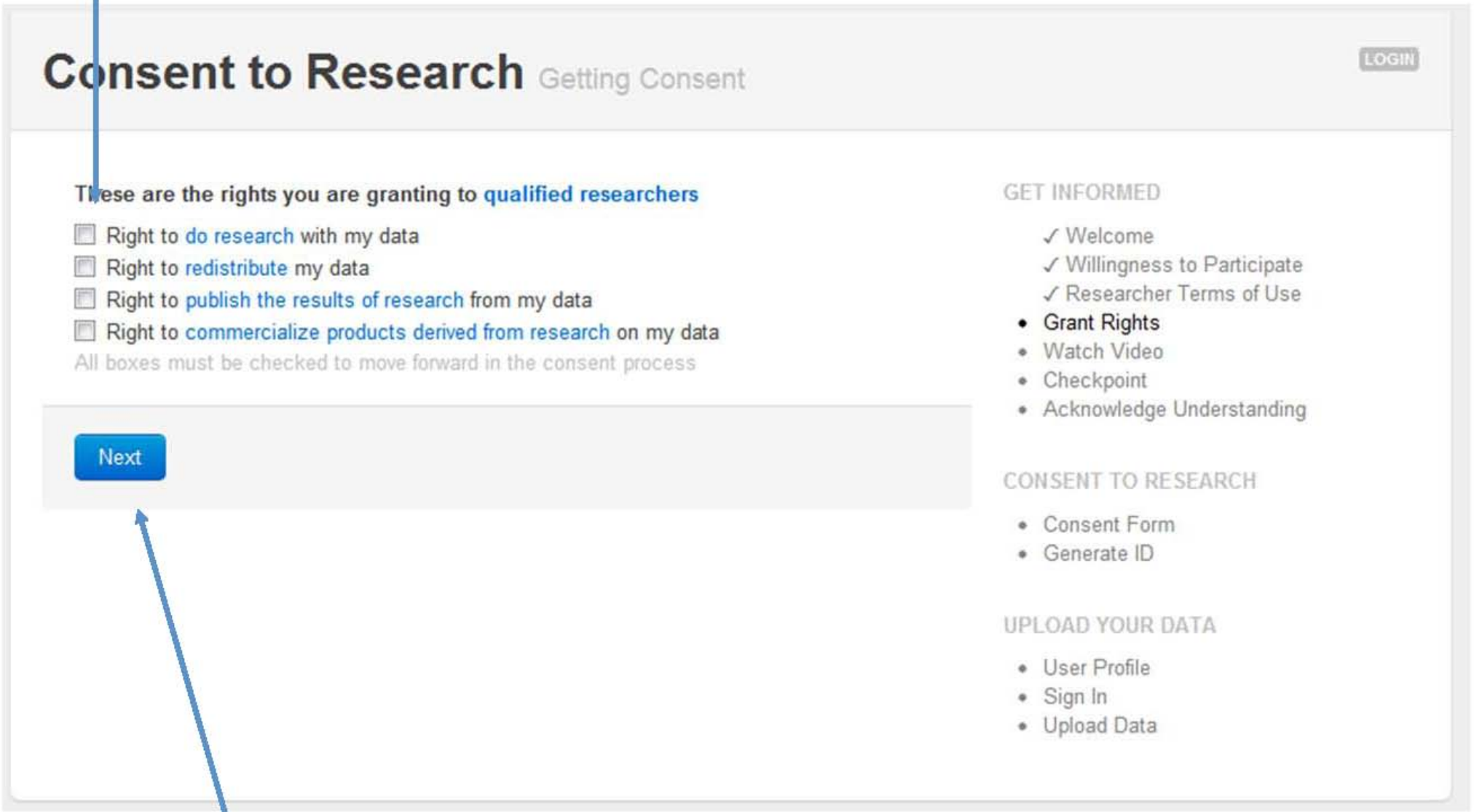
Alert me when cited
Alert me if corrected

Abstract

“eat less and exercise”

the experiment:

all boxes must be checked



volunteer must click to proceed

Genotype- 23andme (syn1418166)

Added by: Xavier Schildwachter on: Mon Oct 01 18:59:24 GMT-700 2012
Modified by: Christine Suver on: Tue Oct 02 09:07:59 GMT-700 2012
Version: 0.0.0 [1] (show all versions)

Description

Genotype from individual 1418165, generated by 23andme using the Illumina OmniExpress Plus genotyping beadchip.

This is a PLC contributed dataset (http://weconsent.us/about)

openSNP News Genotypes Phenotypes SNPs Users Search here Sign in FAQ

jtw's page

jtw has uploaded genotyping rawdata.

- Download this set (23andme)

Description

This user has not entered a description yet.

jtw's variations

This user has not entered any phenotypes yet.

http://opensnp.org/users/615

gs144

4	Magnitude
20120916	Geno time

Male Male.

rs5186(C;C) **7.3x increased risk of hypertension**...more...

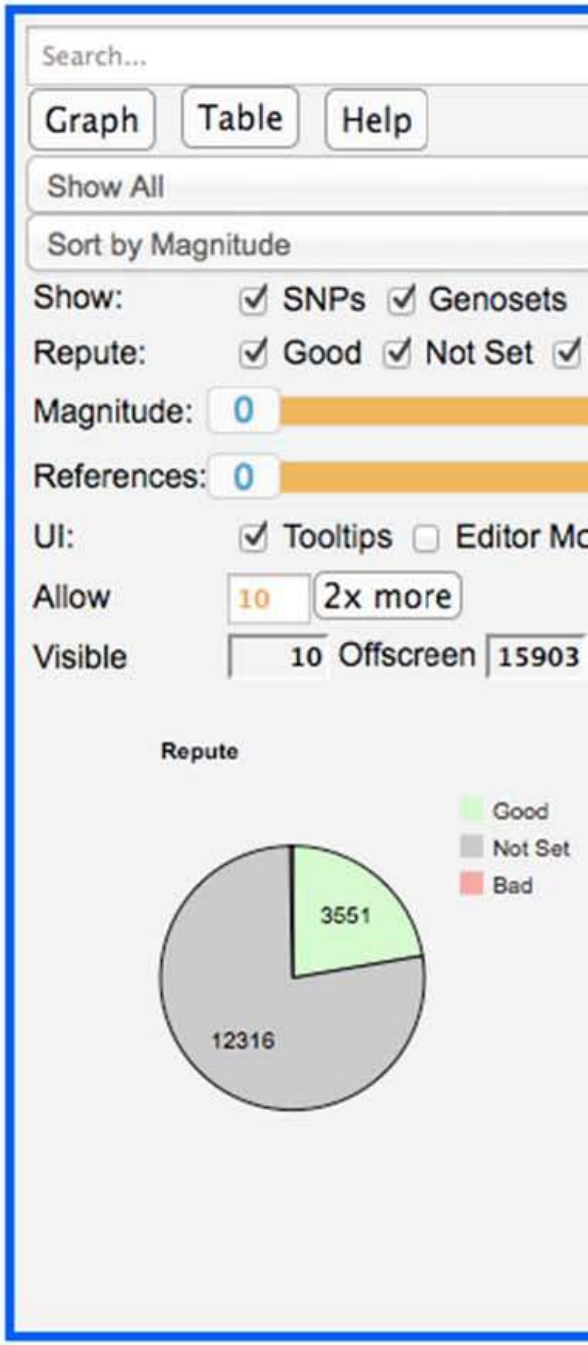
Bad	Repute
4	Magnitude
0.1575	GMAF
54	References
AGTR1	Gene
3	Chromosome
148459988	Position
20120810	Rs time

High blood pressure, Pre-eclampsia

rs6152(A;A) **won't go bald** This genotype seems to prevent baldness ...more...

Good	Repute
4	Magnitude
0.214587	GMAF
11	References
AR	Gene
X	Chromosome
66765627	Position
20120812	Rs time

Baldness



http://files.snpedia.com/reports/promethease_data/genome_jtw_ui2.html

'JTW'

MINOR ALLELE PROGRAM REPORT

'JTW' 'jw' '615' 23andMe Results Chromosomes 1-22 4 October 2012

The program finds about 60 'rare/uncommon' SNPs from the 900,000+ tested by 23andMe.

There is just a single 'homozygous-recessive' result:

'AA' rs11869580 Intergenic

but as this occurs in an Intergenic region it is unlikely to be of significance.

There are no SNPs of special note.

RESULTS

---

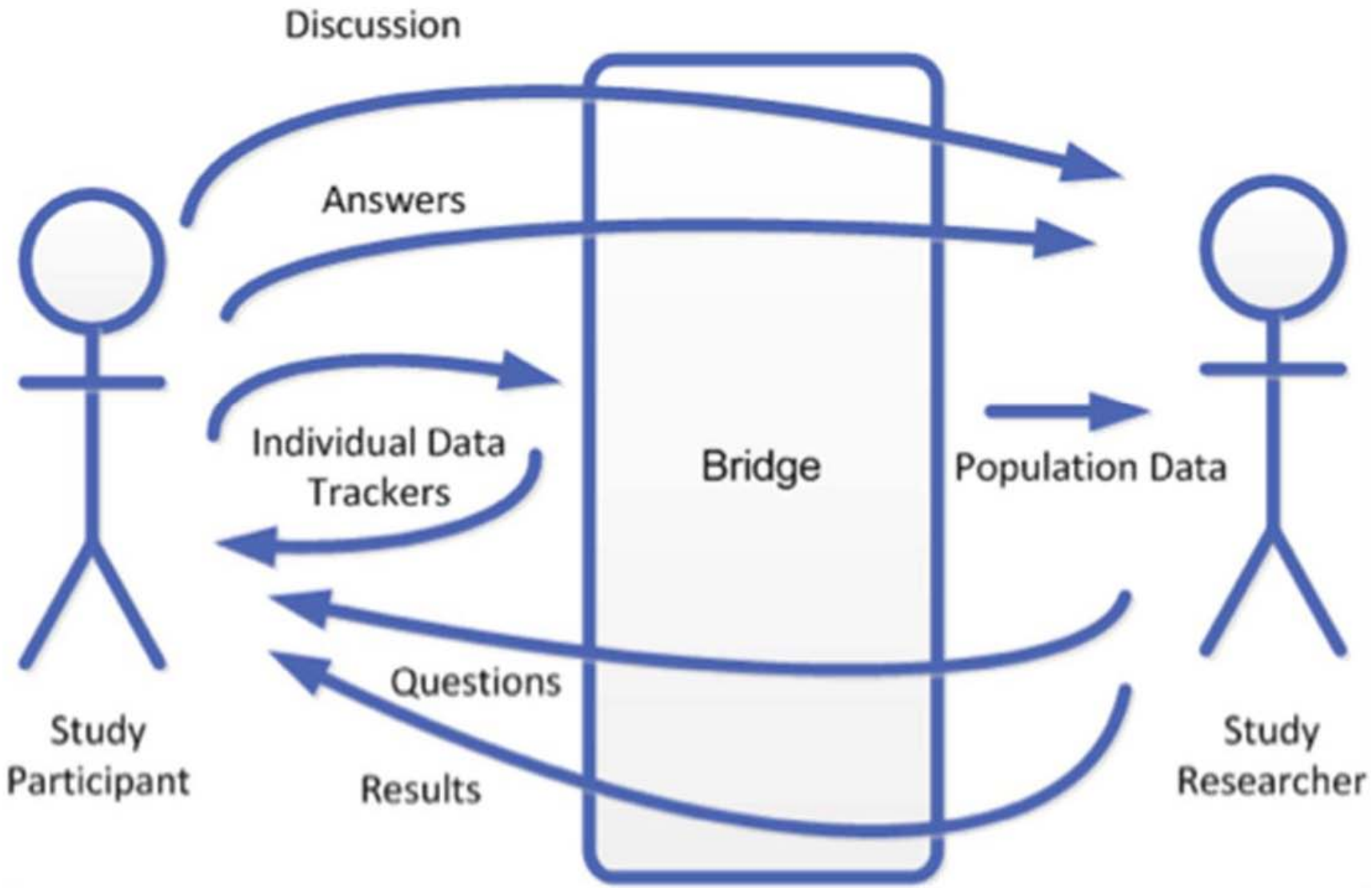
rs56367069	at Chr1a:17326767	gave 'CT'	The minor allele is 'T' with a MAF = 0.00776.
rs4949212	at Chr1a:31961711	gave 'GT'	The minor allele is 'G' with a MAF = 0.00959
rs1181088	at Chr1a:54563039	gave 'AG'	The minor allele is 'G' with a MAF = 0.00959
rs1109918	at Chr1a:67862482	gave 'AG'	The minor allele is 'G' with a MAF = 0.00822.
rs12751479	at Chr1b:98056007	gave 'GT'	The minor allele is 'T' with a MAF = 0.00228
rs35669708	at Chr1b:156851382	gave 'AG'	The minor allele is 'A' with a MAF = 0.00999
rs35698797	at Chr1c:229665958	gave 'CT'	The minor allele is 'T' with a MAF = 0.00502
rs45471294	at Chr2a:31600017	gave 'CT'	The minor allele is 'T' with a MAF = 0.00914.
rs17776702	at Chr2b:103317676	gave 'AG'	The minor allele is 'G' with a MAF = 0.00868
rs17760364	at Chr2c:189631806	gave 'AG'	The minor allele is 'G' with a MAF = 0.00959
rs279552	at Chr3a:9976159	gave 'AG'	The minor allele is 'A' with a MAF = 0.00639
rs460965	at Chr3a:10122927	gave 'CT'	The minor allele is 'T' with a MAF = 0.00594.
rs2067466	at Chr3a:11300780	gave 'CG'	The minor allele is 'C' with a MAF = 0.00319

“Also there is no suggestion of consanguinity in your pedigree.”

http://www.ianlogan.co.uk/

(not so good)

requires coherence and scale - easier to enforce in closed systems…


Discussion
Answers
Individual Data
Trackers
Bridge
Population Data
Questions
Results
Study
Participant
Study
Researcher

4.
someone’s going to achieve coherence and scale.

image via http://jawbone.com/

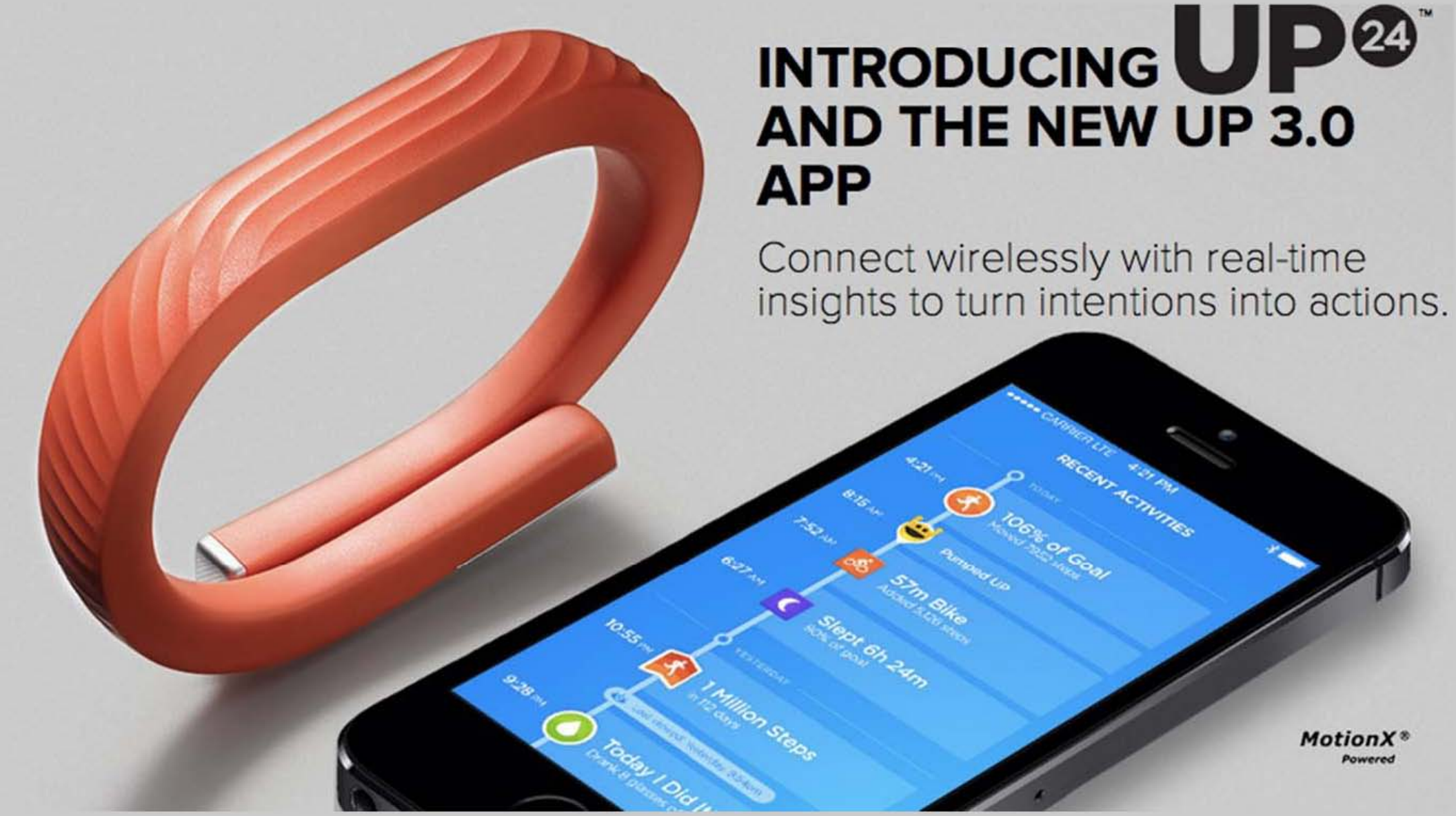
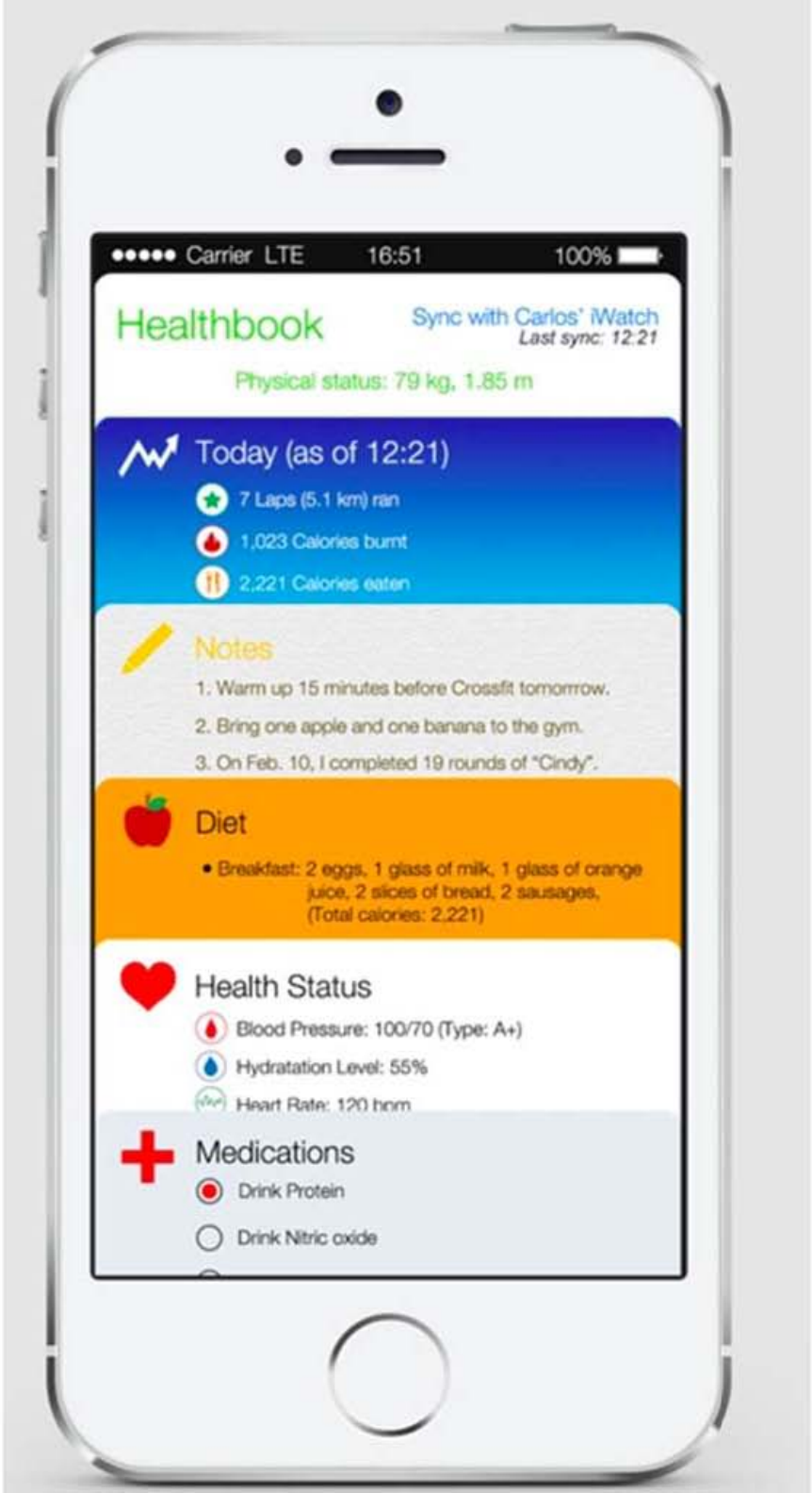
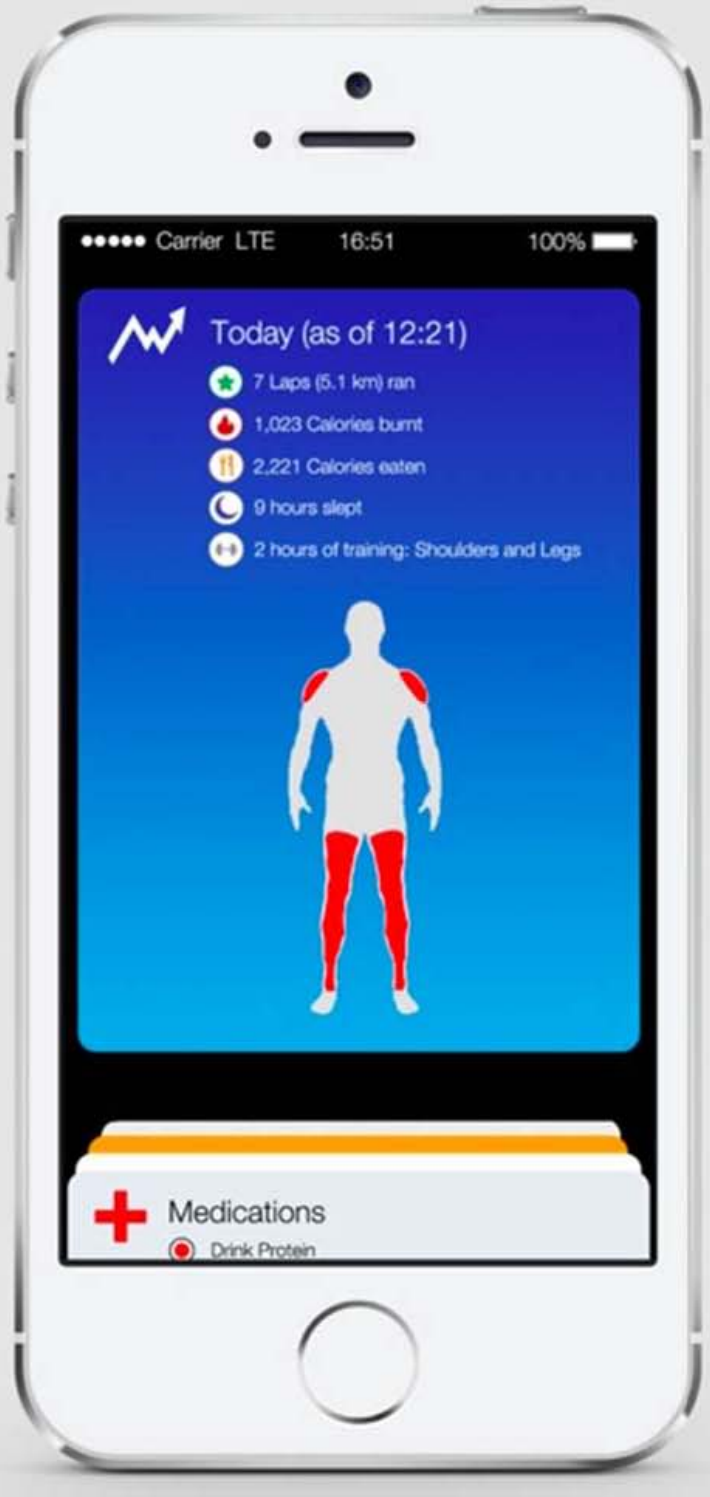


image via http://macrumors.com/





but will we be allowed to opt out?

image via http://gawker.com

thus we have to talk about the politics of data.

three choices for
coherence and scale.

a. “just like now, but moreso”

c. an open system.

Programmatic Clients

Synapse is designed to easily integrate into your current work. That's why we've created the following clients so that you can interact with all of Synapse's functionality programmatically. Create pr
download files, generate provenance, query, create wikis and more all from the comfort of your own code. Don't see your language of choice here? Check out our full REST API documentation.

R Client

```
source('http://depot.sagebase.org/CRA
pkgInstall(c("synapseClient"))
```

API Documentation & Example Code

Python Client

```
# From Terminal Prompt:
pip install synapseclient

# or
easy_install synapseclient
```

Command Line Client

```
# From Terminal Prompt:
pip install synapseclient

# or
easy_install synapseclient
```

Java Client

Sho

API Documentation

National Institutes of Health
Turning Discovery Into Health

Accelerating Medicines Partnership

The Accelerating Medicines Partnership (AMP) is a bold new venture between the National Institutes of Health (NIH), 10 biopharmaceutical companies and several non-profit organizations to transform the current model for developing new diagnostics and treatments by jointly identifying and validating promising biological targets of disease. AMP will begin with three to five year pilot projects in three disease areas: Alzheimer's disease, type 2 diabetes, and the autoimmune disorders of rheumatoid arthritis and systemic lupus erythematosus (lupus).

For each pilot, scientists from NIH and industry have developed research plans aimed at characterizing effective molecular indicators of disease called biomarkers and distinguishing biological targets most likely to respond to new therapies. The ultimate goal is to increase the number of new diagnostics and therapies for patients and reduce the time and cost of developing them.

Through this cross-sector partnership, which will be managed through the Foundation for the NIH (FNIH), NIH and industry partners are sharing expertise and resources –$230 million – in an integrated governance structure that enables the best informed contributions to science from all participants. A critical component of

AMP Partners

Government
- FDA
- NIH

Industry
- AbbVie
- Biogen Idec
- Bristol-Myers Squibb
- GlaxoSmithKline
- Johnson & Johnson
- Lilly
- Merck
- Pfizer
- Sanofi
- Takeda

Non-Profit Organizations

Open Source and Standards

Open Source and Standards
Open Source at IBM
Standards at IBM
Interoperability Specifications Pledge
Links
FAQs

Related links
- Linux at IBM
- DB2 Express-C
- Lotus Expeditor
- Apache OpenOffice
- OmniFind Yahoo! Edition
- Rational Jazz
- Rational Software Delivery Platform
- WAS Feature Pack for Web 2.0
- WebSphere Application Server Community Edition
- IBM Power Architecture
- IBM BladeCenter

Open Source and Standards in the Marketplace

Technology and the Internet revolution have made the world a smaller and "flatter" place. Global innovation continues to bring people around the world closer to one another, but we're now starting to realize that just being connected isn't enough.

Fortunately, a new revolution is beginning: one that holds significant potential. The planet is becoming smarter. Intelligence is being infused into the way the world literally works—into the systems, processes and infrastructure that enable physical goods to be developed, manufactured, bought and sold; that allow services to be delivered; that facilitate the movement of everything from money and oil to water and electrons. Ultimately, this will help to improve how billions of people work and live.

Open Source & Standards are key to making our planet smarter and improving the way we live and work.

Open Source:
Open source in IT is software whose source code is published and made available to the public, enabling anyone to copy, modify and redistribute the source code without paying royalties or fees.

Standards:
A standard is a specification that has been agreed upon by a community, through usage or declaration. Once established, any number of duplicates or variants can be made, while keeping the basic structure or function intact.

IBM is driving reforms for IP, Open Source & Standards

IBM is an industry leader helping governments move toward greater openness and innovation.

Project Data Sphere Overview

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Apply for Access

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- About Us
- Access Data
- Share Data
- User Guide
- Contact Us

Data sharing opens a new world of possibilities for conquering cancer

Apply for Access

2013 goal: 60 data sets

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MK2206 and Paclitaxel in Treating Patients With Locally Advanced or Metastatic Solid Tumors or Metastatic Breast Cancer:nnn...

Detection of Circulating Osteosarcoma Tumor Cells in the Blood of Patients Using the Polymerase Chain Reaction:test

Welcome to Project Data Sphere... a simple idea for transforming innovation in cancer treatment research.

Project Data Sphere enables researchers across industry and academia to share oncology clinical trial data through a single online platform.Sharing data will speed our understanding of the disease and drive efficiencies in the development of new drugs and treatment approaches. Project Data Sphere represents the collaborative effort of industry, academia, and patient advocacy organizations united in their fight against cancer. **Read More >>**

What data sharing means for **COMPANIES** and **INSTITUTIONS**

Why data sharing promotes innovation by **RESEARCHERS**

How data sharing honors **PATIENTS**

c. the cartel.

facebook

Remember Me

Email

Facebook helps you connect and share with the people in your life.

Sign Up

It's free and anyone ca

Full Name:

Your Email:

New Password:

I am: Select Sex:

Birthday: Month:

Why do I need to pro

Sign Up

To create a page for a celebrity, b

thank you

@wilbanks
john.wilbanks@sagebase.org