



Translating a Trillion Points of Data into Diagnostics, Therapies and New Insights in Health and Disease

Atul Butte, MD, PhD

Director, Institute for Computational
Health Sciences

University of California, San Francisco

atul.butte@ucsf.edu

 @atulbutte

Conflicts of Interest

- Scientific founder and advisory board membership
 - Genstruct
 - NuMedii
 - Personalis
 - Carmenta
- Honoraria for talks
 - Lilly
 - Pfizer
 - Siemens
 - Bristol Myers Squibb
 - AstraZeneca
 - Roche
 - Genentech
 - Warburg Pincus
- Past or present consultancy
 - Lilly
 - Johnson and Johnson
 - Roche
 - NuMedii
 - Genstruct
- Tercica
- Ecoeos
- Helix
- Ansh Labs
- Prevendia
- Samsung
- Assay Depot
- Regeneron
- Verinata
- Pathway Diagnostics
- Geisinger Health
- Covance
- Wilson Sonsini Goodrich & Rosati
- Orrick
- 10X Genomics
- Medgenics
- GNS Healthcare
- Gerson Lehman Group
- Coatue Management
- Northrop Grumman
- Aptalis
- Allergan
- Astellas
- Thomson Reuters
- Intel
- SAP
- SV Angel
- Progenity
- Illumina
- Speakers' bureau
 - None
- Companies started by students
 - Carmenta
 - Serendipity
 - Stimulomics
 - NunaHealth
 - Praedicat
 - MyTime
 - Flipora
 - Tumbl.in
- Corporate Relationships
 - Northrop Grumman
 - Aptalis

The Economist

FEBRUARY 27TH-MARCH 5TH 2010

Economist.com

The data deluge

AND HOW TO HANDLE IT: A 14-PAGE SPECIAL REPORT



Obama the warrior

Misgoverning Argentina

The economic shift from West to East

Genetically modified crops blossom

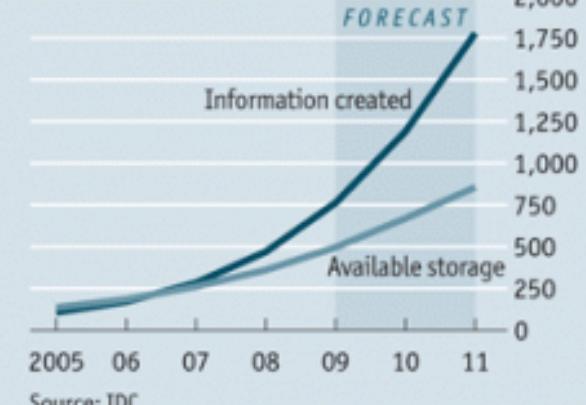
The right to eat cats and dogs

Kilo
Mega
Giga
Tera
Peta
Exa

Zetta

Overload

Global information created and available storage
Exabytes



Source: IDC

The End of Theory: The Data Deluge Makes the Scientific Method Obsolete

By Chris Anderson  06.23.08



Illustration: Manan Bantjes

THE PETABYTE AGE:

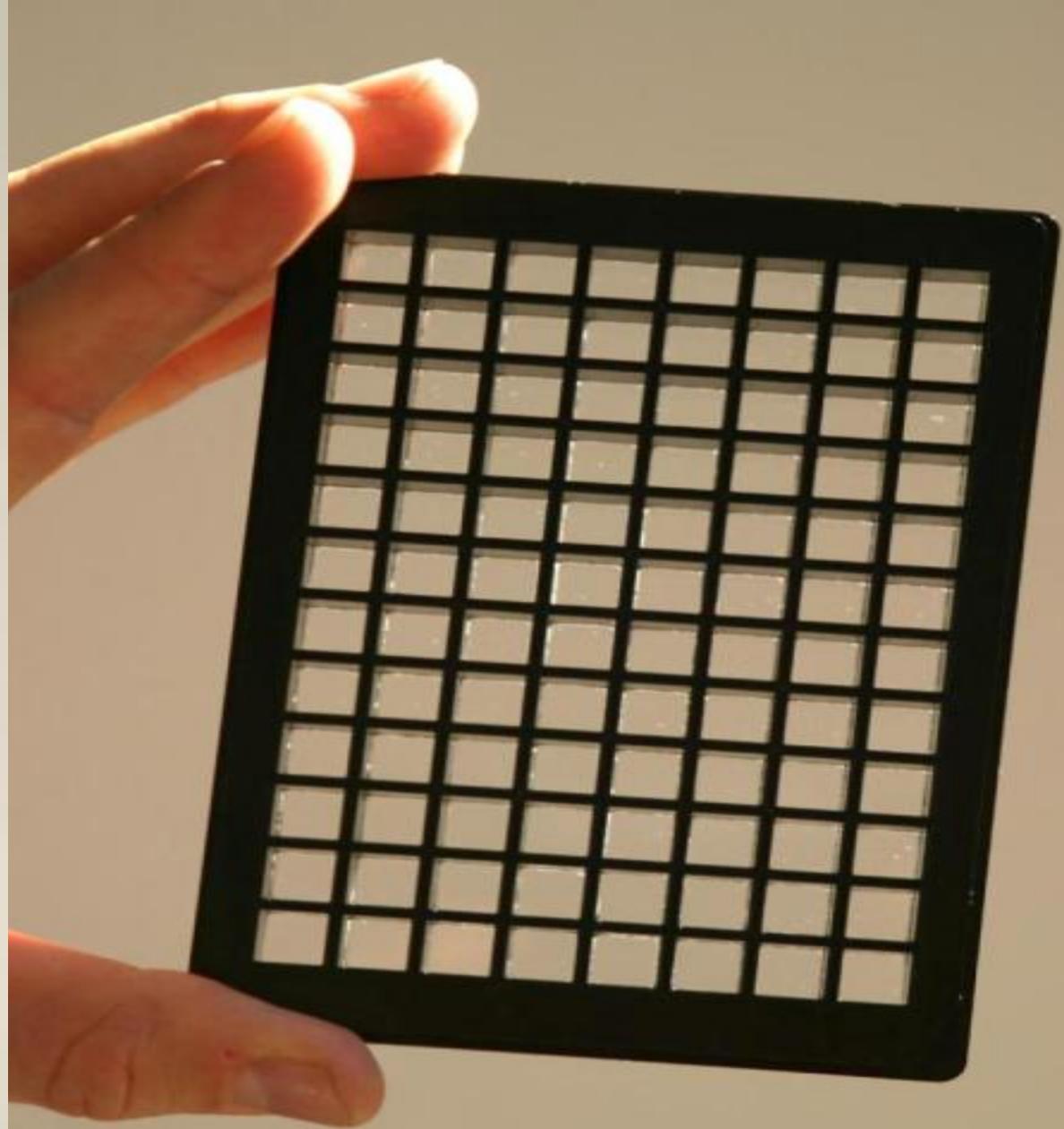
Sensors everywhere. Infinite storage. Clouds of processors. Our ability to capture, warehouse, and understand massive amounts of data is changing science, medicine, business, and technology. As our collection of facts and figures grows, so will

"All models are wrong, but some are useful."

So proclaimed statistician George Box 30 years ago. He was right. But what choice did we have? From cosmological equations to theories of human behavior, seemed to be able to consistently and imperfectly explain the world around us.

@chr1sa

bit.ly/endscience



@affymetrix



DNA microarrays allow researchers to analyse the expression of a huge number of genes simultaneously.

GENOMICS

Gene data to hit milestone

With close to one million gene-expression data sets, researchers can identify disease markers and targets.

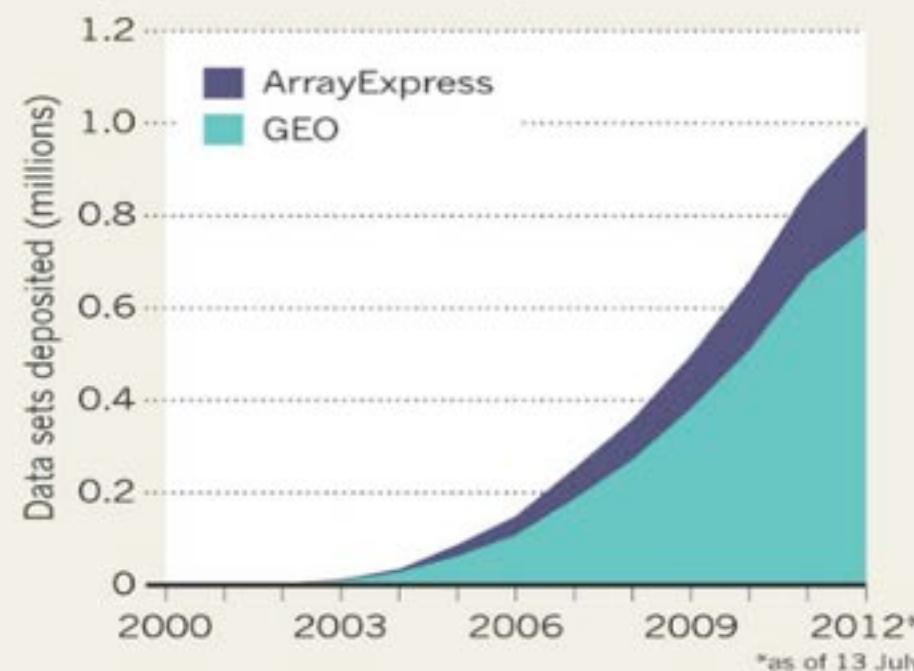
BY MONYA BAKER

Purvish Khatri sits in front of an oversize computer screen, trawling for treasure in a sea of genetic data. Entering the search term 'breast cancer' into a public repository called the Gene Expression Omnibus (GEO), the postdoctoral researcher retrieves a list of 1,170 experiments, representing nearly 33,000 samples and a hoard of gene-expression data that could reveal previously unseen patterns.

That is exactly the kind of search that led Khatri's boss, Atul Butte, a bioinformatician at the Stanford School of Medicine in California, to identify a new drug target for diabetes. After downloading data from 130 gene-expression studies in mice, rats and humans, Butte looked for genes that were expressed at higher levels in

DATA DUMP

The number of gene-expression data sets in publicly available databases has climbed to nearly one million over the past decade.



publicly accessible repositories, without a laboratory.

repository at the European Bioinformatics Institute (EBI) in Hinxton, UK. Some time in the next few weeks, the number of deposited data sets will top one million (see 'Data dump'). The result is an unprecedented resource that promises to drive down costs and speed up progress in understanding disease. Gene-sequence data are already shared extensively, but expression data are more complex and can reveal which genes are the most active in, say, liver versus brain cells, or in diseased versus healthy tissue. And because studies often look at many

bit.ly/genedata

Entry type

DataSets (184)

Series (3,238)

Samples (76,105)

Platforms (49)

Organism

Customize ...

Study type

Expression profiling by array

Methylation profiling by array

Customize ...

Summary ▾ 20 per page ▾ Sort by Default order ▾

Search results

Items: 1 to 20 of 79576

<< First < Prev

[MicroRNA-135b overexpression effect on prostate cancer cell line:](#)

1. Analysis of LNCaP prostate cancer (PCa) cells overexpressing miRNA-135b for 48 hours. LNCaP cells express the androgen receptor (AR). MiRNA-135b overexpression in LNCaP PCa cells results in slower growth compared to AR knockdown. Results provide the basis of this slower growth.

Organism:

Homo sapiens

Entry type

DataSets (184)

Series (3,238)

Samples (76,105)

Platforms (49)

Organism

Customize ...

Study type

Expression profiling by array

Methylation profiling by array

Customize ...

Summary ▾ 20 per page ▾ Sort by Default order ▾

Search results

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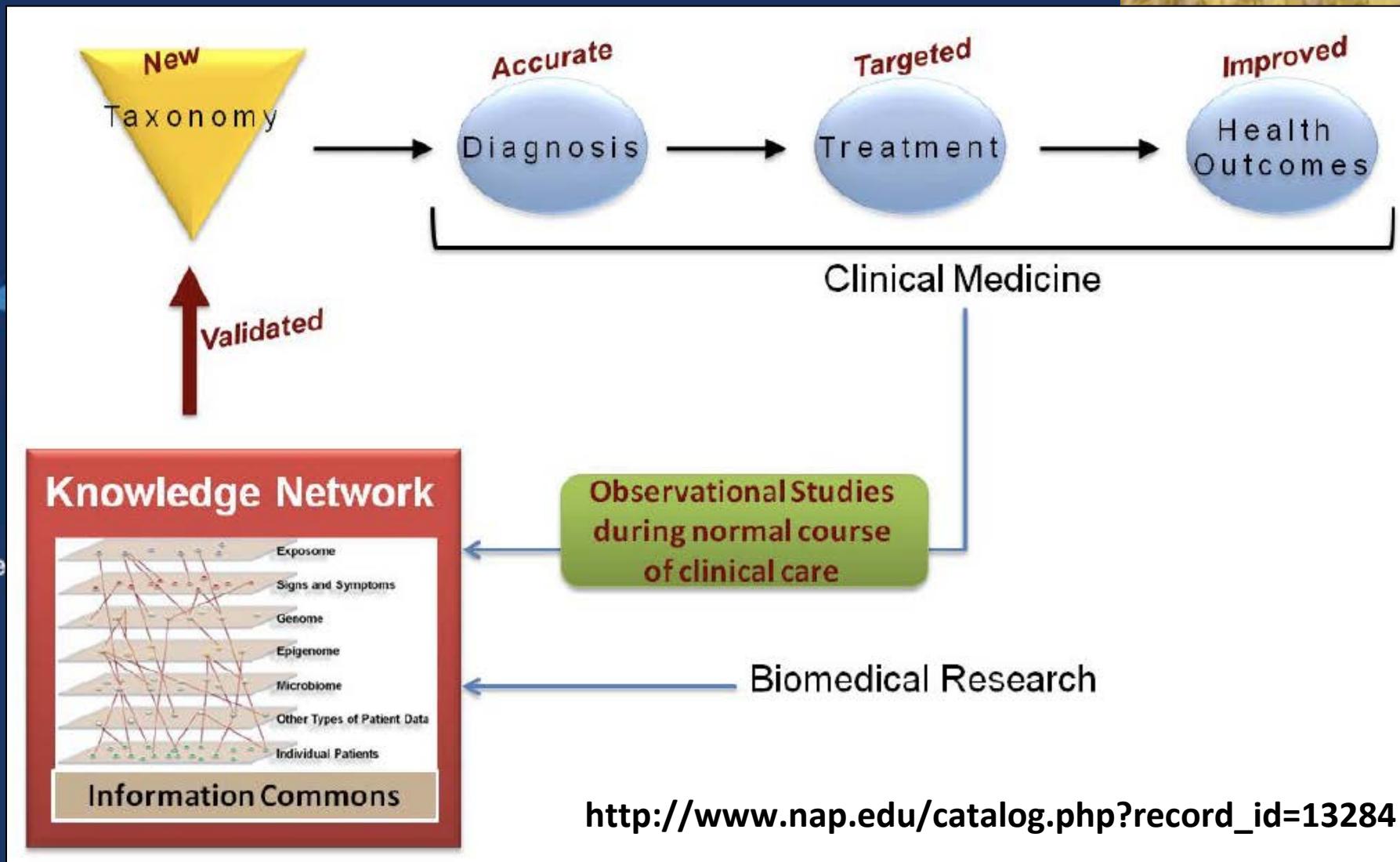
[MicroRNA-135b overexpression effect on prostate cancer cell line:](#)

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[Overview](#)[Home section](#)

Public big data = retroactive crowd-sourcing

THE PRECISION MEDICINE INITIATIVE



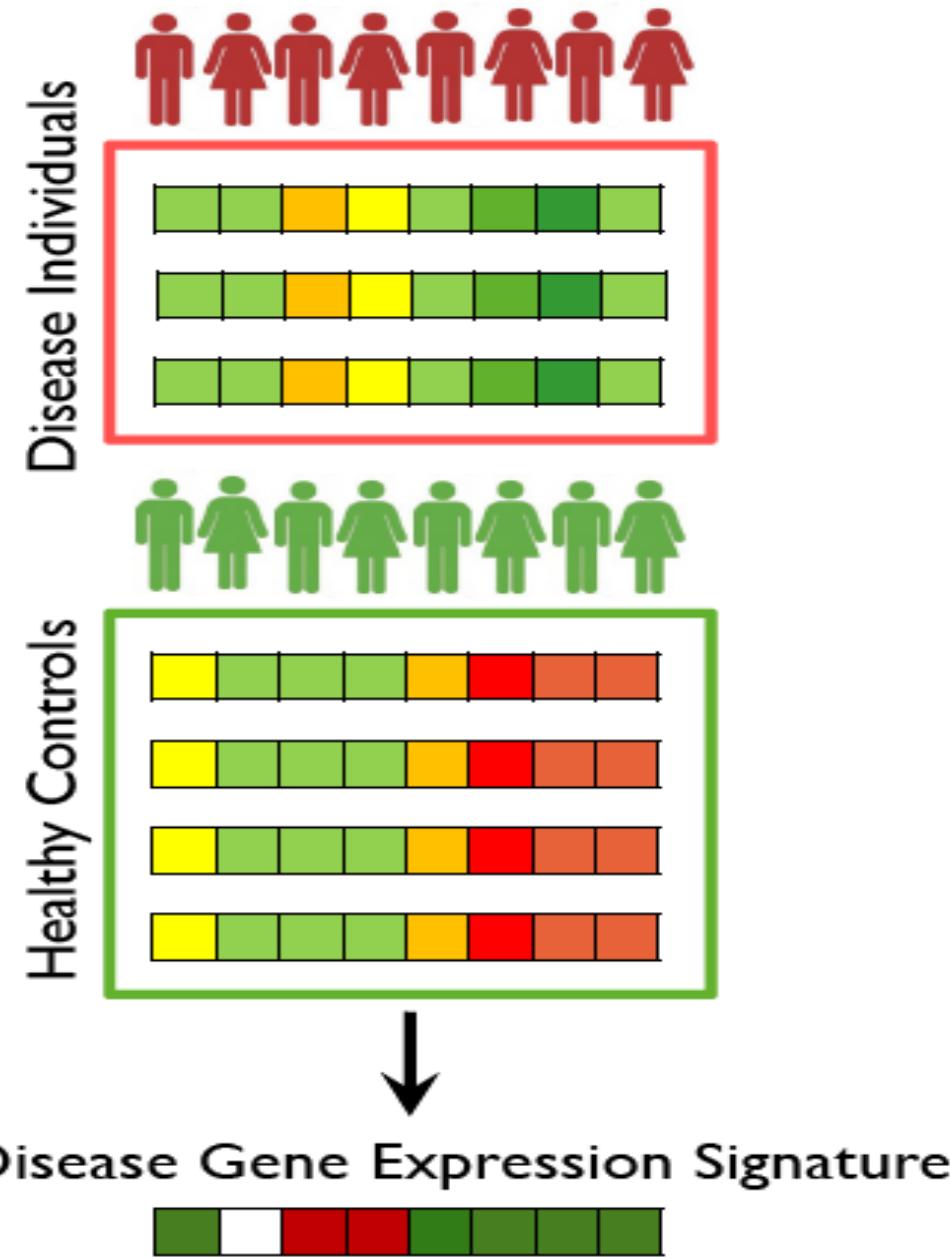
ent Obama's
tiative

In his State of the Union
details about the Precision
revolutionize how we
h a \$215 million investment
edicine Initiative will pioneer a
omises to accelerate
with new tools, knowledge, and
therapies to select which treatments will work best for which patients.

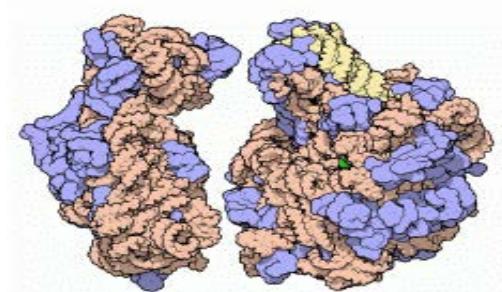
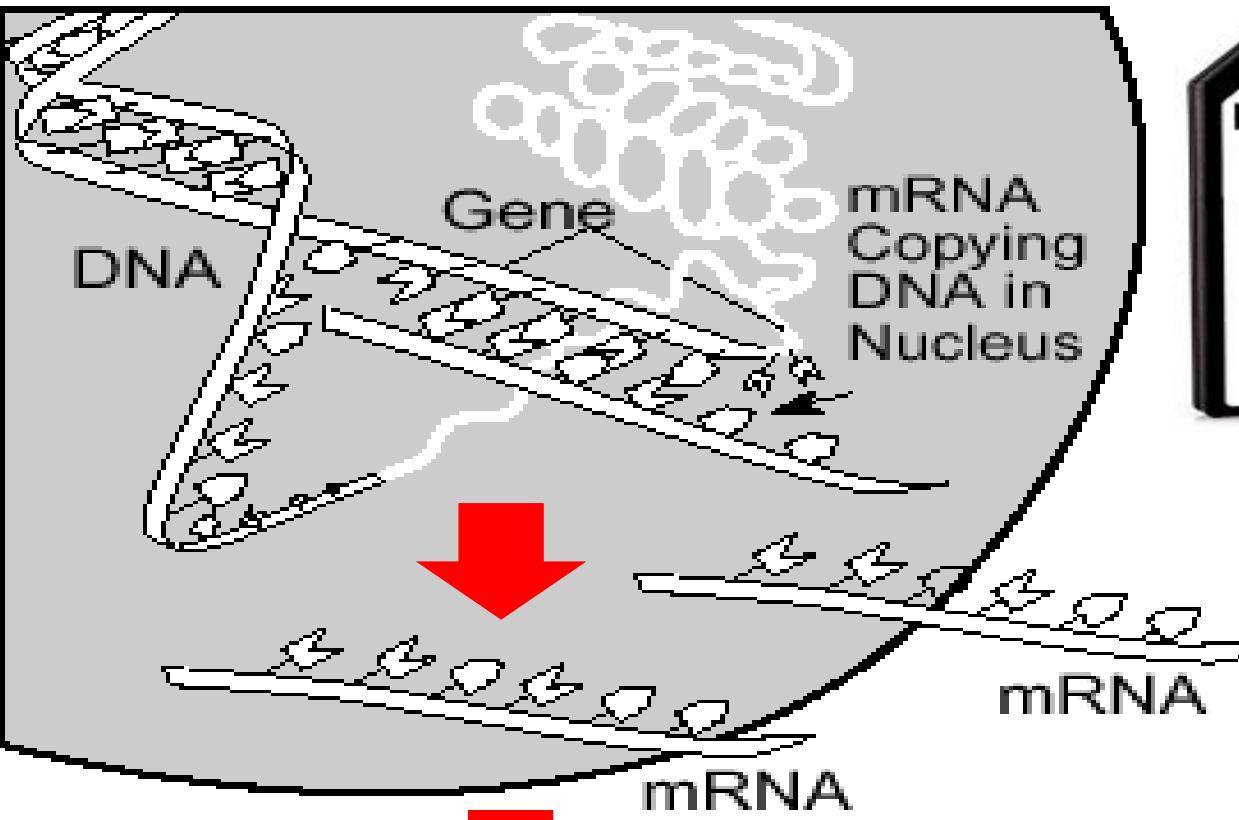
The time is right be

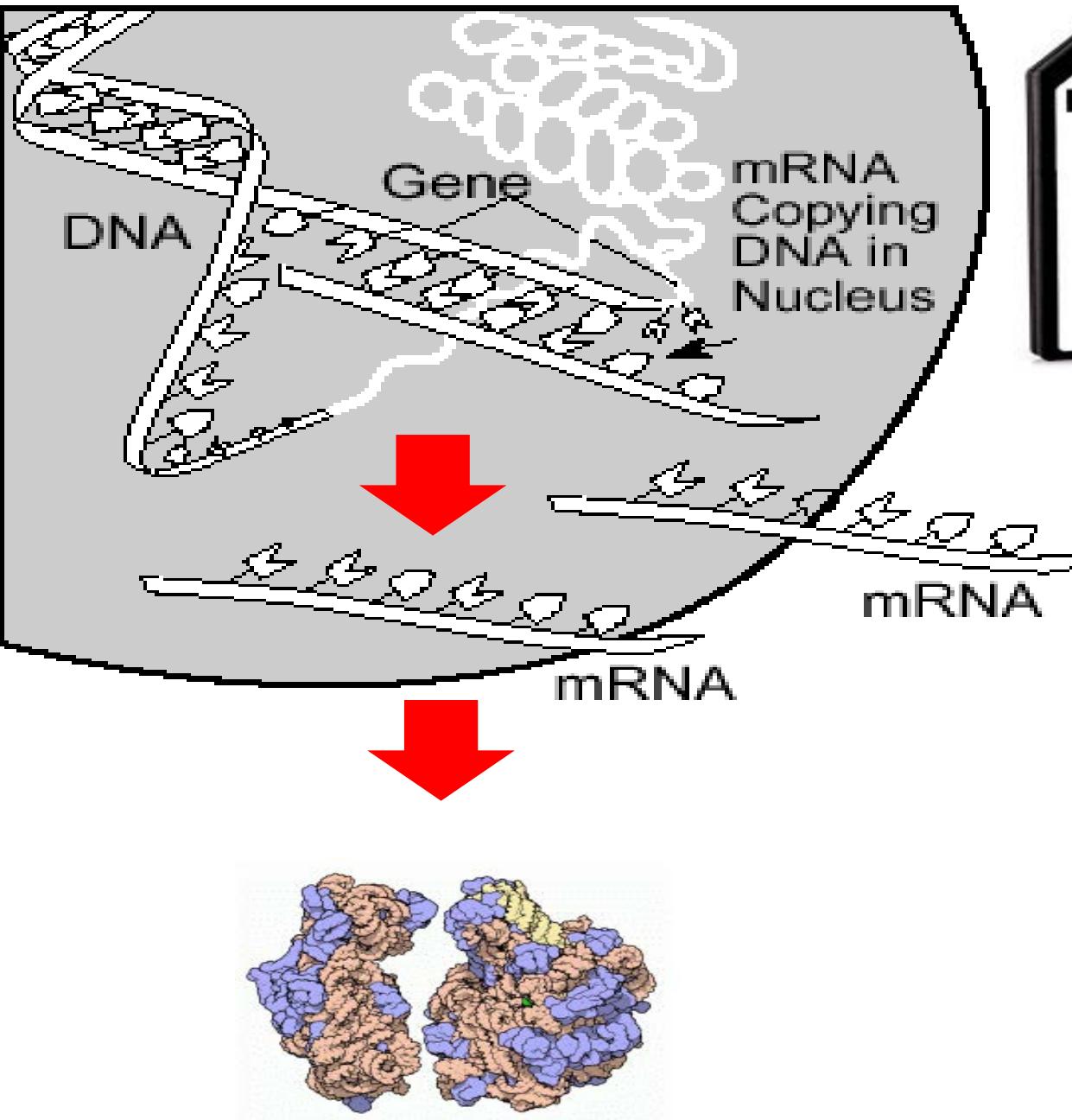
Sequencing
of the human
genome





Marina Sirota

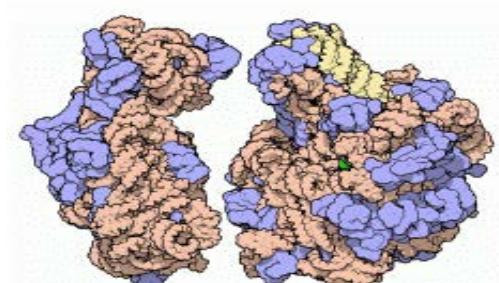
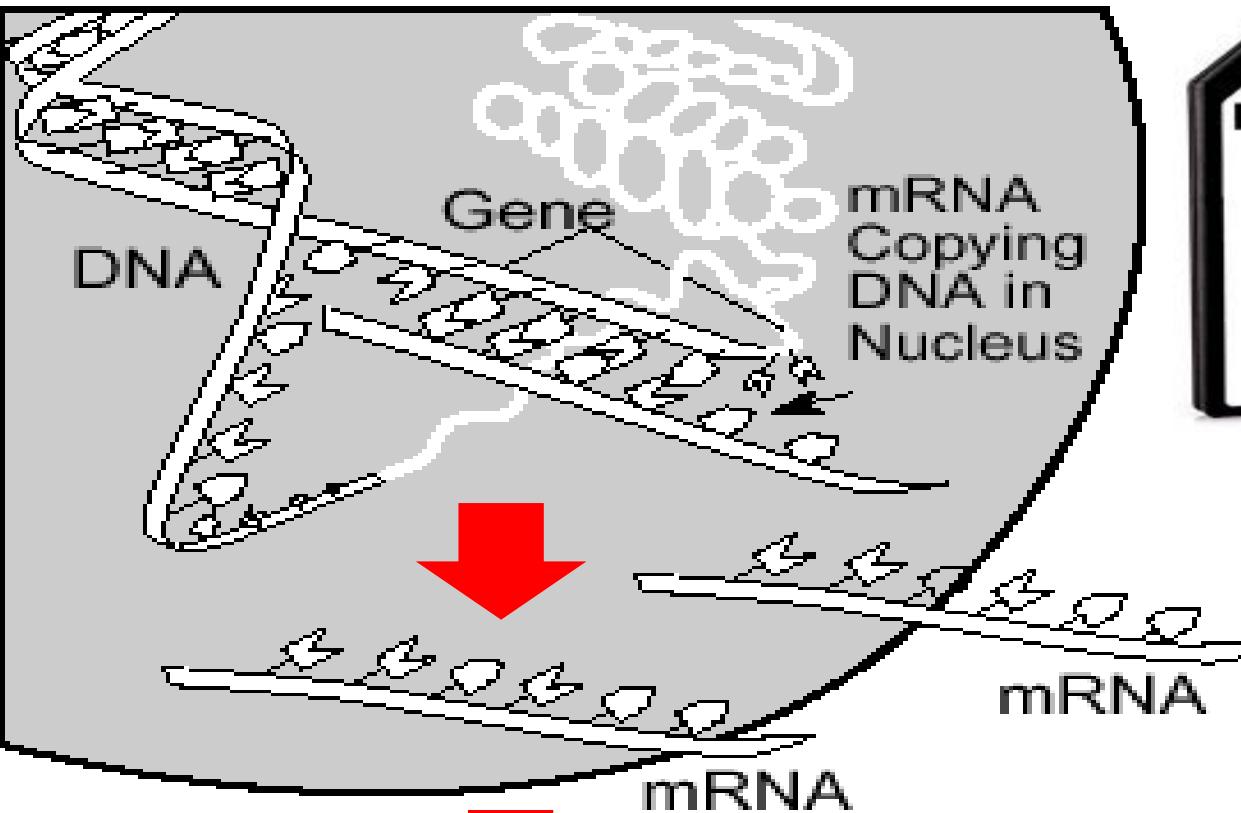




Cancer markers



Haeberle H, Dudley JT, ...,
Butte AJ, Contag CH. *Neoplasia*, 2012.



Chen R, ..., Butte AJ.
PLOS Computational Biology, 2010.



Cancer markers



Transplant Rejection markers



Preeclampsia: large cause of maternal and fetal death

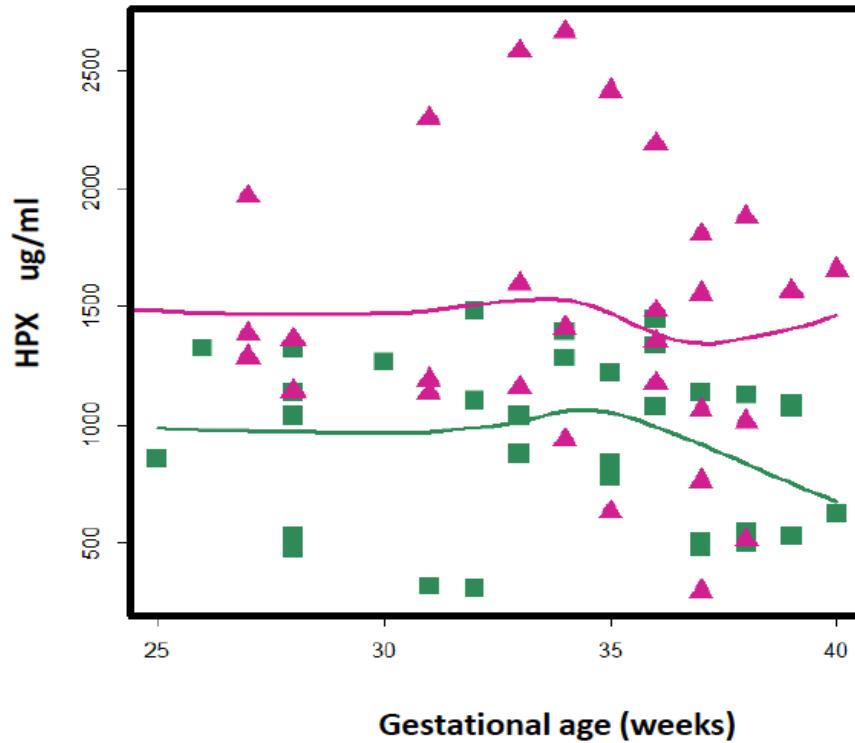
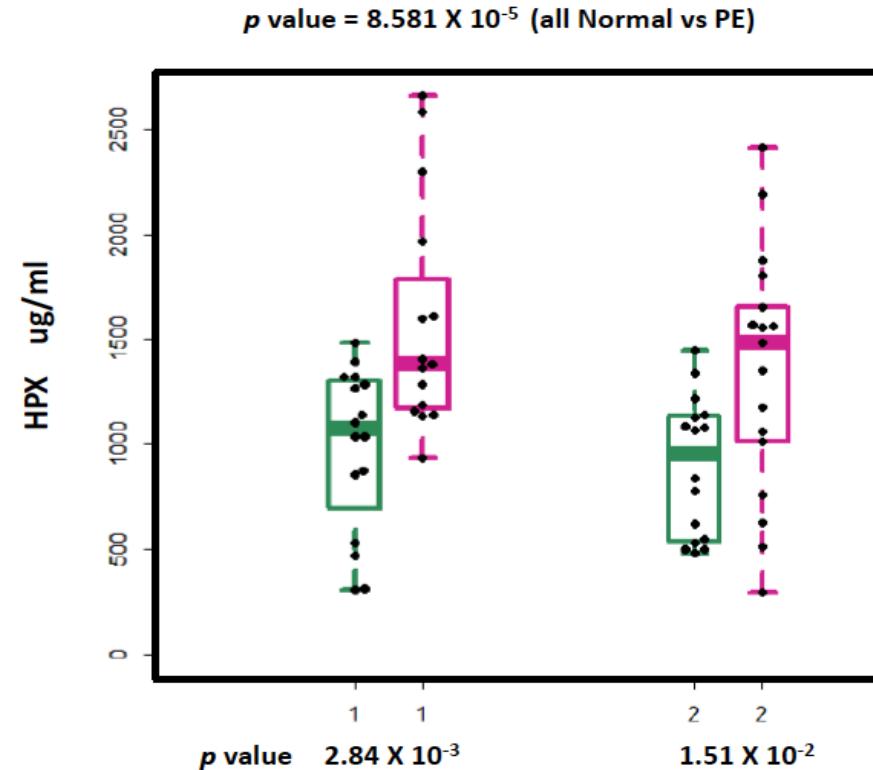
- Incidence
 - 5-8% of all pregnancies in the U.S. and worldwide
 - 4.1 million births in the U.S. in 2009
 - Up to 300K cases of preeclampsia annually in the U.S.
- Mortality
 - Responsible for 18% of all maternal deaths in the U.S.
 - Maternal death in 56 out of every 100,000 live births in US
 - Neonatal death in 71 out of every 100,000 live births in US
- Cost
 - \$20 billion in direct costs in the U.S annually
 - Average hospital stay of 3.5 days



Linda Liu
Bruce Ling
Matt Cooper

Accession	Title	Type	Organism	Assays	Released	Platform
E-GEOD-32472	Oxygen induced complication of prematurity: from experimental data to prevention strategy	transcription profiling by array	Homo sapiens	299	01/11/2011	GEO
E-GEOD-27976	Calvarial osteoblast transcriptome analysis identifies genetic targets and extracellular matrix-mediated focal adhesion as potential biomarkers for single-suture craniosynostosis	transcription profiling by array	Homo sapiens	249	04/03/2012	GEO
E-GEOD-46510	New whole blood gene expression profile predictive of preterm birth	transcription profiling by array	Homo sapiens	154	15/05/2014	GEO
E-GEOD-37210	The application of nonsense-mediated mRNA decay inhibition to the identification of breast cancer susceptibility genes	transcription profiling by array	Homo sapiens	143	11/04/2012	GEO
E-TABM-682	Transcription profiling of human decidua basalis to identify pre-eclampsia susceptibility genes	transcription profiling by array	Homo sapiens	104	07/04/2009	GEO
E-GEOD-35574	Differentially expressed microRNAs revealed by molecular signatures of Preeclampsia and IUGR in human placenta	transcription profiling by array	Homo sapiens	94	07/02/2012	GEO
E-GEOD-41336	Cultured Cyto and Syncytio-trophoblast samples exposed to varying degrees of hypoxia (methylation)	methylation profiling by array	Homo sapiens	90	18/01/2013	GEO
E-GEOD-5999	Transcription profiling of human 27 non- <small>transformed</small> cell lines	transcription	Homo sapiens	72	07/11/2008	GEO

New blood markers for preeclampsia



GA 23-34 weeks
Normal N=16
PE N=15

GA > 34 weeks
Normal N=16
PE N=17

@MarchofDimes
bit.ly/preeclamp

Need a diagnostic for preeclampsia

Public big data available

March of Dimes Center for Prematurity Research

Data analyzed, diagnostic designed

SPARK grant (\$50k)

Life Science Angels, other seed investors (\$2 million)

STOCK WATCH

Express, Wet Seal, Avago Jump

Carmenta Bioscience Secures Over \$2 Million in Oversubscribed Seed Financing

Camille Samuels Accepts Seat on Carmenta Board of Di



Press Release: Carmenta Bioscience, Inc. – Wed, A

BusinessWire
A Berkshire Hathaway Company

Progenity Acquires Carmenta Bioscience for Proprietary Preeclampsia Technology; Appoints Matthew Cooper Chief Scientific Officer

April 29, 2015 08:00 AM Eastern Daylight Time

SAN DIEGO--(BUSINESS WIRE)--Progenity, Inc., a provider of complex molecular and specialized diagnostic testing services, today announced the acquisition of Carmenta Bioscience, a leader in preeclampsia diagnostic development. With this acquisition, Progenity continues its mission of helping families prepare for life, through the development of diagnostic tests for preeclampsia. Preeclampsia, a hypertensive disorder of pregnancy, is often difficult to distinguish

financing will support development and commercialization of a new diagnostic to quickly and accurately diagnose and predict preeclampsia in pregnant women. The test is

@CarmentaBio
progenity.com
bit.ly/carm_prog



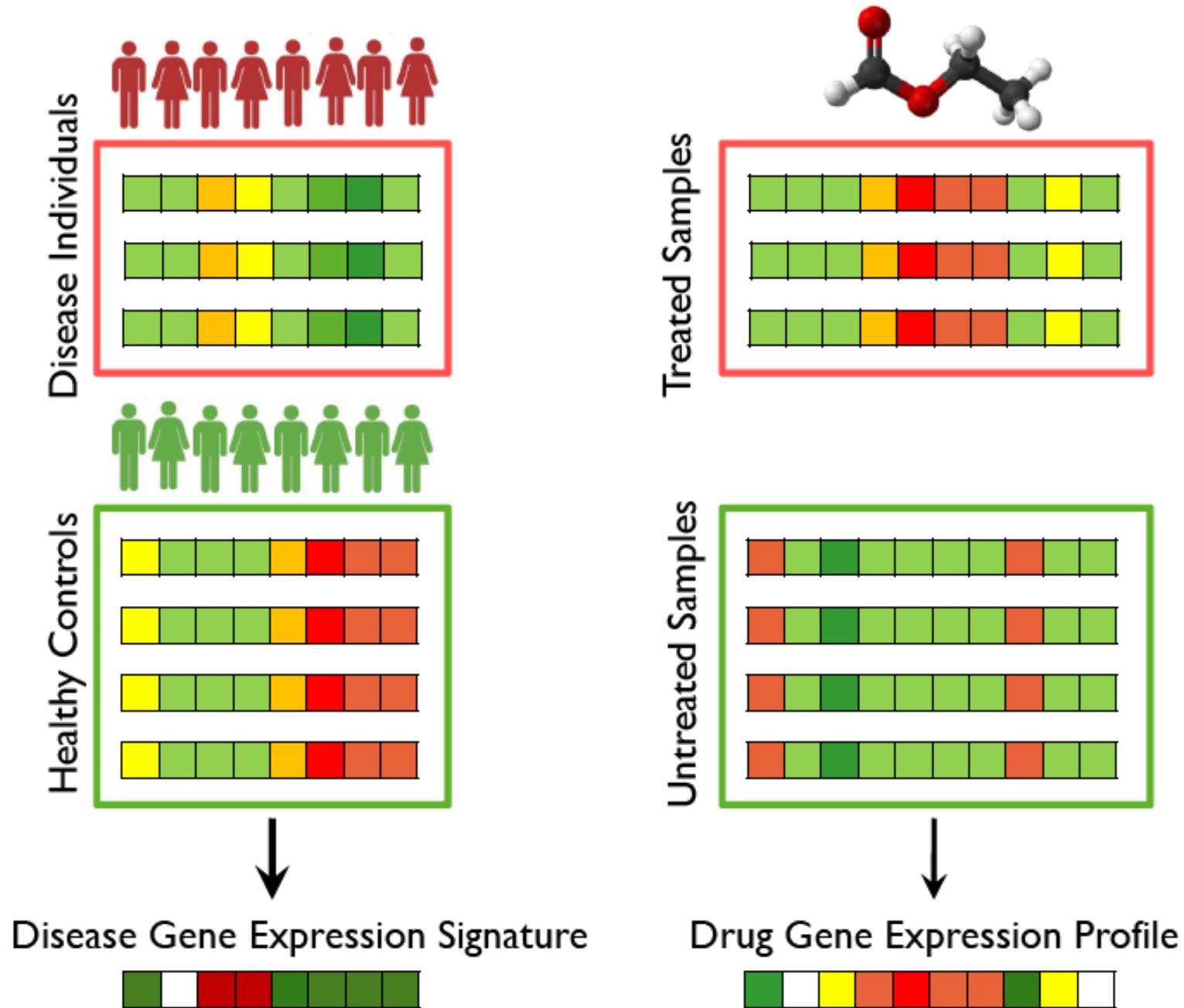
How Much Does Pharmaceutical Innovation Cost? A Look At 100 Companies

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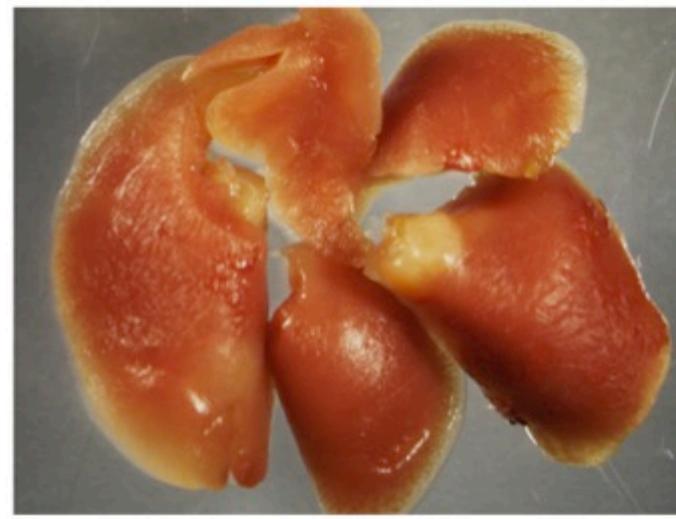
Company	Ticker	Number of drugs approved	R&D Spending Per Drug (\$Mil)	Total R&D Spending 1997-2011 (\$Mil)
AstraZeneca	AZN	5	11,790.93	58,955
GlaxoSmithKline	GSK	10	8,170.81	81,708
Sanofi	SNY	8	7,909.26	63,274
Roche Holding AG	RHHBY	11	7,803.77	85,841
Pfizer Inc.	PFE	14	7,727.03	108,178
Johnson & Johnson	JNJ	15	5,885.65	88,285
Eli Lilly & Co.	LLY	11	4,577.04	50,347
Abbott Laboratories	ABT	8	4,496.21	35,970
Merck & Co Inc	MRK	16	4,209.99	67,260
Bristol-Myers Squibb Co.	BMY	11	4,152.26	
Novartis AG	NVS	21	3,983.13	
Amgen Inc.	AMGN	9	3,692.14	

Sources: InnoThink Center For Research In Biomedical Innovation; The Fundamentals via FactSet Research Systems

@MatthewHerper
bit.ly/newdrug1



Psychiatric Drug Imipramine Shows Significant Activity Against Small Cell Lung Cancer



Vehicle control

Imipramine

*p53/Rb/p130
triple knockout
model of SCLC*

*Mice dosed after
tumor formation*

Joel Dudley
Nadine Jahchan
Julien Sage
Alejandro Sweet-Cordero
Joel Neal
@NuMedii

Cancer Discovery 2013, 3:1.



control food

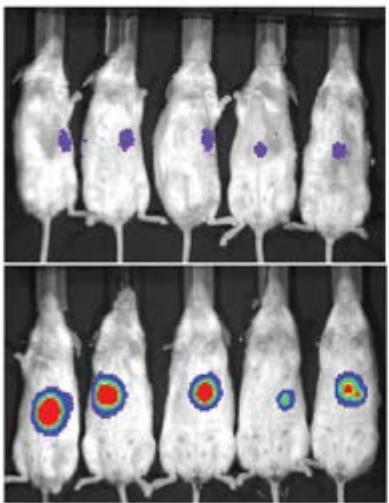


niclosamide



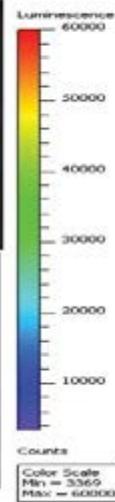
NEN

Before treatment

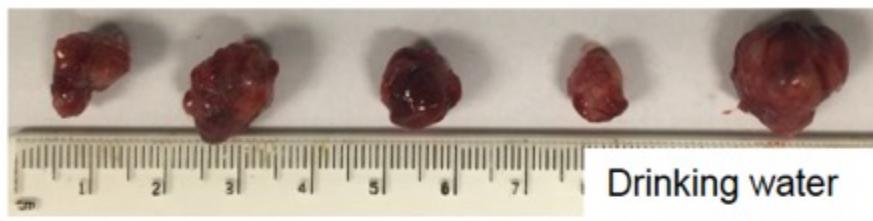
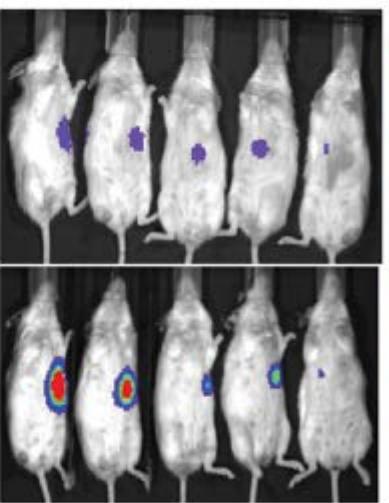


Control food

NEN (0.15%)



After treatment



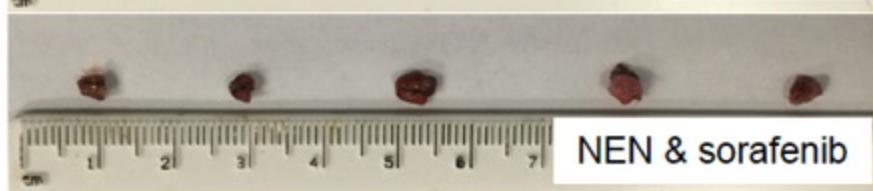
Drinking water



NEN



sorafenib



NEN & sorafenib

Bin Chen

Wei Wei

Li Ma

Bin Yang

Mei-Sze Chua

Samuel So

Gastroenterology, 2017

Need more drugs
for more diseases

Public big data
available

NIH funding

Data analyzed,
method designed

Company launched,
ARRA, StartX,
Stanford license,
first deal

Claremont Creek,
Lightspeed (\$3.5
million)

@NuMedii

Venture capital

'Digital drug development' company NuMedii snags \$3.5 million

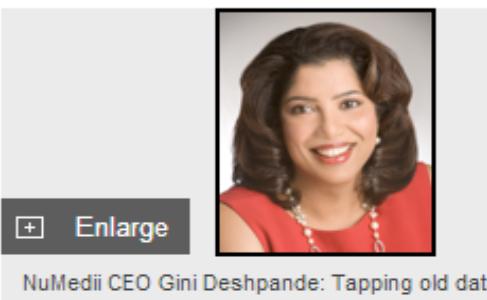


Ron Leuty
Reporter-
San Francisco Business Times
[Email](#) | [Twitter](#) | [Google+](#) | [Twitter](#)

NuMedii Inc., the Palo Alto startup looking to convert pages of drug safety data into faster drug-development times, lined up \$3.5 million in a Series A round.

The oversubscribed round was led by Claremont Creek Ventures and Lightspeed Venture Partners and included Life Science Angels and others.

NuMedii's data-into-gold approach rolls a wide range of data — from public scientific data bases and other sources — into an algorithm to predict if a compound will trans-



NuMedii CEO Gini Deshpande: Tapping old data to find new drugs.



NuMedii

Translating Big Data into new medicines

THE WALL STREET JOURNAL. ≡ | u.s.

TOP STORIES IN U.S.



1 of 12
VA Scandal Is
Shinseki's Latest
Battle

2 of 12

U.S. Economy Contracted
Last Quarter

U.S. NEWS

Researchers Show Gains in Finding Reus

[Email](#) [Print](#)

By AMY DOCKSER
August 18, 2011

In a bit of high-tech combat, scientists have already-approved combat.

The scientists have benefits in t

Astellas hooks up with NuMedii to continue drug repurposing deal drive

January 15, 2016 | By Nick Paul Taylor

SHARE



NuMedii, Inc. Announces New Partnership To Discover And Advance New Treatments For Idiopathic Pulmonary Fibrosis

FierceBiotechIT

Topics: R&D

Allergan taps NuMedii's digital platform for psoriasis R&D

October 5, 2015 | By Nick Paul Taylor

SHARE NuMedii has landed a deal that could validate its platform for psoriasis R&D. Allergan (\$AGN) is the company that developed the psoriasis drug Humira.

ImmPort is funded by the NIH, NIAID and DAIT in support of the NIH mission to share data with the public. Data shared through ImmPort has been provided by NIH-funded programs, other research organizations and individual scientists ensuring these discoveries will be the foundation of future research.



The next big open data: clinical trials

Download 100+ studies today

**Drug repositioning, new patient subsets,
digital comparative effectiveness, more!**

- Analysis Workflow
- Automated Clustering
- Tutorials



Technion
Israel Institute of Technology

UB
University at Buffalo
The State University of New York

Sanchita Bhattacharya
Jeff Wiser

Welcome to Immport.org our
new Beta web site currently
in user review

Data Summary - Studies:
222, Subjects: 37140,
Experiments: 1011

more ➤



**BILL & MELINDA
GATES foundation**

The 10,000 Immunome Project: From the control groups of 242 manually curated experiments



Human Subjects
Control Arms
No Manipulations

Filtering for
Normal Controls
ImmPort Study Design
Inclusion/exclusion criteria
Contact authors
Read protocols

83 Studies
10,344 Subjects
42,000+ Samples



- Automatically find positive and negative populations with MetaCyto
- Assign Standardized Cell Subset Names
- Segregate Sample Types
- Batch Correct
- Validate against gold-standard hand-gated populations

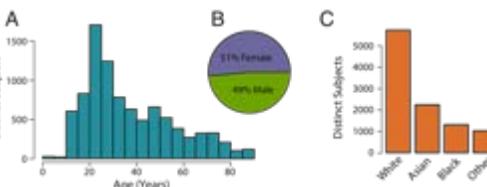
Secreted Immune Proteins

- Standardize Units
- Assign Standardized Cell Subset Names
- Segregate Sample Types
- Correct for Dilution Factor
- Batch Correct

Others (7 Assay Types)

- Standardize Units
- Standardize Names
- Segregate Sample Types
- Correct for Dilution Factor
- Batch Correct where Needed
- RMA Background Correct
- Quantile Normalize
- Log2 Normalize
- Assign Probes to Entrez IDs
- Segregate Sample Types
- Combine data based on Entrez IDs
- Batch Correct with ComBat
- Assign HUGO Gene Names

Gene Expression



Data available in the 10,000 Immunomes Project

Total Samples	42117
Total Distinct Subjects	10344

MEASUREMENT SUBJECTS

Secreted Proteins	
ELISA	4835
Multiplex ELISA	4035
	1286

Virus Titer	
Virus Neutralization Titer	3609
HAI Titer	2265
	1344

Clinical Lab Tests	
Complete Blood Count	2639
Comprehensive Metabolic Panel	1684
Fasting Lipid Profile	664
	664

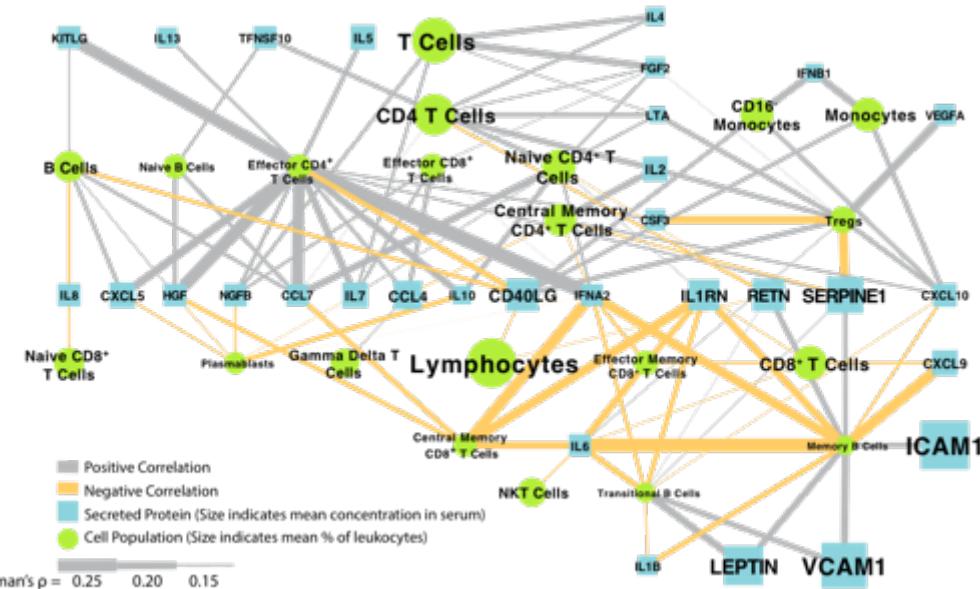
Questionnaire	
	1422

Cytometry	
Flow Cytometry (PBMC)	1415
CyTOF (PBMC)	907
Flow Cytometry (Whole Blood)	583
	164

HLA Type	
	1093

Gene Expression Array	
Whole Blood	476
PBMC	311
	165

Data Dissemination	Web Interface for Data Visualization and Download
	→
	Data Repurposing and Meta-analysis



Kelly Zalocusky
Sanchita Bhattacharya

@ImmPortDB

bioRxiv bit.ly/10kimmu
<http://10kimmunomes.org/>



UCSF

Institute for Computational
Health Sciences

Zuckerberg, Chan give UCSF \$10 million for health data research

By Catherine Ho, San Francisco Chronicle | July 28, 2017

[✉](#) [f](#) [t](#) [p](#) [s](#) [g+](#)

[≡](#) [💬 4](#)





Institute for Computational
Health Sciences

**Build the strongest team in the world in
biomedical computation and health data analytics**

- Academic affinity home for faculty and staff
- Research and development (and spin out technologies)
- Develop new educational plans
- Bring the best new computational and informatics faculty members to UCSF
- Organize infrastructure and operations
- Build and use our new data assets for precision medicine

The next big data: clinical data



Home

Data Explorer

Our Data

Get Started ★

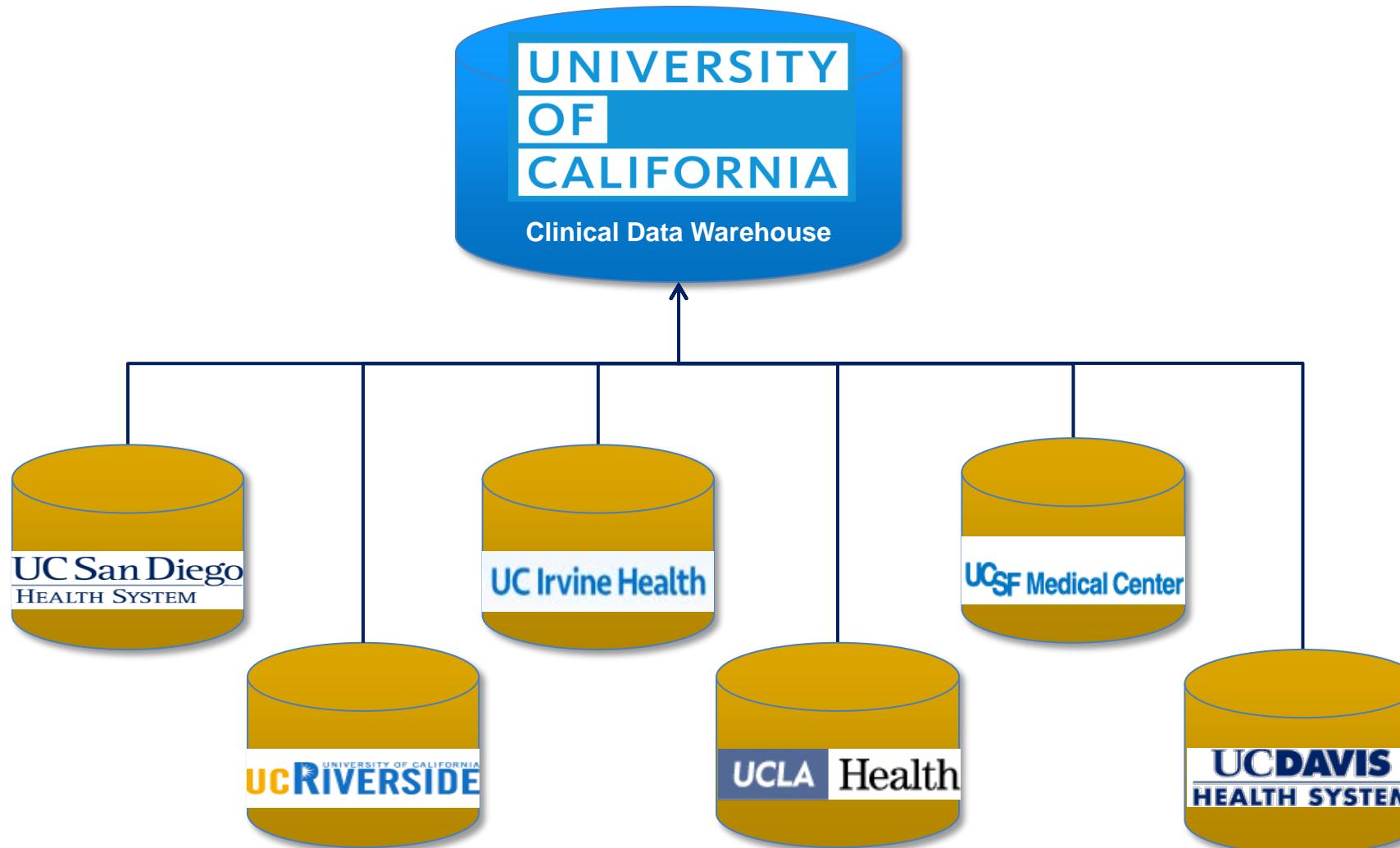
**SEARCH 15 MILLION+ PATIENT RECORDS
FROM THE UNIVERSITY OF CALIFORNIA
WITH THE UC ReX DATA EXPLORER**

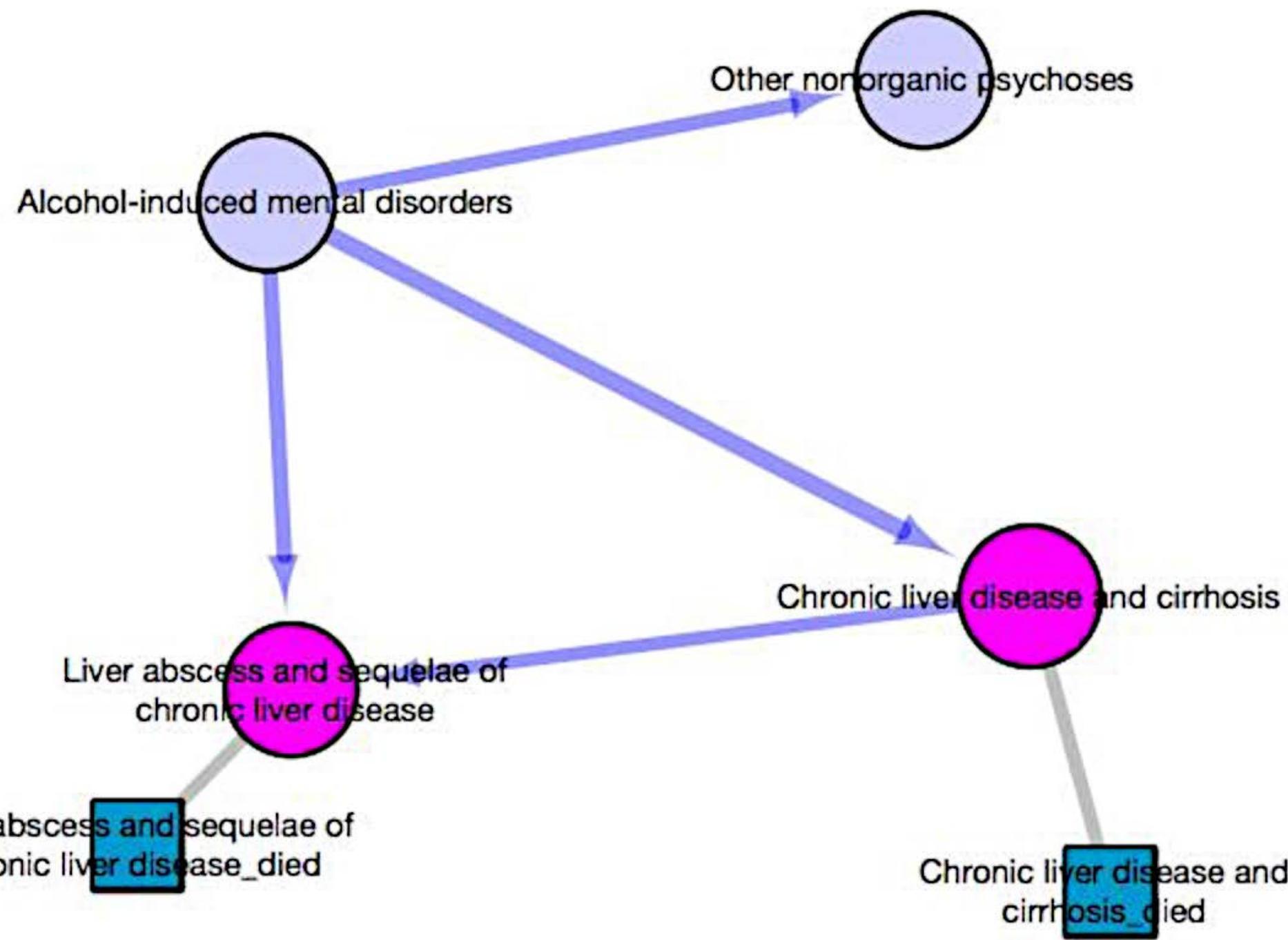
ABOUT THE TOOL

ABOUT THE DATA

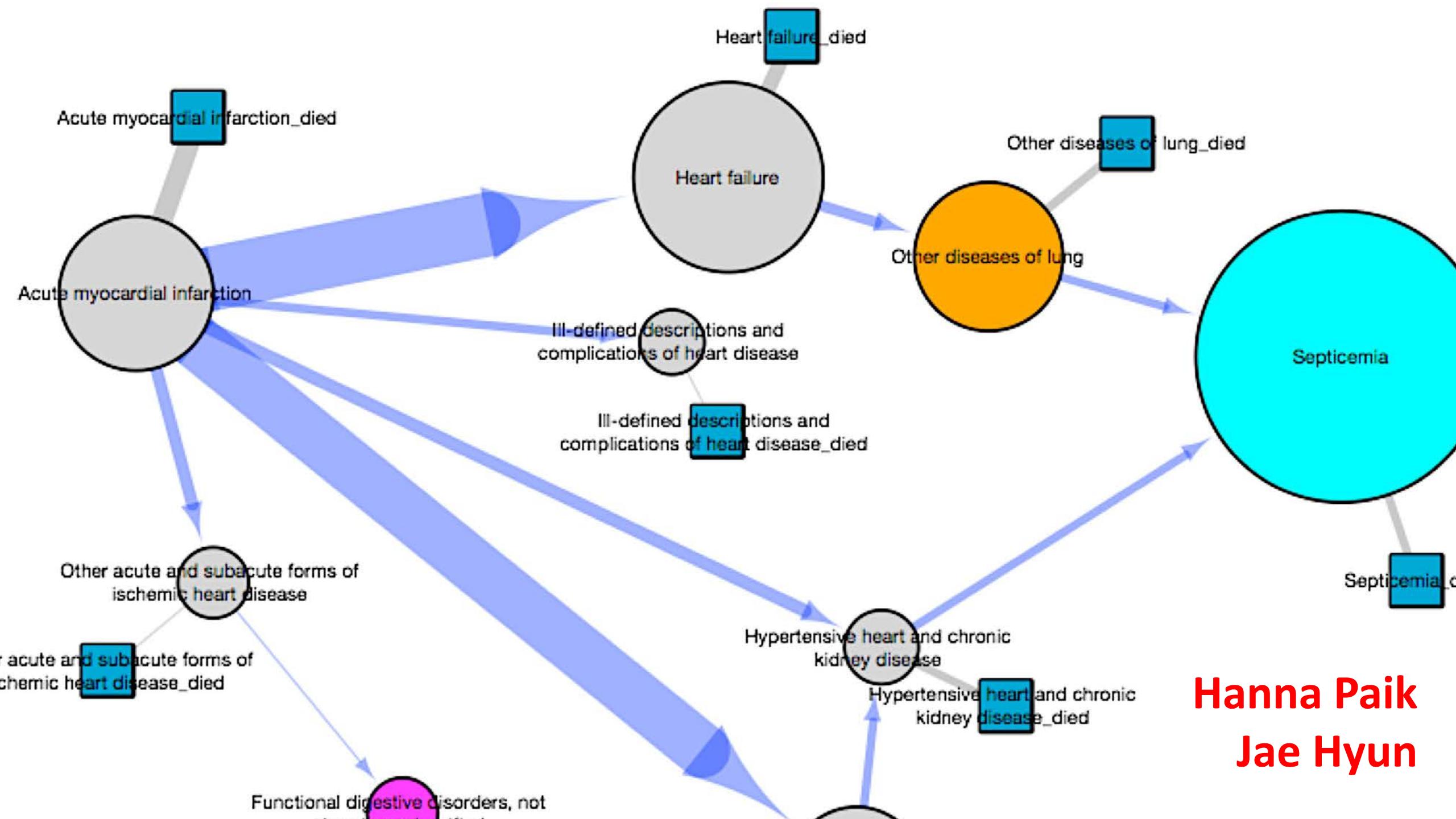
GET STARTED

Combining healthcare data from across the six University of California medical schools and systems





Hanna Paik
Jae Hyun





National Cancer Institute

The Cancer Genome Atlas



Understanding genomics
to improve cancer care



NIH HUMAN
MICROBIOME
PROJECT

CCLE Cancer Cell Line Encyclopedia

HOME BROWSE ANALYSIS TOOLS



fitbit

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News and Publications

Home > For the Scientific Community:Science > Projects > Connectivity Map > Connectivity Map

Connectivity Map



NIH LINCS
PROGRAM

HOME



UK
10K

LINC
of biology by
and other cell
exposed to a



National Cancer Institute



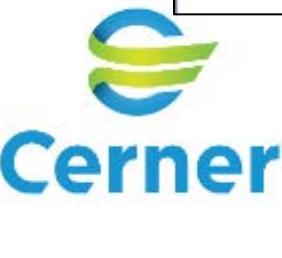
Surveillance Epidemiology and End Results

providing information on cancer statistics to help reduce the burden of these diseases on the U.S. population

Home About SEER Cancer Statistics Datasets & Software Publications

Connectivity Map's unique features is that it allows researchers to screen for drug disease signatures, rather than a pre-selected set of target genes. Drugs using sophisticated pattern-matching methods with a high level of resolution

Connectivity Map Project Website



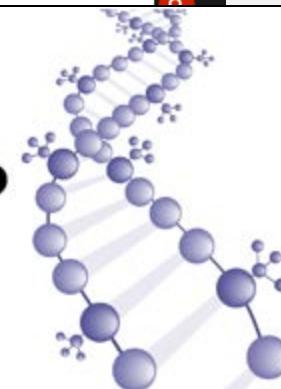
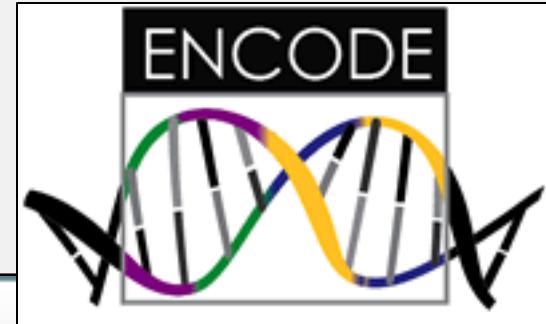
db GaP
GENOTYPE and PHENOTYPE



PharmGKB

GO

Advanced
search





Take home points:

- Plenty of high-quality data already available: some public, some private
- Don't wait for perfection; data always getting better
- Use and intersect data to ask new questions, to innovative new diagnostics and drugs
- Academia and industry are compatible: the science can and will continue in industry



NIH HUMAN
MICROBIOME
PROJECT



HOME ABOUT



LINC
of biology by
and other cell
exposed to a

dbGaP
GENOTYPE and PHENOTYPE



PharmGKB



Advanced
search

UC Clinical Data Warehouse Team

Executive Team

- Atul Butte
- Joe Bengfort
- Michael Pfeffer
- Tom Andriola
- Chris Longhurst

Steering Committee

- Irfan Chaudhry
- Mohammed Mahbouba
- Lisa Dahm
- David Dobbs
- Kent Andersen
- Ralph James
- Jennifer Holland
- Eugene Lee

ETL Team

- Albert Dugan

- Tony Choe
- Michael Sweeney
- Timothy Satterwhite
- Ayan Patel
- Niranjan Wagle
- Ralph James
- Joseph Dalton

Data Harmonization

- Dana Ludwig
- Daniella Meeker

Data Quality

- Momeena Ali
- Jodie Nygaard

Epic

- Kevin Ames
- Ben Jenkins
- Steve Gesualdo

Business Analyst

- Ankeeta Shukla

Hardware

- Sandeep Chandra
- Jeff Love
- Scott Bailey
- Kwong Law
- Pallav Saxena

Support

- Jack Stobo
- Michael Blum
- Sam Hawgood

Collaborators

- Jeff Wiser, Patrick Dunn, Mike Atassi / Northrop Grumman
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- Ken Weinberg / Pediatric Stem Cell Therapeutics
- Mark Musen, Nigam Shah / National Center for Biomedical Ontology
- Minnie Sarwal / Nephrology
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Support

- University of California, San Francisco
- NIH: NIAID, NLM, NIGMS, NCI, NHLBI, OD; NIDDK, NHGRI, NIA, NCATS
- March of Dimes
- Juvenile Diabetes Research Foundation
- Hewlett Packard
- Howard Hughes Medical Institute
- California Institute for Regenerative Medicine
- Luke Evnin and Deann Wright (Scleroderma Research Foundation)
- Clayville Research Fund
- PhRMA Foundation
- Stanford Cancer Center, Bio-X, SPARK

- Tarangini Deshpande
- Kimayani Butte
- Sam Hawgood
- Keith Yamamoto
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