ΕΛΛΗΝΙΚΗ ΦΑΡΜΑΚΕΥΤΙΚΗ ΕΤΑΙΡΕΙΑ

ΗΛΕΚΤΡΟΝΙΚΑ «ΕΡΓΑΛΕΙΑ» ΕΓΚΡΙΤΗΣ ΑΝΑΛΥΣΗΣ ΤΗΣ ΒΙΒΛΙΟΓΡΑΦΙΑΣ

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- fundamental shift of biomedical research domain towards integrative and translational methodologies
- needs related to the collection, management, integration, analysis and dissemination of large-scale, heterogeneous biomedical data sets.
- well-established and broadly adopted theoretical and practical frameworks intended to address such needs are still largely developmental

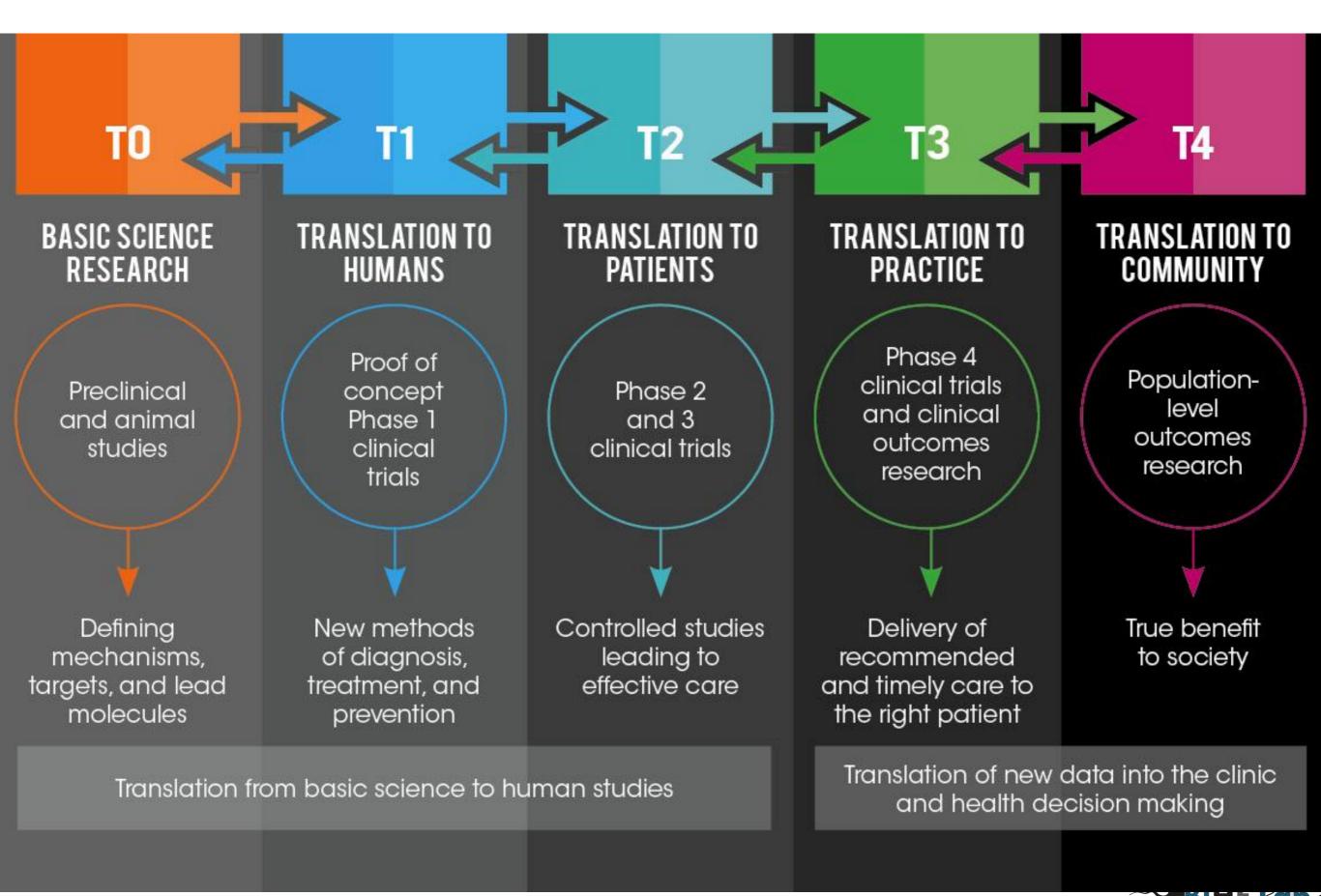


Challenges

- the management of multi-dimensional and heterogeneous data sets
- the size and complexity of data sets that must be managed and analyzed are growing at an extremely rapid rate
- the data management practices currently used in most research settings are both labor intensive and rely upon technologies that have not be designed to handle such multidimensional data
- the translational science community demands the creation and delivery of information management platforms capable of adapting to and supporting heterogeneous workflows and data sources

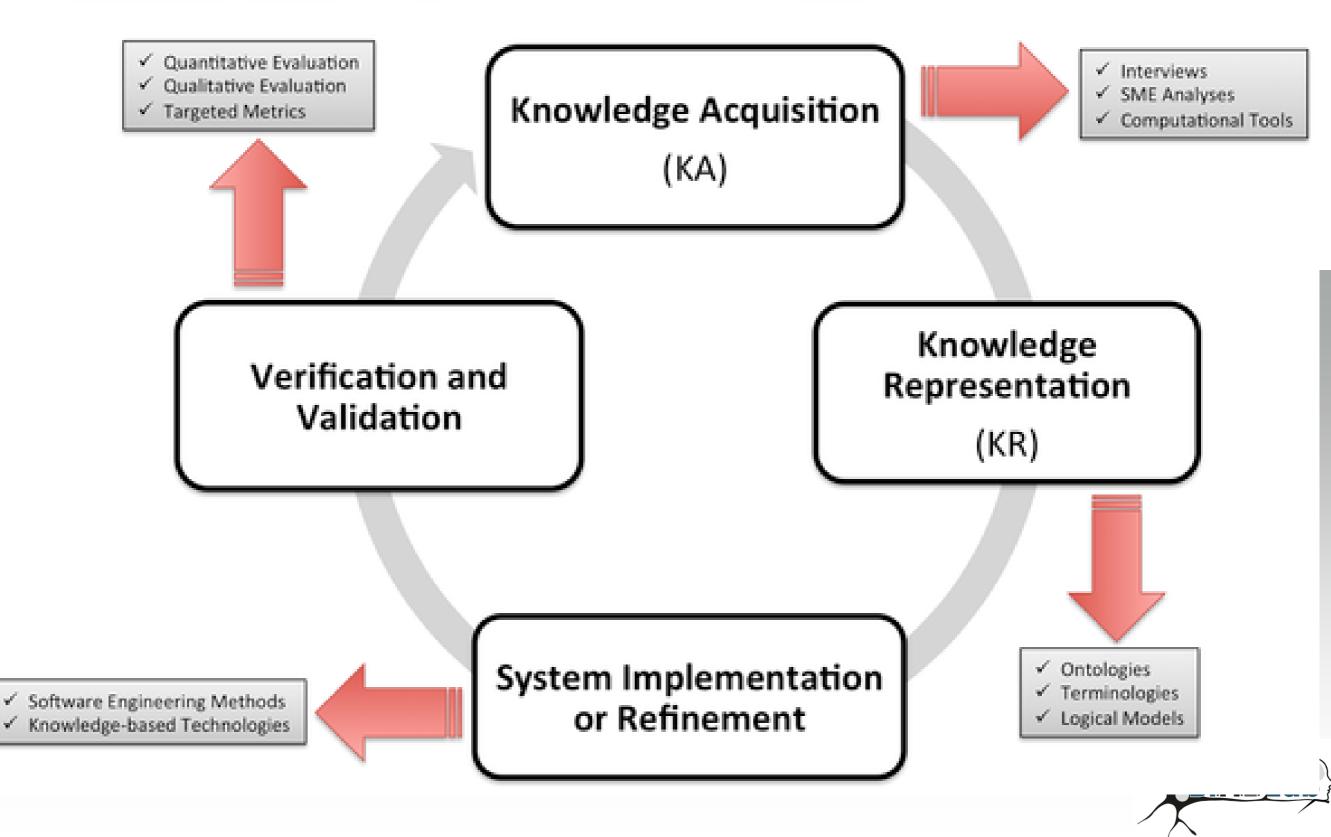
The rise of precision medicine and the availability of high-throughput molecular analyses in the context of clinical care have increased the need for adequate tools for translational researchers to manage and explore these data



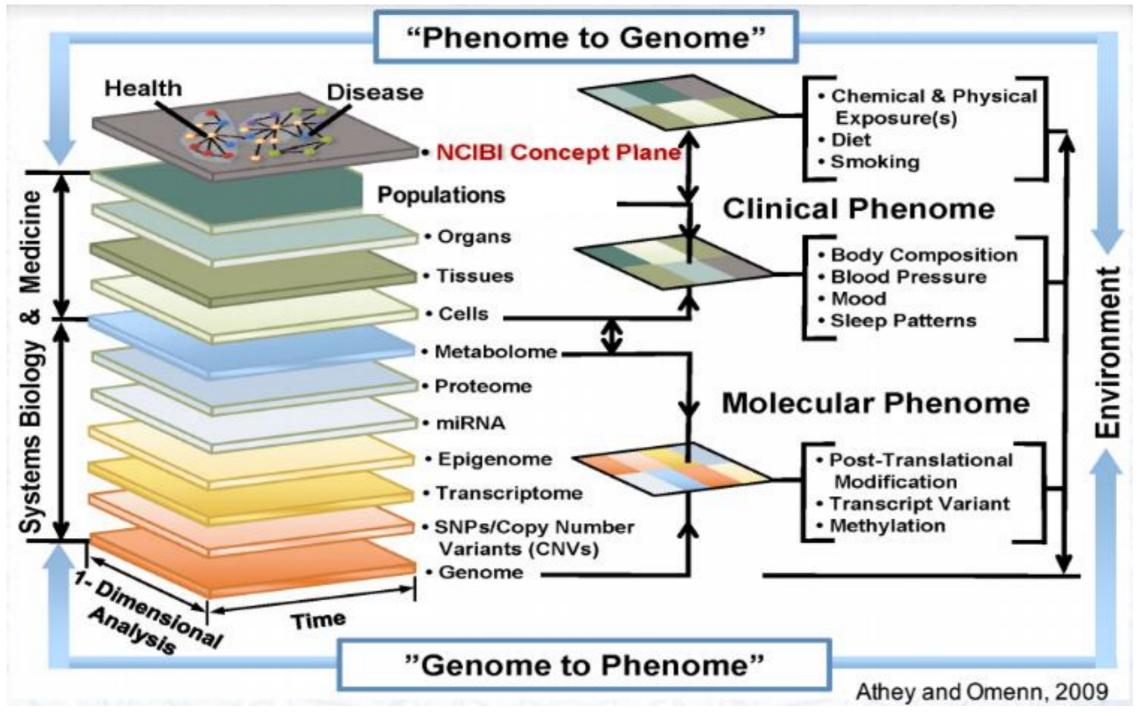


RBIHE LOD

Key Definitions



Translational Research Data is Big Data



Volume, Variety, Velocity





informatics methods

that connect molecular entities to clinical entities

translational research platforms

able to integrate large data sets of clinical information with omics data



Translational research platforms: Overview

should provide

(i) the storage and integration of clinical and omics data;

(ii) an analysis framework, enabling scientists to explore

their data and generate hypotheses; and

(iii) additional information cross-referenced from external

databases



Translational research platforms: Overview

- BRISK: Biology-Related Information Storage Kit (2011)
- iDASH: Integrating data for analysis, anonymization and sharing (201'
- tranSMART (2010)

Cancer

- **+** G-DOC Georgetown Database of Cancer (2012)
- cBio Cancer Genomics Portal (2012)
- iCOD: Integrated Clinical Omics Database (2010)
- caTRIP (2006)



Translational research platforms: Overview

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Γινακας τ									
Platform	tranSMART	cBioPortal	BRISK	iDASH	iCOD	G-DOC	caTRIP		
Community									
Institution/pr oject initiators	Johnson & Johnson, USA	Memorial Sloan- Kettering Cancer Center, NY,	University of British Columbia, Canada	iDASH team, USA	Tokyo Medical Dental University, Japan	Georgetown University, DC, USA	Institution/pro ject initiators		
Funding	Initially Johnson & Johnson funded—now public-private consortia	NIH and industry grants	Public and private consortium	NIH	Public	HSS	NIH		
Software		Free for academic use,	Open	Open	Not	Not	Not		
availability	Open source	commercial	source	SOUICE Canuel,	distributed V., et al, Briefings	distributed in Bioinformatics,	distributed 2014;16:280–290		

Platform	tranSMART	cBioPortal	BRISK	iDASH	iCOD	G-DOC	caTRIP
Clinical data							
Demographics	Yes	Yes	Yes	Yes	Yes	Yes	Yes
Outcomes	Yes	Yes	No	Yes	Yes	Yes	Yes
Biological results	Yes	Yes	Yes	Yes	Yes	Yes	Yes
Images	No	No	No	Yes	Yes	No	Unknown
Structured clinical	Yes	Yes	Yes	Yes	Yes	Yes	Yes
research data		100	100	100	100	100	100
'omics' data							
mRNA expression	Yes	Yes	No	Yes	Yes	Yes	Unknown
miRNA expression	No	Yes	No	Yes	No	Yes	Unknown
SNPs	Yes	Yes	Yes	Yes	No	Yes	Unknown
Copy number variations	Yes	Yes	Yes	Unknown	No	Yes	Unknown
DNA methylation	No	Yes	Yes	Unknown	No	Yes	Unknown

Platform	tranSMA RT	cBioPortal	BRISK	iDASH	iCOD	G-DOC	caTRIP
Clinical data							
Demographics	Yes	Yes	Yes	Yes	Yes	Yes	Yes
Outcomes	Yes	Yes	No	Yes	Yes	Yes	Yes
Biological results	Yes	Yes	Yes	Yes	Yes	Yes	Yes
Images	No	No	No	Yes	Yes	Νο	Unknown
Structured clinical research data	Yes	Yes	Yes	Yes	Yes	Yes	Yes
'omics' data							
mRNA expression	Yes	Yes	No	Yes	Yes	Yes	Unknown
miRNA expression	Νο	Yes	No	Yes	No	Yes	Unknown
SNPs	Yes	Yes	Yes	Yes	No	Yes	Unknown
Copy number variations	Yes	Yes	Yes	Unknown	No	Yes	Unknown

Desiderata for translational research platforms

Privacy

Interoperability and standards

Heterogeneity of granularity of the data models

Deployment and maintenance



The ultimate goal of translational medicine is enabling

personalized care. Nowadays efforts are made to

populate translational research platforms with patient

data to fuel discovery. Allowing real-time data-driven

decision algorithms to leverage translation research

results in the context of clinical care should be a short-

term objective.



caTRIP – 2006 Cancer Translational Research Informatics Platform

Description

Translational research system for the caBIG project (cancer Biomedical Informatics Grid[™]), initiated by the U.S. National Cancer Institute.

Goal

data-integration project with a goal to develop an open-source information network across the United States for secure data exchange on cancer research.

Aims

to create a platform that allows physicians to find patients with similar characteristics, analyze their clinical outcomes and find information about treatments that were administered with success across the caBIG data network.



Oncologists could access a rich live data network that could provide strong statistically significant facts in mere minutes.

This could benefit clinicians to query data from a cohort of preexisting patients to help guide treatment of another patient, rather than relying on single cancer centers or limited facts published in the literature.

caBIG project was cancelled in 2011, few cancer centers were using caBIG's clinical data management tools or its cloud computing infrastructure.

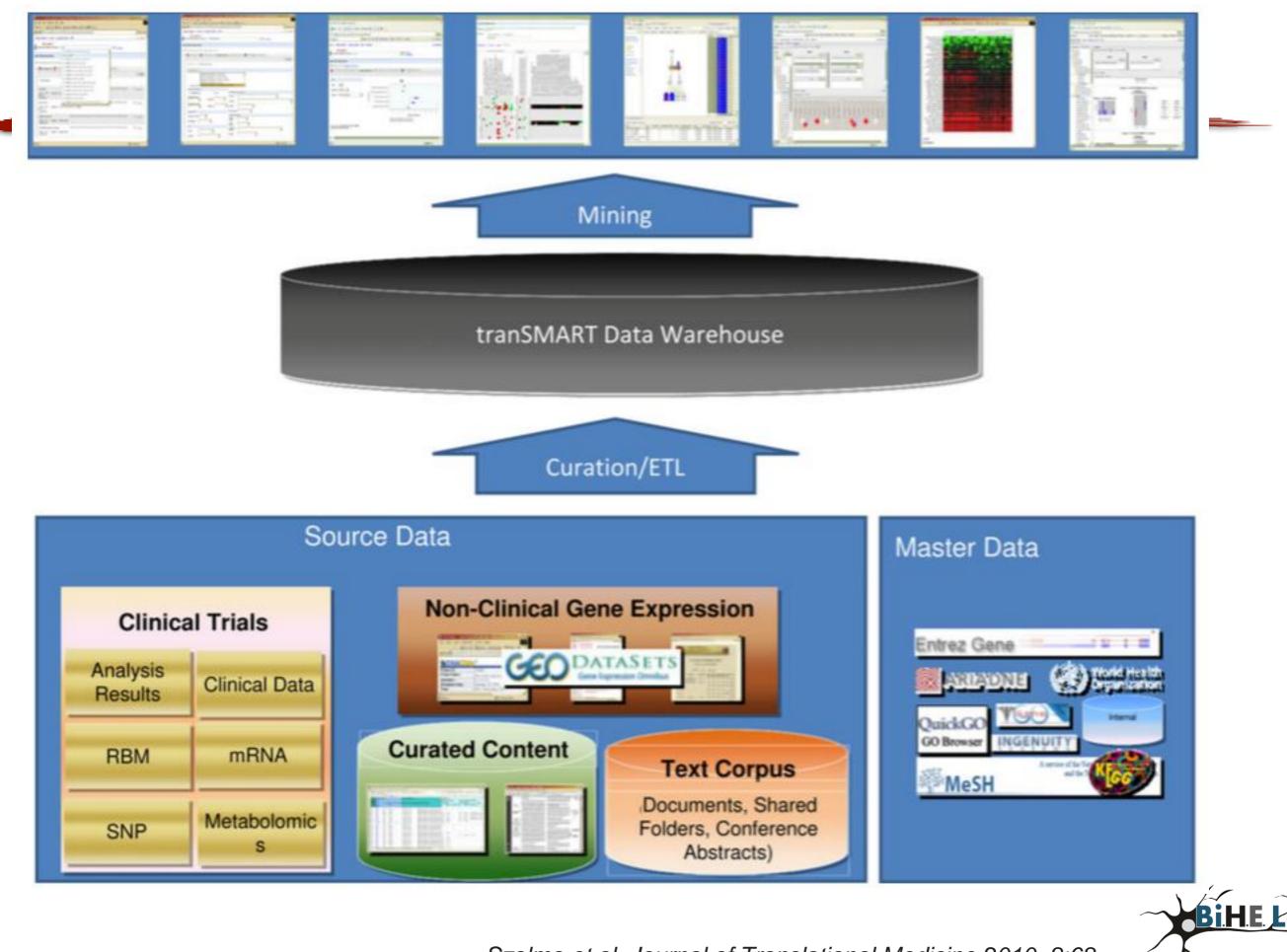
Also caBIG applications cost millions of dollars to build.

The majority of the life sciences research tools developed for caBIG have had **limited** use or impact, according to the report.



tranSMART (2010) - Foundation members





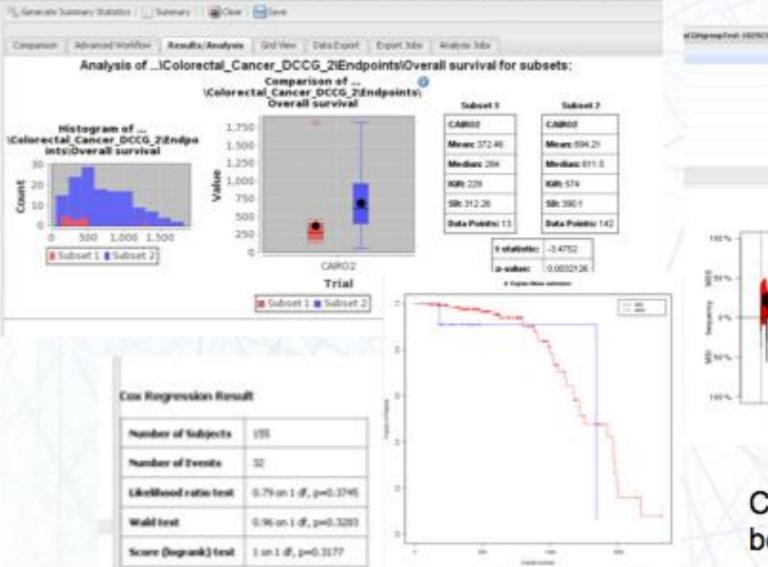
Szalma et al. Journal of Translational Medicine 2010, 8:68

Cohort comparison

- Analysis goals
 - Compare survival and chromosomal abnormalities across disease subtypes
- Available data
 - Clinical data: E.g. staging, age, gender, treatment arm
 - Non-omics data: MSI/MSS (microsatellite instability), mutation data
 - Genomics: Comparative genomic hybridization (arrayCGH)
- Methods
 - Histograms, boxplots, t-test, Kaplan-Meier plot, Cox regression, arrayCGH group test



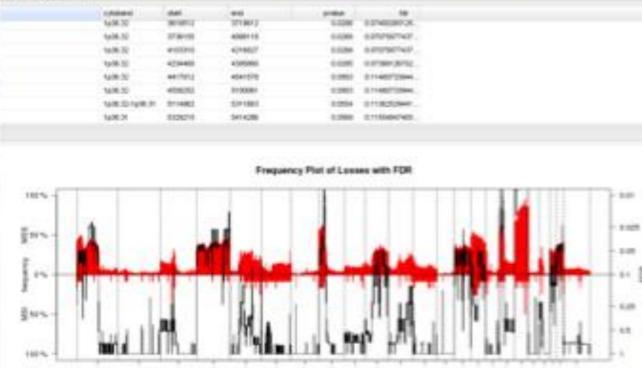
Results: Comparison of cohorts



Comparison of overall survival in subjects with MSI vs MSS



Contributed by Gerrit Meijer, Dutch Translational Research IT (CTMM-TraIT)



Comparison of chromosomal alterations between cohorts

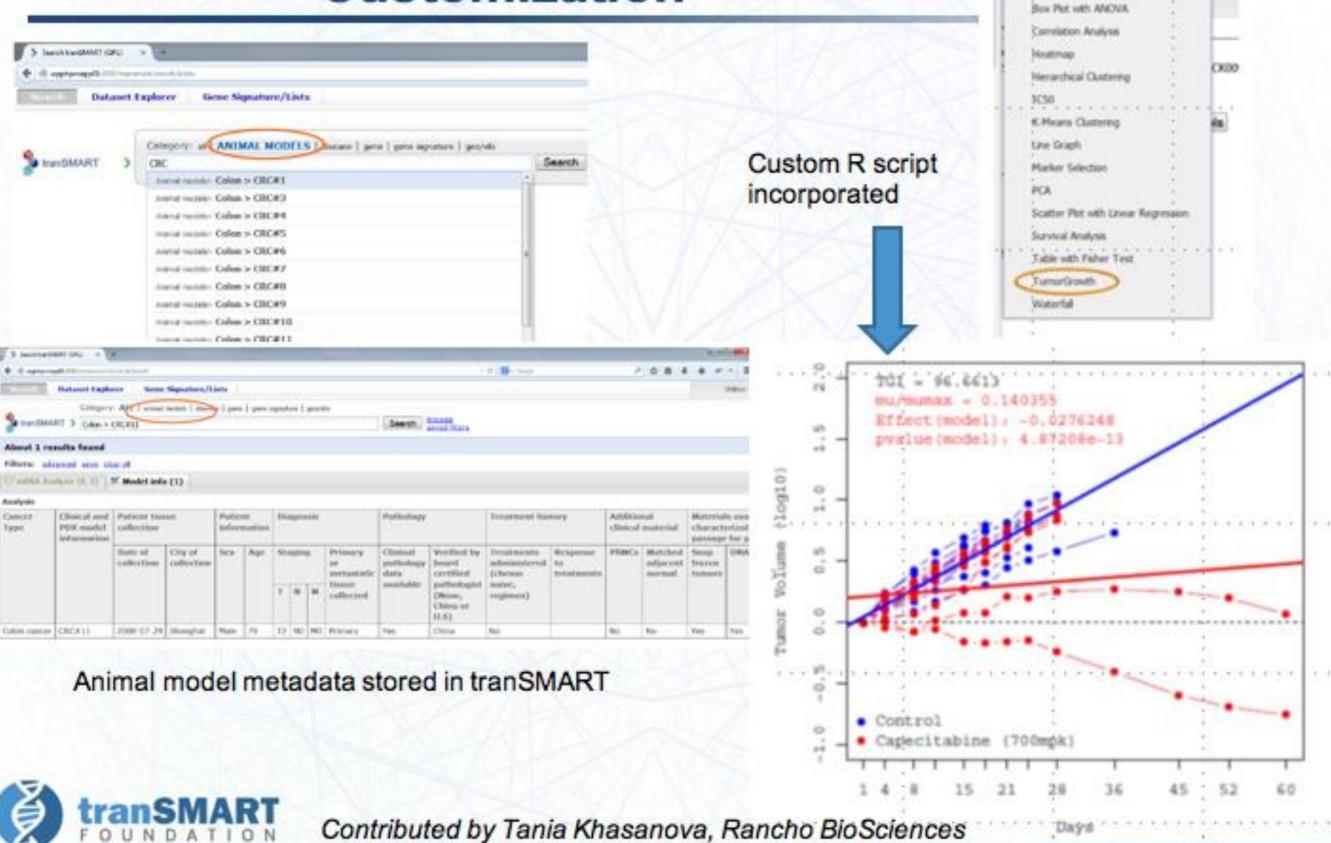
Collaboration, Analysis, Customization

- Goals
 - Create central data storage for a preclinical oncology group at a large pharmaceutical company
 - Incorporate a custom R script that processes tumor volume and weight data
- Available data
 - In vivo studies using animal model
 - animal model metadata



Results: Collaboration, Analysis, Customization

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Comparison Advanced Workflow

Read

Patient Stratification

Analysis goals

- Association between demographic characteristics and Bortezomib response?
- Association between disease subtype and drug response?
- Any gene expression data predictive of drug response?

Available data

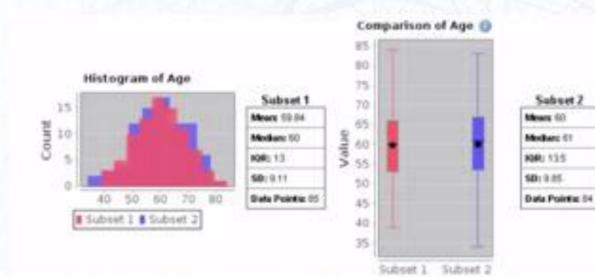
- Clinical study results from Bortezomib multiple myeloma study
 - Treated, untreated, responder, nonresponder patients
 - Demographic information
 - Disease subtype
 - Gene expression data

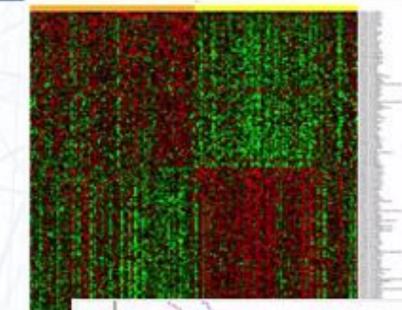
Methods

- Chi-squared
- K-means clustering
- Kaplan-Meier analysis



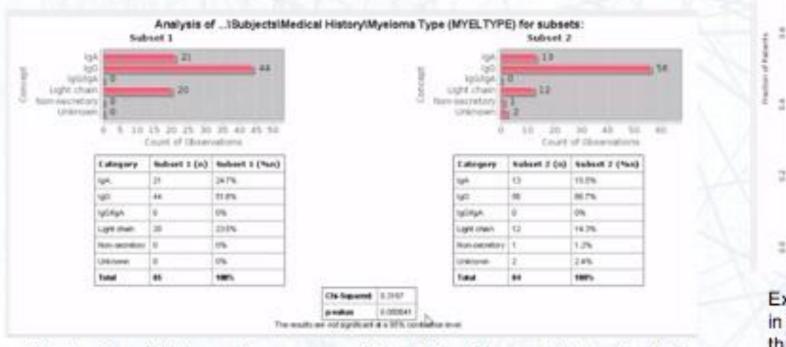
Results: Patient Stratification





Differing gene expression pattern between responders and non-responders

Age distribution of responders and non-responders is similar



Expression of NDUFB1 correlates with OS in intermediate time frames, but not through end of study

No significant difference in response rate for different types of disease tested

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Contributed by Kristen Sweet, Thomson Reuters

tranSMART Foundation Datathon 1.0 (2015) : The cross neurodegenerative diseases challenge

Specific objectives were to identify:

- Common biomarker changes across Parkinson and Alzheimer disease
- Common pathway changes across Parkinson and Alzheimer disease
- The normal distribution of imaging and fluid biomarkers across controls
- Novel hypotheses, research findings or conclusions about these neurodegenerative diseases.



A datathon is an intense 3-day workshop that challenges

researchers to turn data and information into knowledge.

• The datathon format is modeled after hackathons, which are focused on software development. Datathons use research questions and datasets to advance knowledge,

not to develop applications.

At a datathon, participants work in teams to frame research questions, create and implement a research design, mobilize data resources and present their findings in



Open Big Data: Preparing for the Datathon

Alzheimer's Disease Neuroimaging Initiative (ADNI)

Parkinson's Progression Markers Initiative (PPMI)

The Cancer Genome Atlas (TCGA)



Open Big Data: ADNI

The Alzheimer's Disease Neuroimaging Initiative

(ADNI) unites researchers with study data as they work to define the progression of Alzheimer's disease. ADNI researchers collect, validate and utilize data . . . Data. . . including Alzheimer's disease patients, mild cognitive impairment

subjects and elderly controls, are available from



this site.

Open Big Data: PPMI

Since 2002, the Michael J. Fox Foundation has been an

essential driver of PD biomarker development efforts,

funding nearly \$90 million in biomarker research... MJFF

has enabled researchers to identify several promising

biomarker candidates. . . MJFF has invested \$60 million to

develop a solution that would accelerate verification of PD

biomarkers. PPMI is the resulting "collaboration" between

researchers, industry, government and study participants.



The Cancer Genome Atlas (TCGA), a collaboration between the National Cancer Institute (NCI) and National Human Genome Research Institute (NHGRI), aims to generate comprehensive, multi-dimensional maps of the key genomic changes . . . initiated in 2006 . . . showed that a national network of research and technology teams . . . could pool the results of their efforts . . . that the data freely available would making enable

researchers make important discoveries.



Open Big Data: The Reality

Alzheimer's Disease Neuroimaging Initiative (ADNI) Data Use Agreement

I will not further disclose these data beyond the uses outlined in this agreement and my data use application and understand that redistribution of data in any manner is Prohibited.

Parkinson's Progression Markers Initiative (PPMI) Data Use Agreement

I will not further disclose these data beyond the uses outlined in this agreement and my data use application.

I will do my best to ensure that Investigators who utilize PPMI data use appropriate administrative, physical and technical safeguards *to prevent use or disclosure of the data* other than as provided for by this Agreement and will promptly report any use or disclosure of data that does not comply with the guidelines established by this Agreement.

The Cancer Genome Atlas (TCGA) Data Use Agreement

The Requester and Approved Users agree to retain control over the data and further **agree not to distribute data** obtained through this Data Access Request to any entity or individual not covered in the submitted Data Access.



Very interesting preliminary findings

- 4 SNP's that predict Parkinson's progression BETTER than Age
- 3 Biomarkers that cross Alzheimers and Parkinsons
- Sets of biomarkers that predict disease stage

Barash CI, et al 2015;6:42-4.• More "Open" Neurodegenerative Disease Data

- tranSMART Foundation, MJFF and LONI are working together to enable the distribution and access of ADNI, PPMI, LRRK2 and BioFIND datasets in

tranSMART.



Key Outcomes:

- Bringing data scientists, neuroscientists and biostatisticians together to leverage an integrated cross-neurodegenerative disease dataset in tranSMART validated the utility for the platform, and the value of these data when integrated.
- The Datathon produced an innovative approach using machine learning, new biomarker findings, and scientifically thorough pathway analyses.
- It successfully demonstrated that data sharing and the Datathon approach in particular can expedite discovery, as well as offer new fruitful ways to explore datasets. These new approaches are available for the research community to adopt.

BiHE

Key Outcomes:

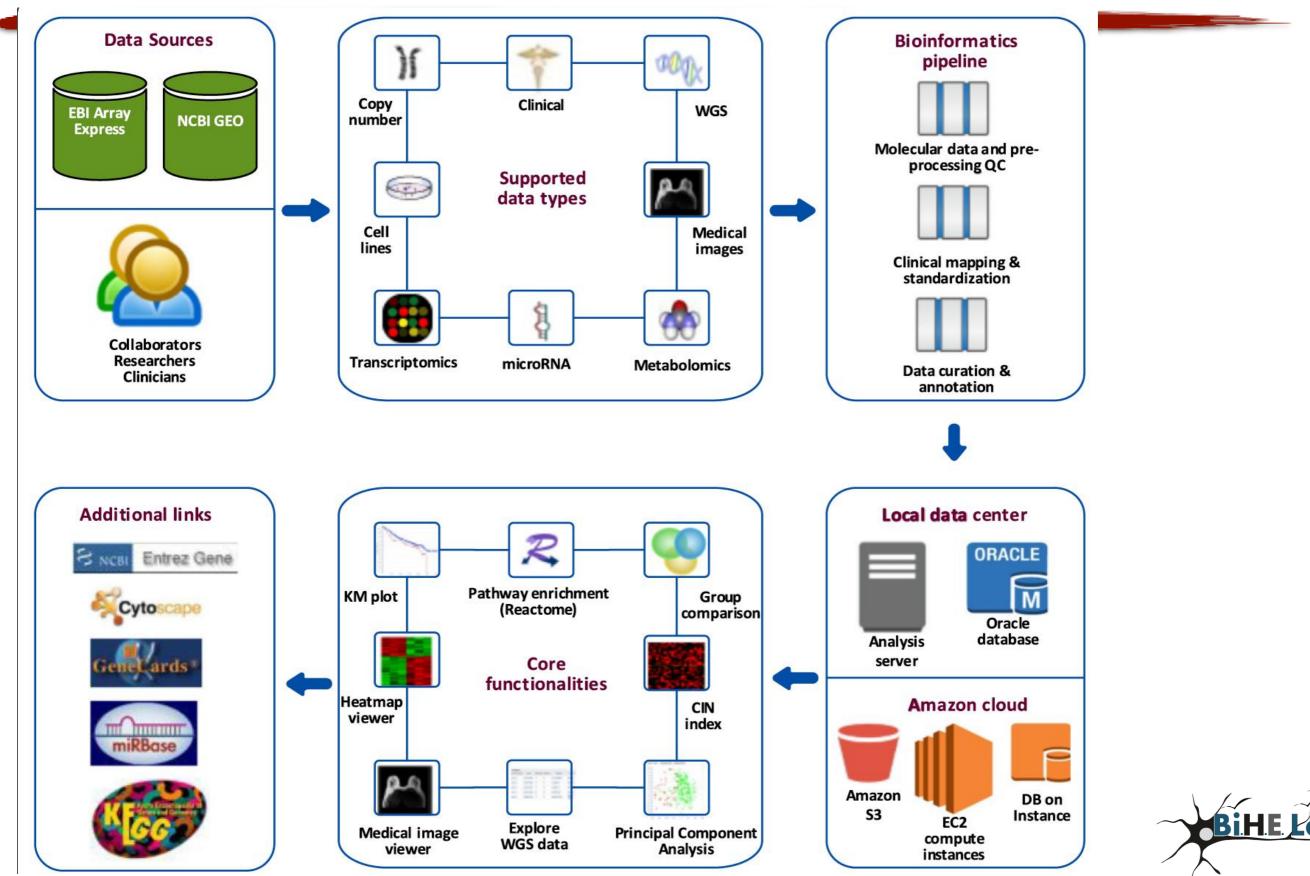
- The tranSMART Platform can support many different large and distributed datasets as well as meet varied end-user needs simultaneously.
- The platform's ability to organize these datasets in useful fashions enabled participants to generate new findings and approaches for future research.
- The Platform proved to be a powerful tool in expediting research in a cost efficient way.
- The value of bringing together experts from different disciplines and organizations to work in newly formed teams on integrated datasets deployed in the tranSMART platform was evident.
- The Datathon also provided excellent technical and scientific feedback on how to improve the tranSMART platform for use by the research community in real scientific projects.

G- Doc Plus uses advanced computational tools to handle a variety of biomedical BIG DATA. It has 3 entry points for the user based on their interest.

- **1. Precision Medicine workflow**
- 2. Translation Research workflow
- **3. Population Genetics workflow**



Summary of G-DOC Plus data management and analysis features



Publications using G-DOC

Madhavan S, Gusev Y, Natarajan T, Song L, Bhuvaneshwar K, Gauba R, Pandey A, Haddad B, Goerlitz D, Cheema A, Juhl H, Kallakury B, Marshall J, Byers S, Weiner L. Genome-wide multi-omics profiling of colorectal cancer identifies immune determinants strongly associated with relapse. *Frontiers in Genetics*. Nov, 2013. PubMed

Madhavan S, Gauba R, Song L, Bhuvaneshwar K, Gusev Y, Byers S, Juhl H, Weiner L. Platform for Personalized Oncology: Integrative analyses reveal novel molecular signatures associated with colorectal cancer relapse. *AMIA Summits Transl Sci Proc.* 2013 Mar 18; 2013:118. PubMed

Madhavan S. The Development of Informatics Platforms to Help Drive Systems Medicine. **Genome-wide multi-omics profiling of** colorectal cancer identifies immune determinants strongly associated with relapse. *Handbook of Personalized Medicine: Advances in Nanotechnology, Drug Delivery and Therapy.* Pan Stanford Publishing (2013).

Gusev Y, Riggins RB, Bhuvaneshwar K, Gauba R, Sheahan L, Clarke R, and Madhavan S. In silico discovery of mitosis regulation networks associated with early distant metastases in estrogen receptor positive breast cancers. *Cancer Informatics* 2013:12 31-51 PubMed

Madhavan S, Gusev Y, Harris MA, Tanenbaum DM, Gauba R, Bhuvaneshwar K, Shinohara A, Rosso K, Carabet LA, Song L, Riggins RB, Dakshanamurthy S, Wang Y, Byers SW, Clarke R, and Weiner LM. **G-CODE: enabling systems medicine through innovative informatics.** *Genome Biology*, 12 (Suppl 1):P38, September 2011. http://www.ncbi.nlm.nih.gov/pmc/articles/PMC3439034/

Elgamal, OA, Park, J, Gusev Y, Azevedo-Pouly AC, Jiang J, Roopra A and Schmittgen TD. Tumor Suppressive Function of mir-205 in Breast Cancer Is Linked to HMGB3 Regulation, PLoS O ne, 2013 Oct 2;8(10):e76402 PubMed

- is to extend translational bioinformatics platforms to stay current with emerging omics technologies and analysis methods to continue supporting novel hypothesis generation, analysis and validation for integrative biomedical research.
- integrating several aspects of the disease and exposing various data elements, such as outpatient lab workup, pathology, radiology, current treatments, molecular signatures and expected outcomes over a web interface, these platforms will continue to strengthen precision medicine research.



- Using former or existing platforms' best practices
- Designing architectures that can survive in time
- Evaluating low cost solutions
- Learning from huge existing databases in other fields of science
- Thinking about metadata
- Believing in future high performance computing



BiHELab – Ελληνική Φαρμακευτική Εταιρεία

HelpDesk for existing translational platforms :

- PhD Candidate : Αντιγόνη Αβραμούλη
- PhD Candidate : Σωτήρης Φωτίου



Focusing on one platform risks missing an obvious signal!!!

