Predictive, Personalized, Preventive and Participatory approach to Medicine: “ P4” Leroy Hood

Precision Medicine: Personalized, Problematic,and Promising

J. Larry Jameson, M.D., Ph.D., and Dan L. Longo, M.D.

NEJM 4 June 2015

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IMPRECISION MEDICINE

For every person they do help (blue), the ten highest-grossing drugs in the United States fail to improve the conditions of between 3 and 24 people (red).

1. ABILIFY (aripiprazole)
Schizophrenia

2. NEXIUM (esomeprazole)
Heartburn

3. HUMIRA (adalimumab)
Arthritis

4. CRESTOR (rosuvastatin)
High cholesterol

5. CYMBALTA (duloxetine)
Depression

6. ENBREL (etanercept)
Psoriasis

7. ADVAIR DISKUS (fluticasone propionate)
Asthma

8. REMICADE (infliximab)
Crohn's disease

9. COPAXONE (glatiramer acetate)
Multiple sclerosis

10. NEULASTA (pegfilgrastim)
Neutropenia

Based on published number needed to treat (NNT) figures. For a full list of references, see Supplementary Information at go.nature.com/4dr78f.

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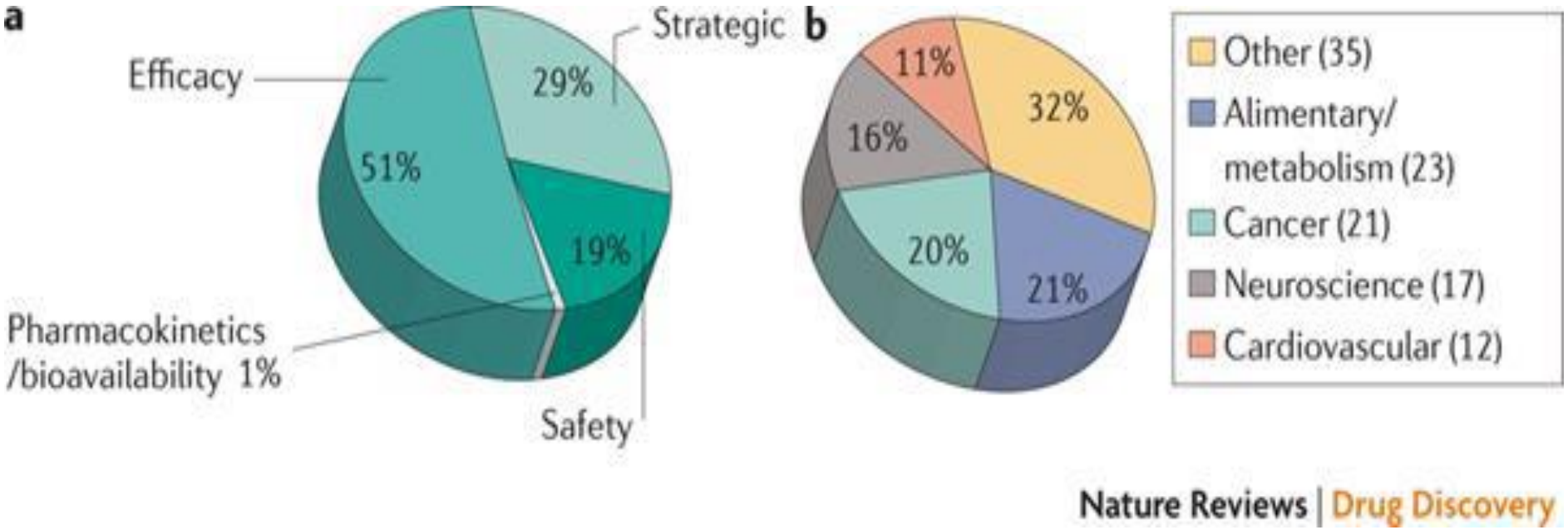
Increasing failures in drug development
Success rates of clinical proof-of-concept have dropped from 28% to 18%
Insufficient efficacy as the most frequent reason

Reason for failure **Therapeutic area**



Source: John Arrowsmith: Nature Reviews Drug Discovery 2011 **Increasing failures in drug development : Analysis of 108 failures in phase II**

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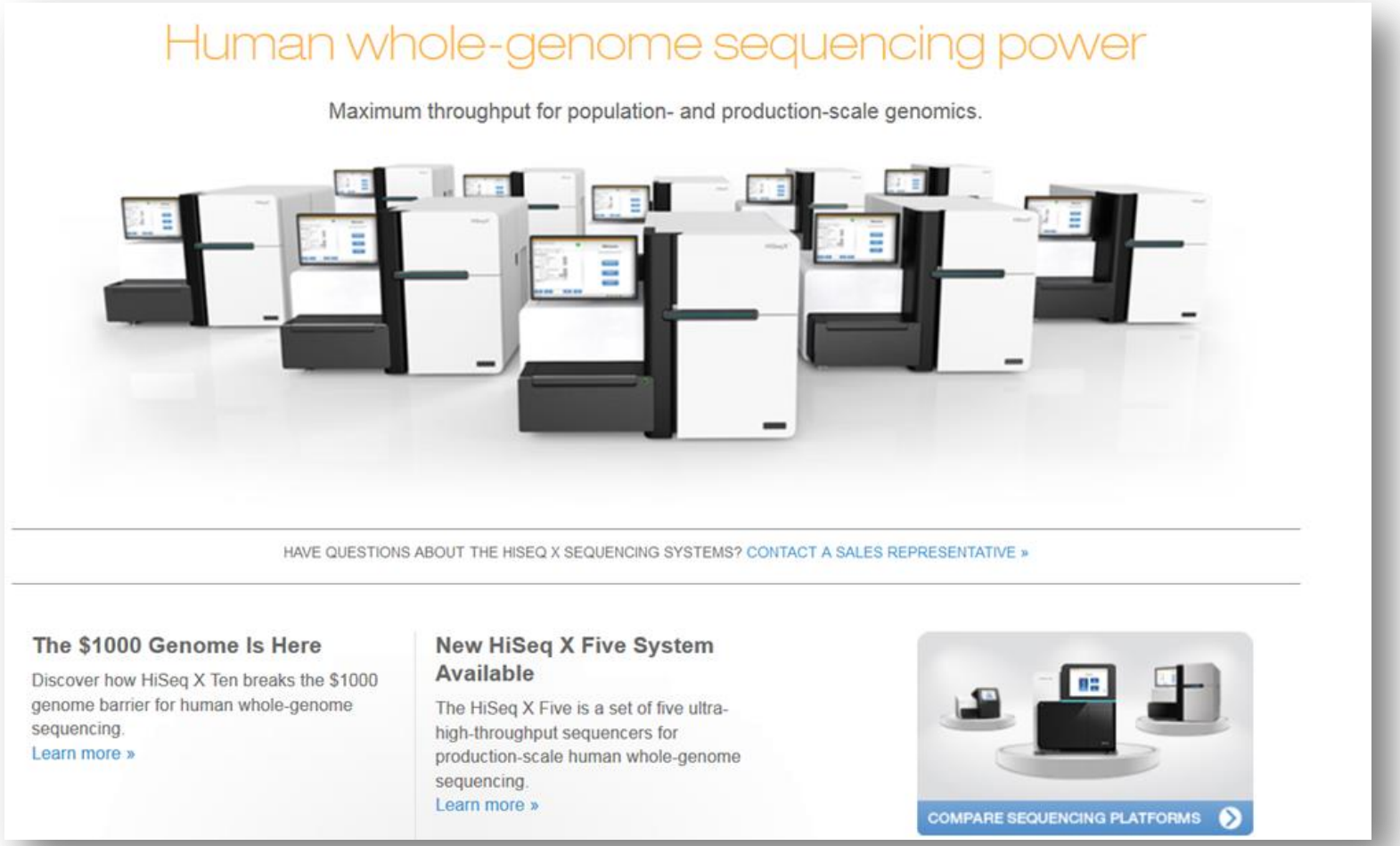
Technology is transforming biomedical science



Example: During 2014 the sequencing company Illumina announced the so called *1000 dollar genome*.

Technical and scientific advances are currently transforming biomedical research, turning an important part of the field into a new modelling and computational science.

High throughput life science data are today affordable and drives important parts of biomedical research. The exploitation of big data is starting to make direct impact in clinical practice.

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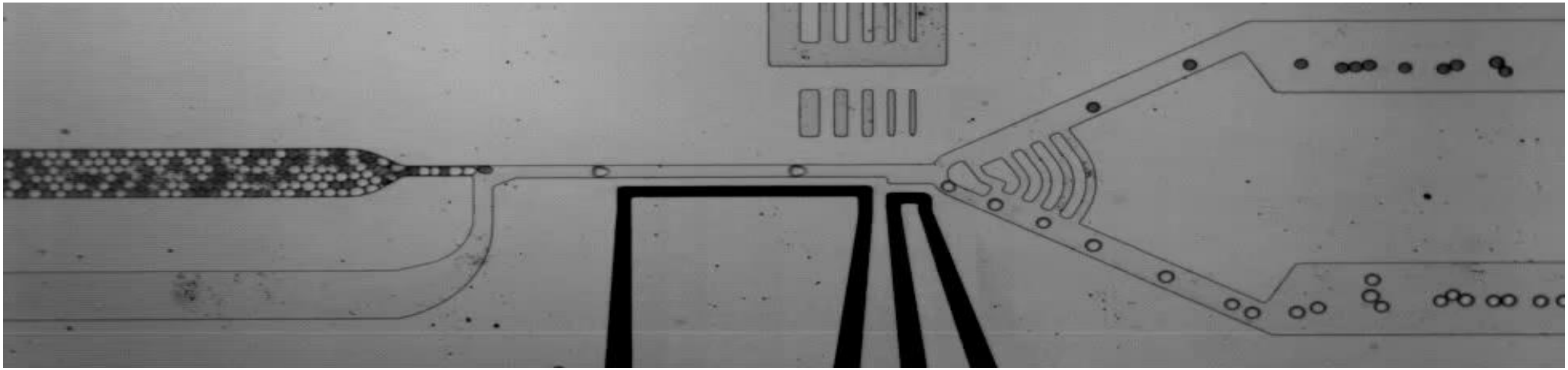
MICROFLUIDIC TECHNOLOGIES TO IDENTIFY PATIENT'S PATHOGENIC ANTIBODIES

Isolate Ab-producing B cells at high-throughput from patients

One cell every 3 droplets



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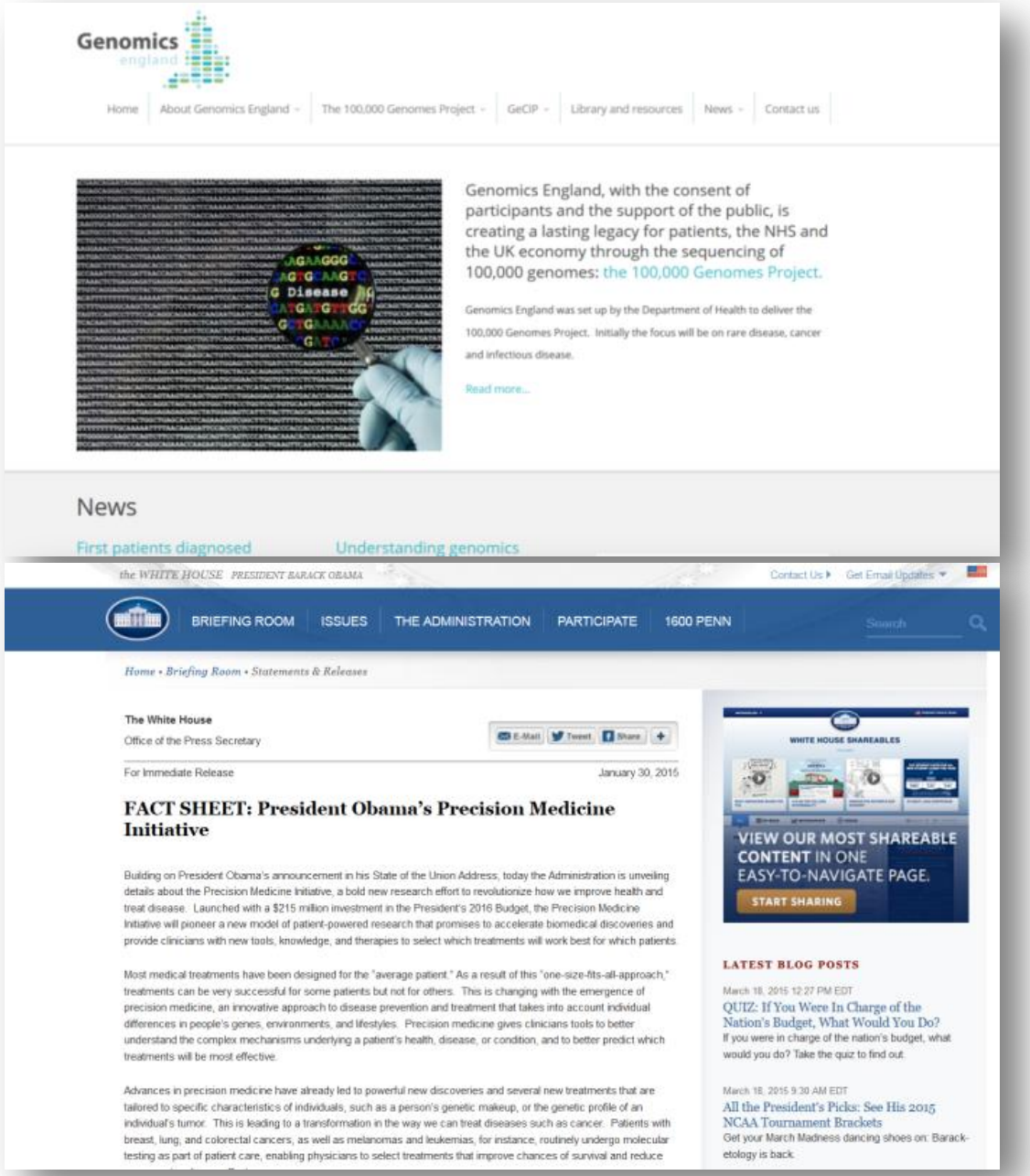
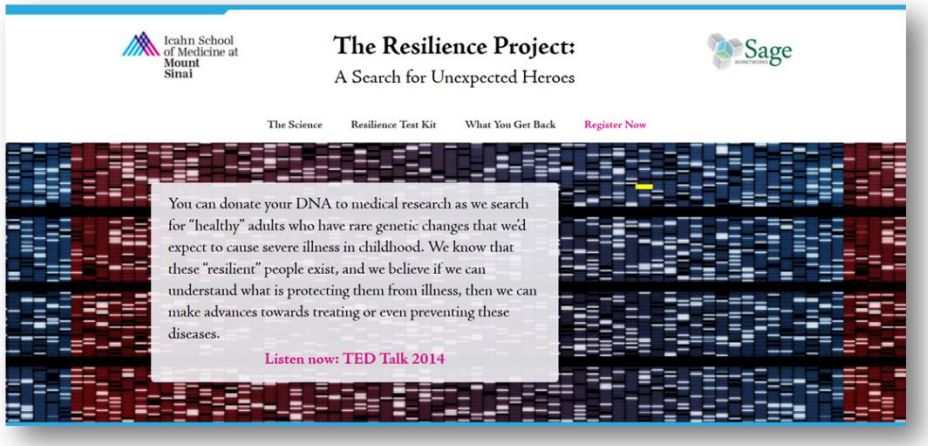
Developing precision medicine. Creating Global Health

Huge efforts to establish national and international baselines, outlining the global biological variation in populations are ongoing or are being initiated. These studies will provide bases for further developments of personalized/precision medicine. Examples include e.g. *Genomics England* and the *Precision Medicine Initiative in the US* as well as targeted projects like *The Resilience project*.





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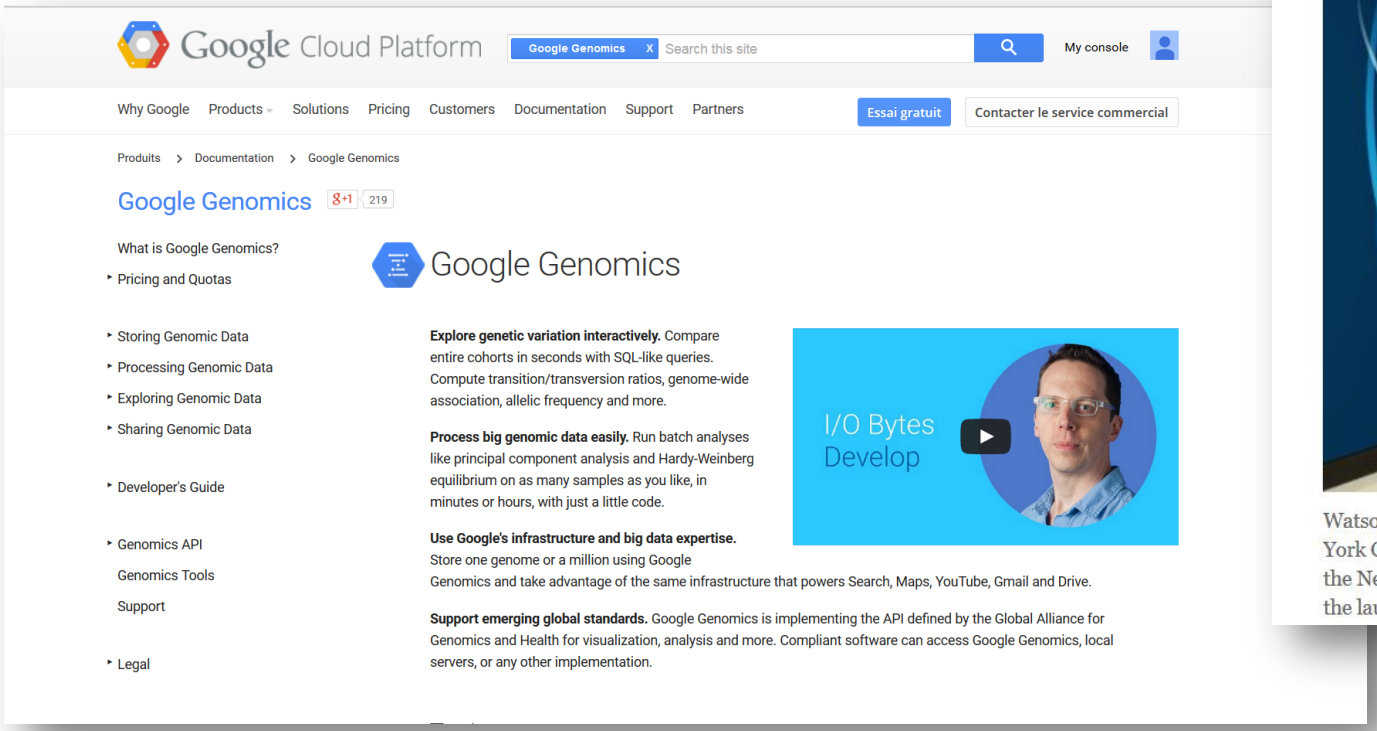
Global companies like Google, IBM, Amazon and Microsoft are currently positioning themselves to provide services around storage, management and analyses of the new big life science data.



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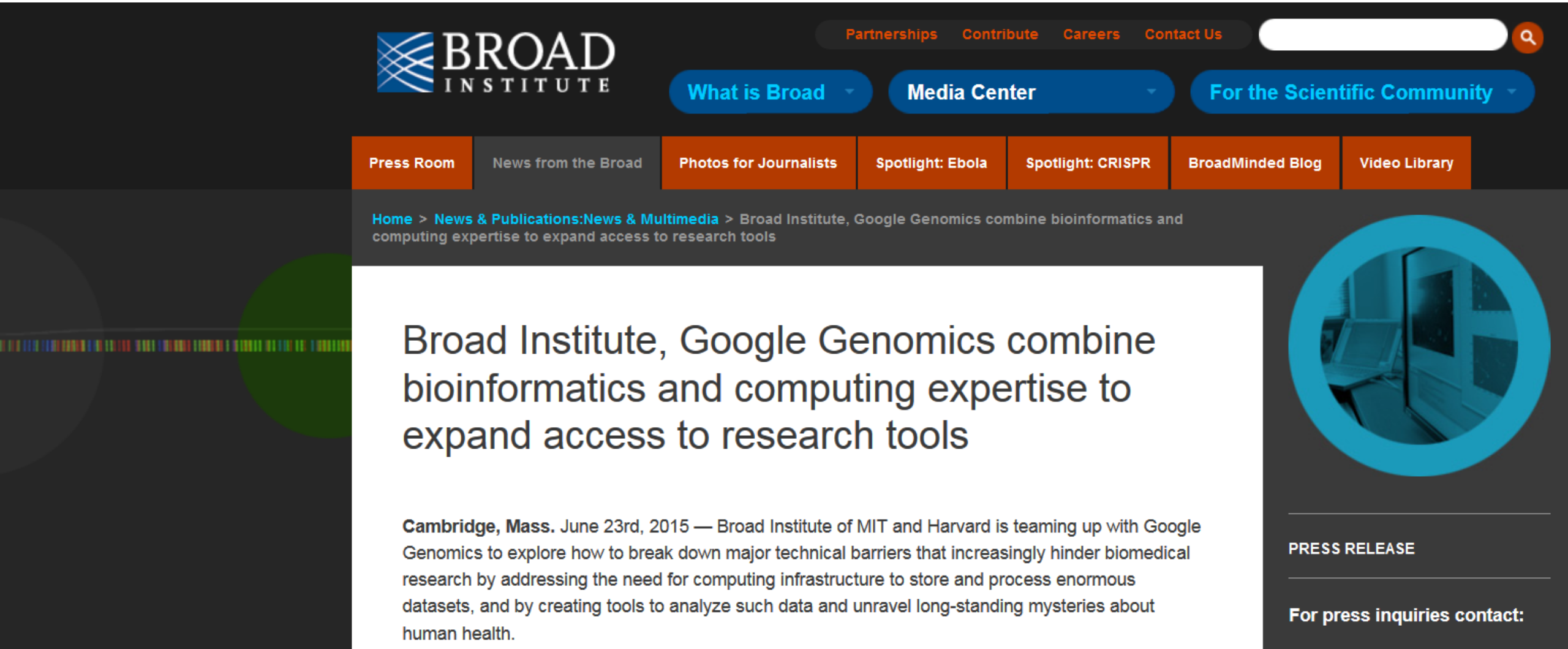
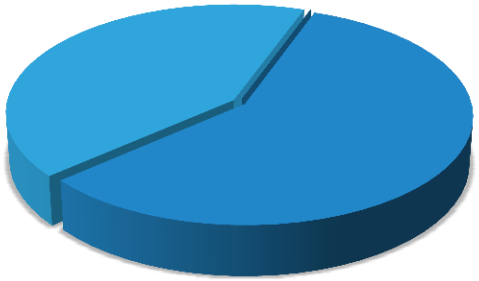
SEARCHING FOR STANDARDIZED PIPELINES FOR HUMAN GENOMICS

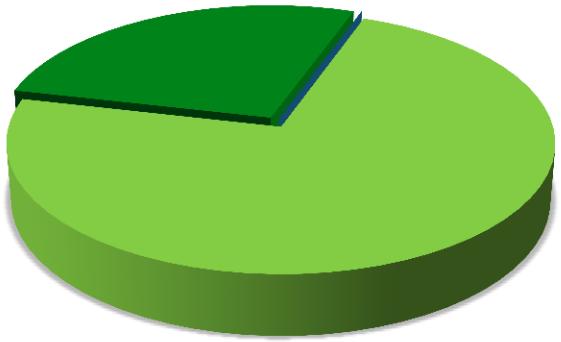


BIOPHARMACEUTICAL COMPANIES ARE COMMITTED TO ADVANCING PERSONALIZED MEDICINES

42% of **new medicines** in the pipeline have the potential to be **personalized medicines**



33% expected increase investment in personalized medicines over the next five years



73% of cancer medicines in the pipeline have the potential to be personalized medicines

69% Expected increase in the number of personalized medicines in development over the next 5 years

Sources: Tufts Center for the Study of Drug Development, "Impact Report," Volume 17, No.3, May/June 2015.

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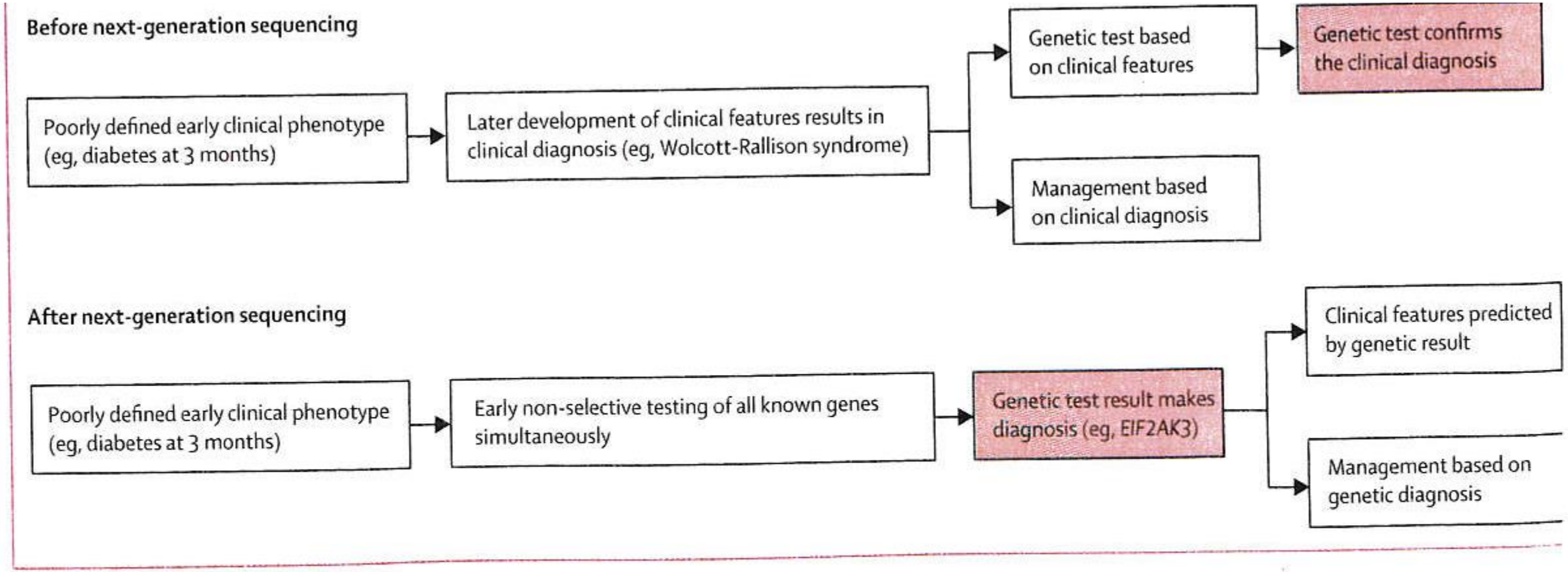
The NEW ENGLAND JOURNAL of MEDICINE

ESTABLISHED IN 1812 NOVEMBER 19, 2015 VOL. 373 NO. 21

Prospective Validation of a 21-Gene Expression Assay in Breast Cancer

J.A. Sparano, R.J. Gray, D.F. Makower, K.I. Pritchard, K.S. Albain, D.F. Hayes, C.E. Geyer, Jr., E.C. Dees, E.A. Perez, J.A. Olson, Jr., J.A. Zujewski, T. Lively, S.S. Badve, T.J. Saphner, L.I. Wagner, T.J. Whelan, M.J. Ellis, S. Paik, W.C. Wood, P. Ravdin, M.M. Keane, H.L. Gomez Moreno, P.S. Reddy, T.F. Goggins, I.A. Mayer, A.M. Brufsky, D.L. Toppmeyer, V.G. Kaklamani, J.N. Atkins, J.L. Berenberg, and G.W. Sledge

The effect of early, comprehensive genomic testing on clinical care in neonatal diabetes: an international cohort study



Lancet 386, September 2015

Figure 1: **The paradigm shift of genetic testing**
Schematic representation of the steps involved in genetic testing before and after the introduction of next-generation sequencing. The red boxes indicate the role c genetic testing.

MULTIPLEX TESTING IS ALREADY AVAILABLE

OncoType DX

Analyzes by qPCR, mRNA expression of a panel of 21 genes within a tumor to determine a Recurrence Score

MammaPrint

Microarray-based prognostic breast cancer mRNA expression profiling test of 70 genes

AlloMap

qPCR-based expression profile of 11 genes to assist physicians in managing heart transplant patients for potential organ rejection

Tissue of Origin

Microarray technology considers 15 common malignant tumor types, including bladder, breast,and colorectal tumors based on mRNA expression on 1,550 genes

GENOMAS

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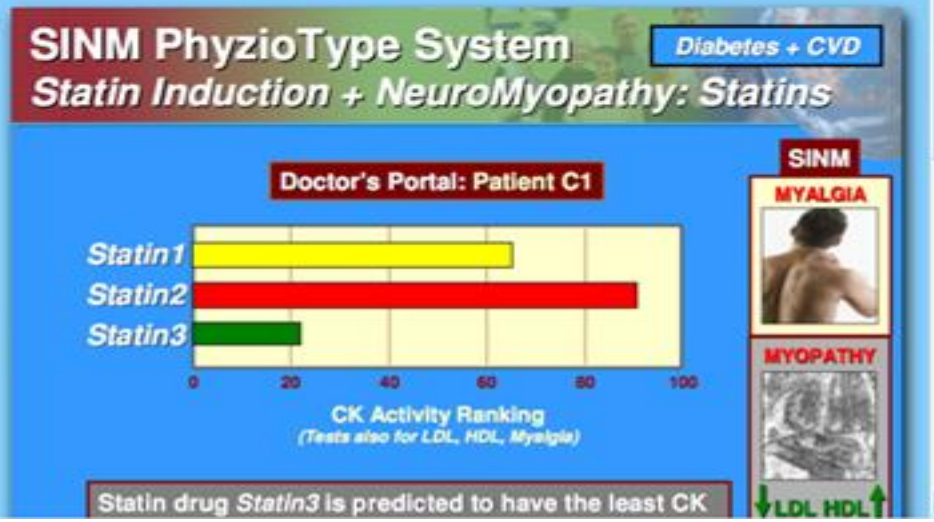
SINM PhyzioType™ System: Statin-Induced Neuro-Myopathy

DIABETES + CVD, Reduction of Cardio-metabolic Risk by Lipid-lowering: *Statins*

The SINM PhyzioType System provides the physician with DNA-guided efficacy predictions for aggressive lipid lowering and risk profiles for neuromuscular side effects of atorvastatin, simvastatin, and rosuvastatin. The information can be employed prognostically before prescribing statin therapy or diagnostically to categorize neuro-myopathy in those statin patients already evidencing neurological or muscular symptoms and seeking remedial treatment. The SINM PhyzioType System consists of 4 tests predicting LDL lowering and HDL raising efficacy, and innate side-effect risk for myalgia and CK activity elevation (mopathy), in response to statins on a class-wide and drug-specific basis. A patent on the SINM PhyzioType product is pending as an application.

Statin Induction + Neuro-Myopathy (SINM), the balance of potency and safety, is the main clinical management challenge of these drugs, particularly in diabetes where treatment targets are aggressive requiring LDL cholesterol levels below 100 mg/dl. In medical practice, Neuro-myopathy presents as a constellation of neuromuscular side effects. Clinical symptoms include myalgia (muscle aches, cramps, weakness) and myopathy (muscular injury monitored by serum elevation of muscle enzymes). Neuro-myopathy is more frequent at the higher doses required for treating advanced cardiovascular disease and varies in extent between individual statins and from patient to patient. Therefore, prescribing the most potent statin on an individual basis is critical as well to avoid maximal doses. Statin usage is ultimately limited by toxicity. Neuro-myopathy is disabling to 10-20% of patients on statins, requires alteration of therapy, burdens healthcare with management costs, and reduces compliance. Only 50% of patients remain on statins 6 months after initiation of therapy.

Statins are the most prescribed drugs in the world. Statins are the most effective



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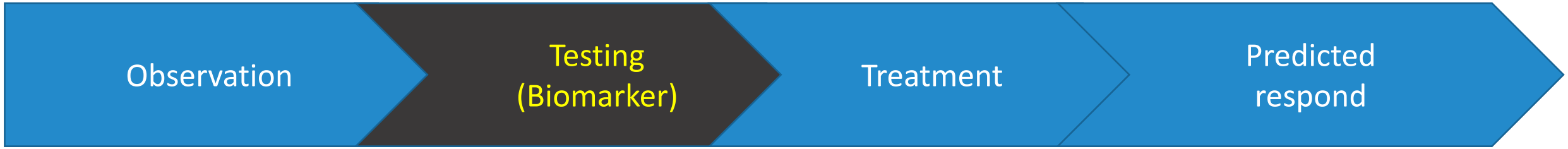
TARGETED THERAPY

Classical

Targeted



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A real increase in the impact of precision medecine in drug development

138

Total number of
FDA-approved drugs with biomarker information
provided on their drug label*

1 in 5 FDA approvals in 2014
were for targeted therapies*

Source: U.S. FDA, "Table of Pharmacogenomic Biomarkers in Drug Labeling," http://www.fda.gov/drugs/scienceresearch/researchareas/pharmacogenetics/ucm083378.htm (accessed Apr 2015), PMC , "More than 20 percent of the Novel New Drugs Approved by FDA's Center for Drug Evaluation and Research in 2014 are Personalized Medicines," http://www.personalizedmedicinecoalition.org/Userfiles/PMC-Corporate/file/2014-fda-approvals-personalized-medicine2.pdf (accessed May 2015).

*As of March 27, 2015

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EXAMPLES OF CONDITIONS IN WHICH PRECISION MEDICINE HAS BEEN USED*

Medical Field	Disease	Biomarker	Intervention
Cancer	Chronic myeloid leukemia	BCR-ABL	Imatinib
	Lung cancer	EML4-ALK	Crizotinib
Hematology	Thrombosis	Factor V Leiden	Avoid prothrombotic drugs
Infectious disease	HIV/AIDS	CD4+ T cells, HIV viral load	Highly active antiretroviral therapy
Cardiovascular disease	Coronary artery disease	CYP2C19	Clopidogrel
Pulmonary disease	Cystic fibrosis	G551D	Ivacaftor
Renal disease	Transplant rejection	Urinary gene signature	Antirejection drugs
Hepatology	Hepatitis C	Hepatitis C viral load	Direct-acting antiviral agents
Endocrine disease	Multiple endocrine neo-plasia type 2	RET	Prophylactic thyroidectomy
Metabolic disease	Hyperlipidemia	LDL cholesterol	Statins
Neurology	Autoimmune encephalitis	CXCL13	Immunotherapy
Psychiatry	Alcohol-use disorder	GRIK1	Topiramate
Pharmacogenomics	Smoking cessation	CYP2A6	Varenicline
Ophthalmology	Leber's congenitalamaurosis	RPE65	Gene therapy

KRAS Colon cancer

BRAF Melanoma

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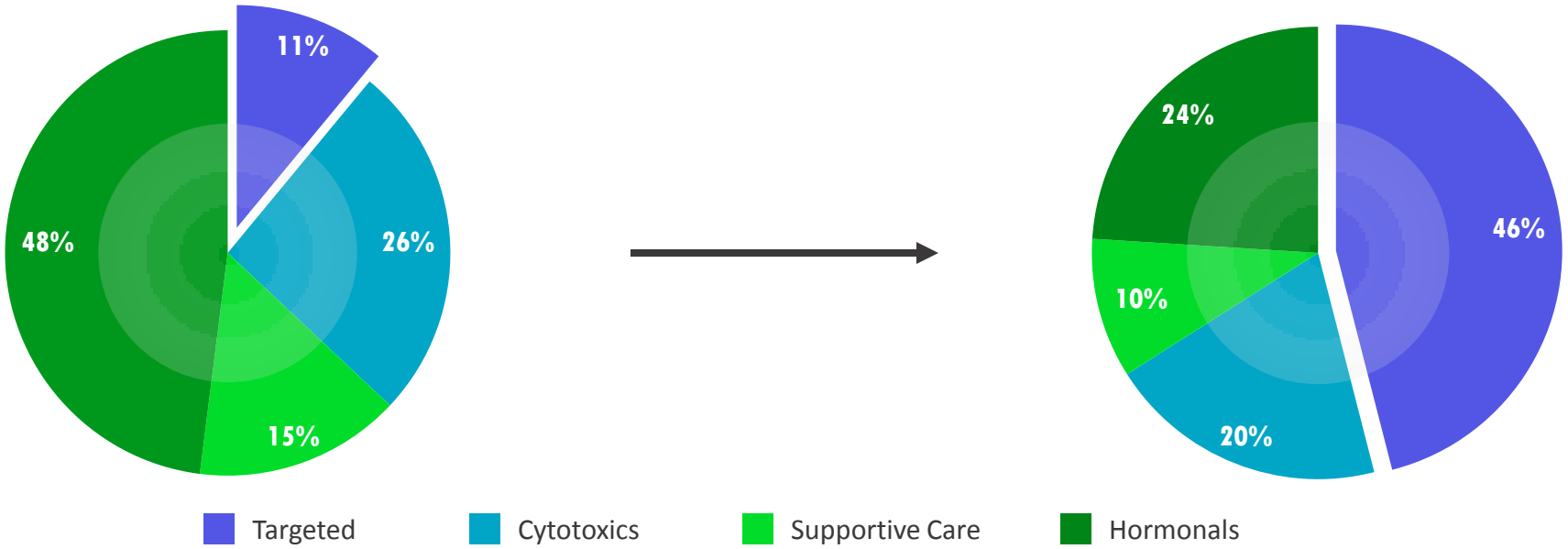
* In the biomarker column, proteins or genes that are probed to find the specific variants of interest are shown. AIDS denotes acquired immunodeficiency syndrome, HIV human immunodeficiency virus, and LDL low-density lipoprotein.

ONCOLOGY IS ON THE LEADING EDGE OF PERSONALIZED MEDICINE

In ten years, cancer patients have seen a four-fold increase in their personalized medicine treatment options.

Breakdown of Oncology Treatment Modalities, Global Market share 2003-2013*



Sources: IMS Institute for Healthcare Informatics, "Innovation in Cancer Care and Implications for Health Systems: Global Oncology Trend Report," May 2014 (accessed May 2015); National Cancer Institute, "NCI Dictionary of Cancer Terms" (accessed May 2015).

Clinical efficacy of Vemurafenib (PLX-4032, Zelboraf) in melanomas

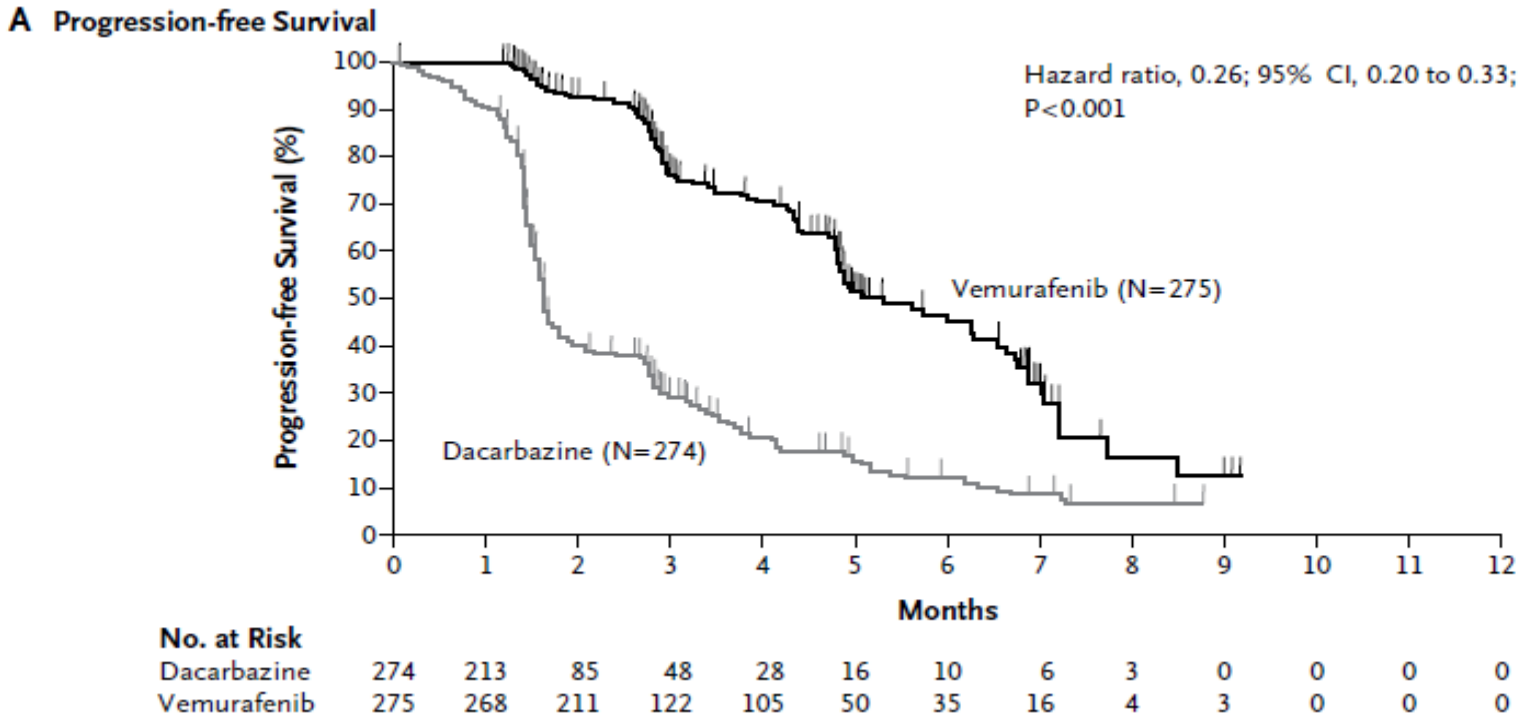
Key biomarkers:

Stratification: BRAFV600E mutation

Mechanism: P-ERK
Cyclin-D1

Efficacy: Ki-67
18FDG-PET, CT

Clinical endpoint: progression-free survival (%)



Chapman et al, NEJM 2011

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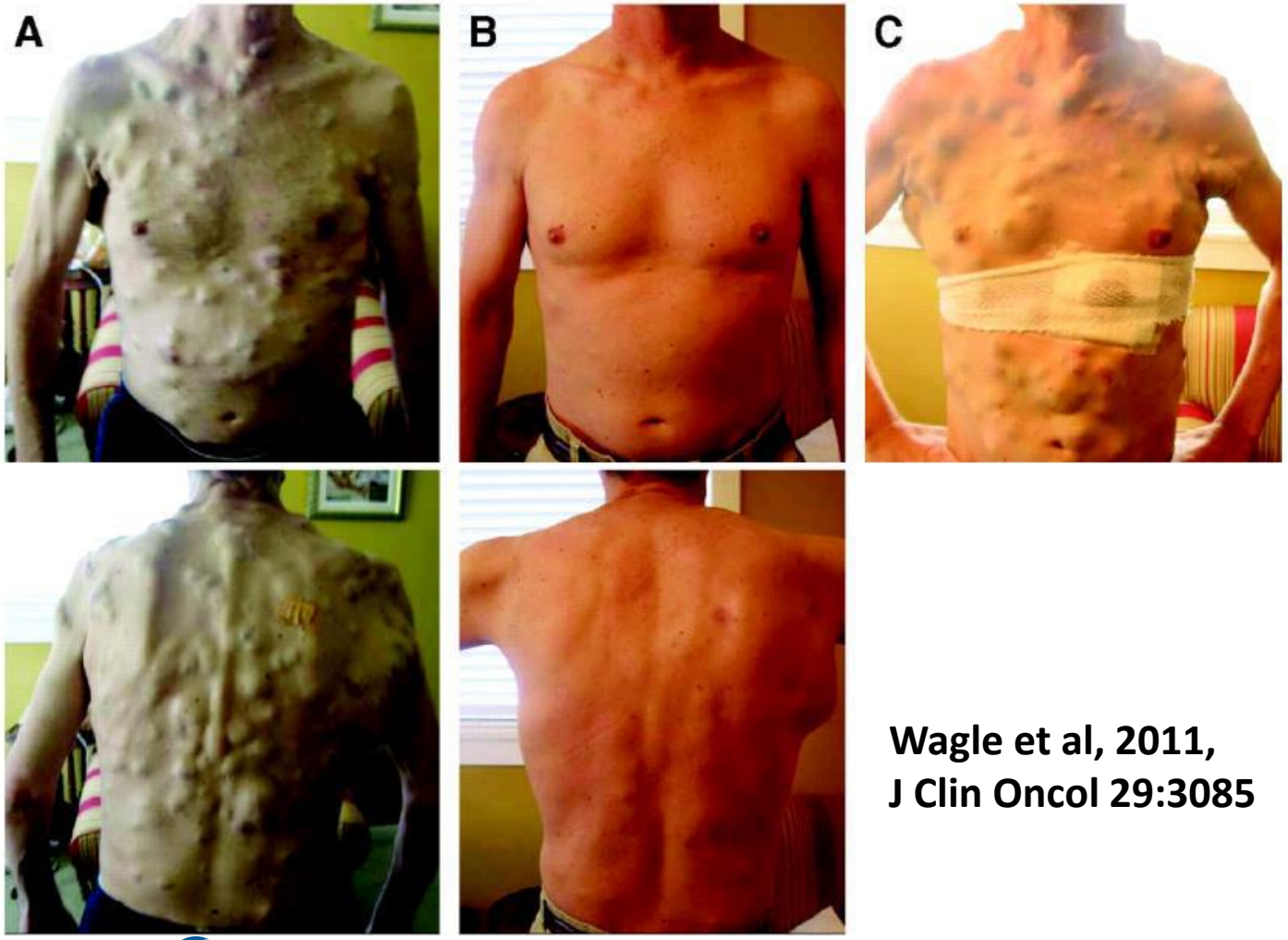
Clinical efficacy of Vemurafenib

Before Rx | Vemurafenib, 15 weeks | Vemurafenib, 23 weeks



Wagle et al, 2011,
J Clin Oncol 29:3085

Strong initial effects vemurafenib

- **Emerging drug resistancy**
- **Recurence of aggressive tumors**

Tumor tissue heterogeneity

- **BRAFV600D/E is driving mutation**

- **However, also no BRAFV600D/E mutation found in regions of a primary melanoma : Molecular heterogeneity in tumor tissue**

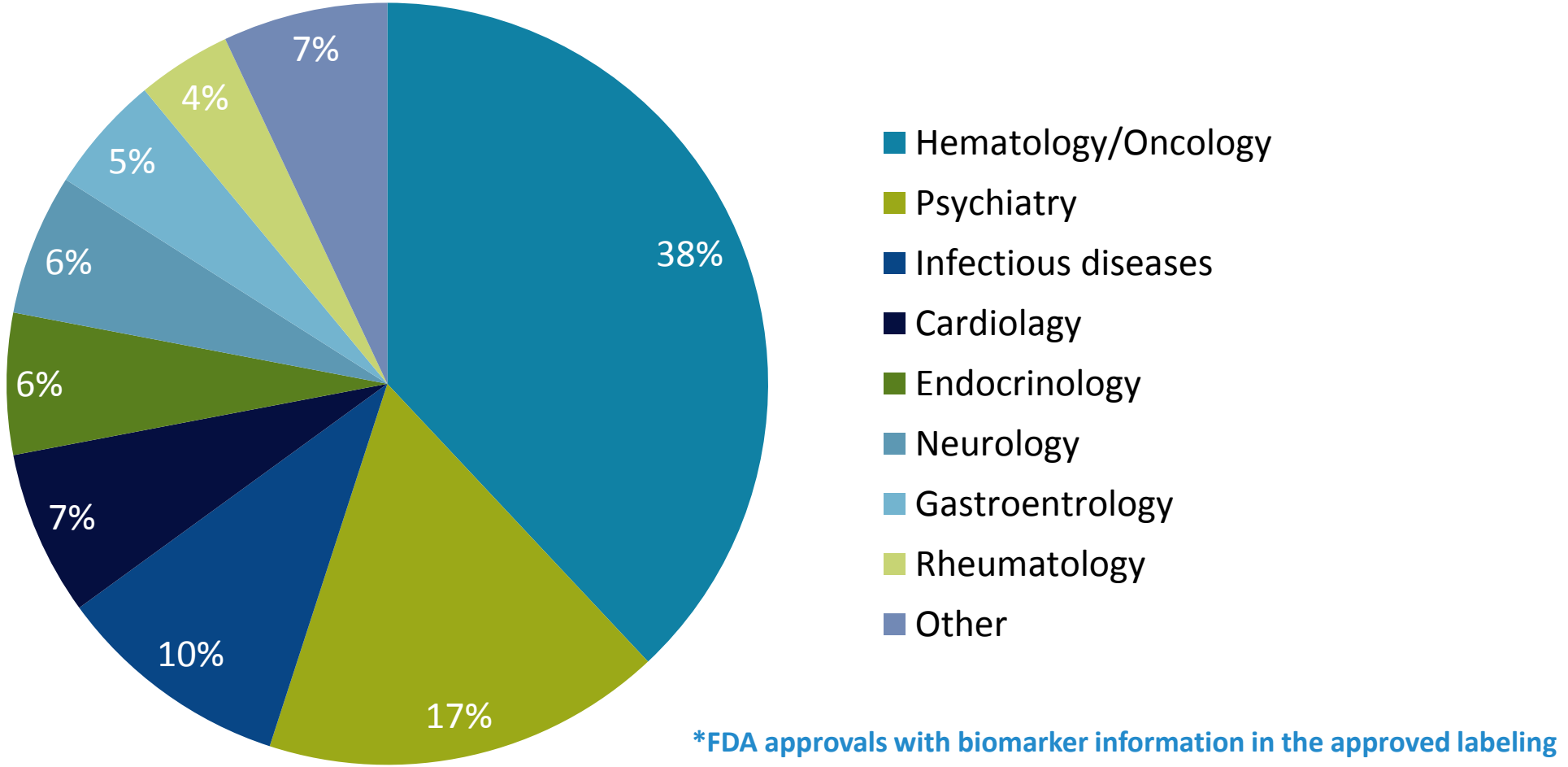
- **Biomarker levels in tissue vary**
  Biomarker levels in body fluids will vary

- **Major challenge for (companion) diagnostics**

{

PERSONALIZED MEDICINES ARE BENEFITTING PATIENTS ACROSS MANY DIFFERENT DISEASES

Across a variety of therapeutic areas, an increasing number of treatments are personalized.*



***FDA approvals with biomarker information in the approved labeling**

Source: U.S. FDA,
"Paving the Way for Personalized Medicine",
Oct 2013.

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PRECISION MEDECINE AND VACCINATION

CD4+ T Cell Autoimmunity to Hypocretin/Orexin and Cross-Reactivity to a 2009 H1N1 Influenza A Epitope in Narcolepsy

Antibodies to influenza nucleoprotein cross-react with human hypocretin receptor 2

HLA-DQB 1*0602

Doses of viral capsid?

(Pandemrix vs Focetria vaccines)

Other genetic determinants?

ScienceTranslational Medecine; 18/12/2013 (1/8/2014); 1/7/2015

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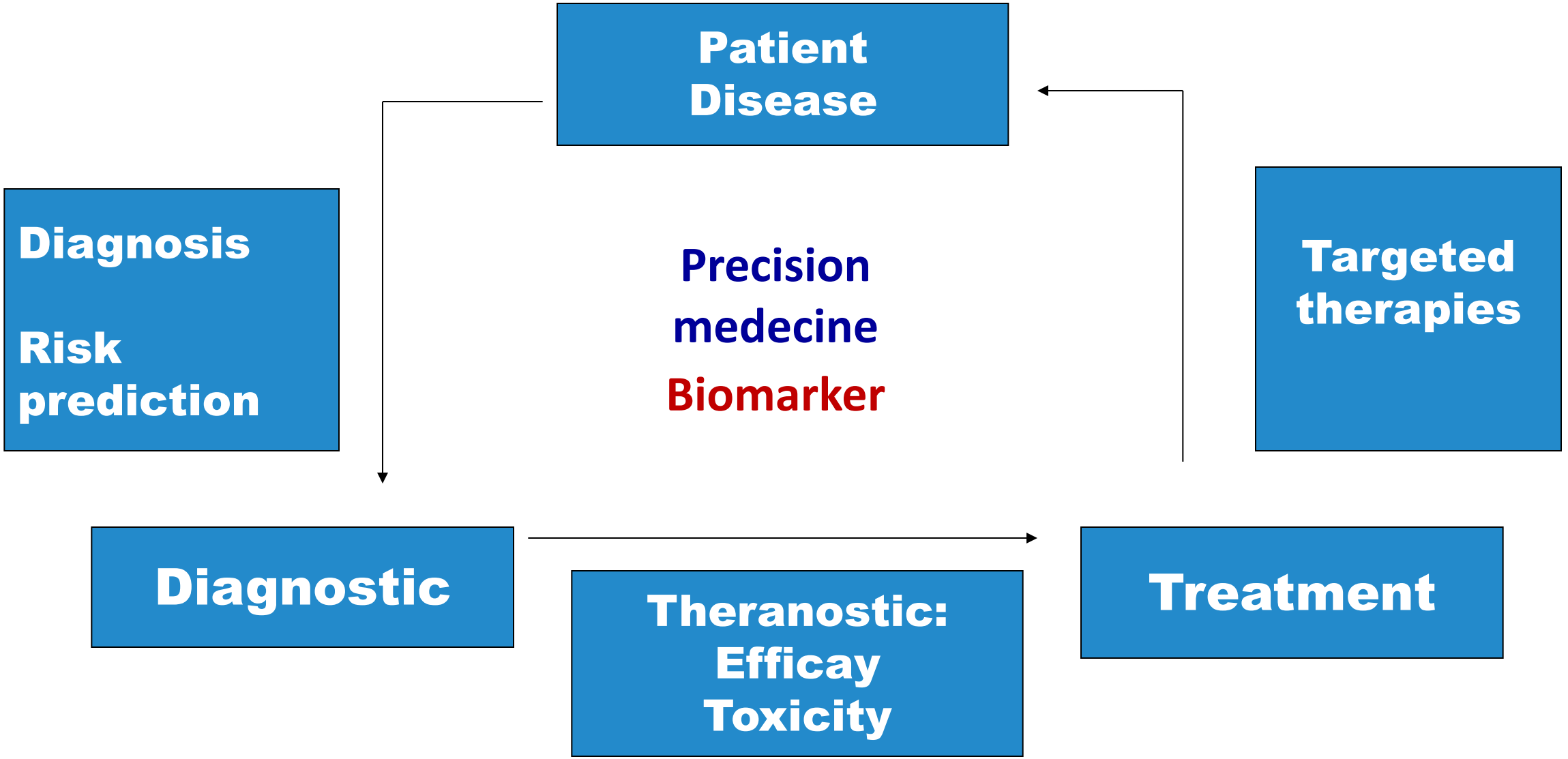

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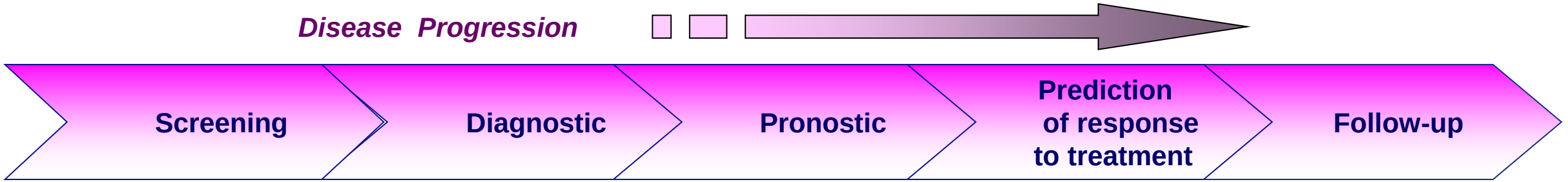
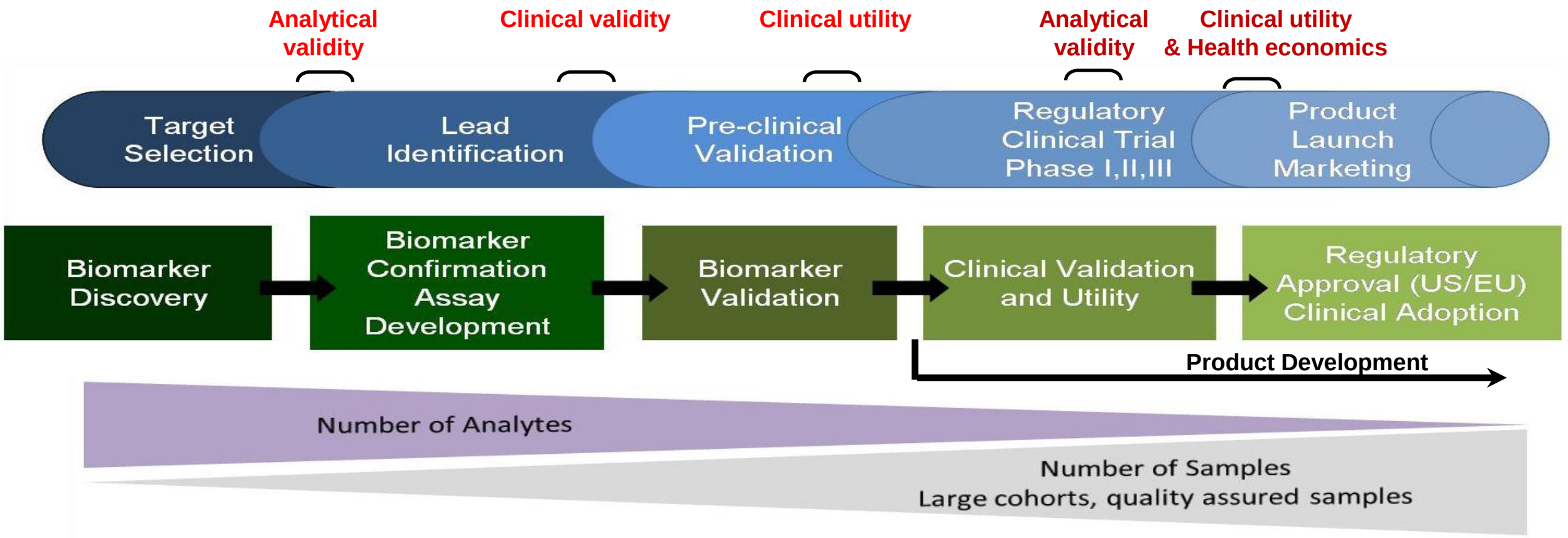
WHAT TYPES OF BIOMARKERS DO WE HAVE ?



1. Screening **(e.g. mammography, fecal occult blood)**
2. Diagnostic **(e.g. cardiac troponin)**
3. Prognosis **(e.g. cytokeratins, estrogen receptors)**
4. Prediction of response to treatment **(e.g. HER2)**
5. Patient follow-up **(e.g. PSA)**

BIOMARKER RESEARCH AND VALIDATION: A LONG JOURNEY



- Analytical and clinical validity drive regulatory approval
- Clinical utility and health economics benefits drive reimbursement

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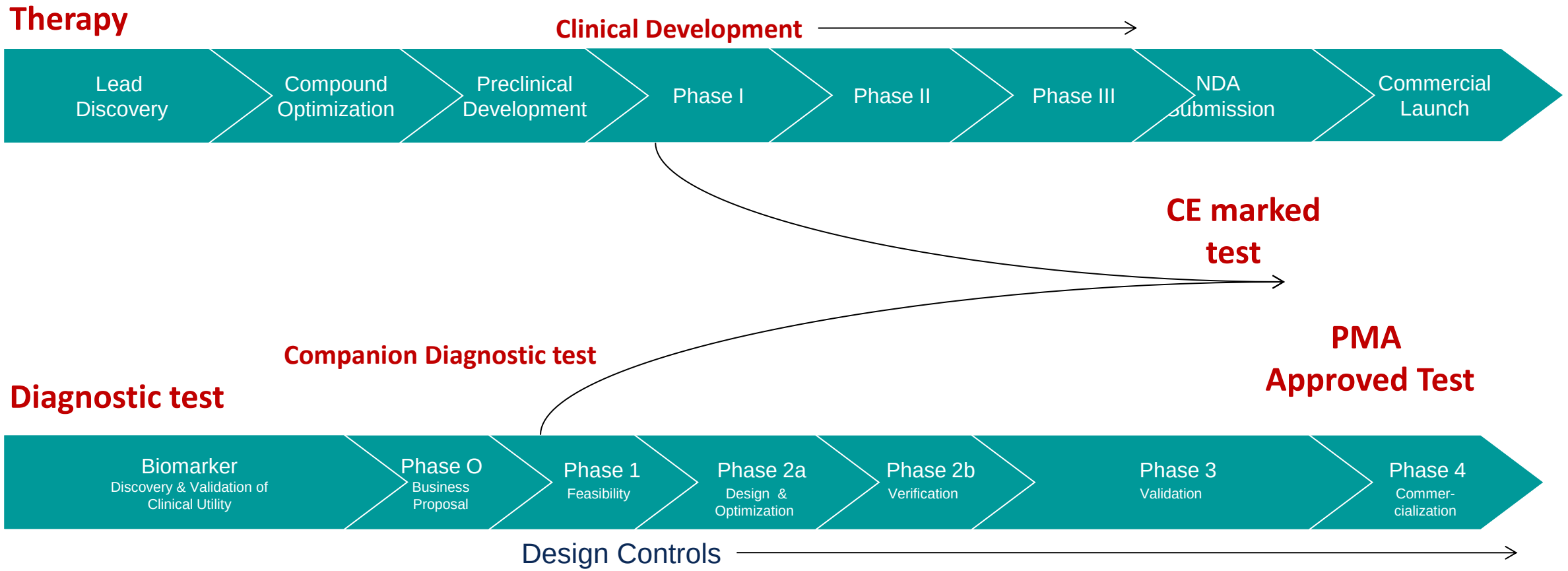
DRUG-DIAGNOSTIC CO-DEVELOPMENT PROCESS: THERANOSTIC



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PARTNERSHIPS AND COLLABORATIONS ARE TRANSFORMING THE RESEARCH AND DEVELOPMENT OF PERSONALIZED MEDICINES

AMP (Accelerating Medicines Partnership)

Developing new diagnostics and biological targets for treatments in Alzheimer's disease, type 2 diabetes, rheumatoid arthritis, and lupus.

The Partners: biopharmaceutical companies, NIH, patient and disease organizations

Biomarkers Consortium

Combining expertise and resources to rapidly identify, develop, and qualify biomarkers, which will then advance new therapies and guide improvements in regulatory and clinical decision-making.

The Partners: biopharmaceutical companies, NIH, CMS, FDA, patient and disease organizations

THE biomarkers CONSORTIUM

Lung-MAP (Lung Cancer Master Protocol)

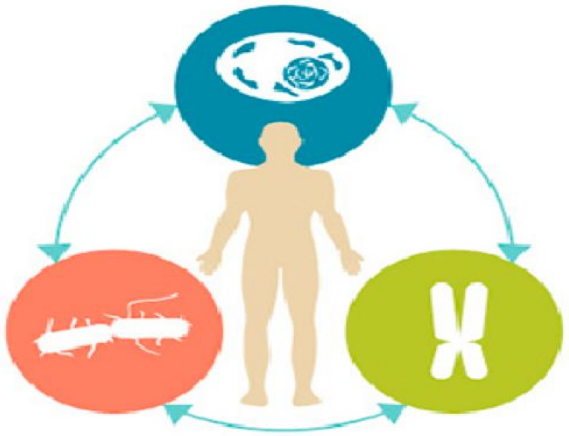
Using comprehensive genetic screening to identify mutations in lung cancer patients in order to direct them to a specific investigational treatment, all operating under a single clinical trial protocol.

The Partners: biopharmaceutical companies, NIH, FDA, patient and disease organizations

LUNG-MAP

Sources: National Institutes of Health, "Accelerating Medicines Partnership," http://nih.gov/science/amp/index.htm; The Biomarkers Consortium, http://www.biomarkersconsortium.org/index.php; Lung Cancer Master Protocol, http://www.lung-map.org/ (all cites accessed May 2015).

INTEGRATING INFORMATION ABOUT IMMUNE RESPONSE, GENETIC & ENTEROTYPE VARIABILITY



→ **Response**

COMMENSAL MICROBIOTA

IMMUNE PHENOTYPING

HOST GENETICS

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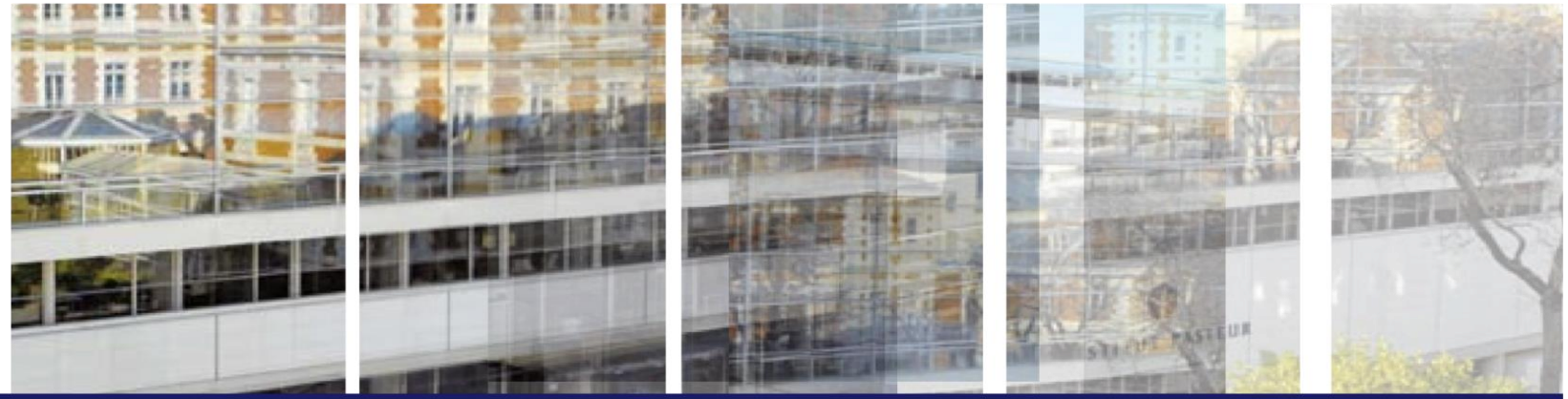
MILIEU INTÉRIEUR CONSORTIUM

Financé par ANR

Milieu Intérieur
Vers une médecine personnalisée



A population based assessment of the Genetic & Environmental Determinants of Immune Phenotype Variance

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Centre d'Immunologie Humaine

Inserm
Institut national de la santé et de la recherche médicale

CNRS
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE

PARIS DESCARTES
IUT

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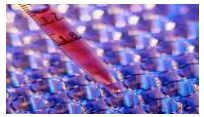
Milieu Intérieur
Vers une médecine personnalisée

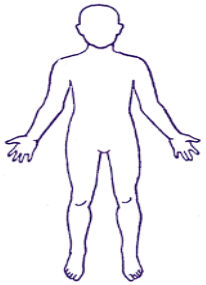
1,000 HEALTHY DONORS COHORT

Clinical data

Serology



Whole blood 20ml



Microbes

Adjuvants

Cytokines

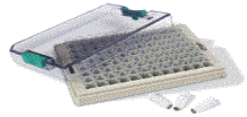
TCR stim

Whole blood 50ml

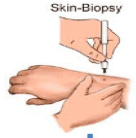
Supernatant

Cell pellets

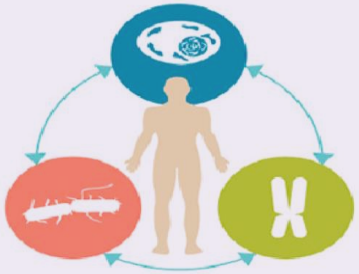
Nasal swabs /Stool



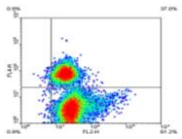
Skin Biopsy



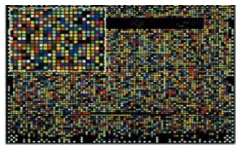
√ Fully recruited
1000 donors
5 decades of life
2 timepoints



1000 eCRF
≥ 300 var / p



10 Panels
15000 FCS files
≥ 500 var / p



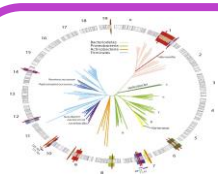
1000 Genotypes
750K var / p

180.000 Supernatant Tubes

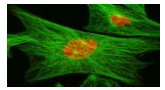
≈ 50 var / tube
≈ 2000 var / p

60.000 RNA profiles

≥ 600 var / tube
≥ 24000 var / d



1000 Enterotypes
16S rRNA NGS



300 fibroblast lines

→ iPS

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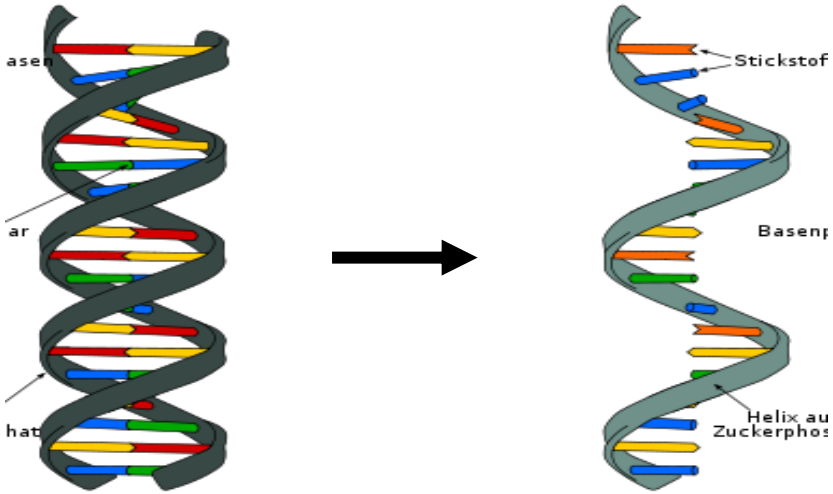
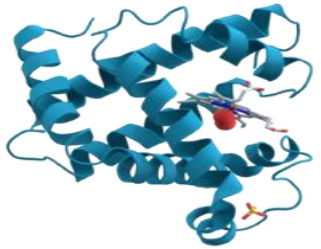
GENETIC SUSCEPTIBILITY ≠ GENETIC DETERMINISM





Disease

Tx response

Etc.

DNA
(static variance)

RNA

Protein

We need functional biomarkers

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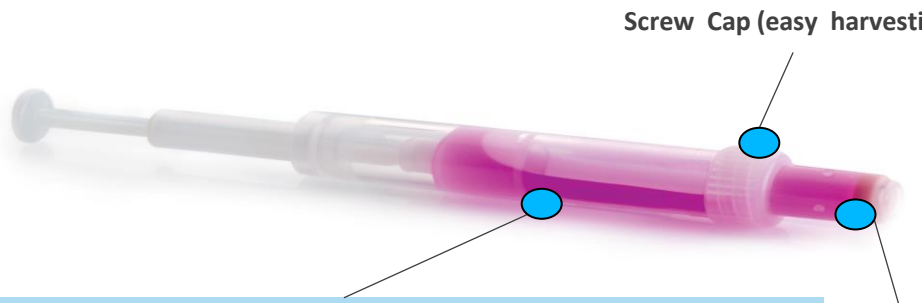
PROFILING INDUCED IMMUNE RESPONSES

Reliable, reproducible results



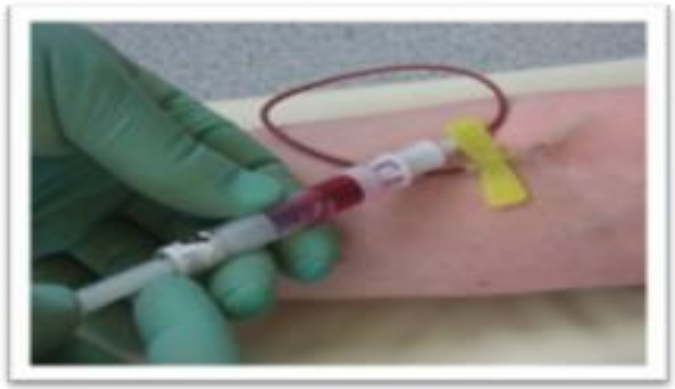
Stimulus	
Null	
HK *E.coli 0111:B4*	Microbe
HK *S. aureus*	Microbe
HK *L. rhamnosus*	Microbe
BCG (Immucyst)	Microbe
HK *H. pylori*	Microbe
HK* *C. Albicans*	Microbe
Influenza A Virus (live)	Microbe
Sendai virus (live)	Microbe
C12-iE-DAP	MAMP
CPPD	MAMP
FSL-1	MAMP
Poly I:C	MAMP
LPS-EB (ultrapure)	MAMP
Flagellin-ST	MAMP
Gardiquimod	MAMP
R848	MAMP
ODN 2216	MAMP
lipoarabinomannan	MAMP
WGP	MAMP
IFNa$_{2b}$ (Intron A)	Cytokine
IFNb (Betaseron)	Cytokine
IFNg (Imukin)	Cytokine
TNFa	Cytokine
IL-1b	Cytokine
IL-23	Cytokine
a-CD3 + a-CD28	TCR
Enterotoxin SEB	TCR

Milieu Intérieur
Vers une médecine personnalisée

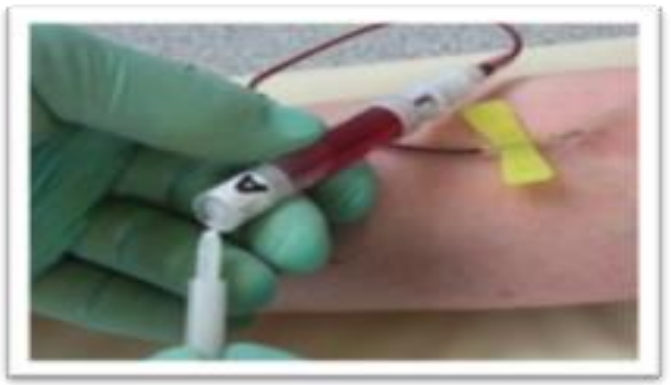
Partnership with Myriad RBM

POINT-OF-CARE FUNCTIONAL IMMUNE ASSAYS PERMITS ON-SITE SAMPLE COLLECTION STANDARDIZATION

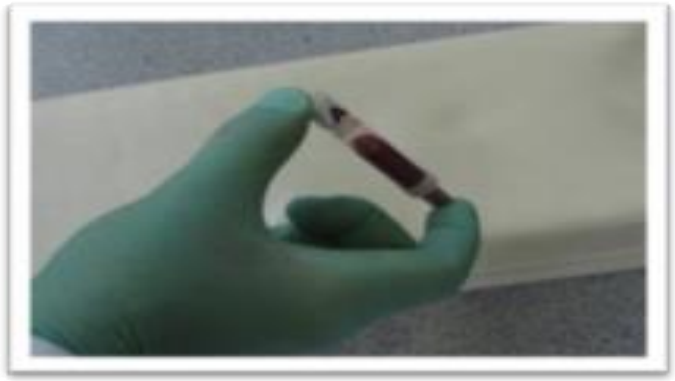
A) Prefill tubing with blood



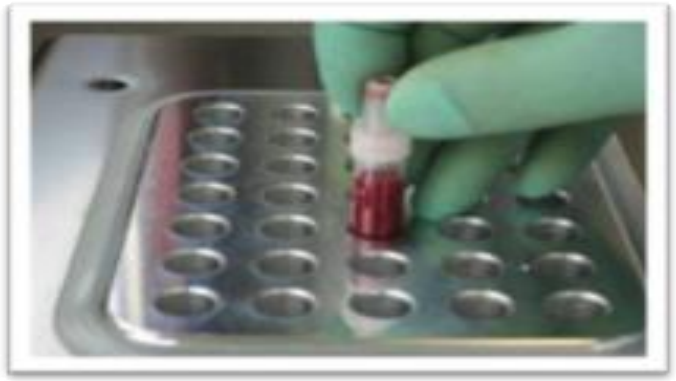
B) Pull, until it “clicks”



C) Break away plunger



D) Mix gently 3x



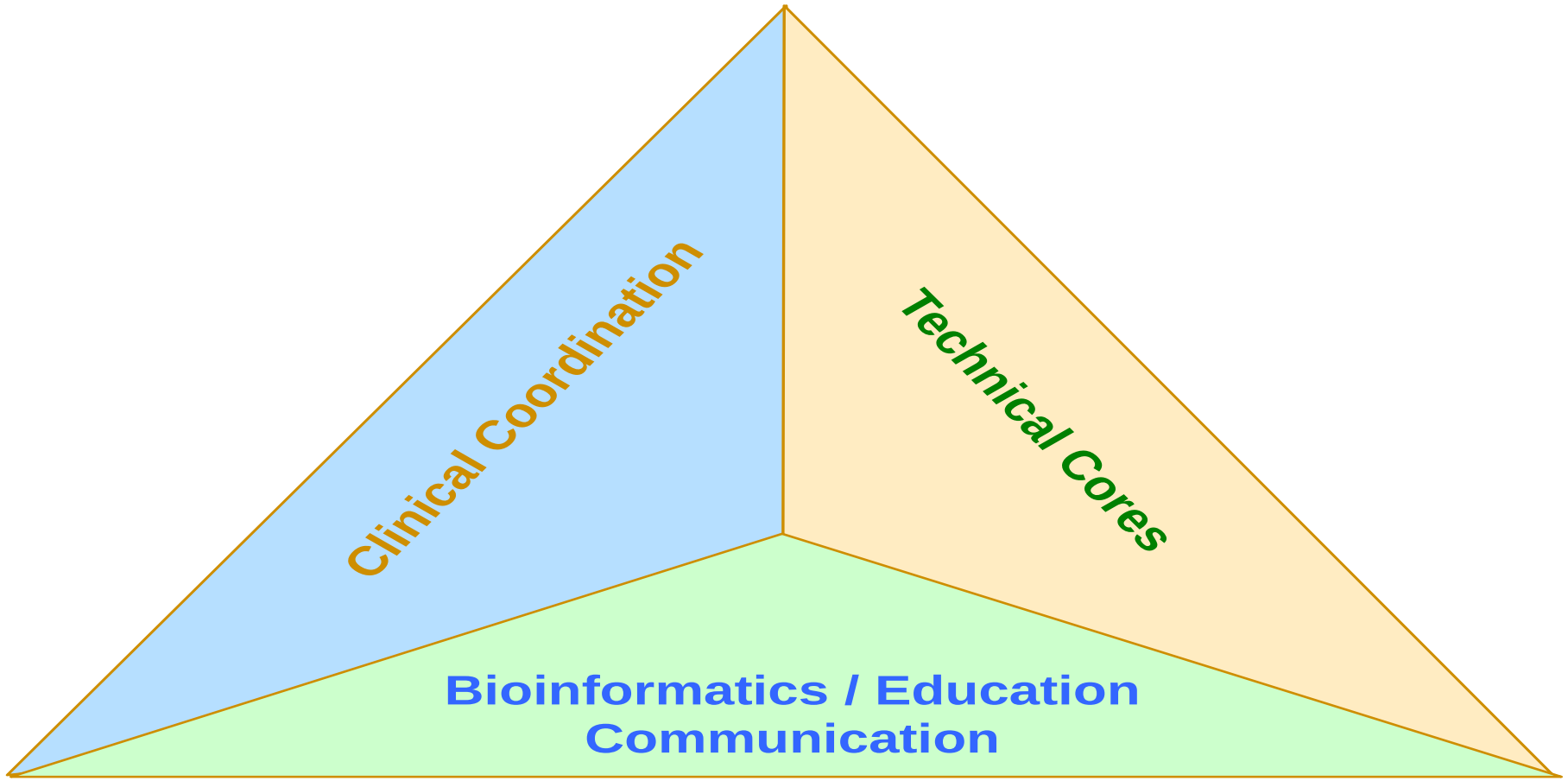
E) Incubate for 4h (mRNA, miRNA analysis) or 22h (protein and lipidome studies)

Milieu Intérieur
Vers une médecine personnalisée

Strategy in place for defining reference values for immunologic variance
380,000 banked samples (1000 donors x 40 TC tubes)

The Center for Translational Science

THE CRT STRUCTURE



Centre de Recherche Translationnelle

Precision Medicine: Personalized, Problematic,and Promising

J. Larry Jameson, M.D., Ph.D., and Dan L. Longo, M.D.

NEJM 4 June 2015

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CURRENT STANDARDIZATION AND COORDINATION EFFORTS

There exist several global coordinated efforts to achieve standardization and sharing of big life science data, notably the Global Alliance for Genomics and Health, but due to heterogeneity, diversity and immaturity of technologies, practices and frameworks the tasks are currently overwhelming.

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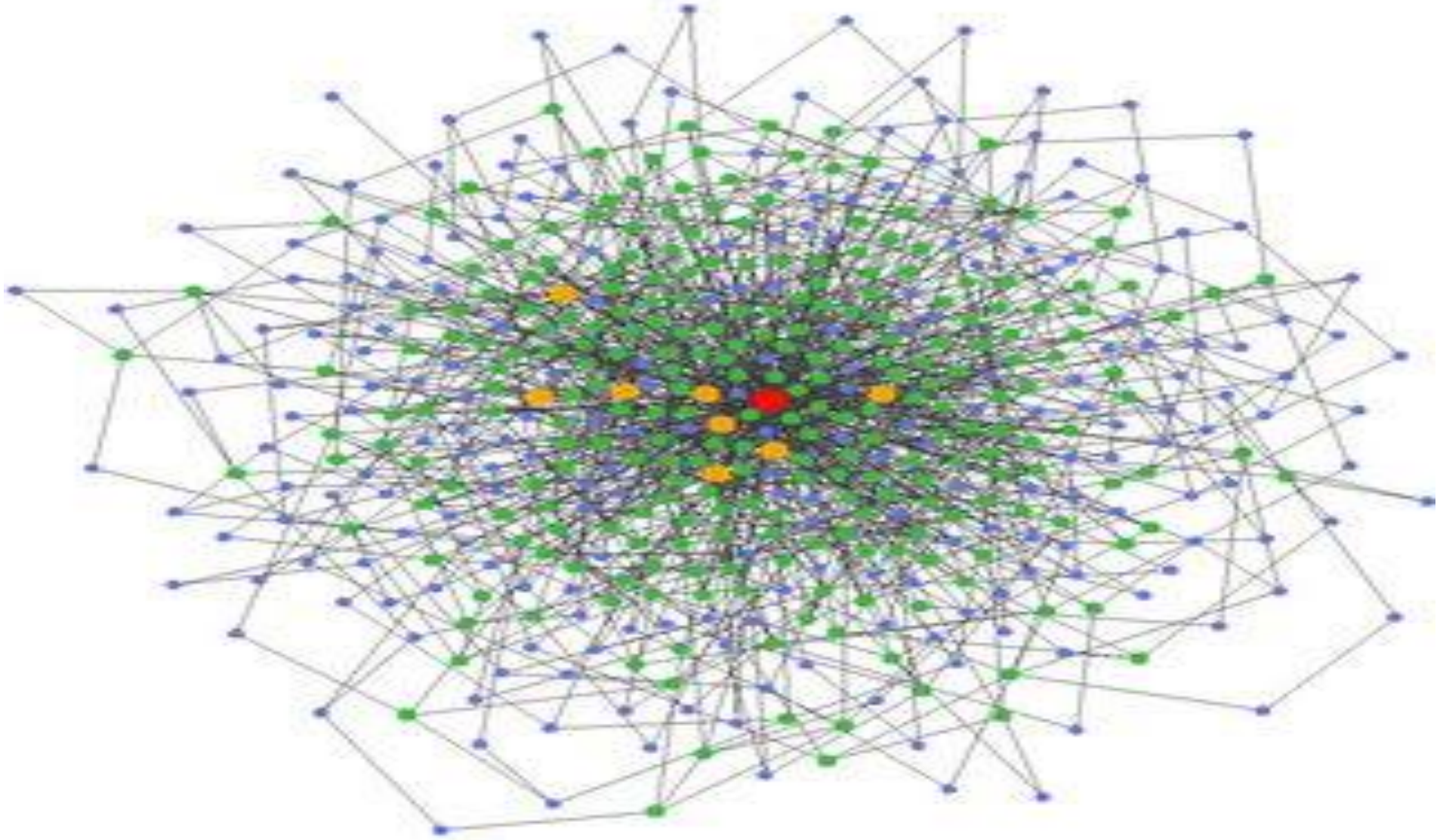
DISEASES ARE THE RESULT OF PERTURBATIONS IN COMPLEX BIOMOLECULAR NETWORKS



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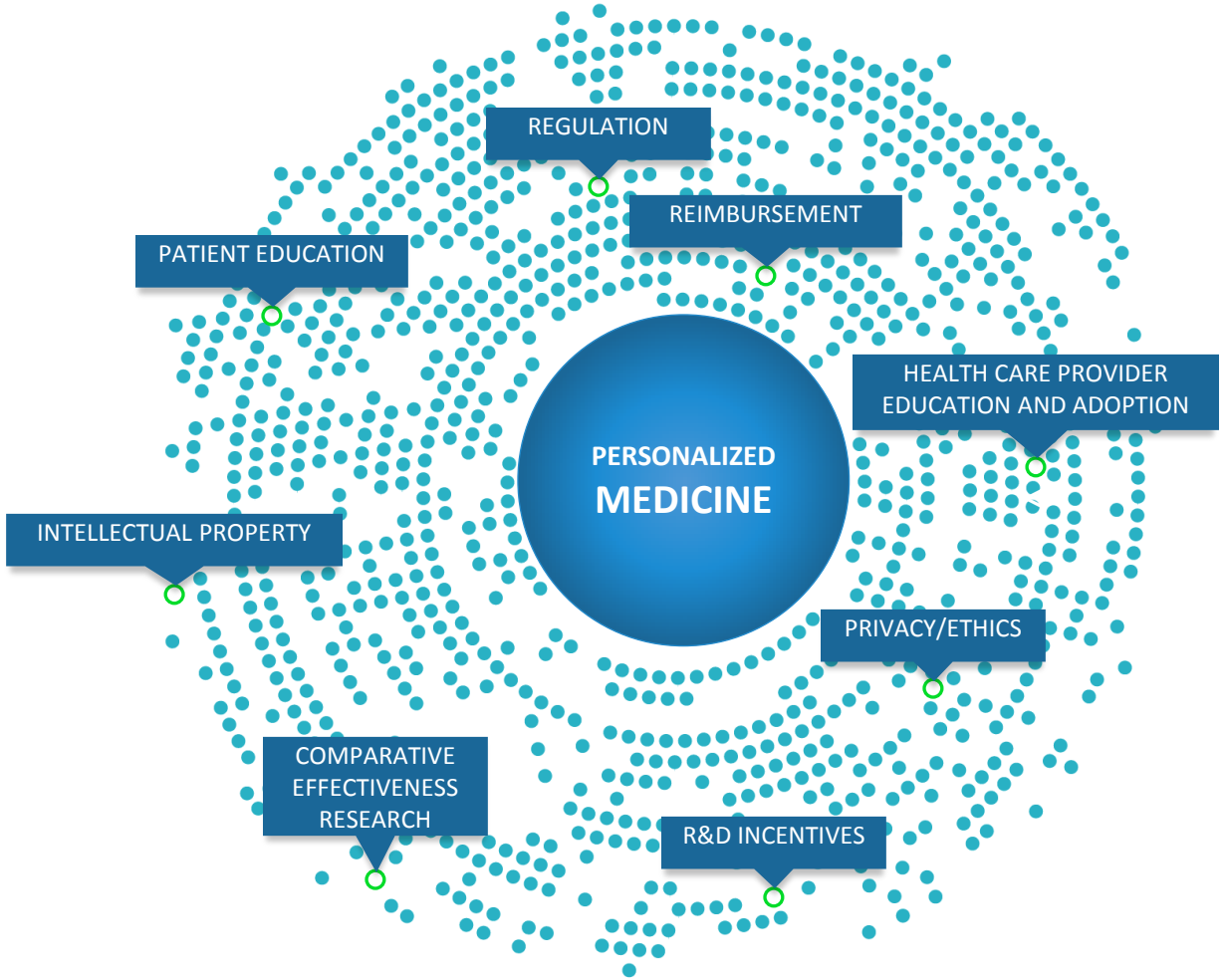
ISSUES WITH AN IMPACT ON PERSONALIZED MEDICINE

The implementation of personalized medicine requires a confluence of multiple factors.
Full implementation of personalized medicine can only be achieved when all sectors converge toward the center.



WE ARE FACING ENORMOUS CHALLENGES AROUND ESTABLISHING REPLICABLE AND REPRODUCIBLE RESEARCH PRACTICES FOR DATA INTENSIVE BIOMEDICAL SCIENCE

Open access, freely available online

Essay

Why Most Published Research Findings Are False

John P. A. Ioannidis

Summary

There is increasing concern that most current published research findings are false. The probability that a research claim is true may depend on study power and bias, the number of other studies on the same question, and, importantly, the ratio of true to no relationships among the relationships probed in each scientific field. In this framework, a research finding is less likely to be true when the studies conducted in a field are smaller; when effect sizes are smaller; when there is a greater number and lesser preselection of tested relationships; where there is greater flexibility in designs, definitions, outcomes, and analytical modes; when there is greater financial and other interest and prejudice; and when more teams are involved in a scientific field in chase of statistical significance. Simulations show that for most study designs and settings, it is more likely for a research claim to be false than true. Moreover, for many current scientific fields, claimed research findings may often be simply accurate measures of the prevailing bias. In this essay, I discuss the implications of these problems for the conduct and interpretation of research.

factors that influence this problem and some corollaries thereof.

Modeling the Framework for False Positive Findings

Several methodologists have pointed out [9–11] that the high rate of nonreplication (lack of confirmation) of research discoveries is a consequence of the convenient, yet ill-founded strategy of claiming conclusive research findings solely on the basis of a single study assessed by formal statistical significance, typically for a *p*-value less than 0.05. Research is not most appropriately represented and summarized by *p*-values, but, unfortunately, there is a widespread notion that medical research articles

It can be proven that most claimed research findings are false.

should be interpreted based only on *p*-values. Research findings are defined here as any relationship reaching formal statistical significance, e.g., effective interventions, informative predictors, risk factors, or associations. "Negative" research is also very useful. is characteristic of the field and can vary a lot depending on whether the field targets highly likely relationships or searches for only one or a few true relationships among thousands and millions of hypotheses that may be postulated. Let us also consider, for computational simplicity, circumscribed fields where either there is only one true relationship (among many that can be hypothesized) or the power is similar to find any of the several existing true relationships. The pre-study probability of a relationship being true is $R/(R+1)$. The probability of a study finding a true relationship reflects the power $1 - \beta$ (one minus the Type II error rate). The probability of claiming a relationship when none truly exists reflects the Type I error rate, α. Assuming that c relationships are being probed in the field, the expected values of the 2×2 table are given in Table 1. After a research finding has been claimed based on achieving formal statistical significance, the post-study probability that it is true is the positive predictive value, PPV. The PPV is also the complementary probability of what Wacholder et al. have called the false positive report probability [10]. According to the 2

PLoS Medicine Vol 2, Issue 8, August 2005

- **Fast technological developments make it hard to establish stable standards.**
- **Both techniques and protocols are constantly evolving.**
- **Holistic and integrative analyses over different platforms and between different datatypes are extremely challenging.**
- **Storage, management, analysis and sharing of data are subject to legal and ethical considerations.**

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THE COMMUNITY IS PUSHING FOR REPRODUCIBLE RESEARCH

nature
International weekly journal of science

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NATURE | EDITORIAL

Announcement: Reducing our irreproducibility

24 April 2013

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Over the past year, *Nature* has published a string of articles that highlight failures in the re
and reproducibility of published research (collected and freely available at go.nature.com/
The problems arise in laboratories, but journals such as this one compound them when th
exert sufficient scrutiny over the results that they publish, and when they do not publish er
information for other researchers to assess results properly.

From next month, *Nature* and the Nature research journals will introduce editorial measur
address the problem by improving the consistency and quality of reporting in life-sciences
To ease the interpretation and improve the reliability of published results we will more
systematically ensure that key methodological details are reported, and we will give more
methods sections. We will examine statistics more closely and encourage authors to be
transparent, for example by including their raw data.

nature biotechnology

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NATURE BIOTECHNOLOGY | EDITORIAL

日本語要約

Rebooting review

Nature Biotechnology **33**, 319 (2015) | doi:10.1038/nbt.3202
Published online 07 April 2015

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***Nature Biotechnology* is reevaluating editorial oversight of papers centered on computational analyses in anticipation of the 'big data' world.**

Computational biology papers pose particular challenges to the peer review process. Often, a computational approach or its software implementation may be insufficiently documented or missing. The version of the software may not match the algorithm described in a paper or produce the published results. And source code associated with software central to the main claims of a paper may not be made available. These issues have prompted *Nature*

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THE CANCER TEST

A nonprofit's effort to replicate 50 top cancer papers is shaking up labs

Science 26 juin 2015

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Repeat failures

6 of 53

Cancer papers that Amgen could reproduce

14 of 67

Biomedical papers that Bayer completely reproduced

55%

MD Anderson researchers who could not reproduce a published study

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Novel methodologies for clinical trials?

Time for one-person trials

Precision medicine requires a different type of clinical trial that focuses on individual, not average, responses to therapy,

Nature 30 Avril 2015

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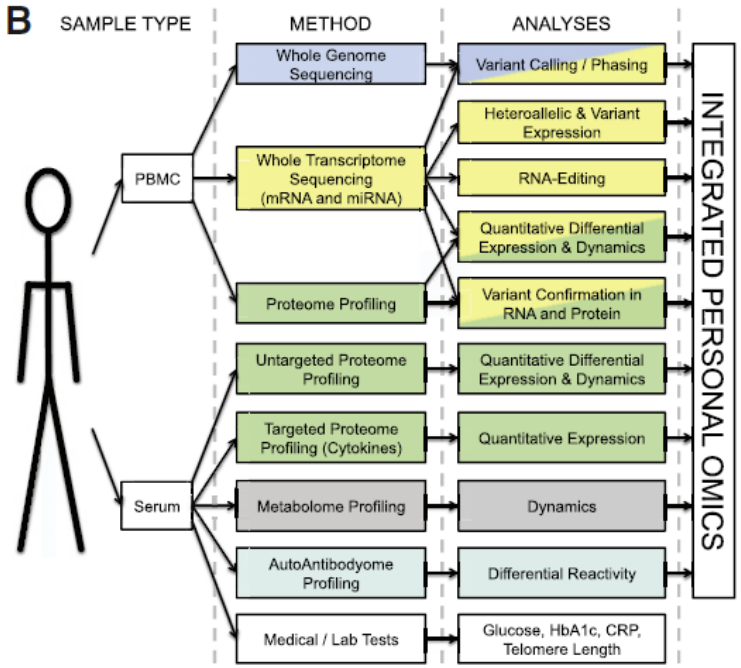
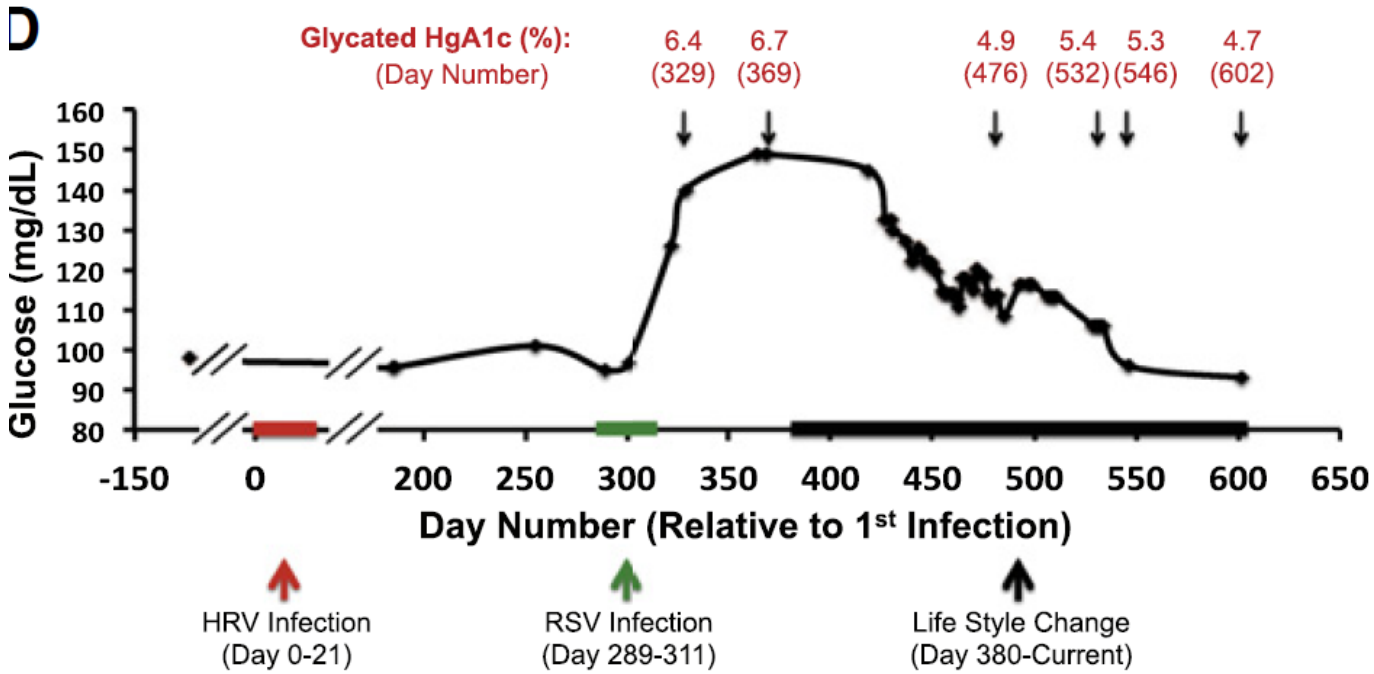
Personal profile-based healthcare

Personal Omics Profiling Reveals Dynamic Molecular and Medical Phenotypes

Rui Chen,[1,11] George I. Mias,[1,11] Jennifer Li-Pook-Than,[1,11] Lihua Jiang,[1,11] Hugo Y.K. Lam,[1,12] Rong Chen,[2,12] Elana Miriami,[1] Konrad J. Karczewski,[1] Manoj Hariharan,[1] Frederick E. Dewey,[3] Yong Cheng,[1] Michael J. Clark,[1] Hogune Im,[1] Lukas Habegger,[6,7] Suganthi Balasubramanian,[6,7] Maeve O'Huallachain,[1] Joel T. Dudley,[2] Sara Hillenmeyer,[1] Rajini Haraksingh,[1] Donald Sharon,[1] Ghia Euskirchen,[1] Phil Lacroute,[1] Keith Bettinger,[1] Alan P. Boyle,[1] Maya Kasowski,[1] Fabian Grubert,[1] Scott Seki,[2] Marco Garcia,[2] Michelle Whirl-Carrillo,[1] Mercedes Gallardo,[9,10] Maria A. Blasco,[9] Peter L. Greenberg,[4] Phyllis Snyder,[1] Teri E. Klein,[1] Russ B. Altman,[1,5] Atul J. Butte,[2] Euan A. Ashley,[3] Mark Gerstein,[6,7,8] Kari C. Nadeau,[2] Hua Tang,[1] and Michael Snyder[1,*]





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THE INSTITUT PASTEUR IN 2015

2500 persons

10 Nobel laureates

14 National Reference centers
8 WHO collaborating centers

More than 60 nationalities
46% « non-french » scientists

130 Research units

500/year students
Master
PhD
postdoc

Microbiology
Infectious diseases
Immunology
Neurosciences
Stem cells
Cancer
Genetics

11 Scientific departments

55 000 square meter campus in the heart of Paris

Industrial partnerships (20 biotech, 4 listed)

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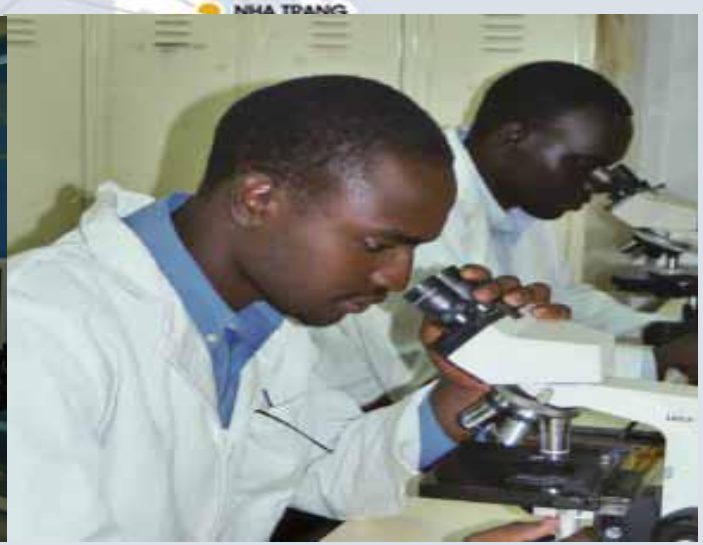

33 institutes Pasteur gather about 9 500 people in 26 countries, over 5 continents

- **in agreement with the local health authorities**
- **within the international network, the institutes share their knowledge, their research programs and keep control of the development of infectious diseases**
- **A major partner for international institutions, Fundations, Governments and industrials**

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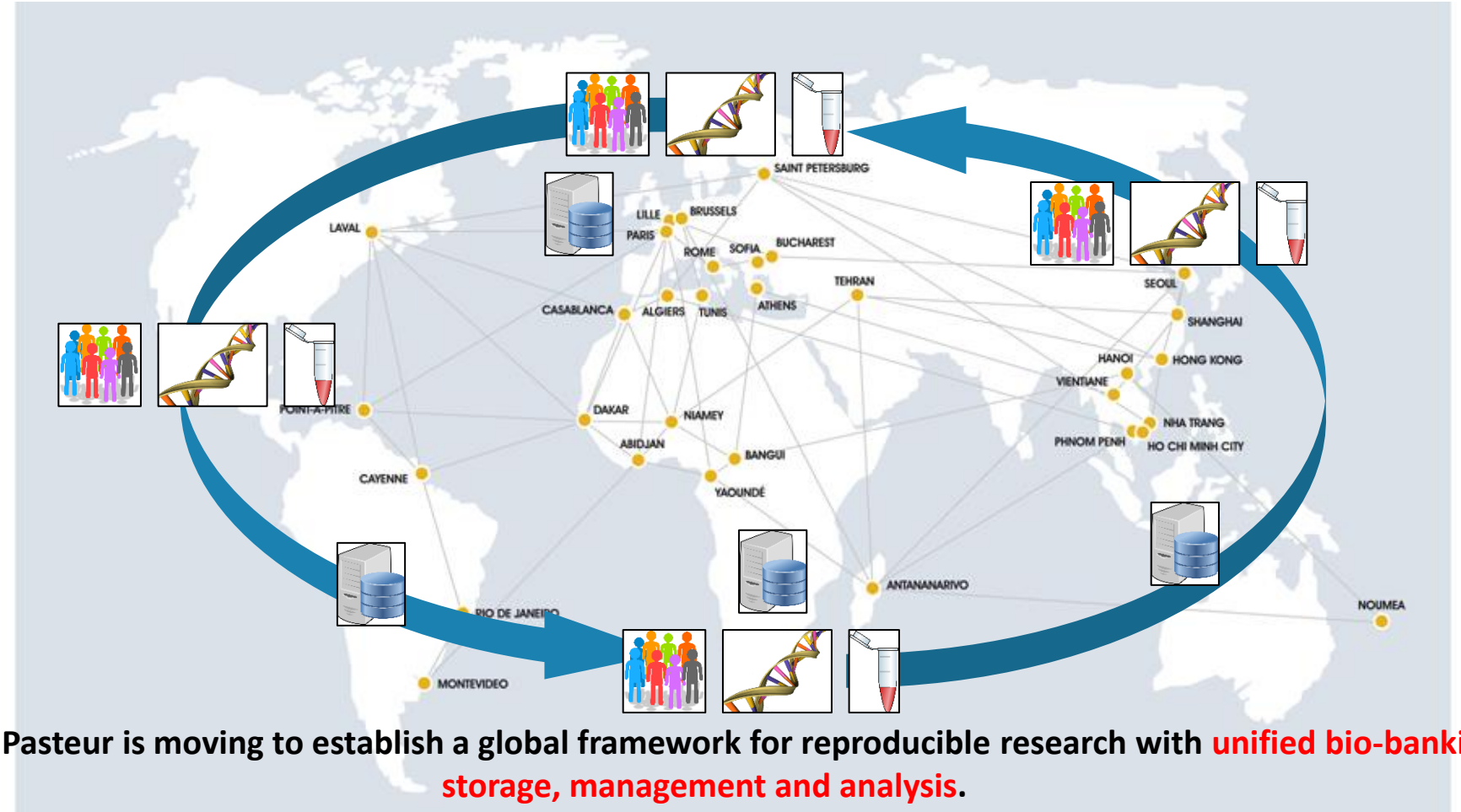
THE GLOBAL VISION FOR THE FUTURE

Cloud for data management and analysis: a Centre for Global Health Genomics



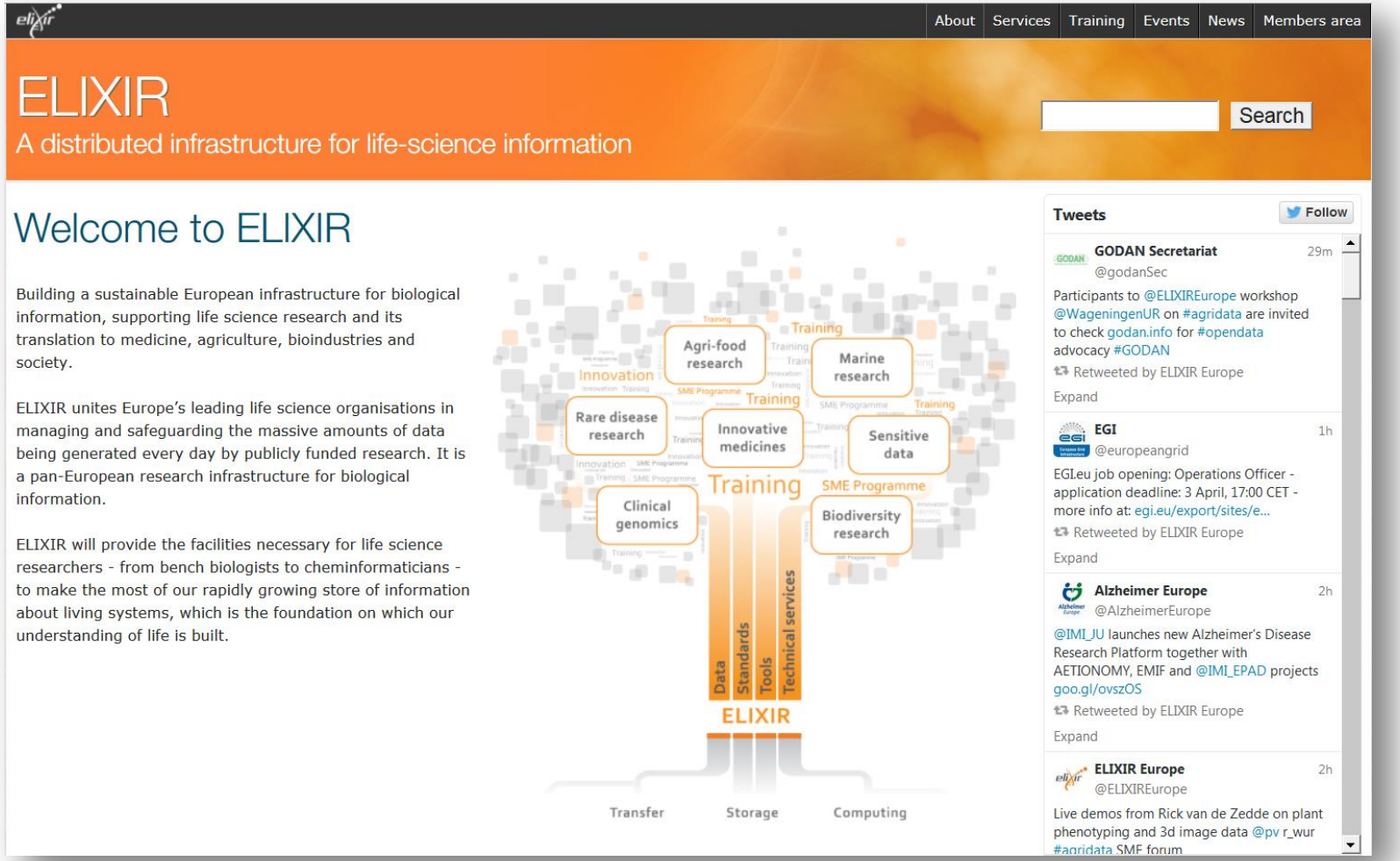
The Institut Pasteur is moving to establish a global framework for reproducible research with unified bio-banking, data storage, management and analysis.

Resources will be connected and shared through the IP cloud for data analysis.

Institut Pasteur INDA

INSTITUT PASTEUR IS CONNECTED TO THE THE EUROPEAN INITIATIVE ELIXIR.

The IP network has the ambition to take a globally leading role to secure alignment around our focus on precision medicine for global health



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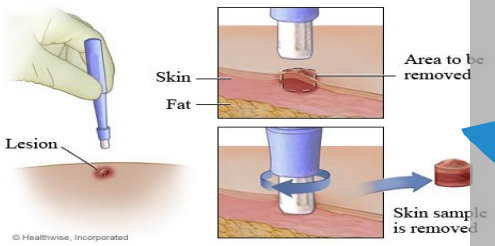
Sample collection

Whole Blood

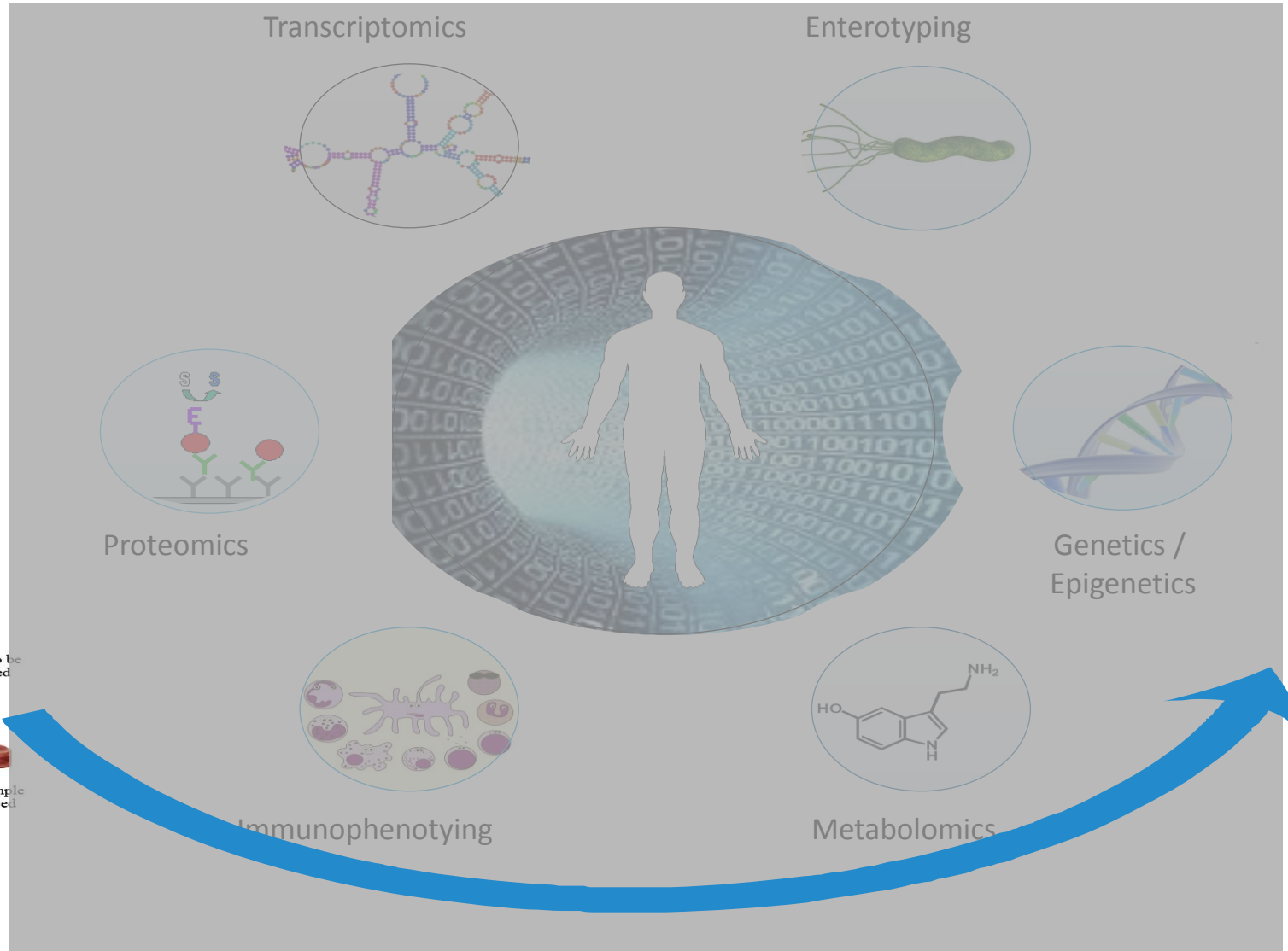
Fecal Sample



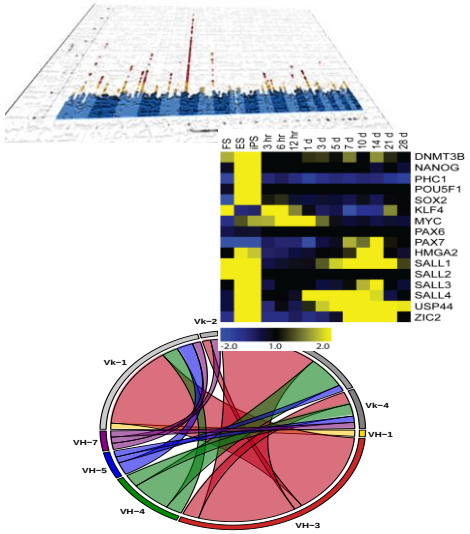
Tissue biopsy

Sample handling*
*and storage

Technical cores

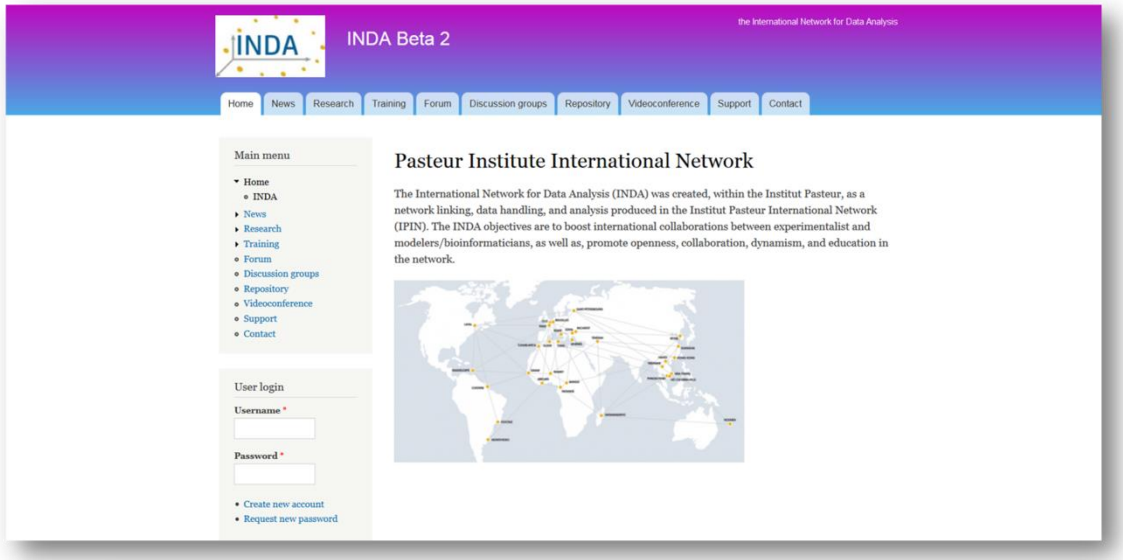


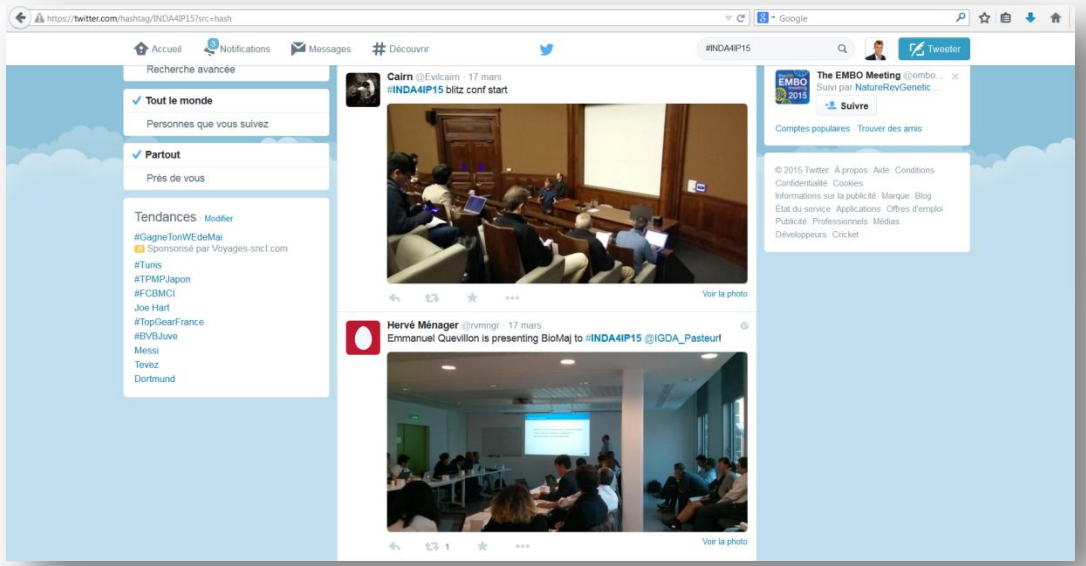
Data analysis



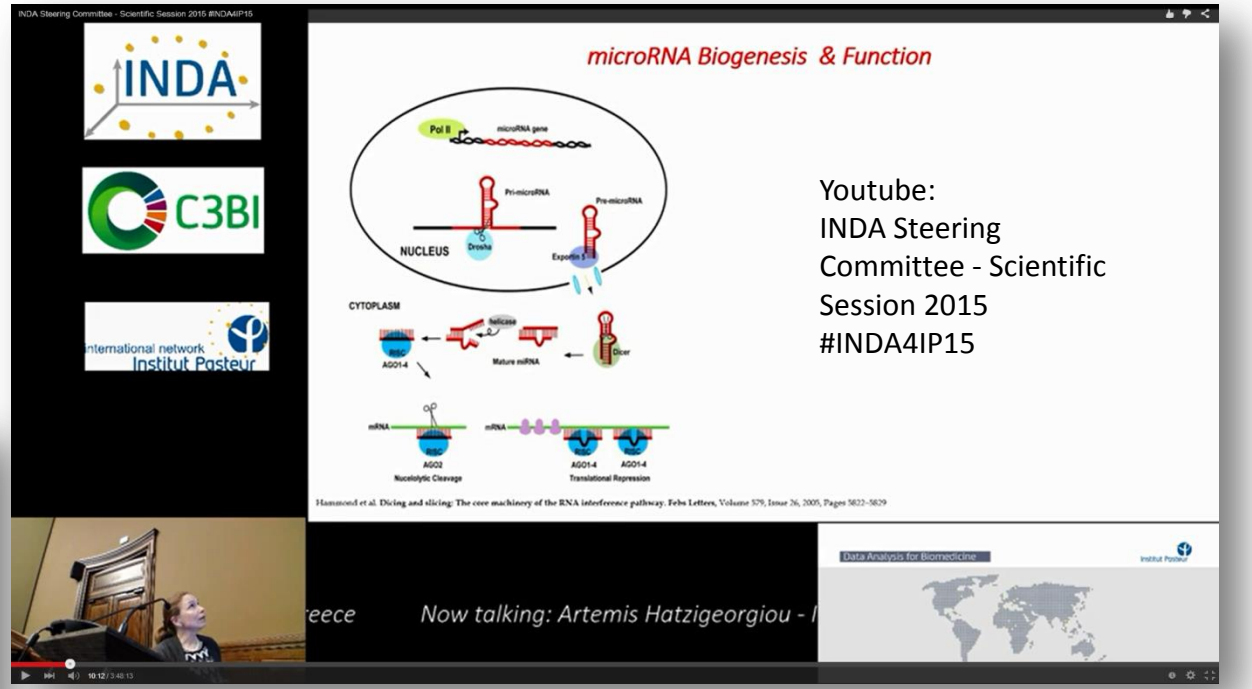
Data storage & access

The Institut Pasteur International Network for Data Analysis (IP-INDA): An aligned global community for data analysis ready for action





Global collaborative dynamism through local adaption



Youtube:
INDA Steering Committee - Scientific Session 2015
#INDA4IP15

Developing and sharing best practices in bioinformatics globally, performing training and engaging in data intensive biomedical research.

Follow us on https://twitter.com/IGDA_Pasteur

Global coordination, example, The Steering Committee INDA 17th March 2015 in Paris

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