

Shaping the future of cancer research from the end of the beginning

Ashok Venkitaraman

The Ursula Zoellner Professor of Cancer Research & Director,
Medical Research Council (MRC) Cancer Unit at the University
of Cambridge



1994-2019

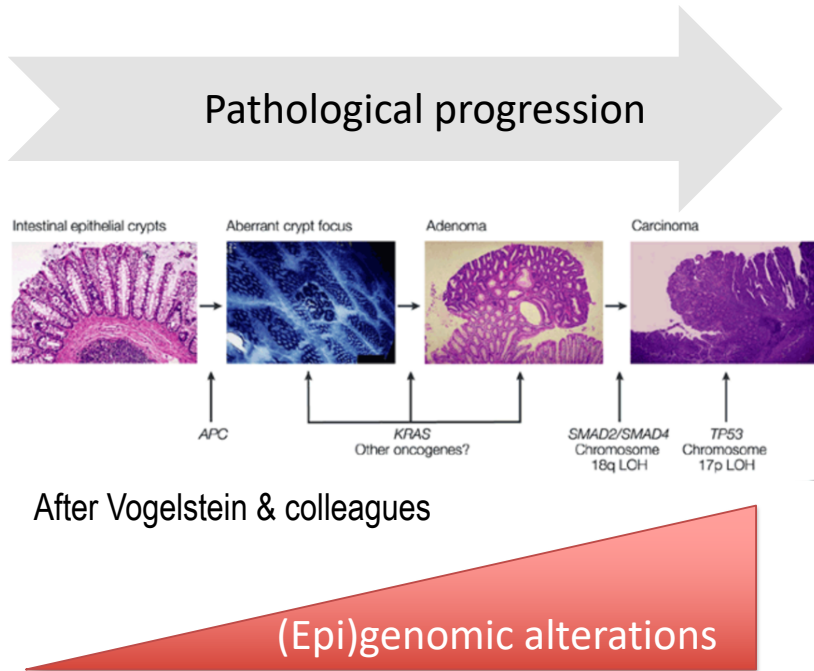


Shaping the future of cancer research from the end of the beginning

Cancer will affect ~1 in 4 of us. Its incidence is increasing worldwide with aging populations. Cancer has a larger economic impact than any other disease.

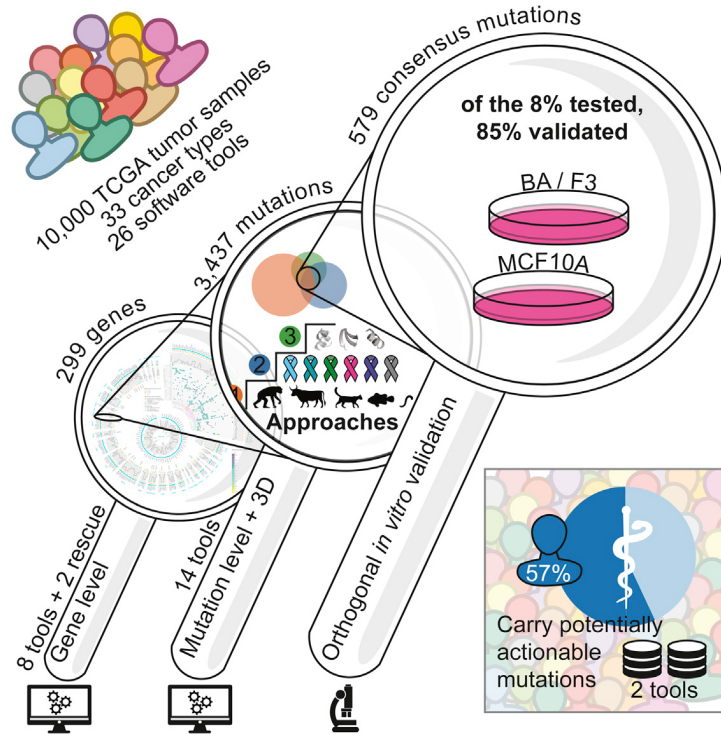
- Why are we at the 'end of the beginning' in understanding and treating cancer?
- What are the future horizons for cancer research?
- What will it take to reach them – in Singapore and elsewhere?

Cancer: the end of the beginning

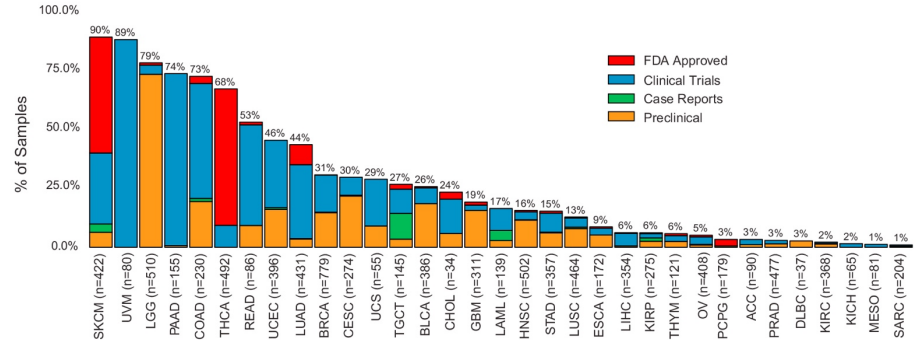


- 2005 - first cancer genome
- 2010 - about a hundred cancer genomes, information used for scientific research & discovery
- 2018 - 1000s of cancer genomes - translation to the clinic underway (eg., stratification of patients in clinical trials based on 'actionable' genotypes)

Cancer: the end of the beginning



Bailey et al., *Cell* (2018)



- The Cancer Genome Atlas (TCGA) reported in 2018 the analysis of 10,300 cancers from 33 different tissues
- About 300 genetic alterations collude to drive the most common cancers
- ~60% are potentially 'actionable' in the clinic **if** new treatments can be devised

The end of the beginning: approaching the premise of personalized medicine

Integration of molecular research with clinical data from individual patients to develop a more accurate **molecular taxonomy of diseases** that enhances diagnosis and treatment and **tailors disease management to the individual** characteristics of each patient.

(US Nat Acad of Sciences, 2011)

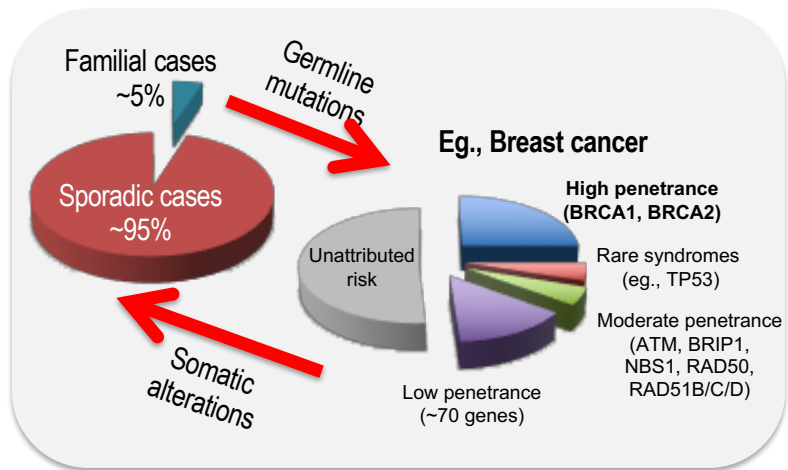
Matching therapies with specific patient population characteristics **using clinical biomarkers**.

(Trusheim et al, 2007)

Shaping the future: delivering the clinical impact of personalized cancer medicine

- Formulation of a new taxonomy of human cancers, based on the integration of their molecular and clinical features
- Discovery and validation of robust, clinically applicable biomarkers to individualize patient management
- Creation of an enhanced repertoire of drugs and clinical interventions suited to individual patients
- Beyond personalized therapy towards EARLY intervention in cancer

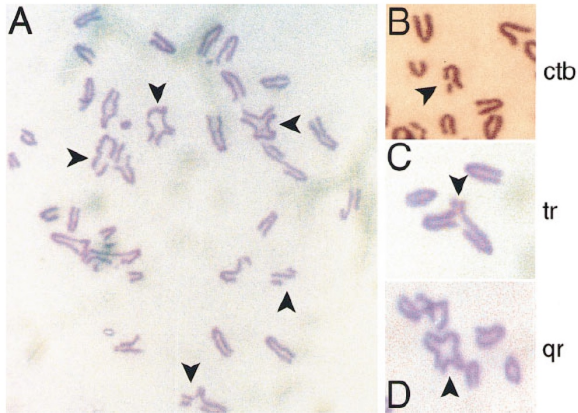
From taxonomy to treatment: germline mutations in the breast cancer gene, *BRCA2*



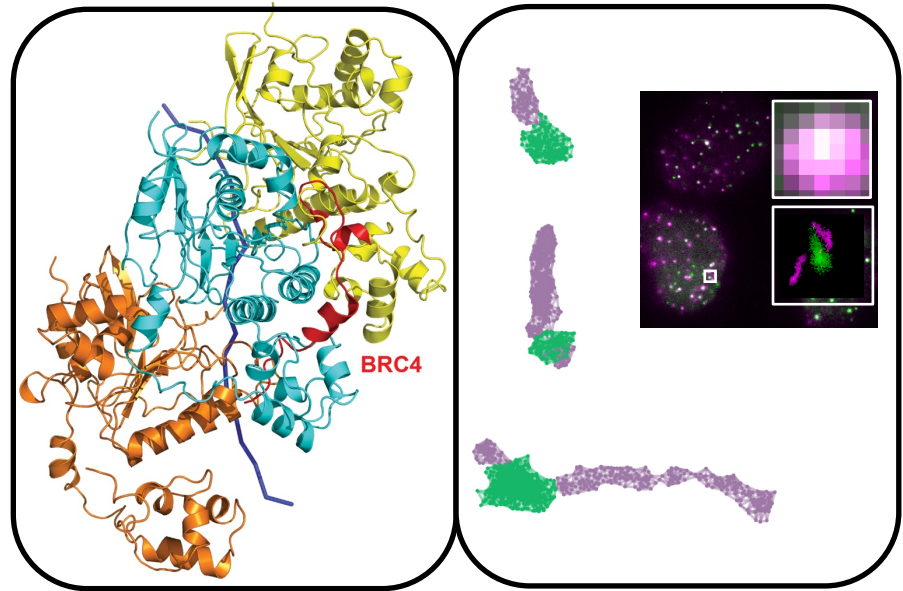
Reviewed in Venkitaraman *Science* (2014)

- Germline *BRCA2* mutations affecting a single allele predispose to breast, ovarian, pancreatic, prostatic and other cancers
- Carriers exhibit a cumulative risk of ~70% for breast cancer, and ~25% for ovarian cancer, by age 80 yrs. (ie., **highly penetrant**)
- Cancer risk increases rapidly until ~45 yrs. (ie., **early onset**)

From taxonomy to treatment: germline mutations in the breast cancer gene, *BRCA2*



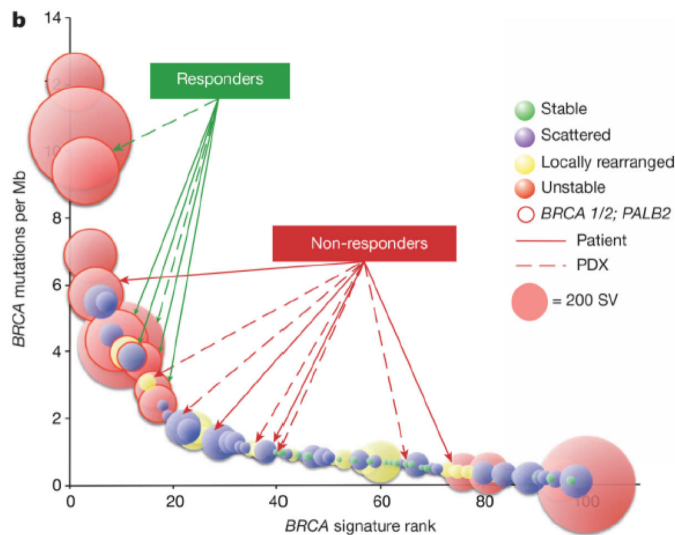
Patel, Yu et al. (1998)



Jude Short, Yang Liu (2016)

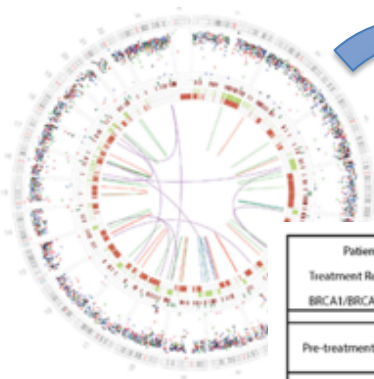
Kalina Haas, Ale Esposito (2018)

From taxonomy to treatment: germline mutations in the breast cancer gene, *BRCA2*



Modified from Waddell et al, *Nature* 2014

Responsiveness to DNA
damaging agents



The “HR Detect”
biomarker predicts
responsiveness

Modified from Davies et al, *Nat Med* 2017

Patient	PD9768	PD9769	PD9770	PD9771	PD9777	PD9772	PD9774	PD9775	PD9776
Treatment Response	RD	RD	RD	RD	RD	CR	CR	CR	CR
<i>BRCA1/BRCA2</i> status						<i>BRCA1</i>	<i>BRCA1</i>	<i>BRCA1</i>	<i>BRCA1</i>
Pre-treatment Biopsy 1	PD9768c 0.02	PD9769c 0.22	PD9770c 0.01	PD9771c 0.00	PD9777c 0.55	PD9772a2 1.00	PD9774c 1.00	PD9775c 1.00	PD9776c 1.00
Pre-treatment Biopsy 2			PD9770d 0.14	PD9771a 0.01	PD9777a 0.03			PD9775a 1.00	PD9776a 1.00
Post-treatment specimen from surgical block		PD9769a 0.16	PD9770a 0.39	PD9771d 0.03	PD9777d 0.07				

RD = residual disease

CR = complete response

Numbers indicate HRDetect probability score for each specimen

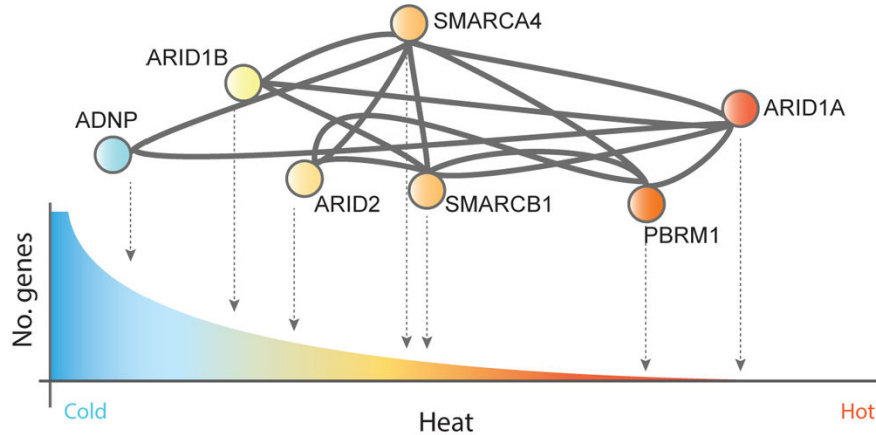
Reviewed in Venkitaraman *Science* (2014)

But translating cancer taxonomy to mechanism generally remains challenging



Venkitaraman *Science* (2014)

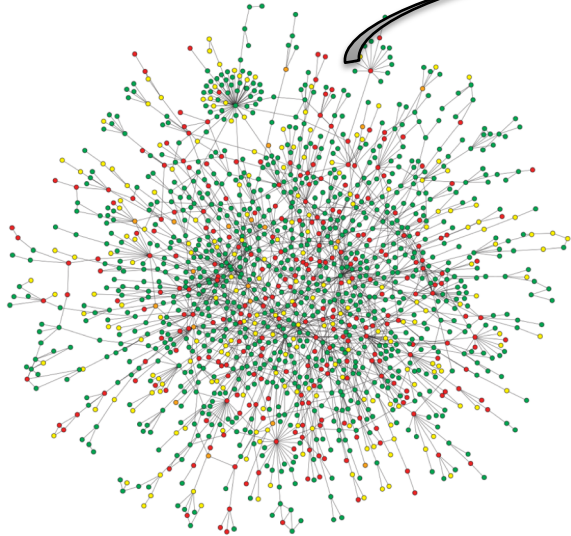
16 functional networks with 150 genes



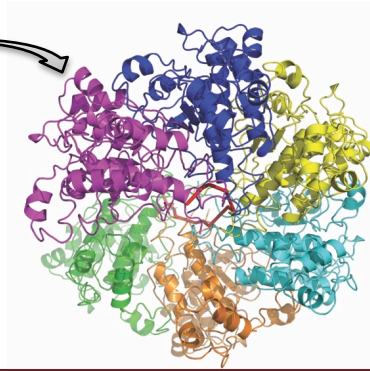
Leiserson et al. *Nature Gen* (2015)

- Many genomic alterations that characterize cancer are rare, and difficult to distinguish from “background”
- Multiple genes in multiple functional networks are affected even in the most significant clusters of alterations
- These features pose challenges in translating taxonomy to treatment

As is the translation of mechanism to cancer therapy



S. cerevisiae protein interaction network
(Jeong et al., *Nature* (2011))



- Biological processes altered in human disease are enacted by complex networks of interactions between proteins & other macromolecules (MMIs)
- Of >500K potential MMI targets, only a handful have been successfully 'drugged'
- Our limited ability to parse MMI networks using selective chemical tools impedes chemical biology & the development of new therapies

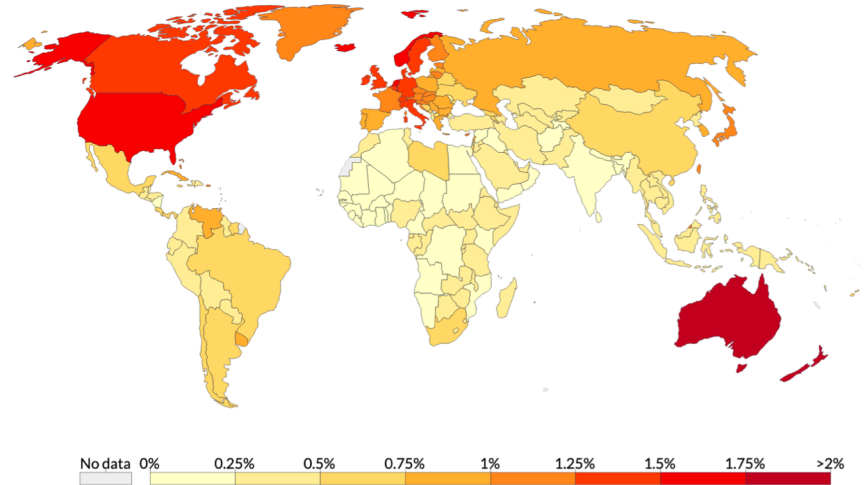
The *status quo* is not an option

- The cost of bringing a new medicine to market is estimated by pharma companies to exceed \$1BN. The time taken exceeds 10 years. Yet, the failure rate may approach 70-90%.
- *The status quo is not an option*We need to more rapidly and cheaply develop 'next generation' drugs to fuel the personalized treatment of diseases like cancer.

Yet the global unmet need is acute

Share of population with cancer, 2016

Share of total population with any form of cancer, measured as the age-standardized percentage. This share has been age-standardized assuming a constant age structure to compare prevalence between countries and through time.



Source: IHME, Global Burden of Disease

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Accelerating next-generation medicines – our work at the MRC Cancer Unit in Cambridge

New genetic tools

to identify rate-limiting steps



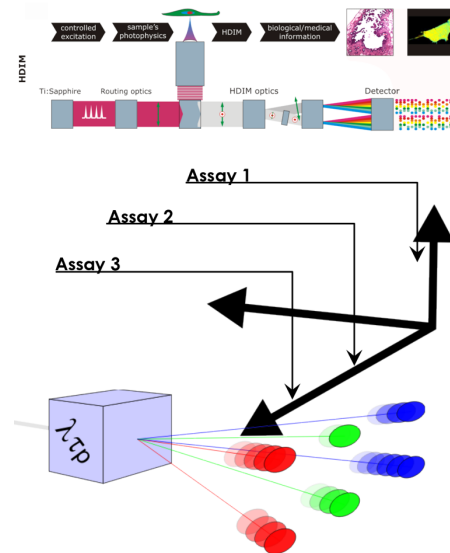
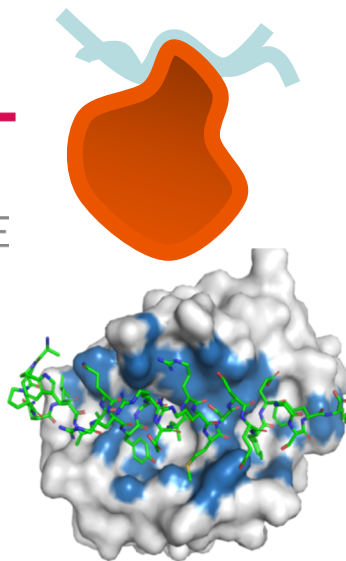
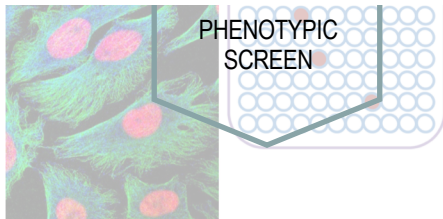
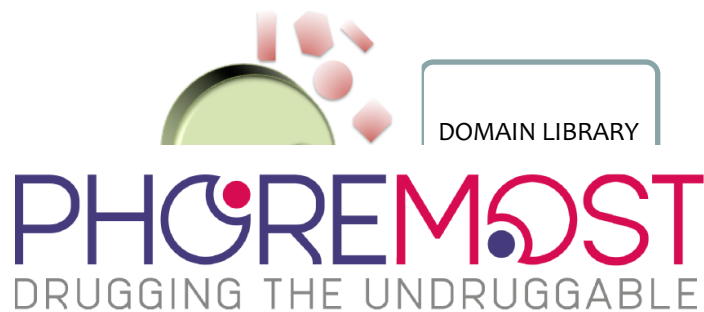
Structure-guided chemical lead

discovery as a starting point for new drugs

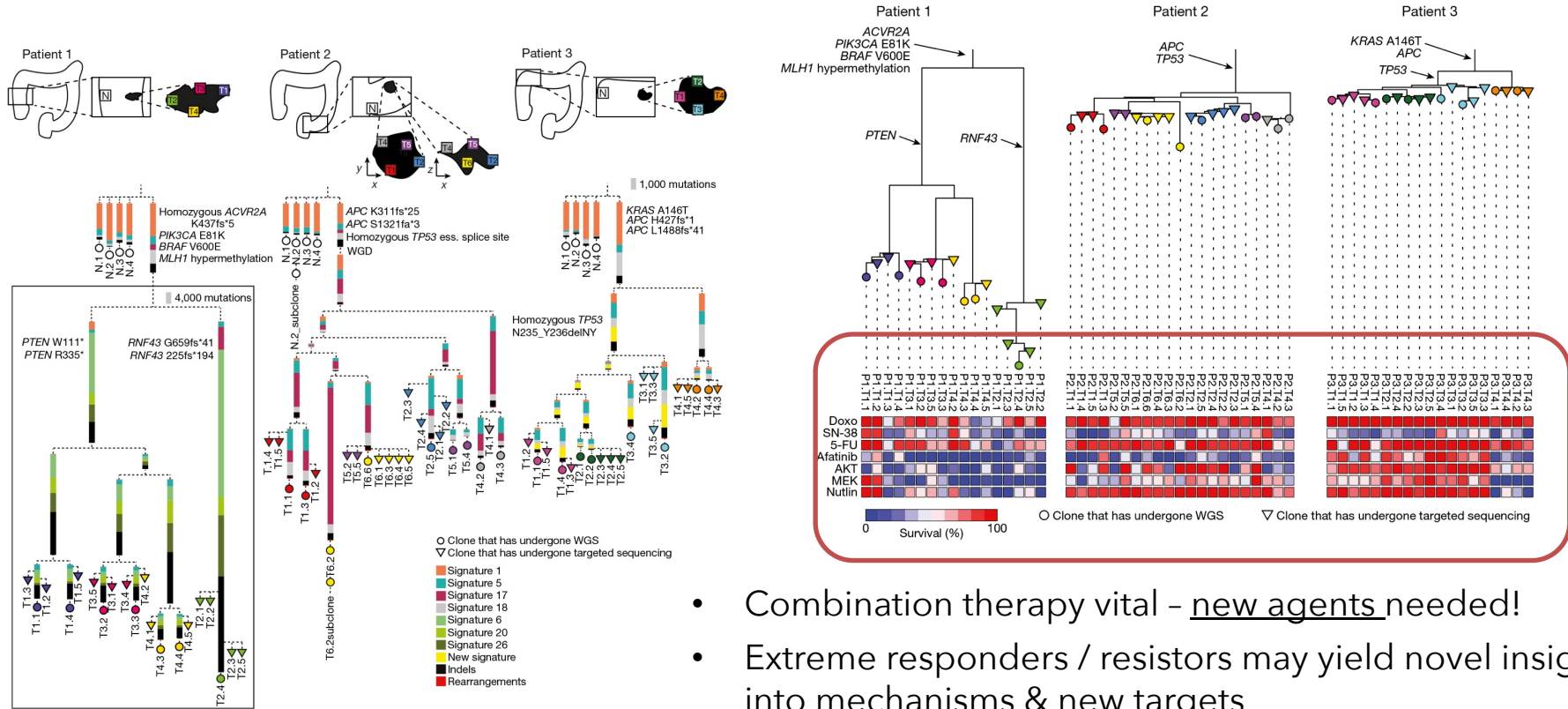


Systems microscopy

to reveal how new drugs work



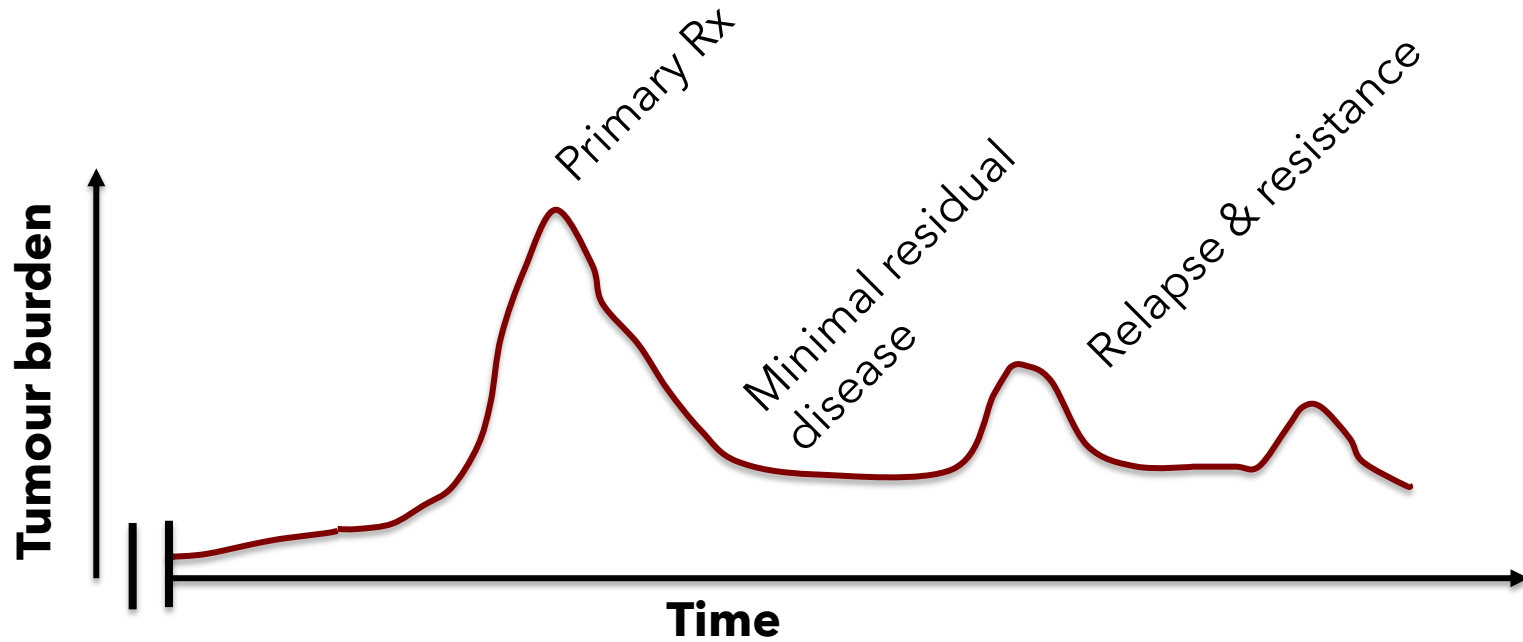
Clonal heterogeneity & therapy resistance



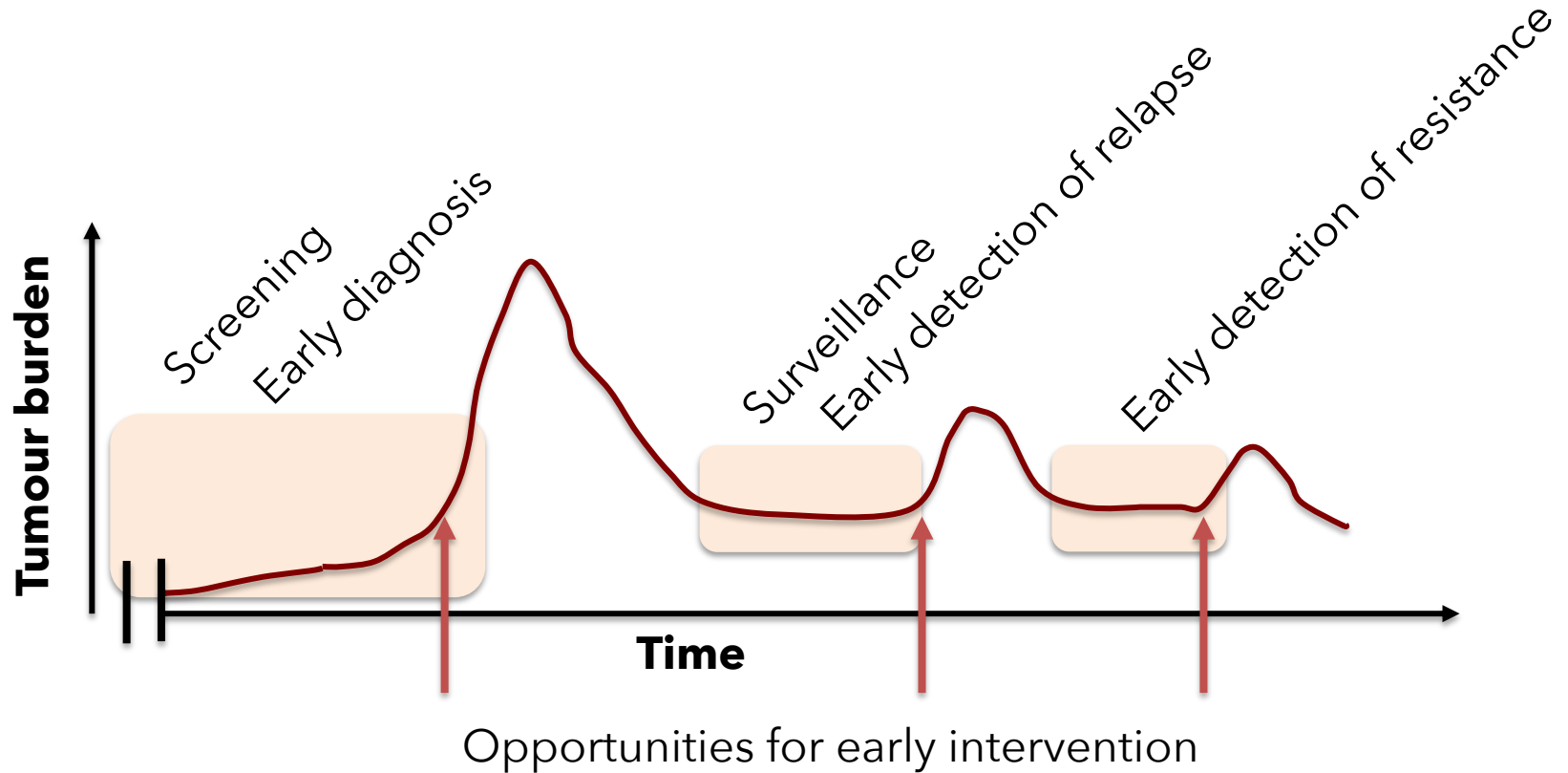
Roerink et al., *Nature* (2018)

- Combination therapy vital – new agents needed!
- Extreme responders / resistors may yield novel insight into mechanisms & new targets
- Needs a change in clinical *mindset*? Cancer as a chronic disease

Beyond personalized therapy?



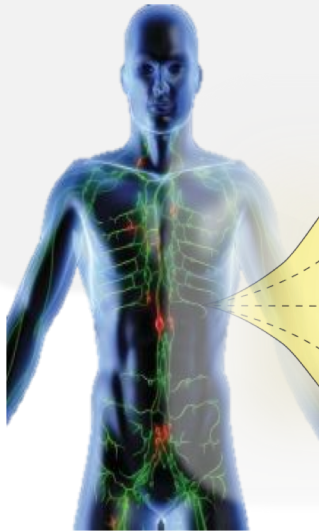
Beyond personalized therapy? Early intervention across disease progression



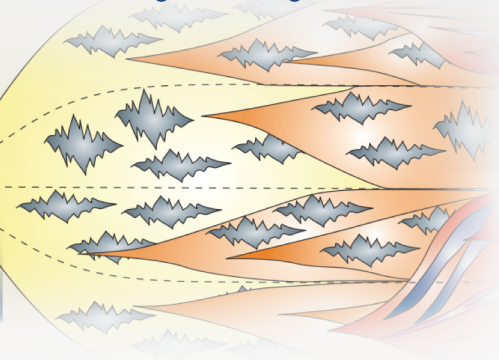
The MRC Cancer Unit: Advancing early intervention in cancer

- Early detection
- Risk stratification
- New approaches for therapy and prevention

Genetic & environmental risk



Molecular & cellular events
during carcinogenesis



Enabling technologies



MRC

Cancer
Unit

Brief reflections – What will it take in
Singapore and elsewhere?

Paradigm-shifting clinical translation is impossible without fundamental research

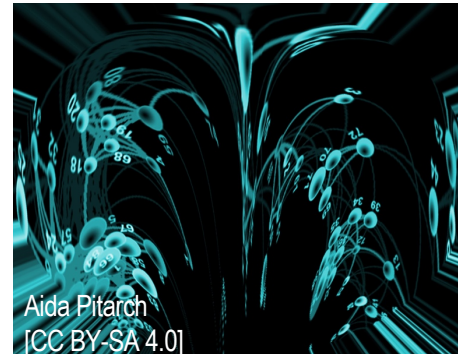
Richard Doll, A.B. Hill



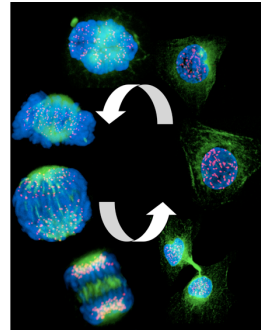
Peter Mansfield



Cesar Milstein,
Greg Winter



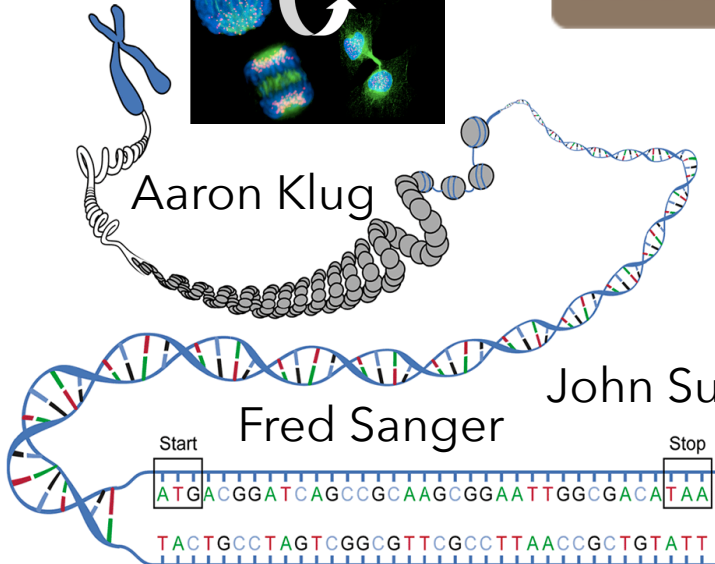
Aida Pitarch
[CC BY-SA 4.0]



Aaron Klug

John Sulston

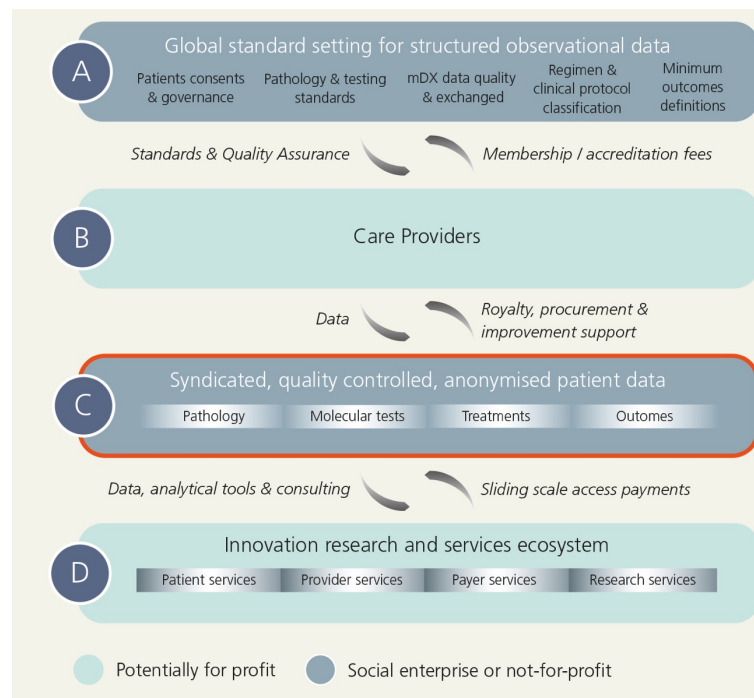
Fred Sanger



The growing need for “game changing” information bases

“Game changing” information bases may potentially require:

- 100K to 1000K cancer genomes including *longitudinal* collections
- Deep linkage to clinical phenotypes and associated samples (eg., blood)
- Standardized mechanisms for collection, analysis and reporting



Mahon & Tenenbaum *J Precis Med* (2015)
Andrew Morris, Health Data Research UK

Singapore: does size matter?

Millions of patients tested to identify 250 cases/year
assuming X% biomarker prevalence

Incidence Rank	Site	Incidence (per m)	Mortality	X=30%	X=10%	X=5%	X=1%
3	Lung	530	83%	1.6	4.7	9.4	47
8	Pancreas	111	94%	7.5	23	45	226
14	Kidney	82	46%	10	31	61	306
17	Ovary	62	62%	13	40	81	405
25	Brain	38	81%	22	66	131	657

Mahon & Tenenbaum *J Precis Med* (2015)

Singapore needs an integrated clinical infrastructure, with managed points of entry into clinical trials, to compete globally in academic or industrial cancer research that requires clinical material

Singapore

- Strong clinical base
- Multiethnic genetics
- Good research infrastructure

BUT

- ~5.8M population
- ~15K cancer cases/yr
- Insufficient integration between clinical centers

Leveraging the 4th Industrial Revolution

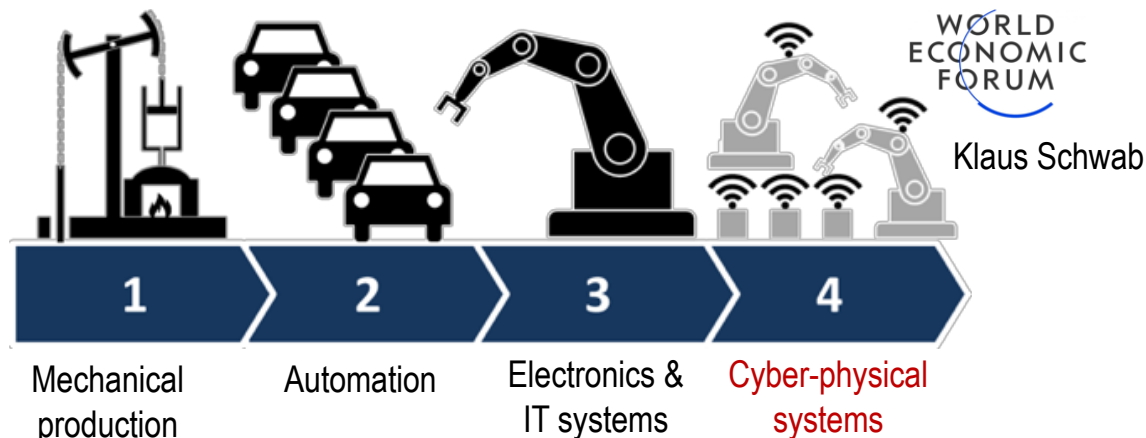
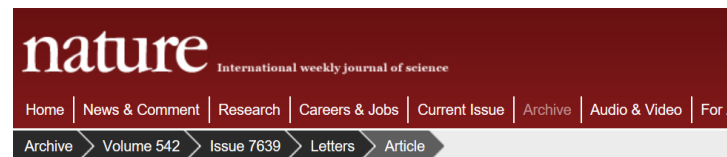


Image courtesy Christopher Rossner

Cancer diagnosis by mobile phone

- ~130K images of skin lesions analysed using deep neural networks; algorithm outperforms specialist dermatologists in diagnosis of malignancy
- >6 billion mobile telephones by 2020

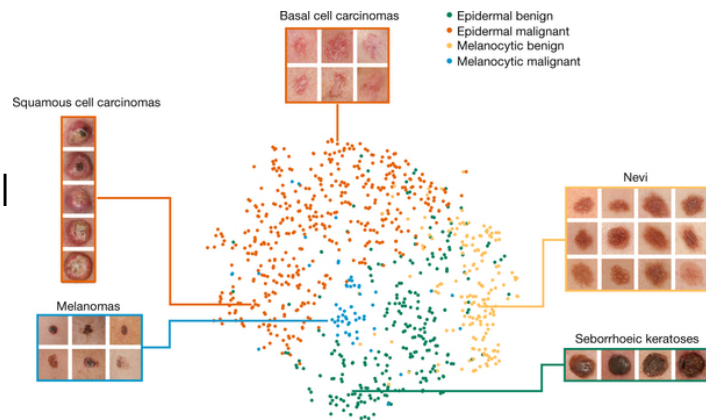


NATURE | LETTER

日本語要約

Dermatologist-level classification of skin cancer with deep neural networks

Andre Esteva, Brett Kuprel, Roberto A. Novoa, Justin Ko, Susan M. Swetter, Helen M. Blau & Sebastian Thrun



Shaping the future of cancer research from the end of the beginning

- What are the future horizons for cancer research?
 - Disruptive technologies to discover clinically stratified new therapeutics
 - Deep fundamental understanding & innovation for early intervention across all disease stages
- What will it take to reach them?
 - Build disease-centric multidisciplinary communities of fundamental, applied & clinical researchers addressing key challenges together
 - Devise assessment metrics that encourage paradigm shifts
 - Support the creation, accessibility & analysis of multidimensional, *longitudinal* clinical datasets
 - Nurture mutually beneficial external collaborations

The Medical Research Council Cancer Unit



UNIVERSITY OF
CAMBRIDGE



The mission of the MRC Cancer Unit is to discover the fundamental mechanisms underlying early steps in carcinogenesis, and to exploit this knowledge for early intervention in the clinic, using innovative enabling technologies.