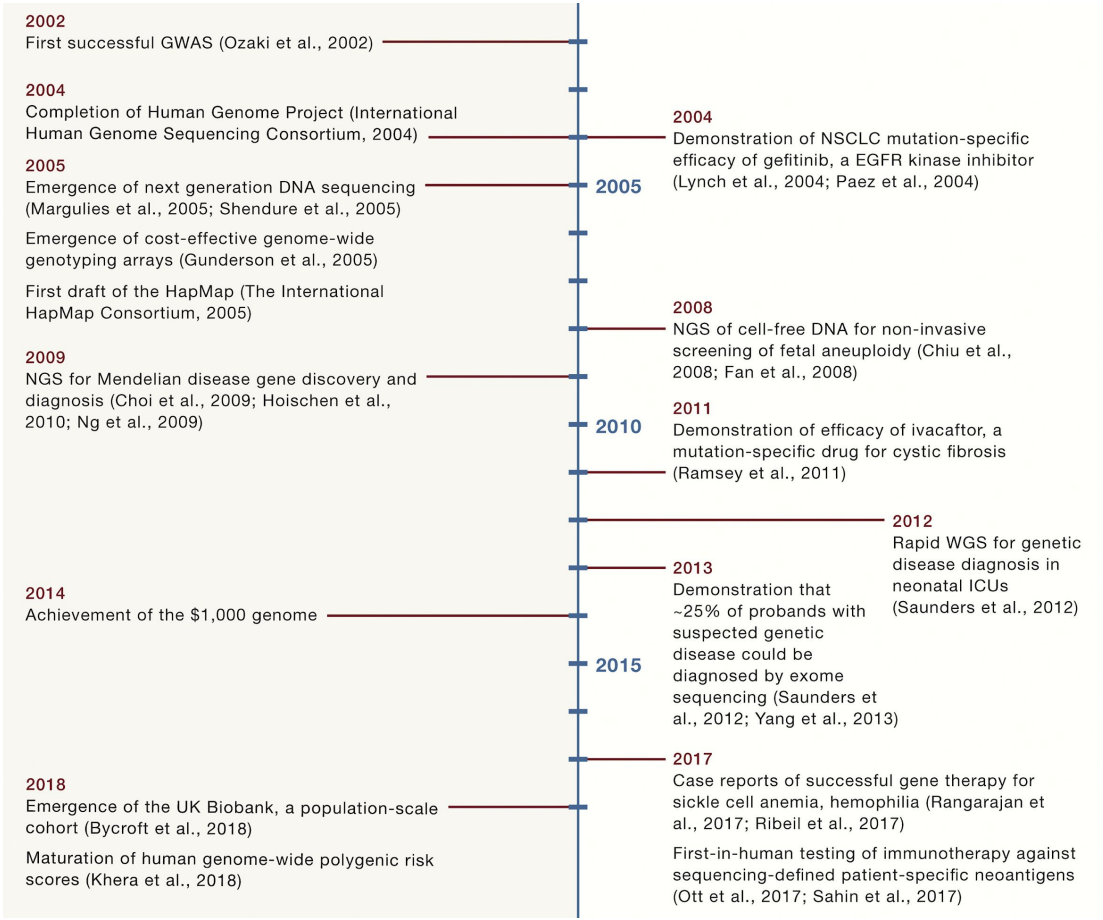
Lecture 29: Personal genomics

Milestones in genomic sciences & genomic medicine

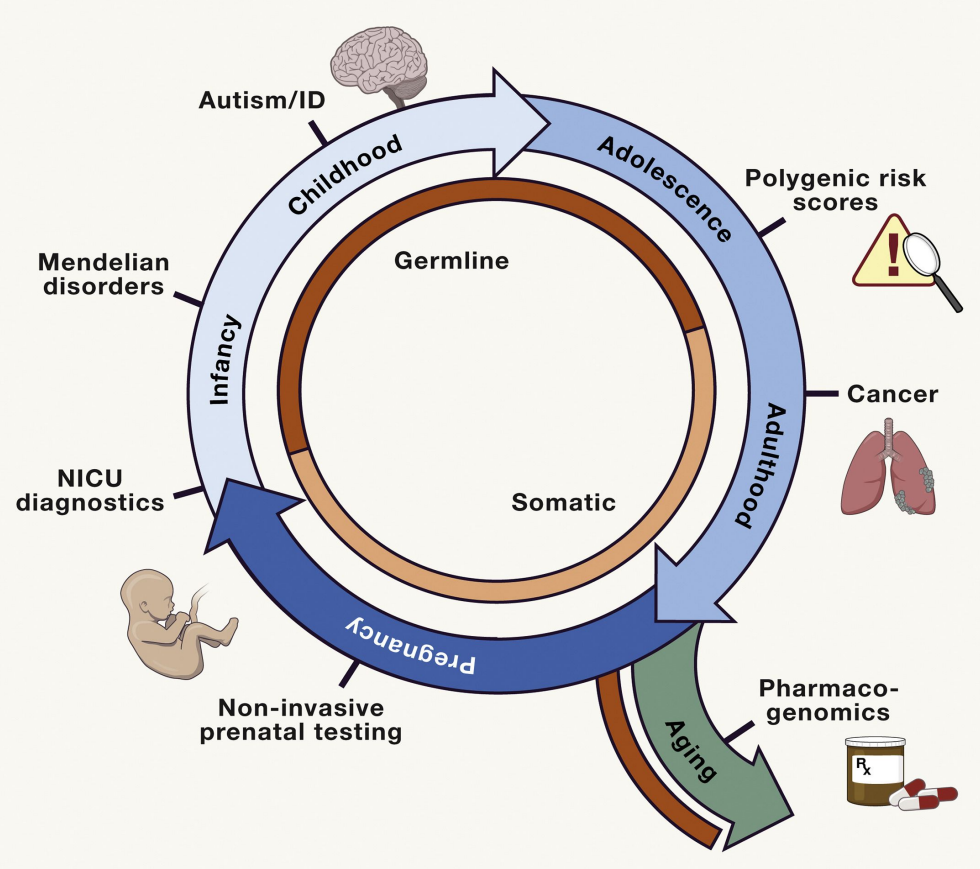
Science



Medicine

Schendure (2019) Cell

Genomic-medicine throughout the human life cycle

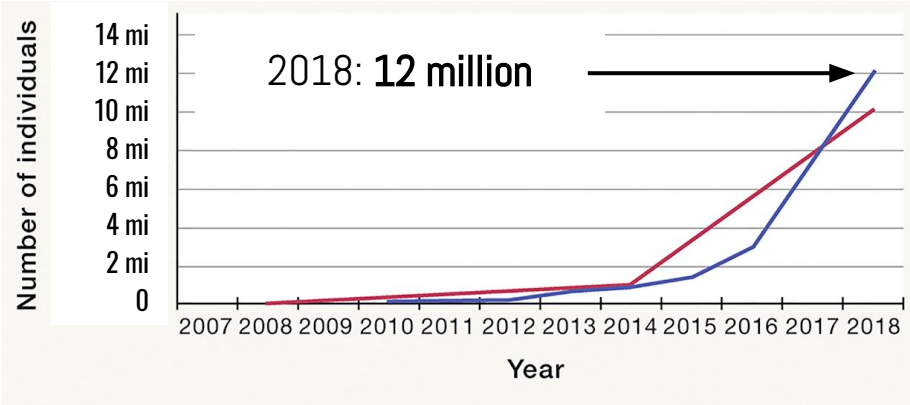


Schendure (2019) Cell

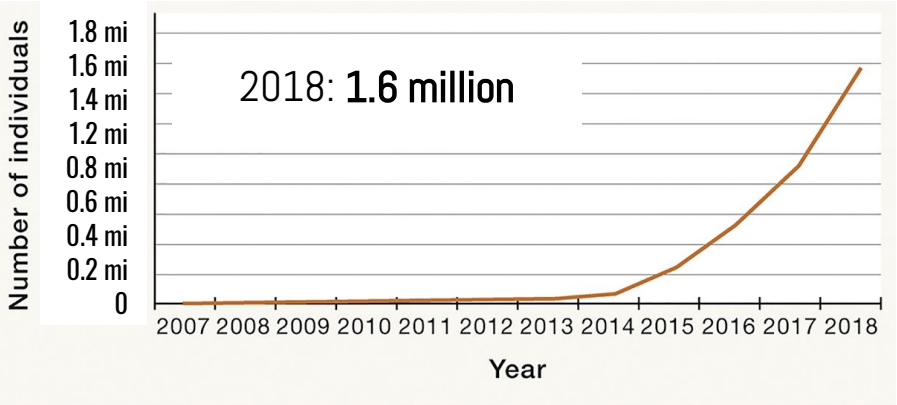
Exponential growth in genomic testing

Direct to consumer testing

Non-invasive prenatal testing

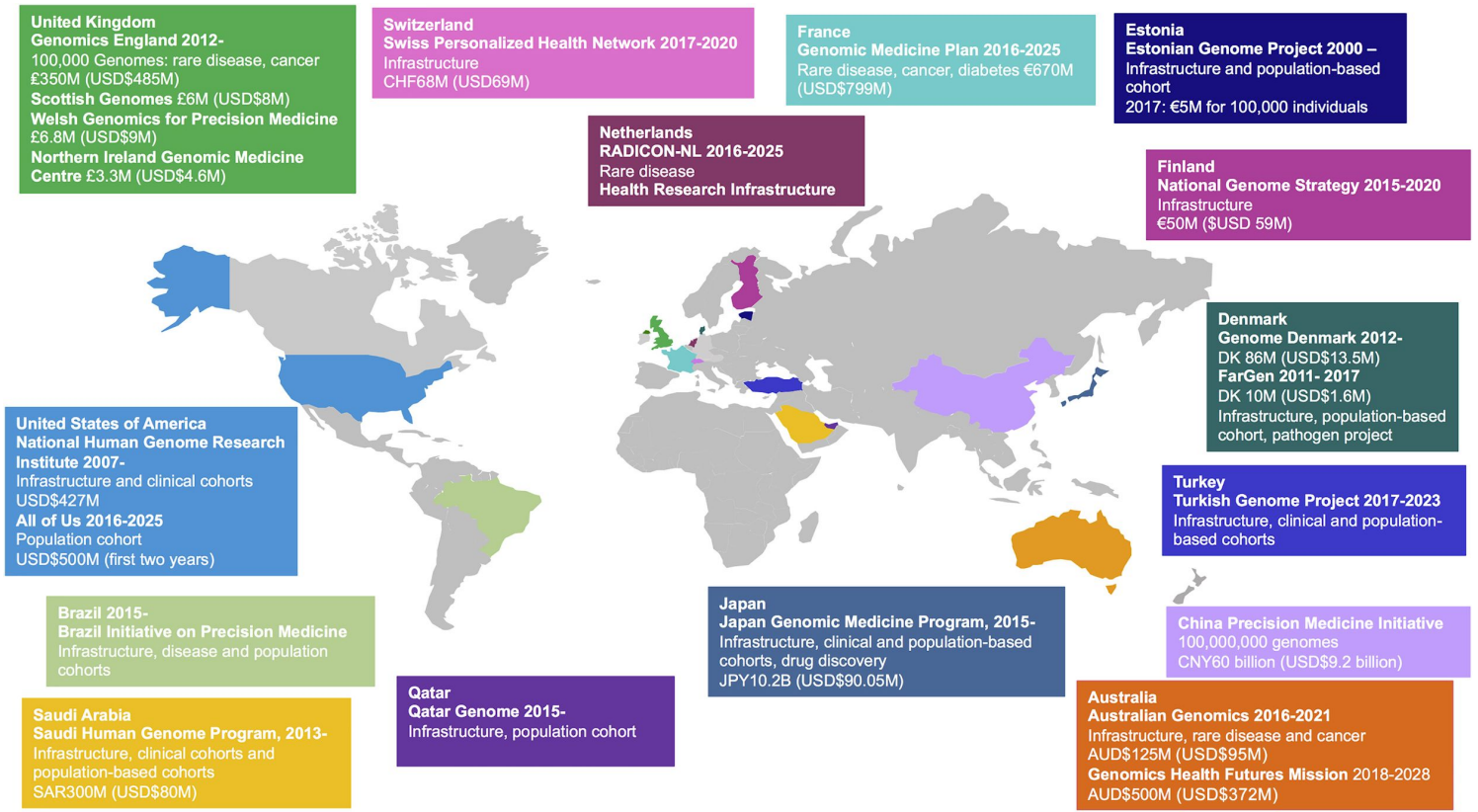


Genome sequencing



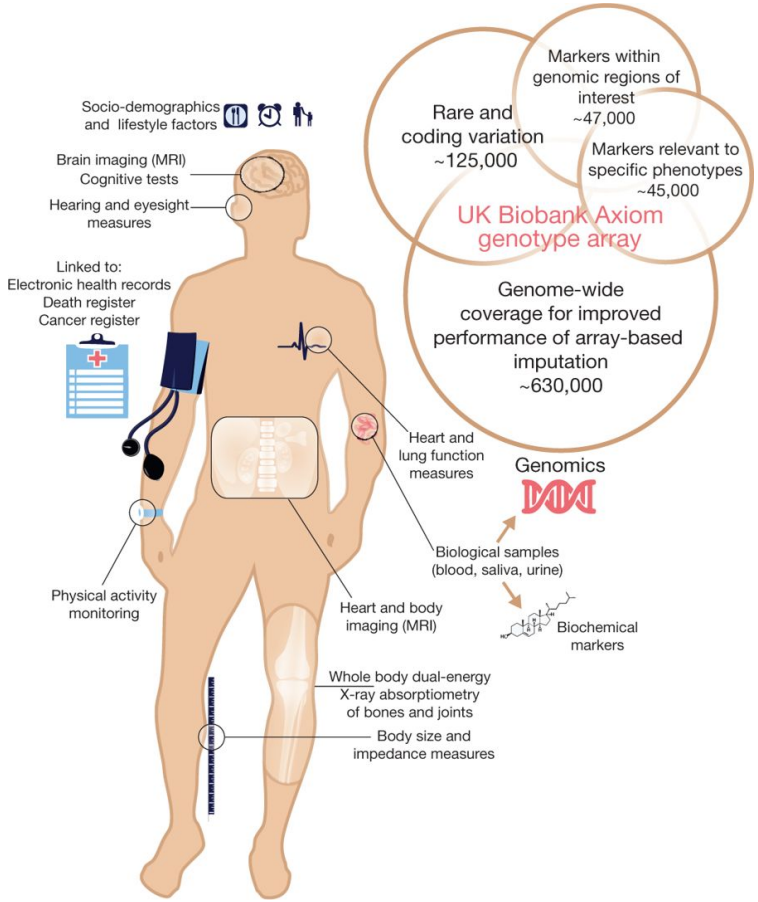
Schendure (2019) Cell

Govt-funded national genomic medicine initiatives



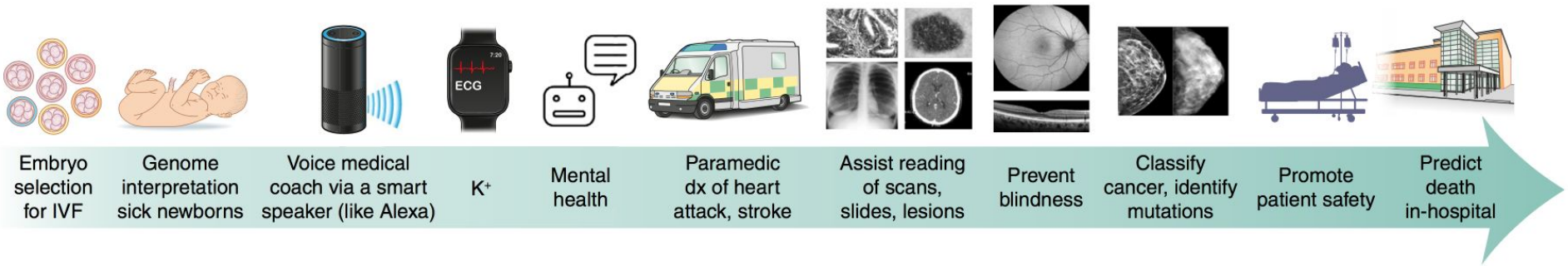
Stark (2019) Amer. Jour. Hum. Genet.

Govt-funded national genomic medicine initiatives



Bycroft (2018) Nature

ML applications across the human lifespan



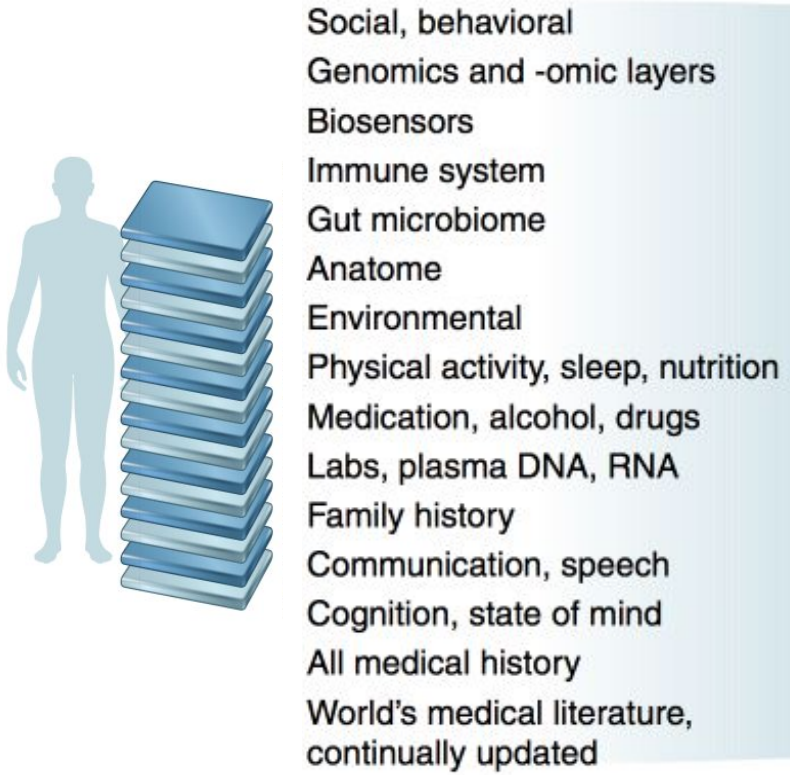
Topol (2019) Nat. Med.

FDA-approved ML algorithms

Company	FDA Approval	Indication
Apple	September 2018	Atrial fibrillation detection
Aidoc	August 2018	CT brain bleed diagnosis
iCAD	August 2018	Breast density via mammography
Zebra Medical	July 2018	Coronary calcium scoring
Bay Labs	June 2018	Echocardiogram EF determination
Neural Analytics	May 2018	Device for paramedic stroke diagnosis
IDx	April 2018	Diabetic retinopathy diagnosis
Icometrix	April 2018	MRI brain interpretation
Imagen	March 2018	X-ray wrist fracture diagnosis
Viz.ai	February 2018	CT stroke diagnosis
Arterys	February 2018	Liver and lung cancer (MRI, CT) diagnosis
MaxQ-AI	January 2018	CT brain bleed diagnosis
Alivecor	November 2017	Atrial fibrillation detection via Apple Watch
Arterys	January 2017	MRI heart interpretation

Topol (2019) Nat. Med.

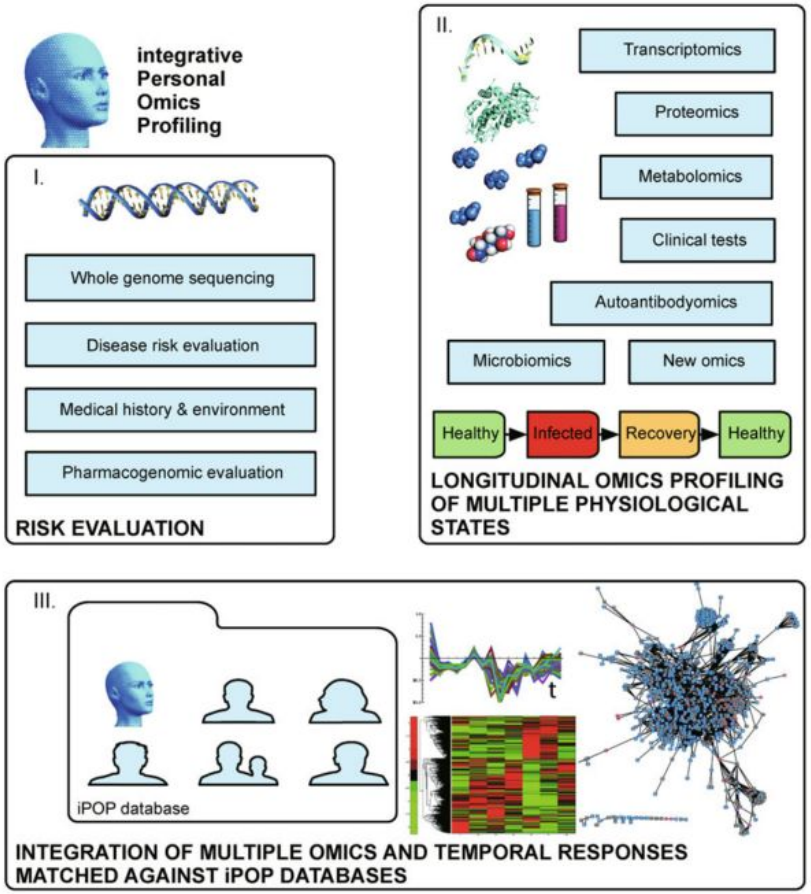
ML/AI-driven personalized health guidance



Topol (2019) Nat. Med.

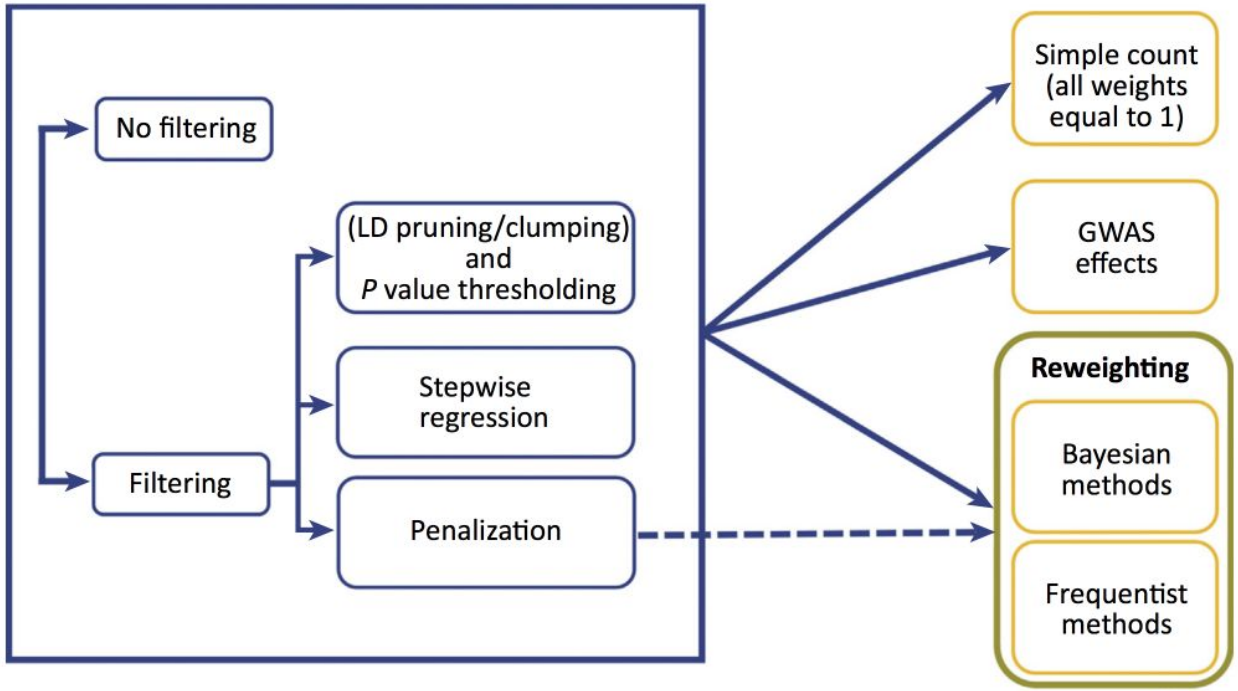
Personal genomics @ MSU

George Mias



Mias (2013) Quant. Biol.

Polygenic risk score

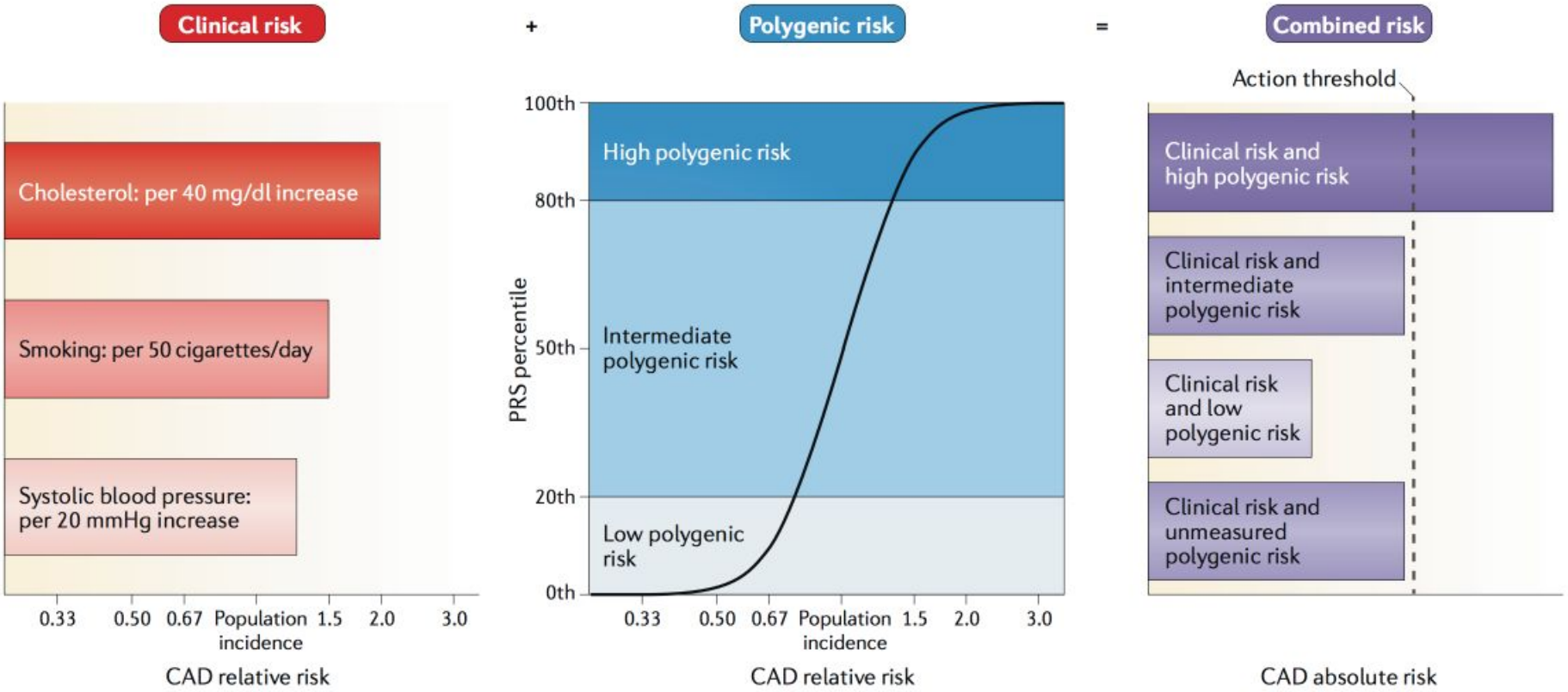


$$PRS_i = \sum_{j \in SNPs} d_{ij}$$

$$PRS_i = \sum_{j \in SNPs} \beta_j d_{ij}$$

Chasioti (2019) Trends. Genet.

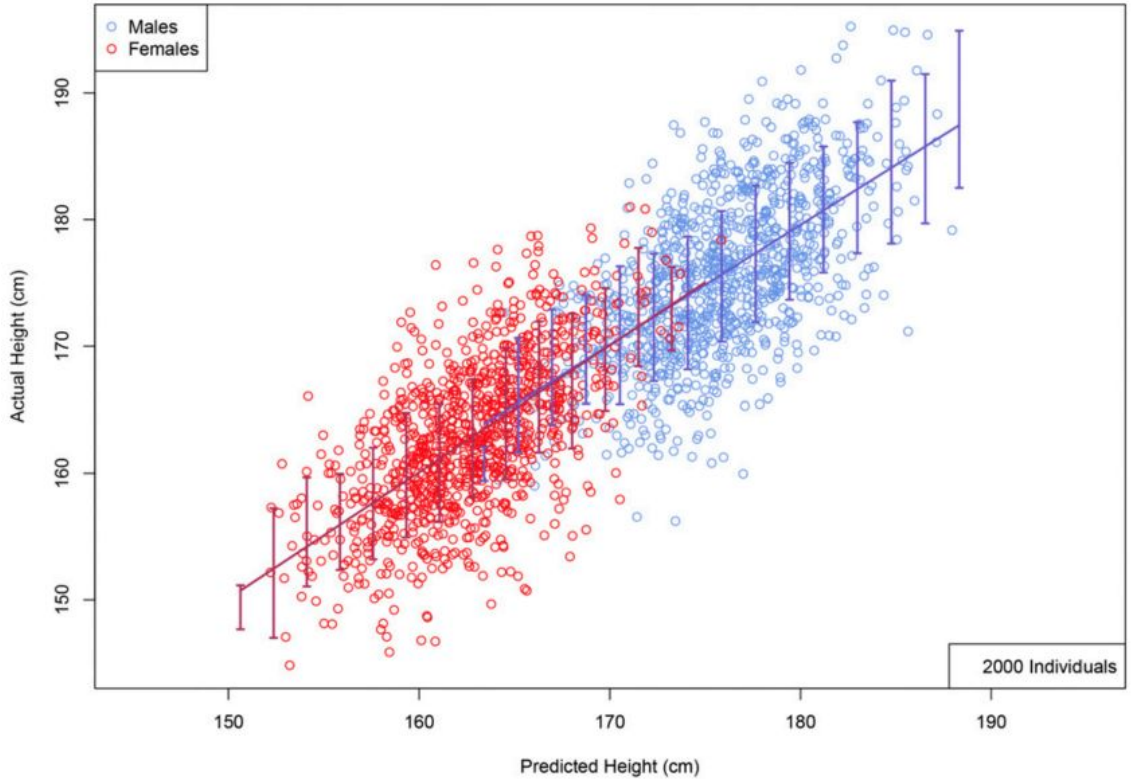
Polygenic risk score



Torkamani (2018) Nat. Rev. Genet.

Polygenic risk score @ MSU

Gustavo de los Campos & Stephen Hsu



Lello (2018) Genetics

Grand challenges in genomic sciences & genomic medicine

Science

- A spatiotemporally resolved molecular atlas of all human cell types, throughout the lifecycle, and in both health and disease
- A comprehensive catalog of common genetic variants in which all human populations, as well as all classes of genetic variation, are well represented
- A "telomere-to-telomere" ungapped reference representation of the human genome
- A functionally validated catalog of human regulatory elements, annotated with the gene(s) that they regulate and the cellular, developmental, and/or disease contexts in which they are active
- The definitive identification of causal variants and genes for thousands of GWAS associations
- A comprehensive understanding of the genetic basis of all Mendelian disorders
- A basic understanding of the primary function(s) of every human gene
- Algorithms that can accurately predict the consequences of arbitrary genetic variants at the molecular/cellular level

Medicine

- A database of whole genome sequences for at least 0.1% of living humans, integrated with electronic medical records and other phenotypes, and broadly accessible for research
- The routine use of exome or genome sequencing to diagnose the vast majority of suspected cases of Mendelian disease
- The routine use of genome-wide genotyping and polygenic risk scores for common disease risk prediction
- The generation of catalogs of clinically meaningful functional scores for all possible SNVs in all "clinically actionable" genes
- The routine use of exome or genome sequencing to guide cancer treatment, including for patient-specific immunotherapy
- The successful exploitation of cell-free DNA for early (or at least earlier) detection of common cancers
- Algorithms that can accurately predict the consequences of arbitrary genetic variants at the organismal level

Schendure (2019) Cell