

iMinds Department MEDICAL IT

Health
Data Analytics
and
Decision Support



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Department Med IT

Trends

P3 x P4 medicine

Decision support
cases



MEDICAL IT DEPARTMENT

207

PhD students

10

PhDs /
year

200

papers / year

4

Nature papers

21

10

PIs

PI H-index > 25

9

RM

8

Patents

8

Health spinoffs



Department Med IT

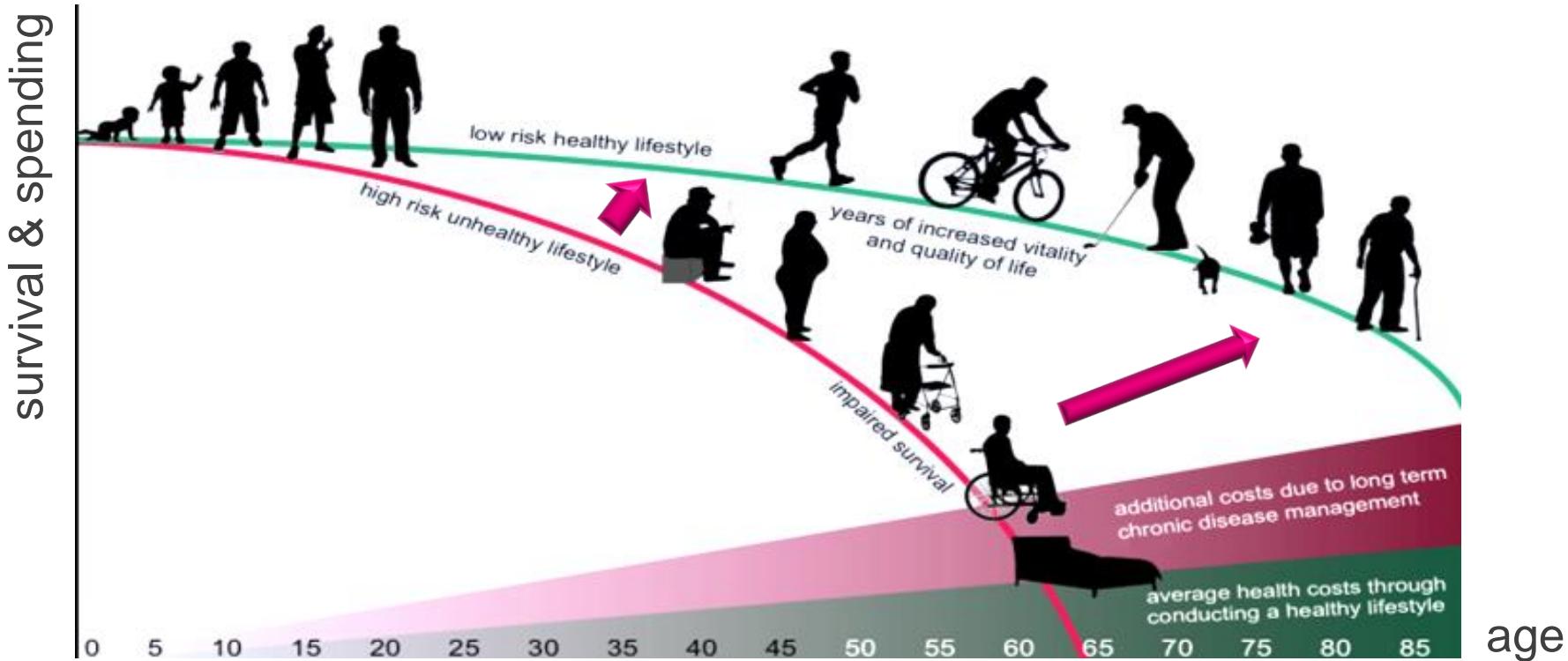
Trends

P3 x P4 medicine

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DEMOGRAPHY & COSTS



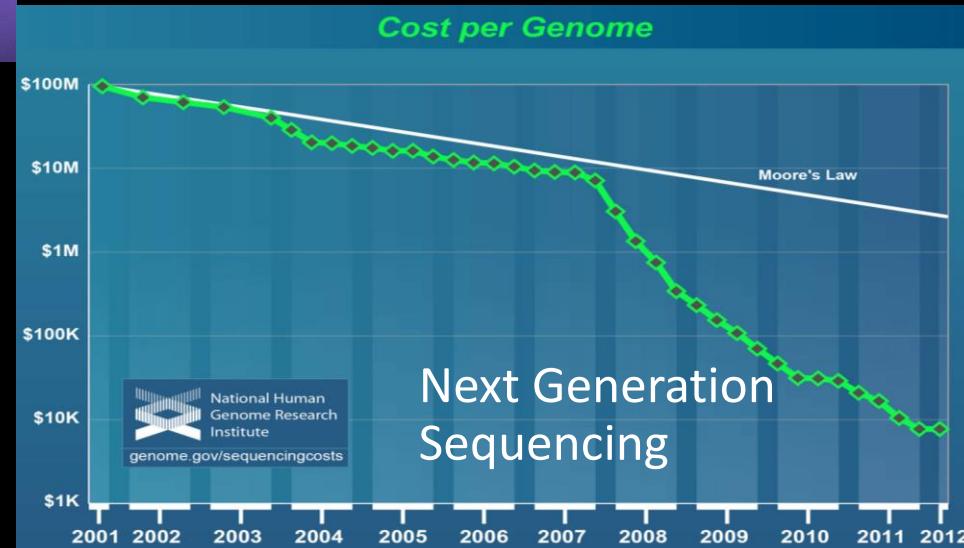
TECHNOLOGY FOR EVOLVING NEEDS



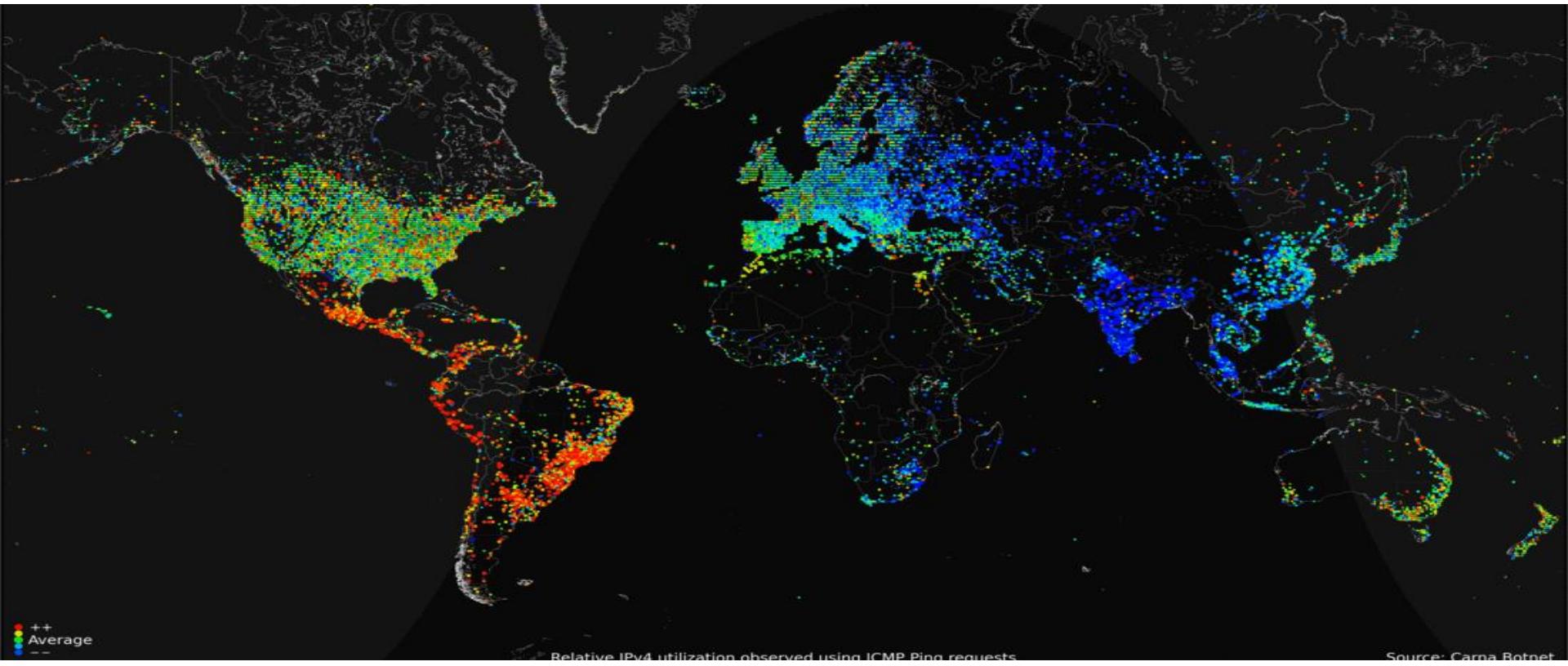


Carlson's law:
complexity/cost
evolves
exponentially

Moore's law:
computing power
doubles
every 18 months



WWW





Grains of rice the world consumes annually: **27.5 quadrillion**



Amount of data the world consumes every 30 minutes: **40.4 petabytes**

We consume more bytes on the internet in 30 minutes than grains of rice in a year.

1 million = 1 000 000

1 kB = 1 000

1 TB

1 billion = 1 000 000 000

1 MB = 1 000 000

= large university library

1 trillion = 1 000 000 000 000

1 GB = 1 000 000 000

= 212 DVD discs

1 quadrillion =

1 TB = 1 000 000 000 000

= 1430 CDs

1 000 000 000 000 000

1 PB = 1 000 000 000 000 000

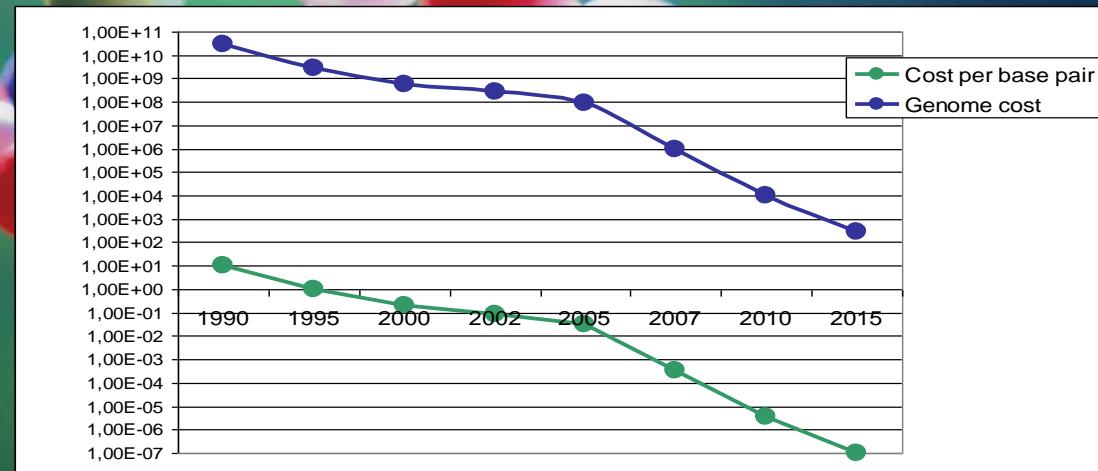
= 3 year music in CD quality

GENOME DATA

- Human genome project (2003)
 - 13 year project
 - \$300 million value with 2002 technology
- Personal genome (2007)
 - Genome of James Watson, 2 months
 - \$1 000 000
- €1000-genome
 - Expected 2012-2020



GS-FLX Roche
Applied Science 454
Sequencers



TSUNAMI OF MEDICAL DATA

sequencing all newborns
by 2020 (125k births /
year)

125 PetaByte / year

index of 20
million
Biomedical
PubMed
records

23 GigaByte

1 small
animal
image

1
GigaByte

raw NGS data
of 1 full genome
1 TeraByte

1 slice mouse
brain MSI at
10 µm
resolution

81 GigaByte

PACS
UZ Leuven

1,6 PetaByte

Genomics core
HiSeq 2000 full
speed exome
sequencing

1 TeraByte / week

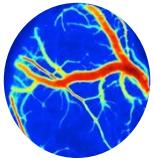
1 CD-ROM

750
MegaByte

3P x 4P MEDICINE



DATA-DRIVEN 3P MEDICINE



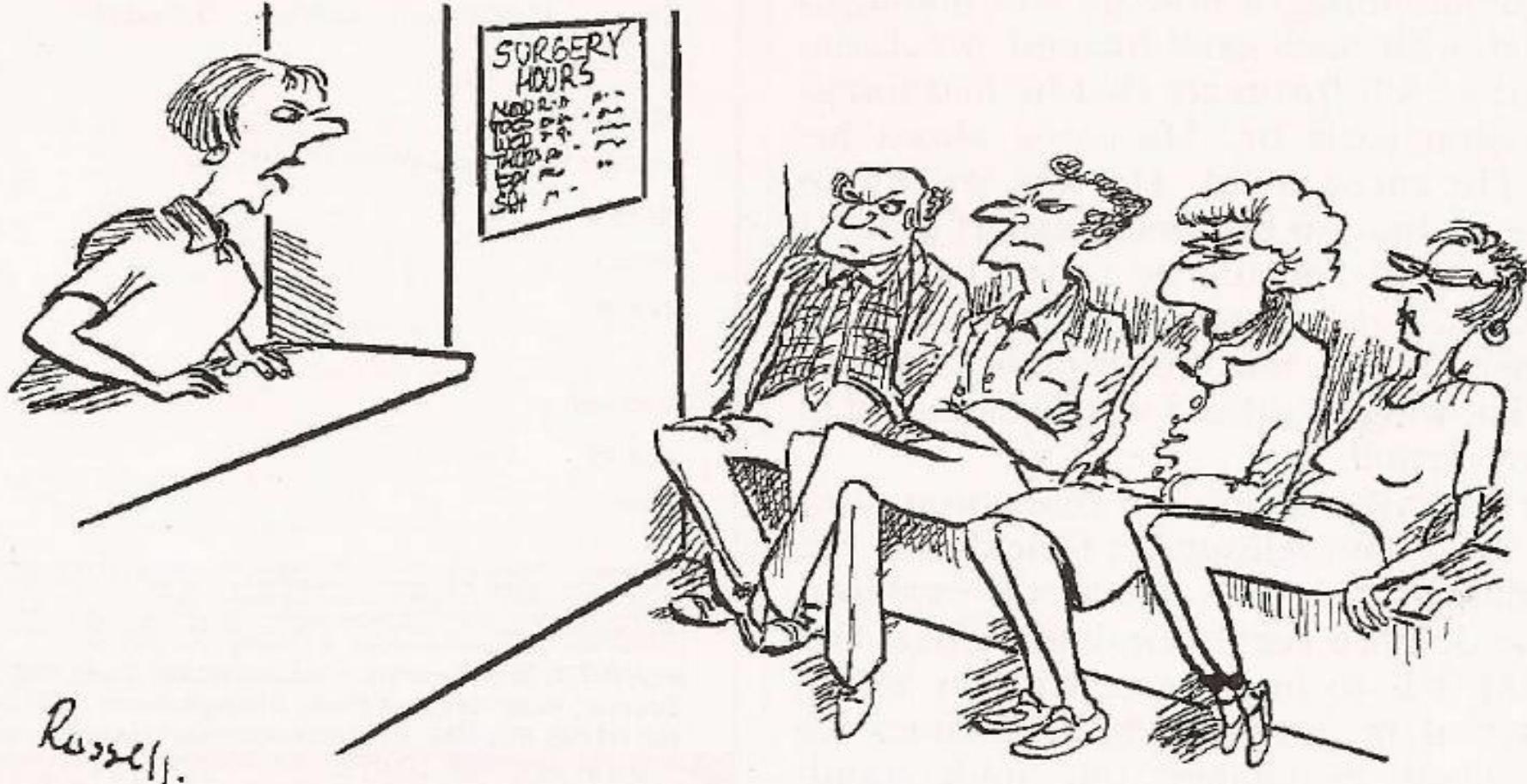
PROFESSIONALS: Clinicians, Researchers, ...



PATIENTS: Empowerment, Associations, ...



POLICY MAKERS: Hospitals, Health Insurance, Social Security, ...



'The doctor will see anyone who hasn't already self-diagnosed on the internet.'

DATA-DRIVEN 4P

MEDICINE



PERSONALIZED "customized" diagnosis and treatment



PREVENTIVE better than curation



PREDICTIVE determine risk profiles & predict outcome



PARTICIPATORY involve the patient

Department Med IT

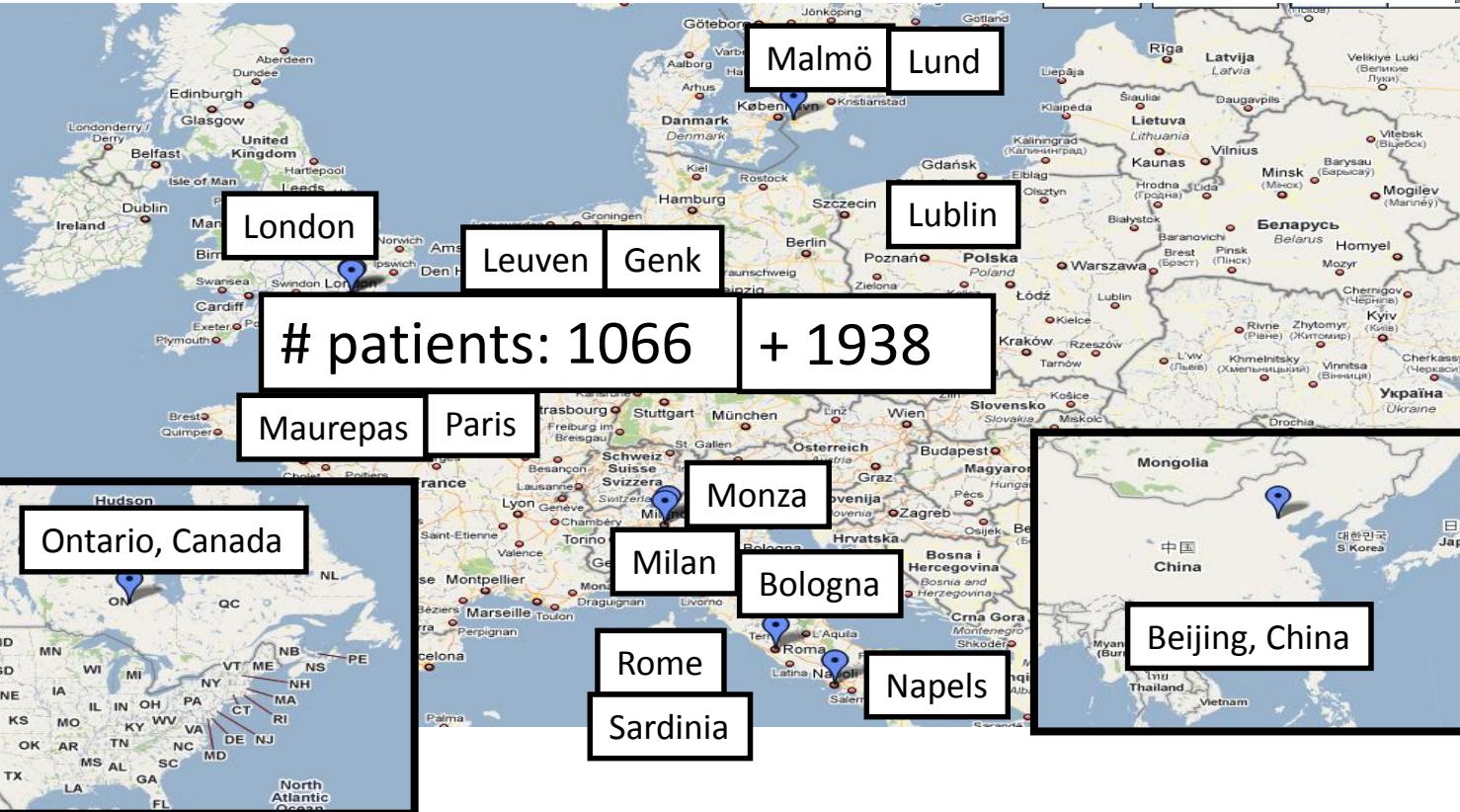
Trends

P3 x P4 medicine

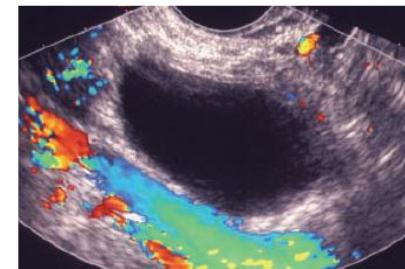
Decision support
cases



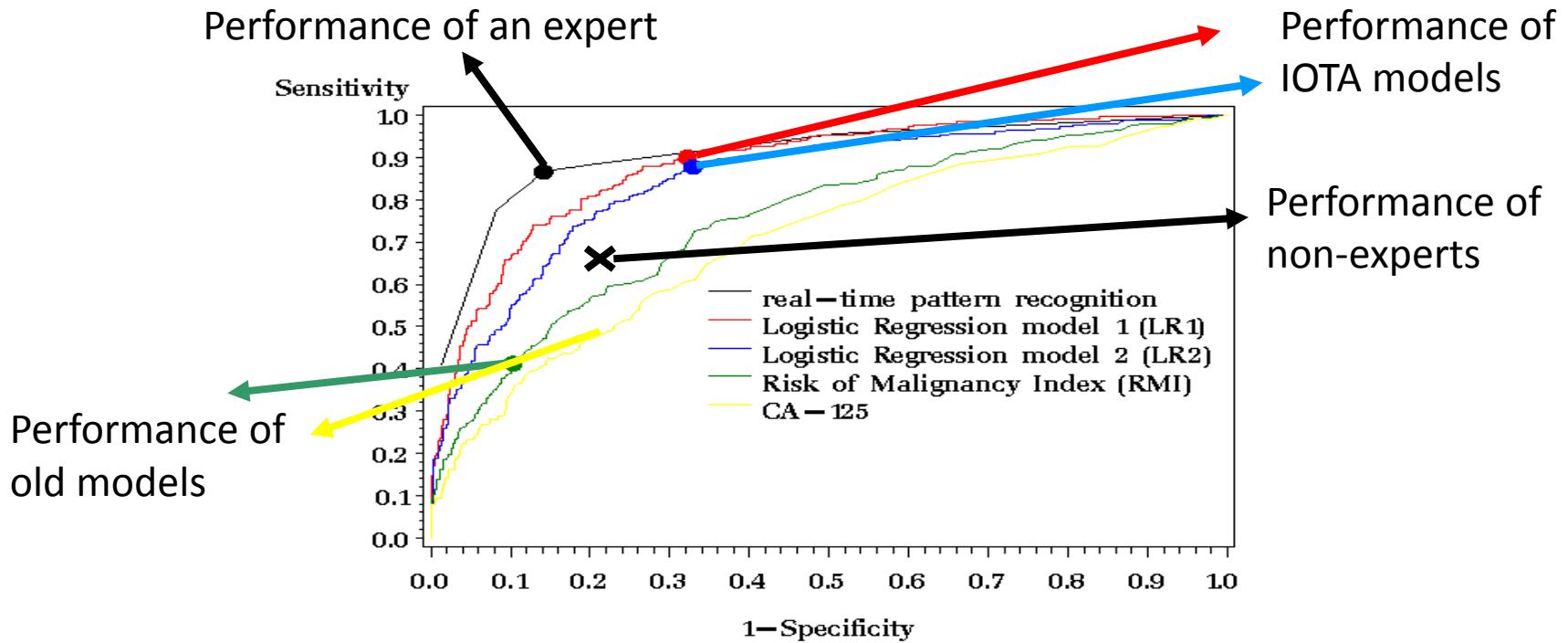
PARTICIPATORY



IOTA app:
population
based
assessment
of ovarian
tumour malignancy:

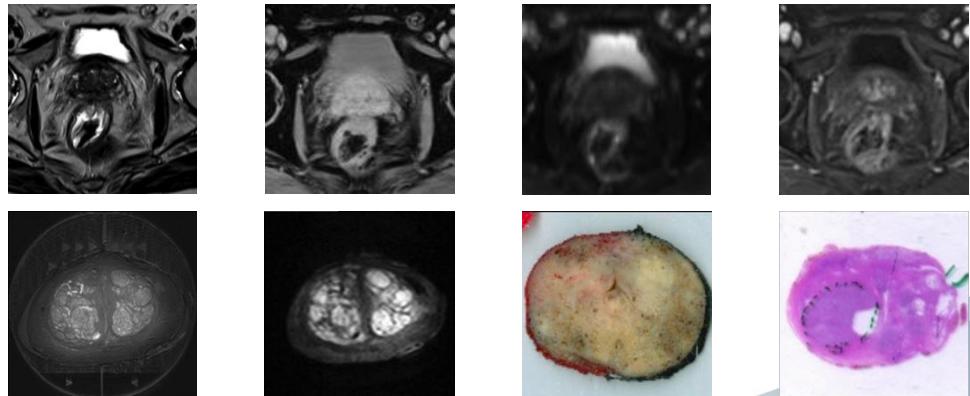
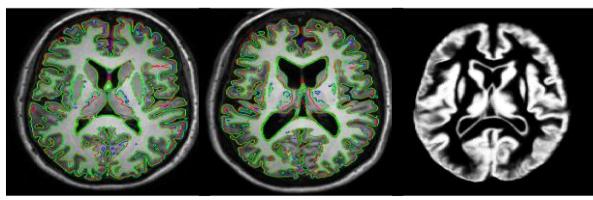
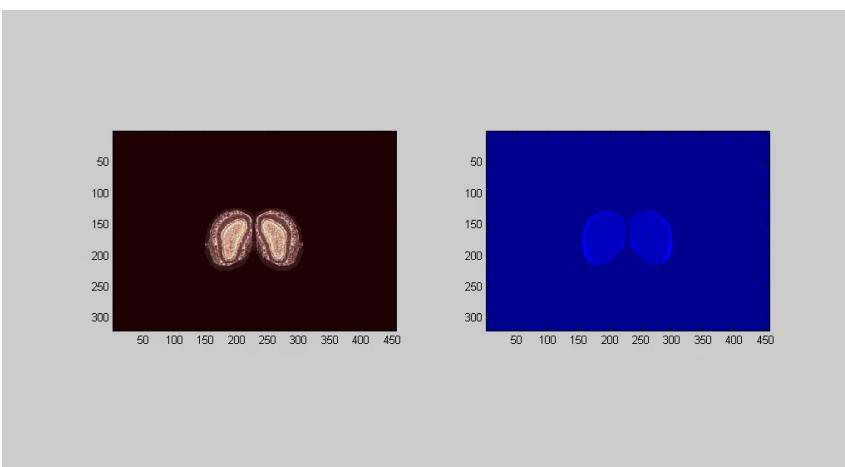
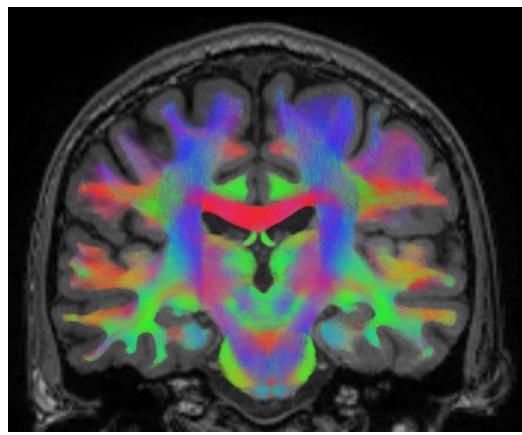
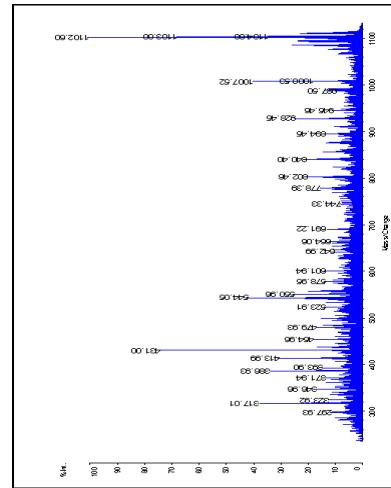


PERFORMANCE



You share, we care !

PREDICTIVE



PERSONALIZED

with



LOGIC-Insulin

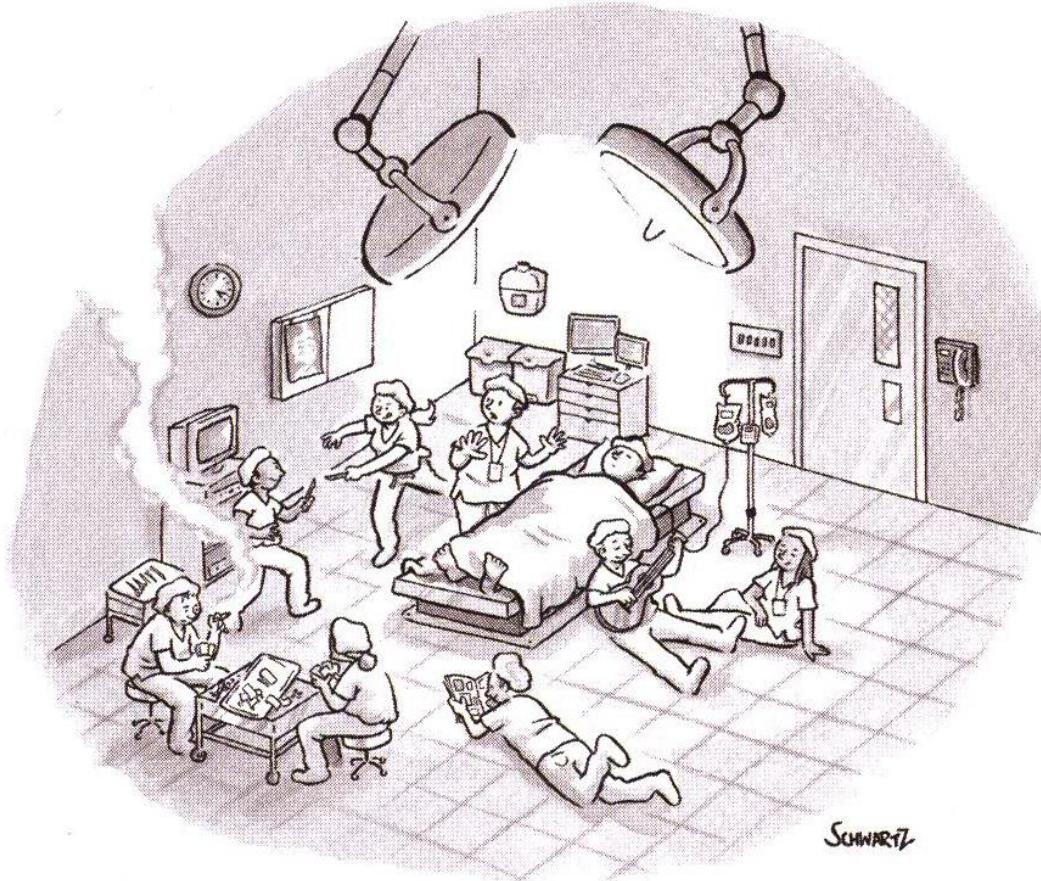
Tight Glycemic Control in intensive care lowers mortality

Control algorithm LOGIC-Insulin ('automated customized patient pilot')

400 clinical trials



GEPLUKT UIT THE NEW YORKER



'Hij wordt wakker! Iedereen terug op zijn plaats!'

PREVENTIVE



ACACATTAATCTTATGCTAAAAGGGTCTCGT
TTAGGGATGTTATAACCATCTTGAGATTATTGA
TGCATGGTTATTGGTTAGAAAAAATACGCTTGT
TTCTTCCTAGGGTATTGACTCATACATGTGTT
CATTGAGGAAGGAACCTAA
ACTTAAAGTGTCAAAGTA
AATATAAAGACATTGTTCAA
ACAATATCAAGAACAGACAAAAA
TCAGGAAGGCATATATTACA
TTTTGTAATCACACCCGACCA
ACATTAATCTTATGCTAAA
TAGGGATGTTATAACCATT
CATGGTTATTGGTTAGAAAAA
CTTCTAGGGTATTGA



ACACATTAATCTTATGCTAAAAGGGTCTCGT
TTAGGGATGTTATAACCATCTTGAGATTATTGA
TGCATGGTTATTGGTTAGAAAAAATACGCTTGT
TTCTTCCTAGGGTATTGACTCATACATGTGTT
CATTGAGGAAGGAACCTAAACAAAGGGTCTCGT
TCAACGTCAAGCTACTTAAAGTGTCAAAGTA
TATCAAGAACGCTTAATATAAAGACATTGTTCAA
GGTTCTGAAGTGCACAATATCAAGAACAGACAAAAA
TGACTAATTGTTCTCAGGAAGCATATATTACA
CGAACACAAATCTTGTAAATCAACACCGACCA
TGGTCGATTACACACATTAATCTTATGCTAAA
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TGAGATTATTGATGCTGGTTATTGGTTAGAAAAA
TATACGCTTGTGTTCTTCCTAGGGTATTGA

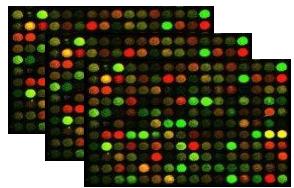


ACACATTAATCTTATGCTAAAAGGGTCTCGT
TTAGGGATGTTATAACCATCTTGAGATTATTGA
TGCATGGTTATTGGTTAGAAAAAATACGCTTGT
TTCTTCCTAGGGTATTGACT
CATTGAGGAAGGAACCTAA
TCAACGTCAAGCTACTTAA
TATCAAGAACGCTTAATATA
GGTTCTGAAGTGCACAAT
TGACTAATTGTTCTCAGGAAGCATATATTACA
CGAACACAAATCTTGTAAATCAACACCGACCA
TGGTCGATTACACACATTAATCTTATGCTAAA
ACTAGGTCTCGTTAGGGATGTTATAACCATT
TGAGATTATTGATGCTGGTTATTGGTTAGAAAAA
TATACGCTTGTGTTCTTCCTAGGGTATTGA



GENOMIC DATA FUSION

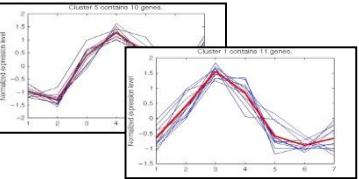
High-throughput
genomics



Validation



Data analysis



Information sources

Candidate genes

Name	Ensembl
TTR	ENSG000000118271
PAH	ENSG000000171759
G6PC	ENSG000000131482
IGF1	ENSG000000017427
ALB	ENSG0000000163631
CRP	ENSG000000032693
HABP2	ENSG0000000148702
IF	ENSG0000000138799
FST	ENSG0000000134363
ARAF1	ENSG000000078061
HMGA2	ENSG000000049948
C9	ENSG000000113600
PCBP2	ENSG0000000111406
HOXB6	ENSG000000108511
RERE	ENSG000000142599
HOXA11	ENSG00000005073
CLIC1	ENSG000000096238
ERCC3	ENSG000000163161
ERCC3	ENSG000000063161
TLL2	ENSG000000095587
SYT4	ENSG000000132872
SYT4	ENSG000000132872
PIK4CB	ENSG000000143393
PKD2	ENSG000000118762
ANKRD3	ENSG000000081026
F13A1	ENSG000000124491
BPAG1	ENSG000000151914
KCNN3	ENSG000000143603
GRIN2A GRIN2B	ENSG000000150086
SIM1	ENSG000000112246
C14orf10	ENSG000000174891
STX8	ENSG000000089195
MSH5	ENSG000000092024
CRH	ENSG000000107030
MID1	ENSG000000107671
	ENSG000000096474
	ENSG000000147571
	ENSG000000101871
	ENSG000000184508
	ENSG000000113460
TGFB3	ENSG000000196999
C1QR1	ENSG000000125810
NR4A2	ENSG000000153234
PDGFC	ENSG000000145431
PDGFC	ENSG000000145431
NR3C2	ENSG000000151623
NFYA	ENSG00000001167
	ENSG000000018989
C8orf4	ENSG000000176907
TM4SF13	ENSG000000106537
MMMP3 MMMP1	ENSG000000149968

Candidate prioritization

Rank	En	Ex	Ip	Ke	GO	Te	Avg	Pval
1	TTR	G6PC	PAH	36PC	IGF1	TTR		TTR
2	IGF1	TTR	IGF1	PAH	PAH	IGF1		PAH
3	CRP	ALB	TTR	RERE	36PC	CRP		G6PC
4	HOXB6	HABP2	ALB	ERCC3	TTR	HOXB6		IGF1
5	ALB	PAH	HDC	ERCC3		ALB		ALB
6	NR4A2	IF	TLL2	ANKRD3				CRP
7	PAH		C1QRT	ARAF1	HDC	NR4A2		HABP2
8	HOXA11	IGF1	G6PC	PKD2	F13A1	PAH		IF
9	NFYA	CRP	HABP2	MMPR1	KCNN3	HOXA11	C14orf7	FST
10	C9	ARAF1	IF	HDC	CLIC1	NFYA	TTR	ARAF1

PROFESSIONA

genomic data fusion:
trace disease-causing variants
20x more accurate



Sifrim, Popovic et al,
Nature Methods, 2013

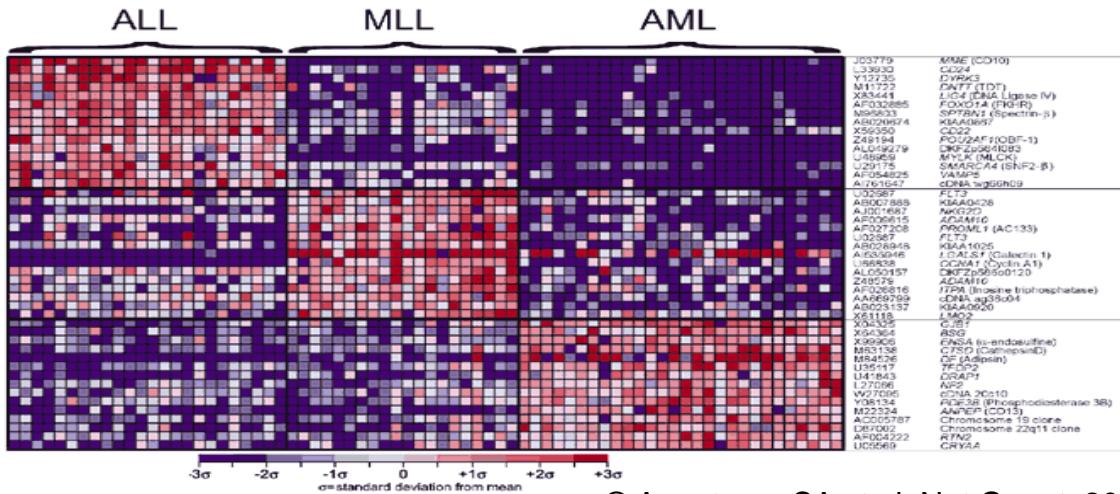
ONDERZOEK

Vlamingen sporen genetische ziektes accurater op

Onderzoekers van iMinds (het vroegere IBBT) en de KU Leuven hebben software ontwikkeld die enorme hoeveelheden genetische data kan doorzoeken en die aanbevelingen doet over de meest waarschijnlijke oorzaak van een erfelijke ziekte. Het 'eXtasy' maakt gebruik van artificiële intelligentie en werkt tot twintig keer beter dan andere software. Volgens professor Yves Moreau zit de software nog in de onderzoeksfase en is nog één tot twee jaar nodig voor de technologie commercieel beschikbaar is.

Bron:
De Tijd, woensdag 23 oktober 2013

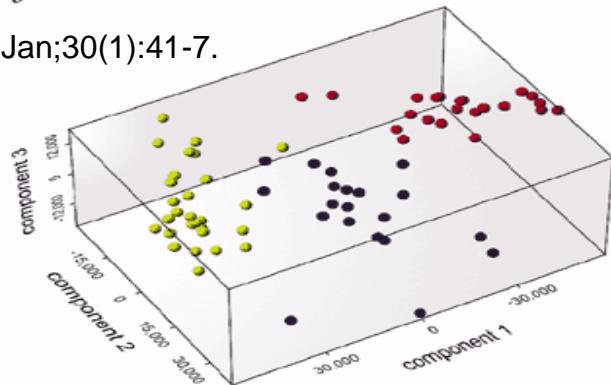
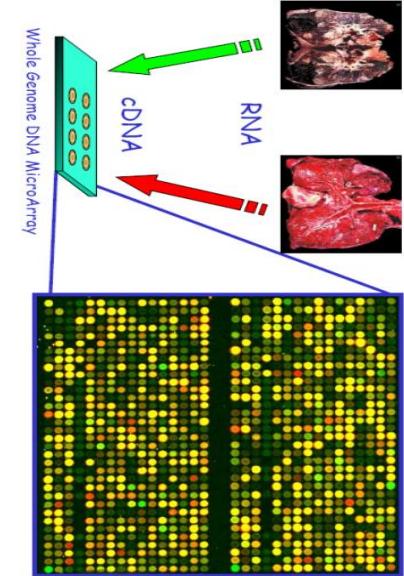
PREDICTIVE Genetic Biomarkers For Leukemia



12 600 genes
72 patients

- 28 Acute Lymphoblastic Leukemia (ALL)
- 24 Acute Myeloid Leukemia (AML)
- 20 Mixed Linkage Leukemia (MLL)

© Armstrong SA et al. Nat Genet. 2002 Jan;30(1):41-7.



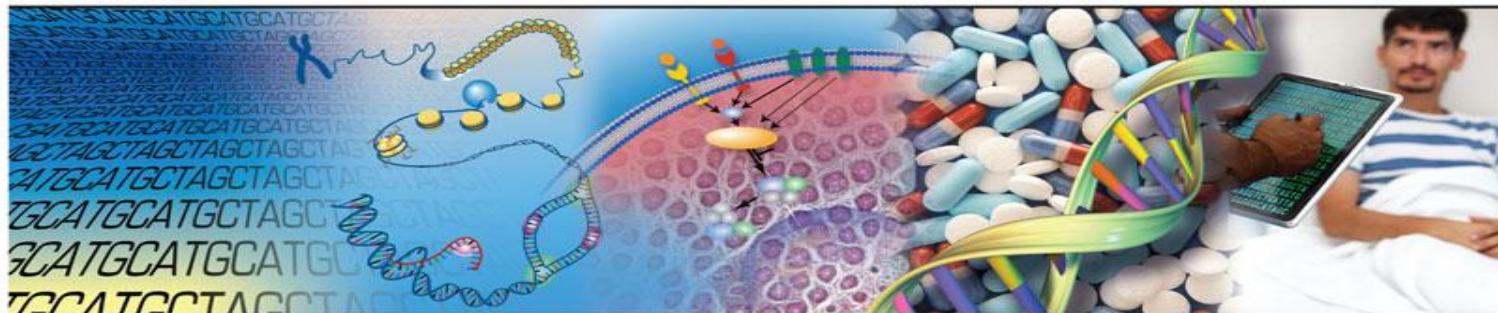
Understanding
the structure of
genomes

Understanding
the biology of
genomes

Understanding
the biology of
disease

Advancing
the science of
medicine

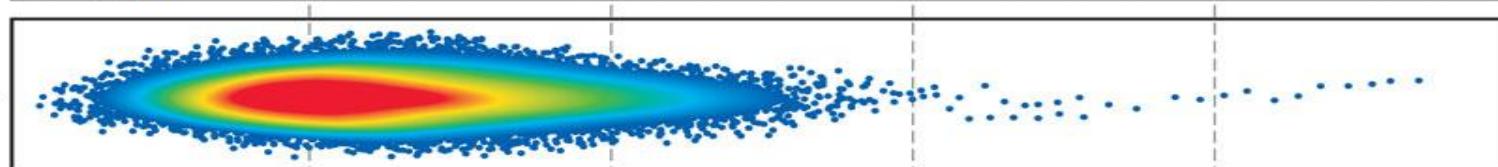
Improving the
effectiveness of
healthcare



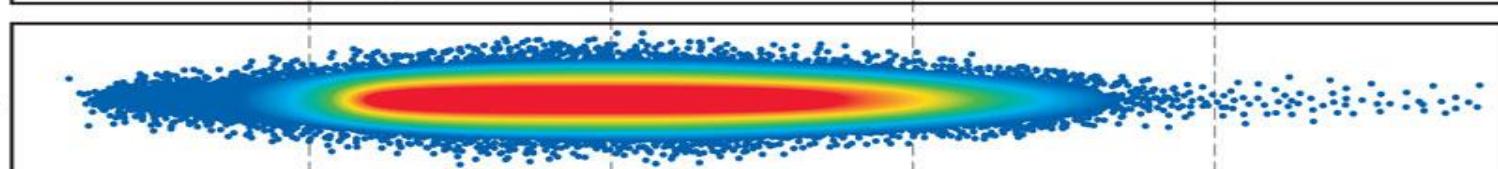
1990–2003
Human Genome Project



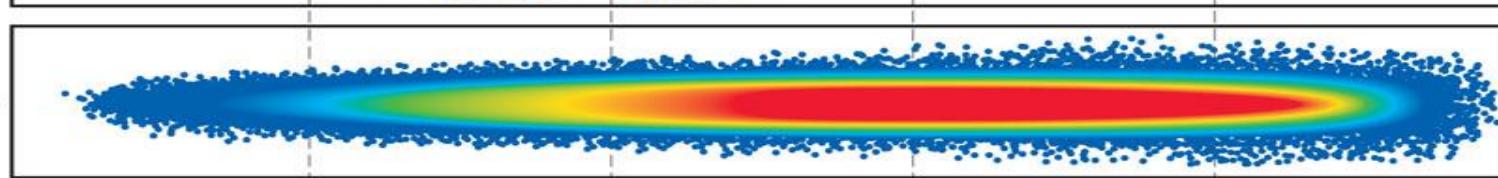
2004–2010



2011–2020



Beyond 2020



POLICY

Social security data mining
for **evidence-based policy decision making**



- Mining @ CM to detect diabetes risk from billing data
- Model & visualize current health care mechanisms (resources, consumption, outliers, ...)
- Deduce optimal policy changes & best practices (in e.g. prescription behaviour)
- Mine RIZIV ? !

iMinds MEDICAL IT



Trends

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KU LEUVEN

Universiteit
Antwerpen



www.iminds.be/medicalit

