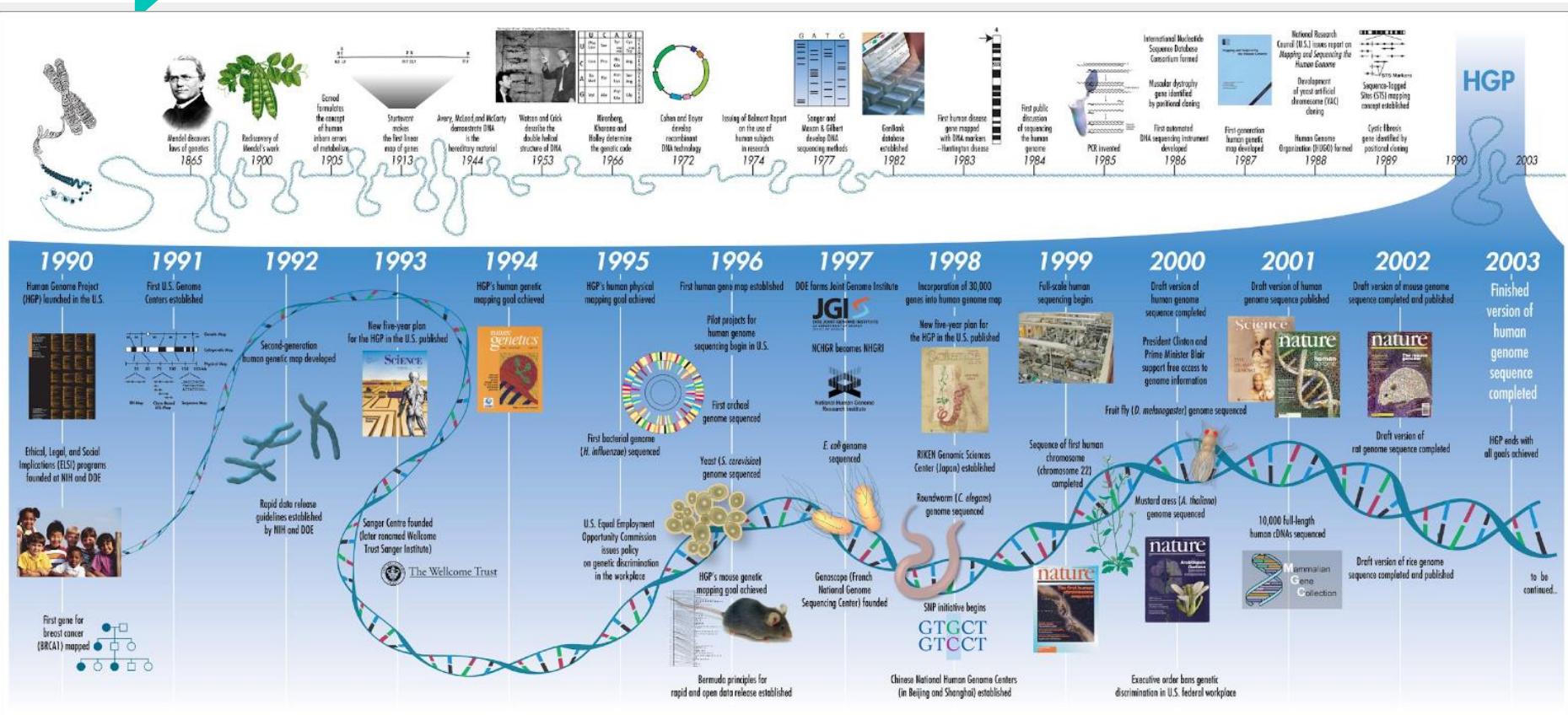


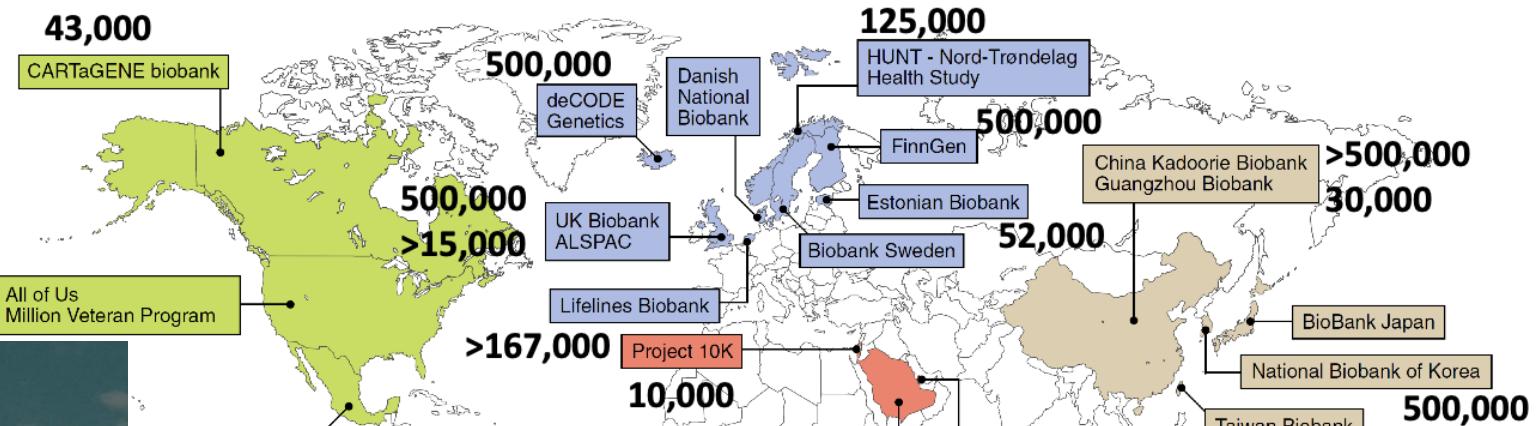
Taiwan Biobank

Su Ming-Wei wei@ibms.sinica.edu.tw

Human Genome Project



Global biobanks



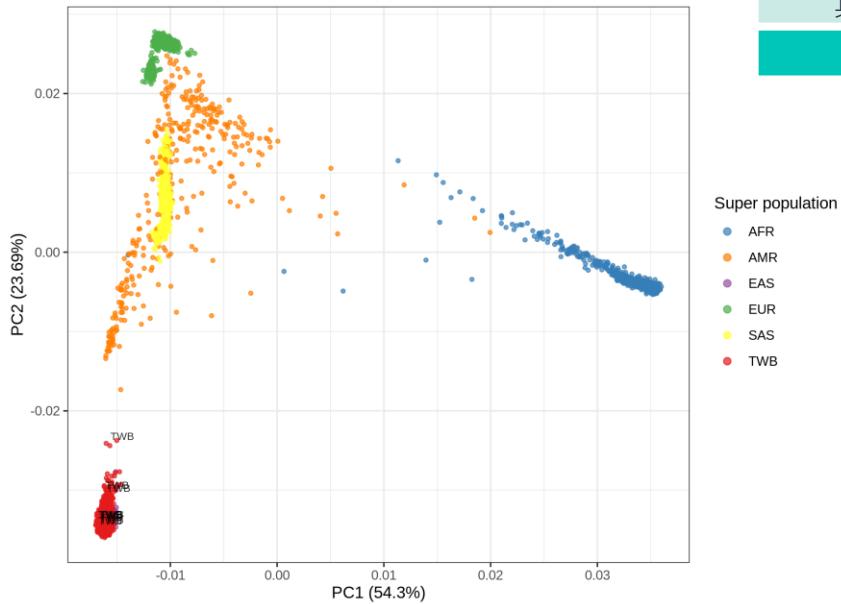
enjoy

每個人都會經過這個階段，
見到一座山，
就想知道山後面是什麼。
我很想告訴他，可能翻過山後面，
你會發現沒什麼特別。回望之下，
可能會覺得這一邊更好。

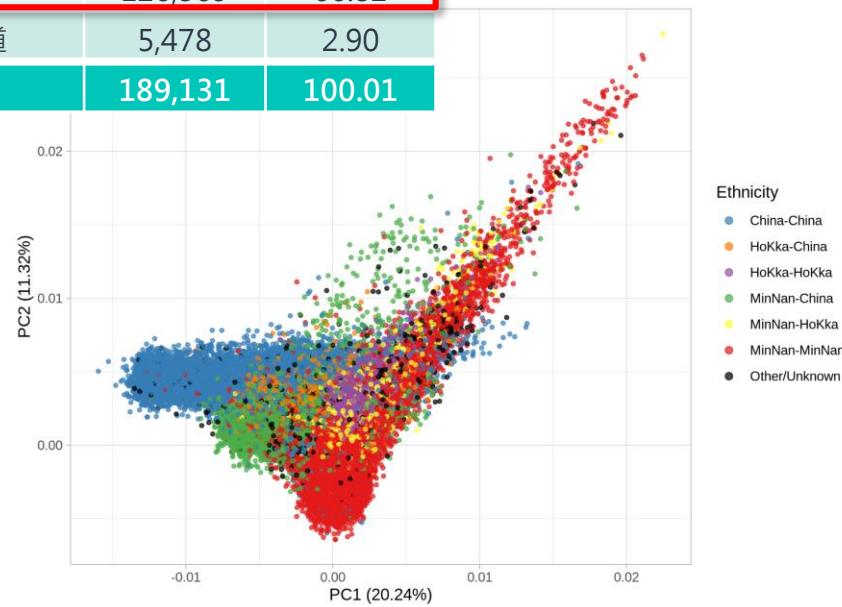
東邪西毒

族群遺傳結構

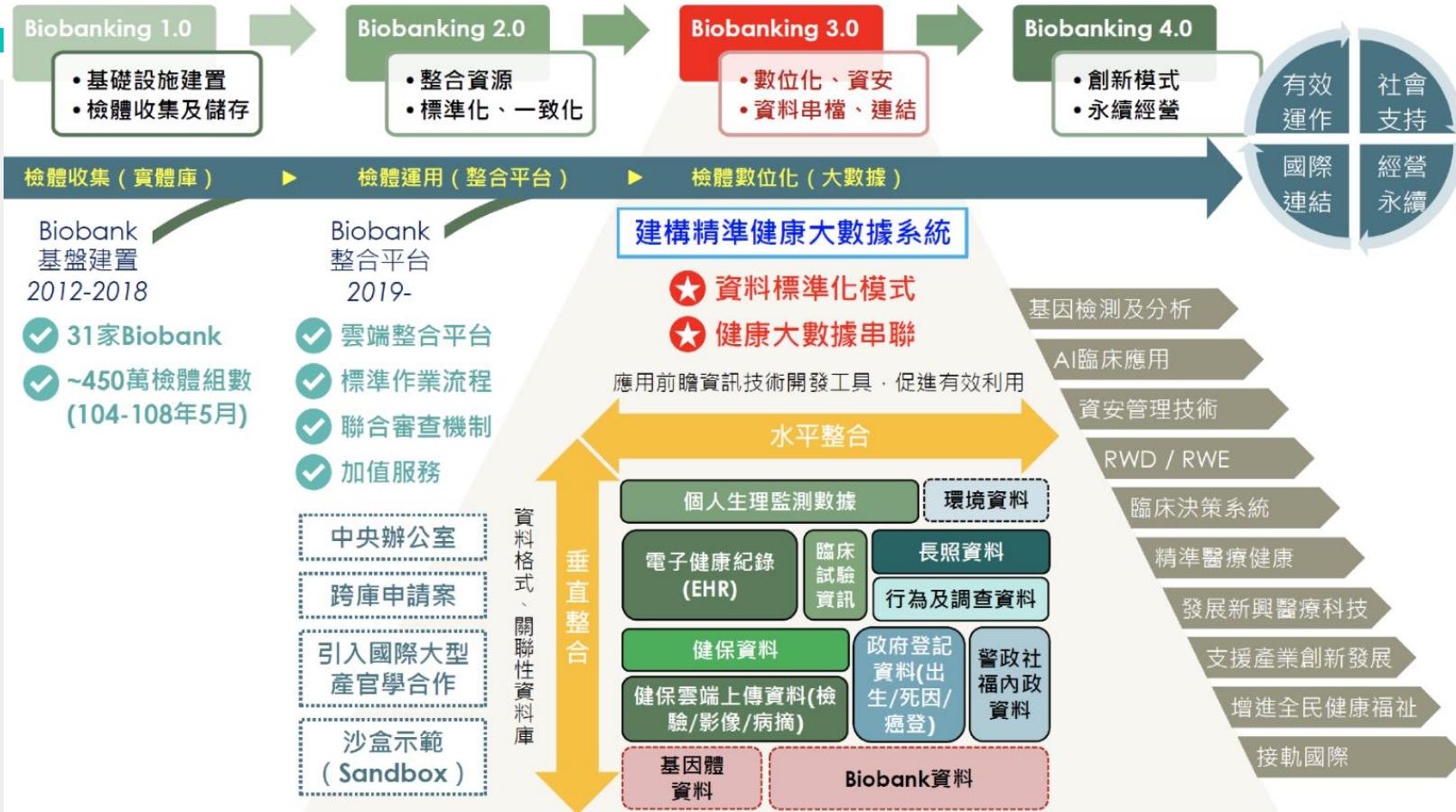
TWB samples + 1000GP samples



自述父母親籍貫	人數	百分比
中國各省-中國各省	12,032	6.36
客家-中國各省	2,895	1.53
客家-客家	18,152	9.60
閩南-中國各省	12,795	6.77
閩南-客家	11,410	6.03
閩南-閩南	126,369	66.82
其他/不知道	5,478	2.90
加總	189,131	100.01



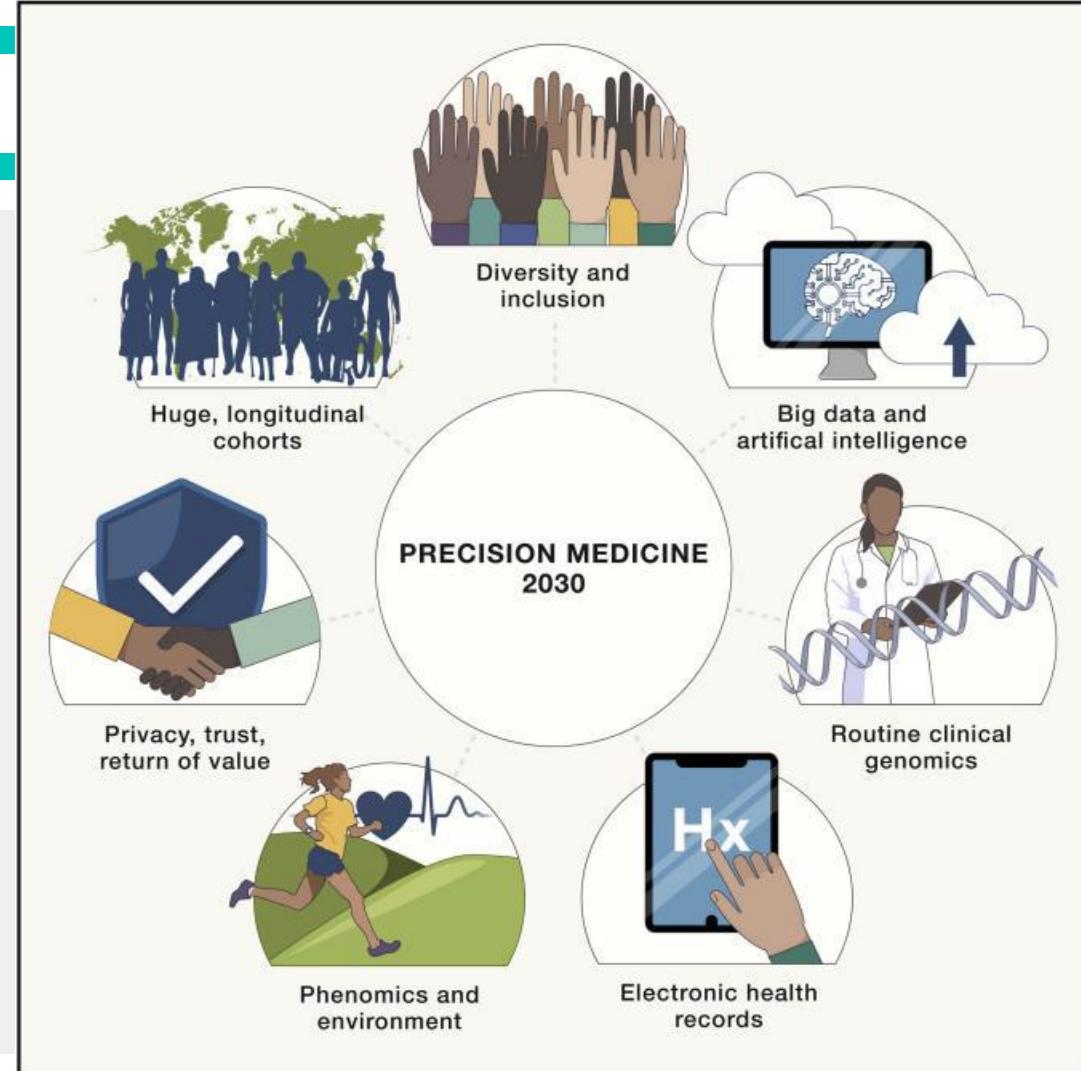
建構以大數據為基礎之國家精準健康架構



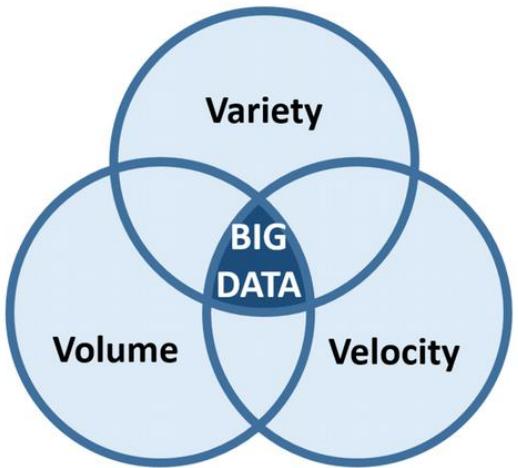
Commentary

Precision medicine in 2030—seven ways to transform healthcare

Joshua C. Denny ^{1, 3}  , Francis S. Collins ²



Data v.s. **Big** data in a geek way

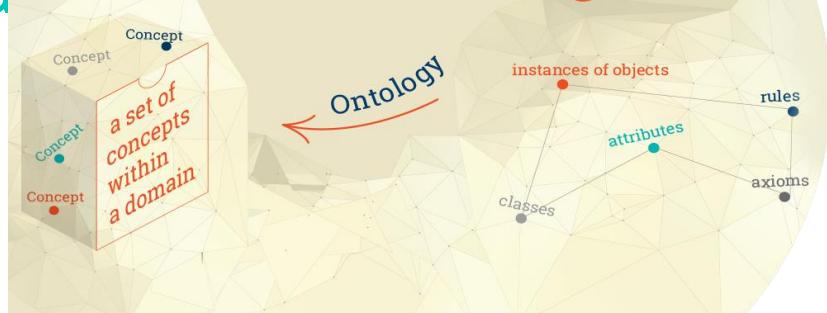


BAYERN 1-0 HAMBURG

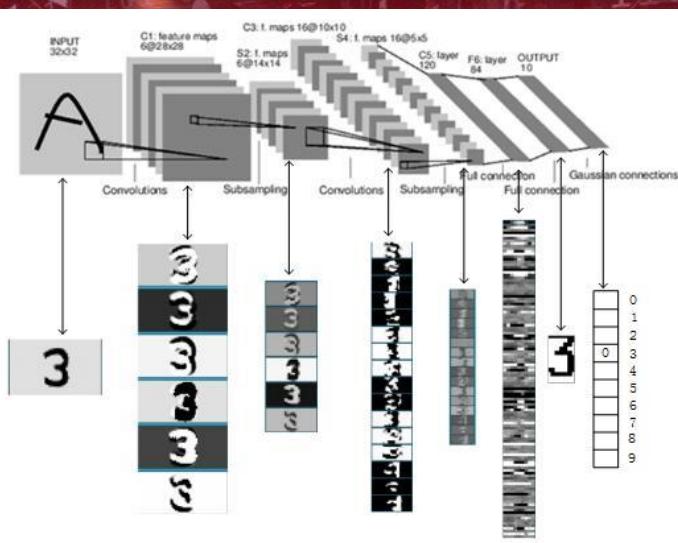


Big data

What are Ontologies?



Deep Learning Meets Big data



Data = World



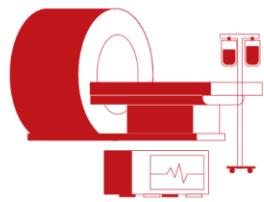
Why Taiwan ?

- Holo Taiwanese
- Hakka Taiwanese
- Mainlanders
- Taiwanese indigenous peoples

Why Taiwan's Health Care System
is the Best in the World



Well-trained
medical personnel



New equipment



Diverse professions



www.president.gov.tw

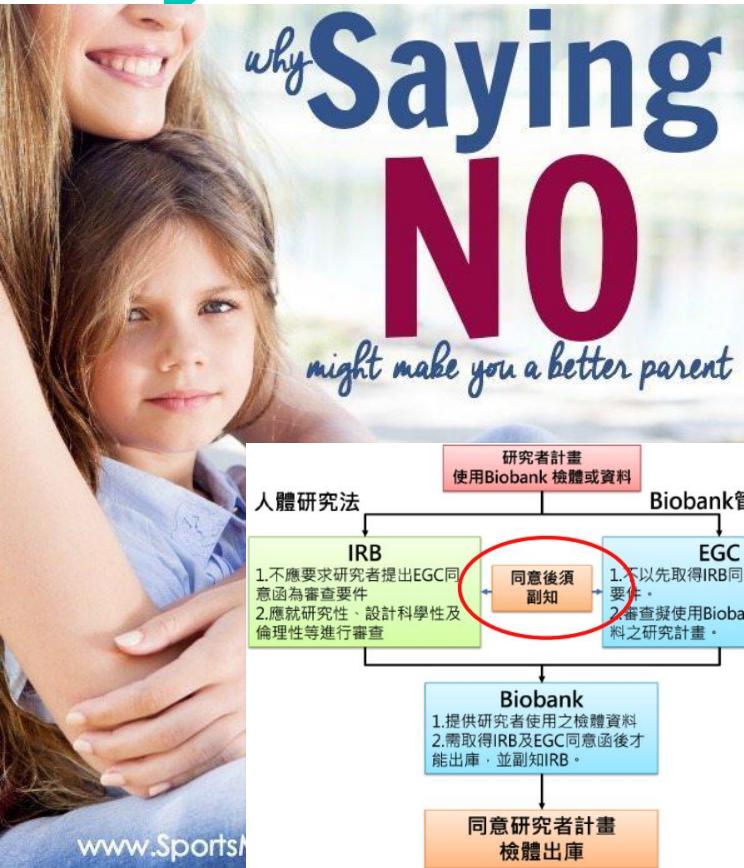
<https://ogme.edu.tw/lc/culturalGroups>

<https://tendashsix.com/taiwan-medical-service-ranked-first/>

- 主管機關：衛生福利部
- 設置者：中央研究院
- 依2010.2.3 總統府頒布執行之《人體生物資料庫管理條例》設置
- 設有倫理委員會，針對資料庫之管理等有關事項進行審查及監督
- 2012.10.24 取得設置許可
- 第一個主管機關核准設置之人體生物資料庫
- 2012.11.8 開始正式收案 預計目標20萬社區民眾

NOT ONLY YOU CARE!!

why Saying NO might make you a better parent



我們是誰？在做什|

Taiwan Biobank 整體概念圖

我們是中央研究院臺灣人體生物資料庫 (Taiwan Biobank)，欲透過結合生活習慣、環境因子、臨床醫學與基因生物標幟等資訊，為生物醫學研究蒐集龐大的生物檢體與健康資訊，提供國內學者申請使用，目前已有諸多成果。

為籌建多元化的國家型健康大數據，因應多樣性研究，我們自2012年取得設立通過後即開始邀請20萬名一般民眾與部分疾病別之患者加入，收集其身體檢測、檢體、醫藥史、家族史、生活環境與習慣等健康相關資料、資訊，除了提供基礎研究資源外，更希望最終回饋於民，讓民眾共享健康碩果。





4 回饋於民、自主健康



<https://www.biobank.org.tw/index.php>



首頁 最新消息 收案統計 關於資料庫釋出 ▾ 檔案下載 使用者註冊/登入

Taiwan Biobank 最新消息

2021.01.28 數位資料集線上下載更新檔案功能上版！

發表日期：2021-01-25 觀看：245 次

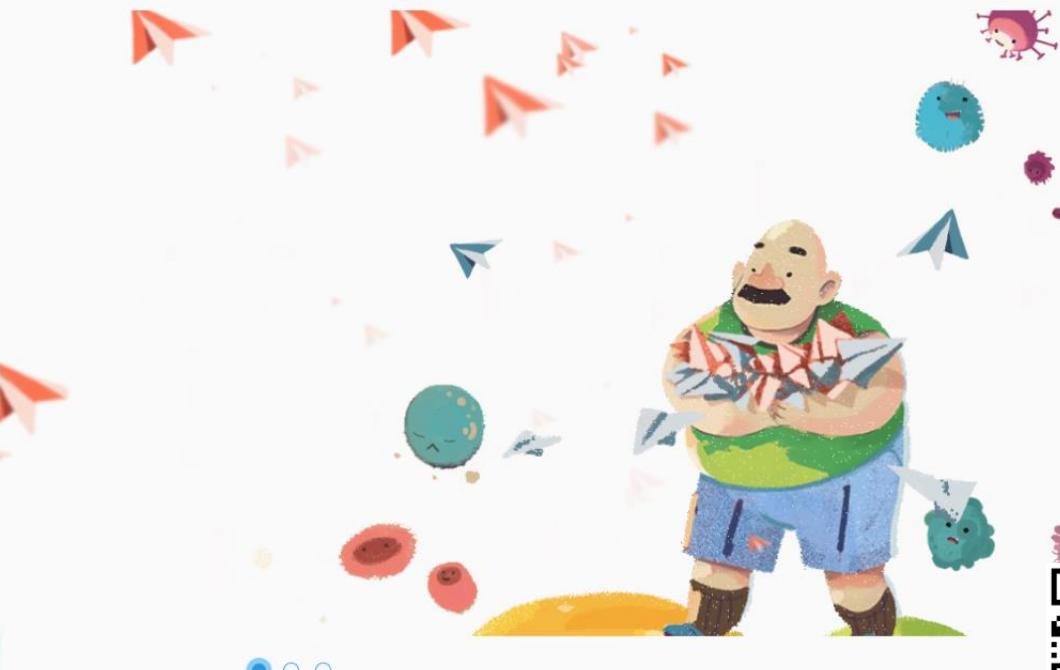
2021.01月份「檢體與數位資料釋出管理系統」停機
公告

發表日期：2021-01-07 觀看：147 次

進階追蹤：醫學影像資料資料集開放釋出！

發表日期：2020-10-21 觀看：401 次

了解更多



TWB

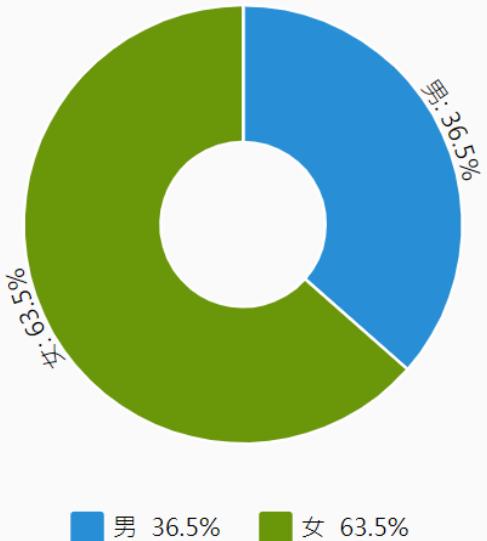
<https://reurl.cc/jjqjqNZ>

目前成果

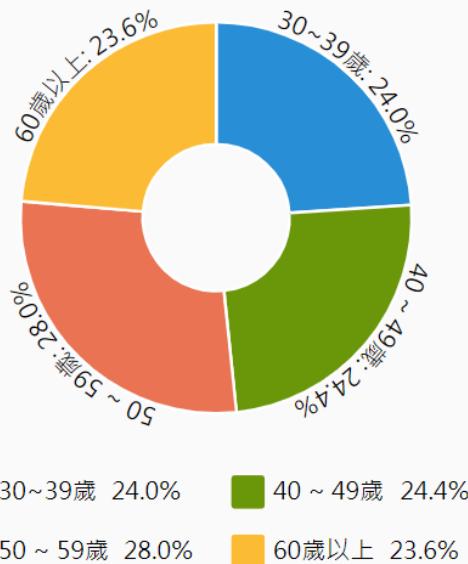
✓ 已累計超過 25萬多人次參與



01. 性別分布



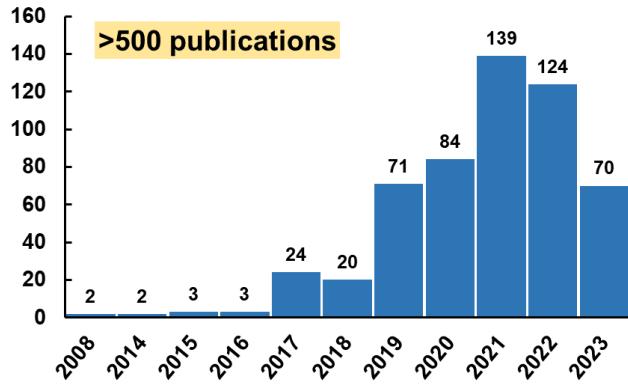
02. 年齡分布



✓ 透過Taiwan Biobank資料研究發表至國際期刊之文章已高達522篇以上

累計至 2023年7月

No. of papers



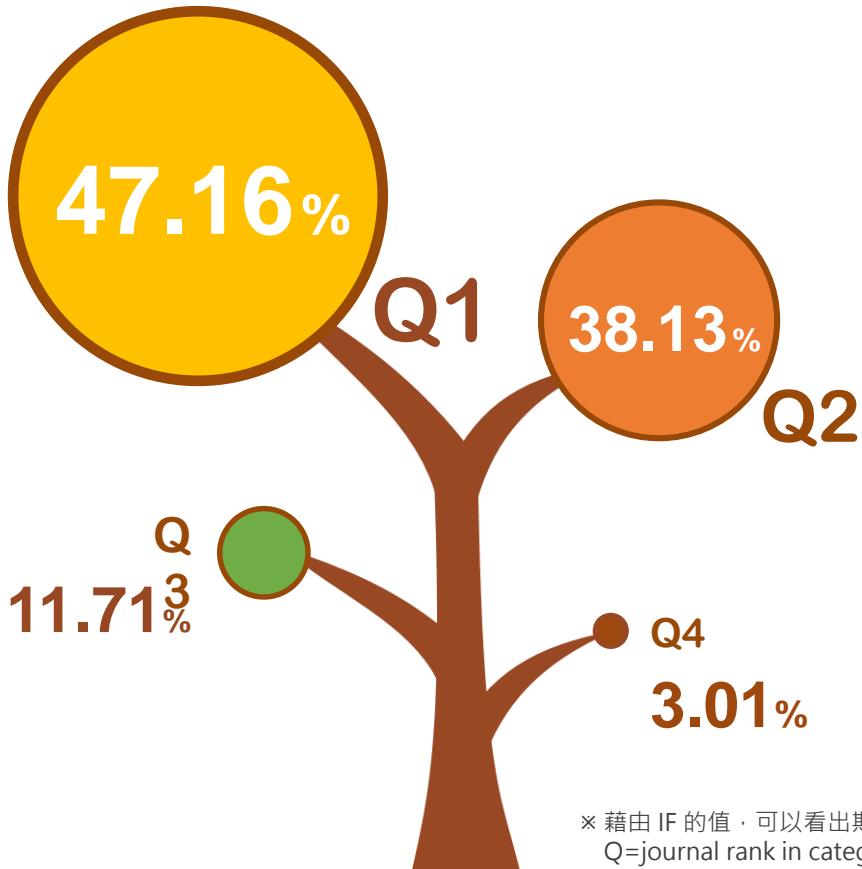
>500 publications

資料釋出成果 - 2023年

- Int. J. Mol. Sci. Splice-Site Variants in the Gene Encoding GABA-A Receptor Delta Subunit Are Associated with Amphetamine Use in Patients under Methadone Maintenance Treatment.
(2023) Lin, Y.-F., et al.
- J. Pers. Med. Whole-Exome Sequencing Identifies Genetic Variants for Severe Adolescent Idiopathic Scoliosis in a Taiwanese Population.
(2023) Lin, M.-R., et al.
- Mol Ther Oncolytics. Zika virus cleaves GSDMD to disseminate prognosticable and controllable oncolysis in a human glioblastoma cell model.
(2023) Kao, Y.-T., et al.
- J. Oncol. Clinicopathological Features and Oncological Outcomes of Early and Late Recurrence in Stage III Colorectal Cancer Patients after Adjuvant Oxaliplatin-Based Therapy.
(2023) Chang, Y.-T., et al.
- Am J Hum Genet. 15 years of GWAS discovery: Realizing the promise.
(2023) Abdellaoui A., et al.

https://www.biobank.org.tw/dt_release.php

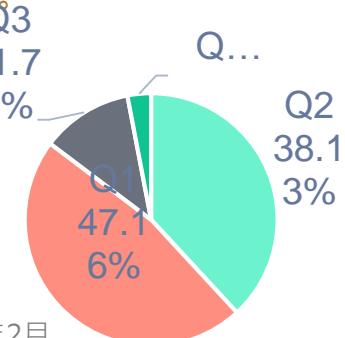
Taiwan Biobank 研究量能之基石



目前透過 Taiwan Biobank 資料研究發表至國際之期刊排名：

Q1高達47.16%、Q2達38.13%；
更有50.33%↑篇數Impact Factor(IF)>5。

我們擁有完整時序性且精確可靠的健康大數據，可以增強學研能量之產值、減少研究者之人力時間成本，極具國際影響力



資料統計截至2023年2月



世界是一切發生的事情
世界是事實的總和，而非事物的總和
發生的事情，即事實，就是諸事態的存在

DATA QUALITY



Completeness

All data sets and data items
are recorded?

缺失值

Uniqueness

Is there a single view of the
data set?

某些資料須具獨特性，如身份證

Timeliness

Does data represent the
correct time frame of events

Validity

Does data match the
business rules?

Accuracy

Is data a proper reflection of
the data set?

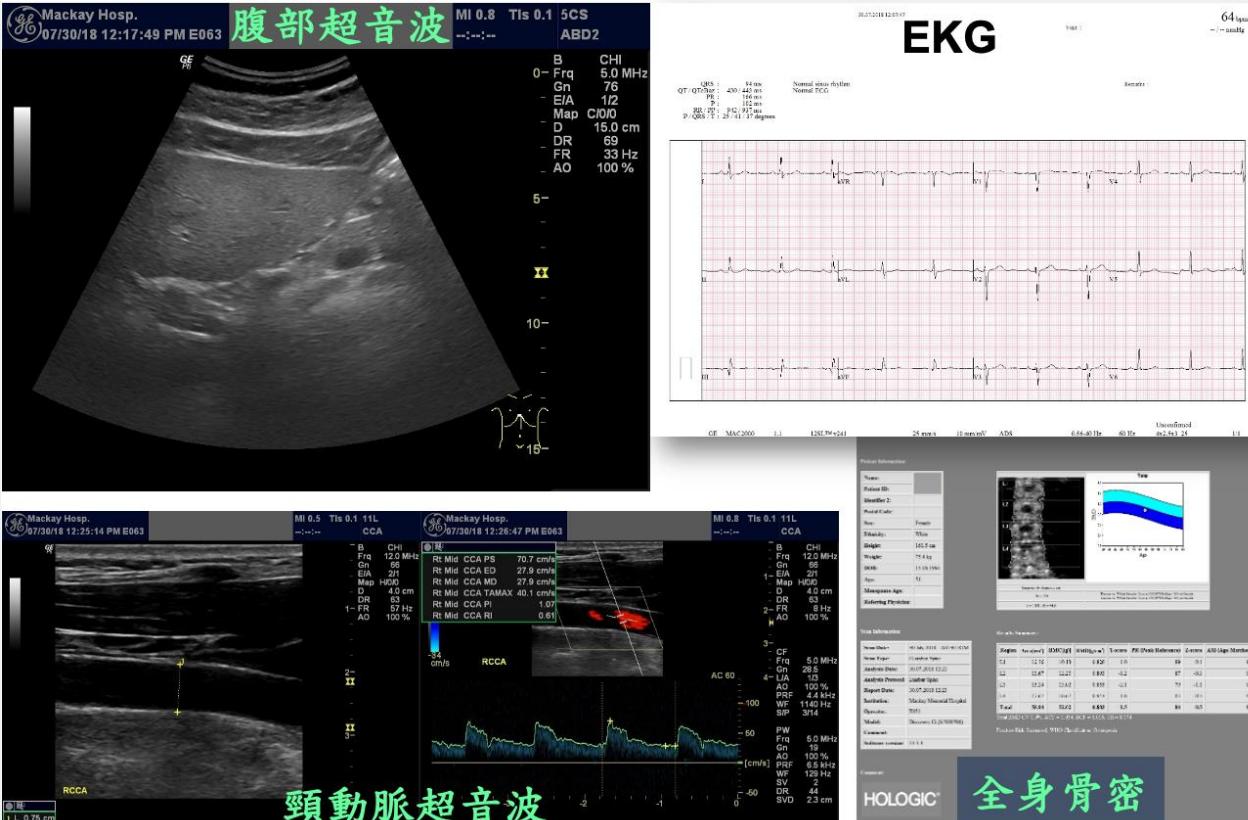
BMI > 100 ?

Consistency

Is the data homogenous, can
be compared across?

資料需有一致性描述，如胖 or 肥胖

advance follow-up program



Taiwan View

Source: Healthy controls
Type and platform: Genome-Wide Genotyping
Number of subject: 128775

PheWeb

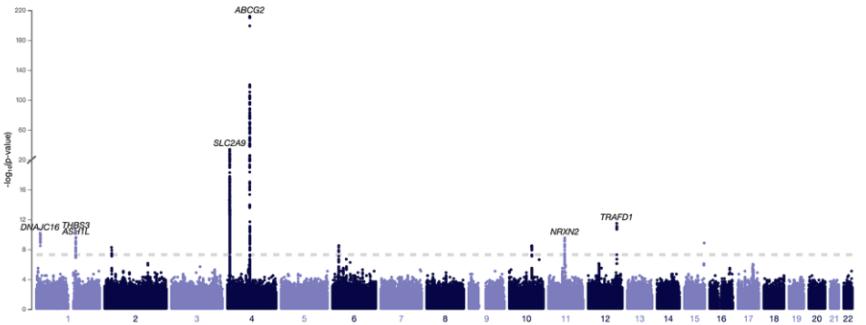
Phenotypes Top Hits Random About

Browse GWAS results using SAIGE

Search for a variant, gene, or phenotype

GOUT: Gout

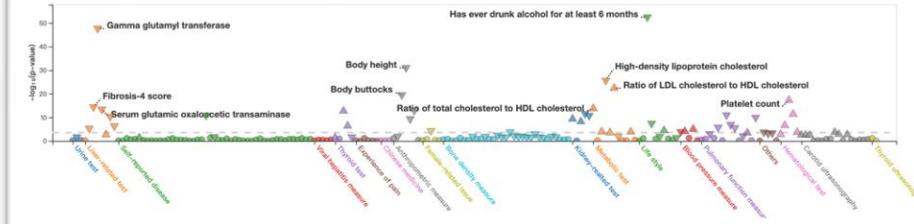
964 cases, 122474 controls
Category: Self-reported disease
Manhattan QQ Correlated phenotypes



Query by a phenotype

12 : 111,803,962 G / A (rs671)

nearest gene: ALDH2
 β ranges from 0.27 to 0.29
View on UCSC , GWAS Catalog , dbSNP , PubMed (256 results) , Clinvar



Search... "427-21", "Diabetes", etc.

Category	Phenotype	P-value	Effect Size (se)	Number of samples
Life style	Has ever drunk alcohol for at least 6 months	$\leq 1e-320$	-0.86 (0.0)	11013 / 117015
Liver-related test	Gamma glutamyl transferase	1.9e-48	-0.056 (0.0038)	127571
Anthropometric measure	Body height	9.0e-32	-0.033 (0.0028)	128242

Query by a gene

ALDH2

Phenotypes with the most-significant associations for this locus:

Top p-value in gene	Phenotype
$\leq 1e-320$	Has ever drunk alcohol for at least 6 months
8.4e-64	Platelet count
1.9e-48	Gamma glutamyl transferase
2.2e-45	Fibrosis-4 score
5.6e-32	Body height
6.5e-27	High-density lipoprotein cholesterol
1.3e-23	Ratio of LDL cholesterol to HDL cholesterol
1.7e-22	Red blood cell count
2.9e-20	Body buttocks
7.4e-15	Ratio of total cholesterol to HDL cholesterol

健康數據酷

<https://healthy.twbiobank.org.tw/>

臺灣人體生物資料庫官方網站

性別：全部

年齡：40歲

身高：170公分

體重：85公斤

體脂肪率：30%

BMI

提交

芭弟 身體代表

身體質量指數 (BMI) 是普遍用來衡量體..... 閱讀更多

BMI, 性別：全部

年齡：40, BMI: 29.41

數量

年齡 % 量度 % 主因 %

年齡

性別：全部

20-29歲

30-39歲

40-49歲

50-59歲

臺灣

甜心 心臟代表

總膽固醇：176mg/dL

高密度脂蛋白膽固醇：72mg/dL

低密度脂蛋白膽固醇：117mg/dL

提交

芭弟 身體代表

芭弟是你的身體夥伴，代表了人的身體整體。進入體質測評外觀的關鍵部位，提供運動工作所必要的營養，並帶走二氧化的廢物。

甜心 心臟代表

甜心是你的動力中心，是維持人類各項運作正常運作的關鍵器官，提供運動工作所必要的營養，並帶走二氧化的廢物。

血寶 血液代表

血寶是你的代謝MOVE，可以將營養送給各器官，並把她的代謝废物帶離這些器官。別忘記血寶的任務：白蛋白球蛋白。

臺灣人體生物資料庫官方網站

性別：全部

年齡：40歲

總膽固醇：176mg/dL

高密度脂蛋白膽固醇：72mg/dL

低密度脂蛋白膽固醇：117mg/dL

提交

總膽固醇：為血液中脂肪的一種，提供人體中..... 閱讀更多

總膽固醇，性別：全部

年齡：40, 總膽固醇：176

數量

年齡 % 量度 % 主因 %

年齡

性別：全部, 總膽固醇：176

20-29歲

30-39歲

40-49歲

50-59歲

百分比

臺灣人體生物資料庫官方網站

data and tubes

<https://www.youtube.com/watch?v=LmHJ1KFIW1s&t=2s>



~1.5
PB



~3 million
liters

ISO certificate

ISO/IEC 27001 for management system



ISO/IEC 29100 for personal information protection



TWB-NHIRD



身分證號+Release ID
實體加密後傳輸



Release ID + TWB data

1. Release ID + TWB data 加密傳輸
2. email Key to 申請者



Diseases	Sex	TWB (%)	NHIRD (%)
Diabetes	Male	10.98	12.53
	Female	7.25	8.84
Hypertension	Male	29.12	26.7
	Female	16.86	17.08
Hyperlipidemia	Male	26.69	26.09
	Female	20.51	21.05

- 臺灣人體生物資料庫為生物醫學研究的目的而建立，且經參與者「事前同意」及完善的「事後退出」流程，保障參與者權利
- IRB EGC 雙重保障

Genomics data = new experience = new world

健保資料庫是不同來源資料的合集

- 1. 非屬病歷、醫療及健康檢查的個人資料
- 2. 由醫院儀器所產生的健康檢查資料
- 3. 由醫師依其個人經驗判斷的病歷及醫療"資訊"

什麼是健保資料庫？



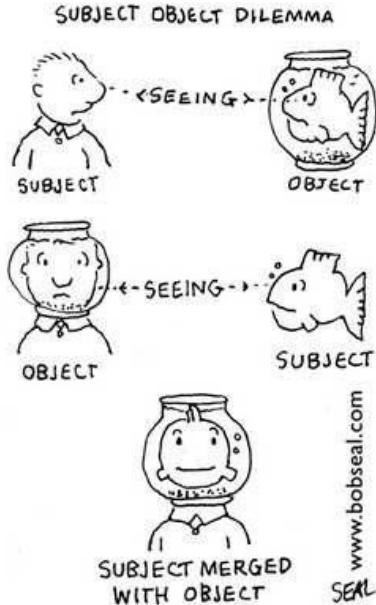
”

資料庫除國人的就醫、健保、出生、死亡紀錄外，加入更多社會福利相關資料，包括低收入戶家庭檔、原住民檔案等。

健保資料庫
醬行嗎？

台灣人權促進會

- 不同醫師依其不同的經驗對該個人的疾病狀態判斷可能不同
- 醫師的判斷又與該個人的自我認知不同
- 健保資料紀錄的是與醫療費用有關的資料



Why medical image Ai growing so rapidly?? Traditional experience



Evidence-based medicine

“心靈是塊白板，”

理性主義

經驗主義

德國觀念論（上）

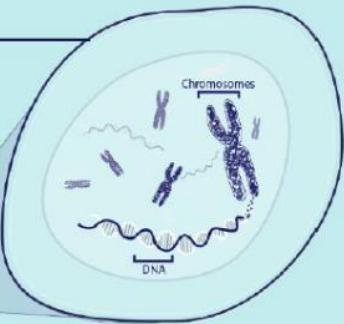
一切知識和觀念都起源於經驗。人們能夠經驗外界事物，並對所觀察的事物加以反省，我們便得到知識。



Genetics 101

Human cell

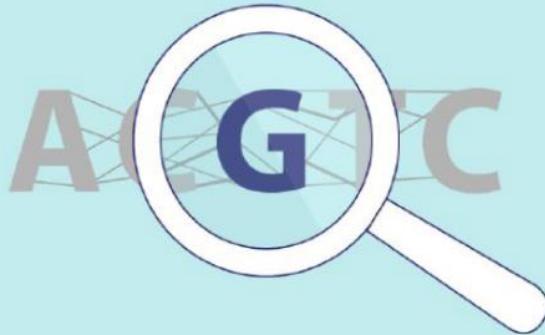
Most cells in the human body have a **complete** set of genes



Your **genome** is one whole set of all your genes plus all the DNA between your genes.

There are around **20,000** genes in your genome

Now



We know that the non-gene (non-coding) parts of your genome may have a role to play so we look at the whole thing, every single letter, and how the different parts work together.

5%

were analysed

Only the active genes were looked at



Your genome

with

3 Billion

pairs of letters in the human genome

AAGTAATATGC
TTCTAGGC GTC
TCAAGATGC AT
CTAGCACAGC
GCCCTTATT A
TCTCTATACTCA
ACTACTAGGGC
TATTTCATATCT
AAATACGCTCG
AGGCTACTGAC
TTATGCTATCG
ATCTCGAGCGC
TDCCGTAATT T
TCGCGAATCAG
AAGTAATATGC
TTCTAGGC GTC
TCAAGATGC AT
CTAGCACAGC
GCCCTTATT A

95%

were unused

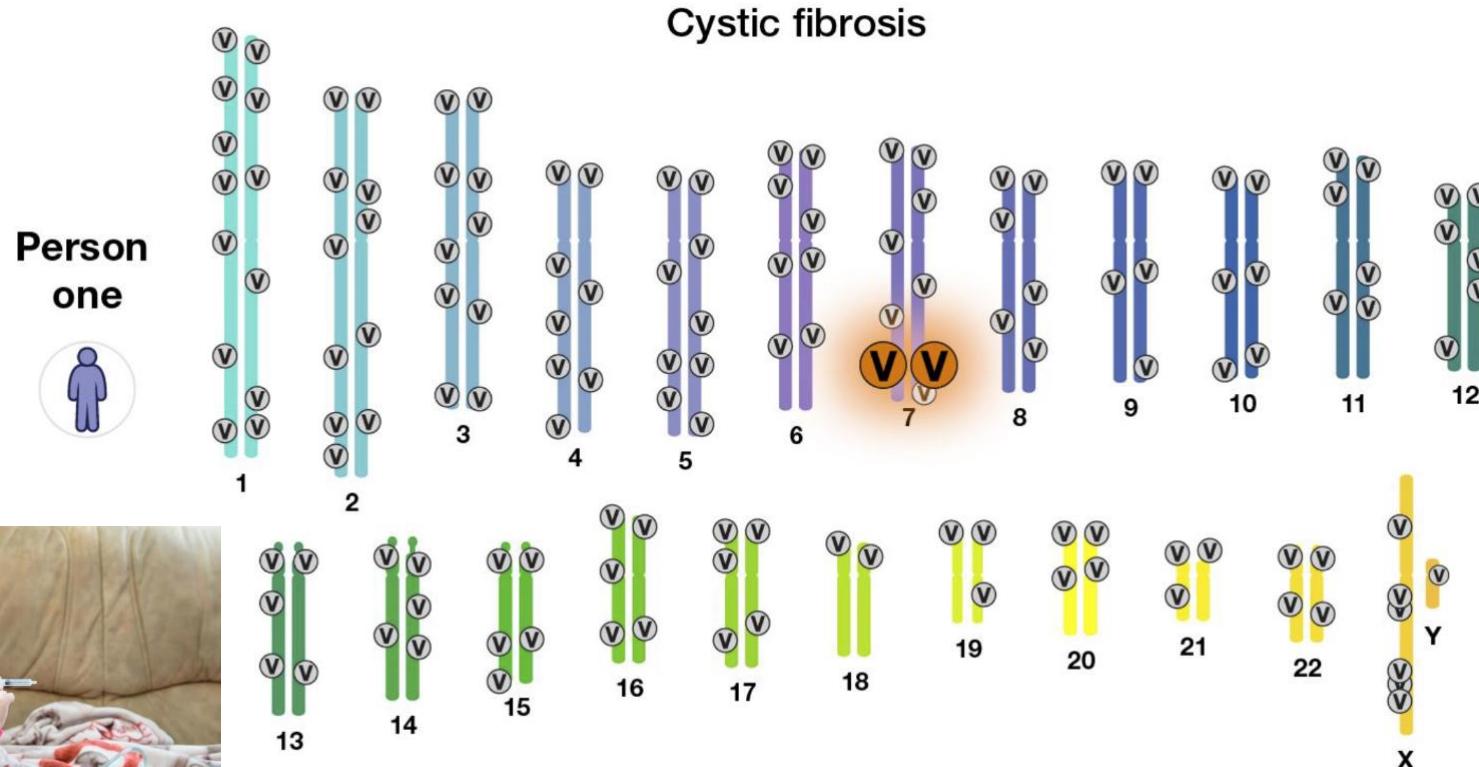
All the non-gene sections that we didn't understand were disregarded as useless



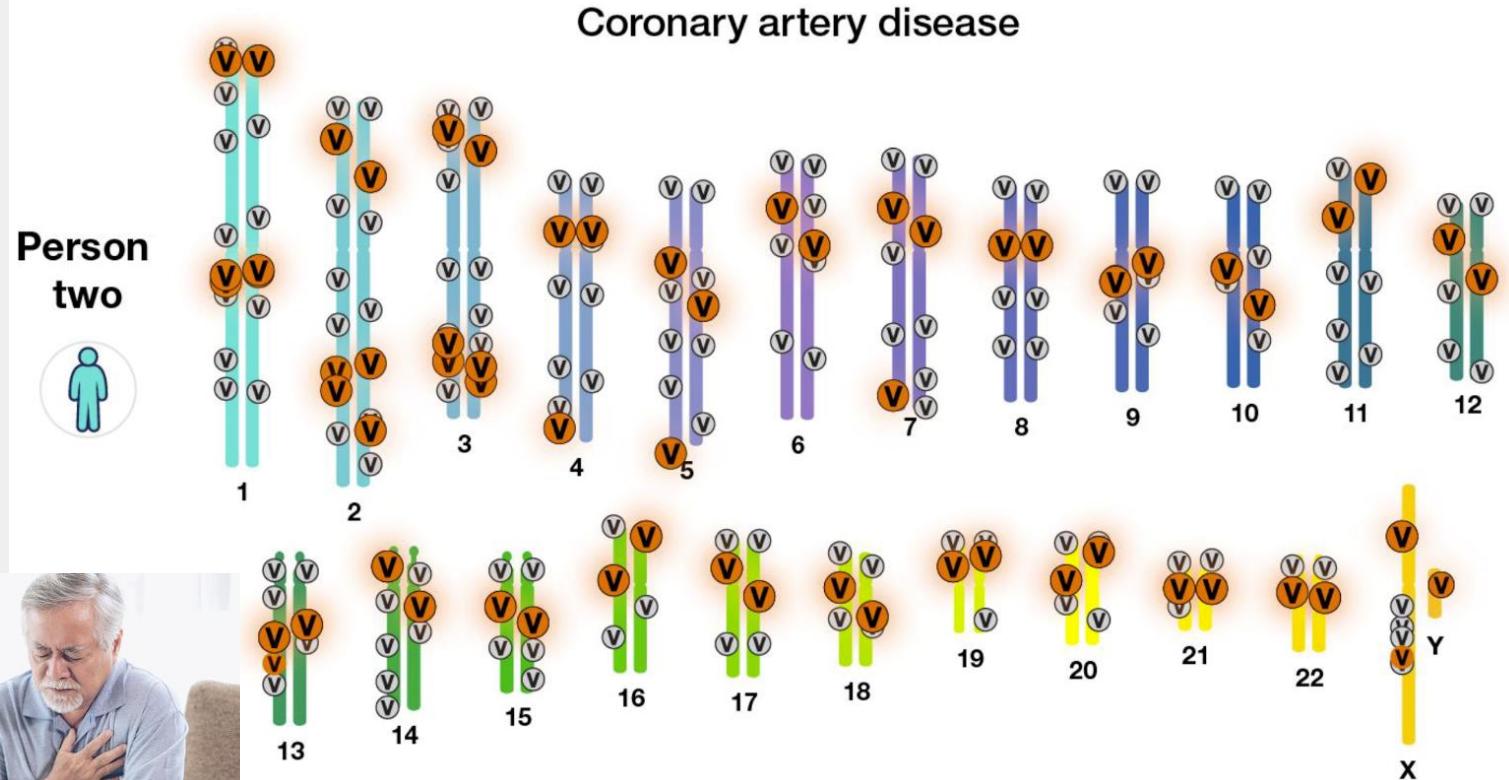
BIOBANK • 健康世代

中央研究院・臺灣人類生物資料庫

cystic fibrosis (囊狀纖維化) → transmembrane conductance regulator (CFTR) gene on chromosome 7.

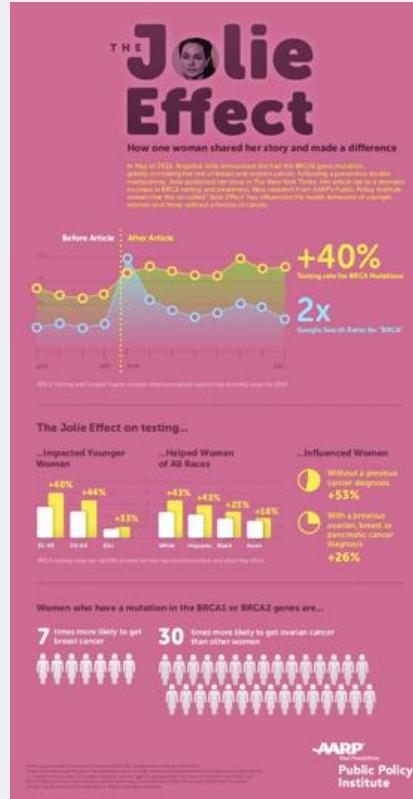


complex diseases (polygenic disease)



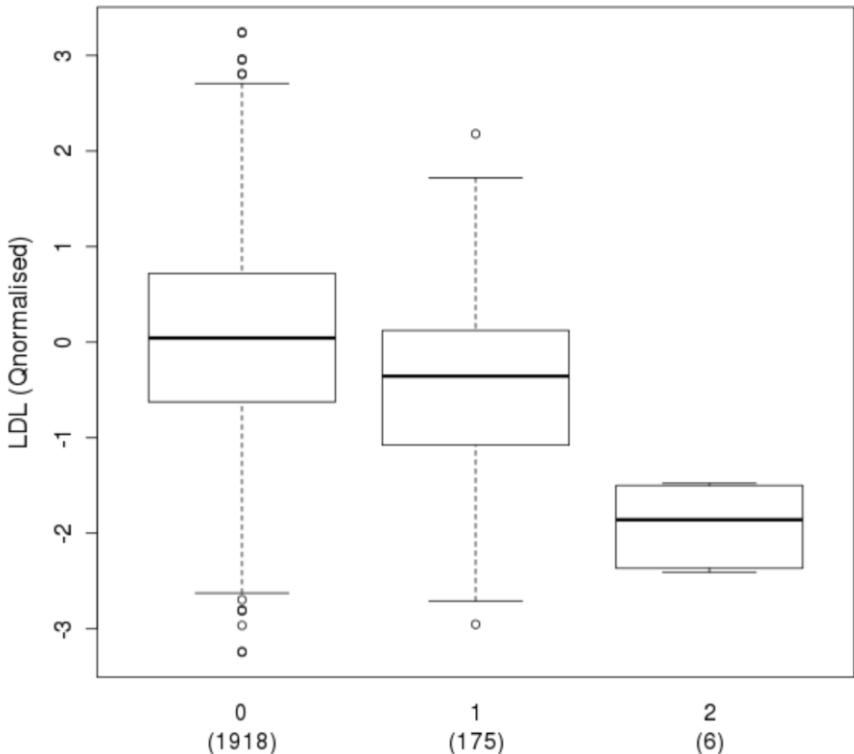
single gene

Jolie Effect



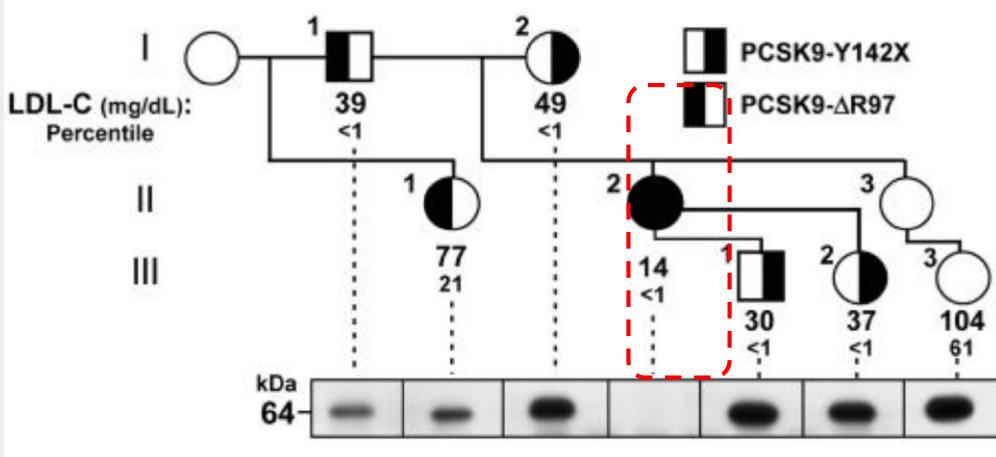
GENETIC VARIANT “RS11591147” IN PCSK9

PCSK9 NONSYN; $b=-0.57$, $p=1e-14$; $N=2099$



- Carriers of T variant have lower levels of LDL cholesterol than carriers of G variant
- LDL is a strong risk factor for heart disease

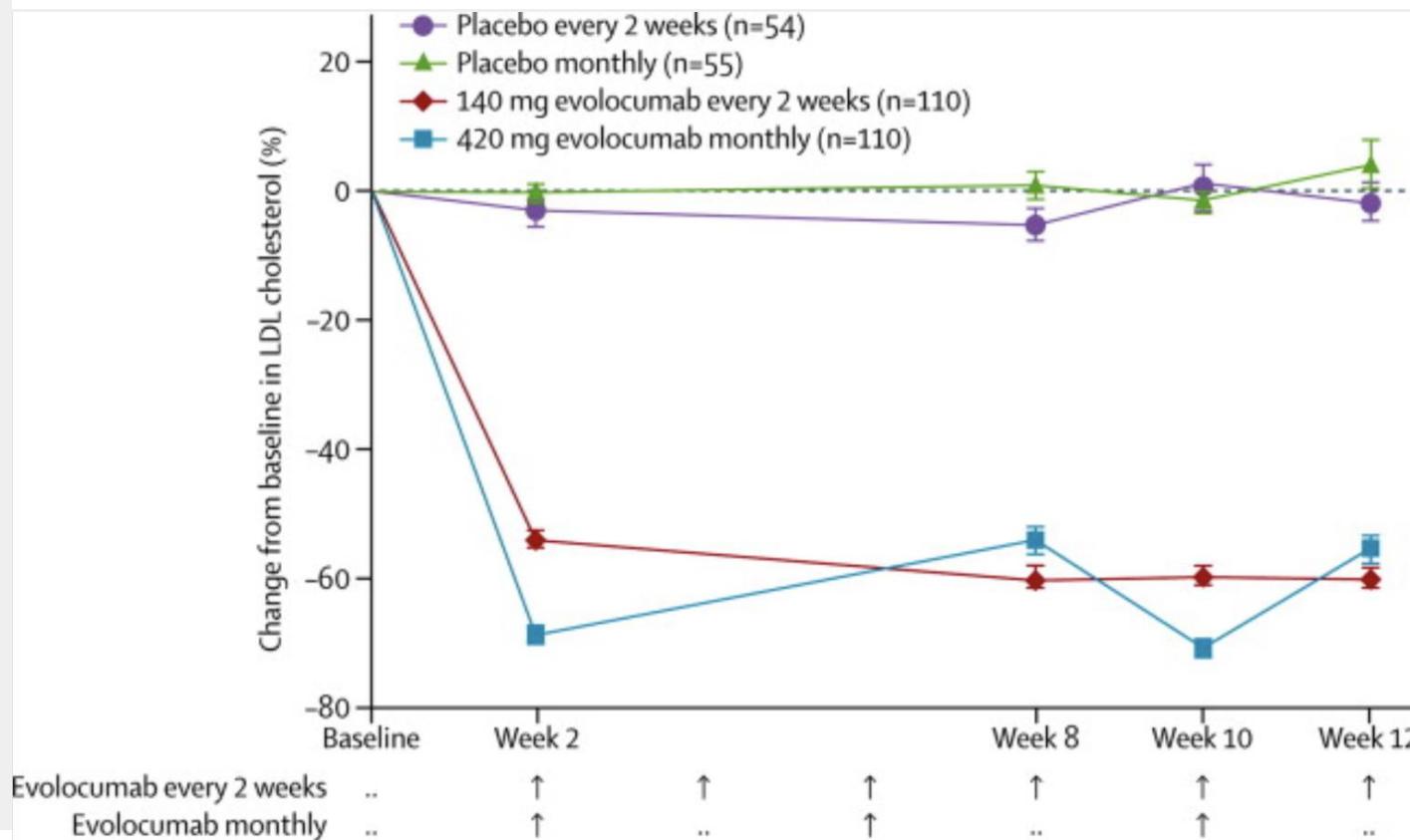
A HUMAN KNOCK-OUT OF PCSK9 (2006)



Individual II.2 has zero working copies of PCSK9 gene

- no circulating PCSK9 and an LDL-C of only 14 mg/dL
- apparently healthy, fertile, normotensive, college-educated woman with normal liver and renal function tests who works as an aerobics instructor
- Why is this very interesting observation?
Inhibiting PCSK9 might be a safe way to reduce LDL

PCSK9 inhibition with evolocumab (AMG 145) in heterozygous familial hypercholesterolaemia (RUTHERFORD-2): a randomised, double-blind, placebo-controlled trial



Evolocumab and Clinical Outcomes in Patients with Cardiovascular Disease

Marc S. Sabatine, M.D., M.P.H., Robert P. Giugliano, M.D., Anthony C. Keech, M.D., Narimon Honarpour, M.D., Ph.D., Stephen D. Wiviott, M.D., Sabina A. Murphy, M.P.H., Julia F. Kuder, M.A., Huei Wang, Ph.D., Thomas Liu, Ph.D., Scott M. Wasserman, M.D., Peter S. Sever, Ph.D., F.R.C.P., and Terje R. Pedersen, M.D. for the FOURIER Steering Committee and Investigators*

FDA Approves Amgen's Repatha (evolocumab) to Prevent Heart Attack and Stroke



Dec 1 2017

In the Repatha cardiovascular outcomes study (FOURIER), Repatha reduced the risk of heart attack by 27%, the risk of stroke by 21% and the risk of coronary revascularization by 22%..

precision medicine in Taiwan

Use of HLA-B*58:01 genotyping to prevent allopurinol-induced severe cutaneous adverse reactions in Taiwan: national prospective study

BMJ 2015;351:h4848 Sep 23, 2015

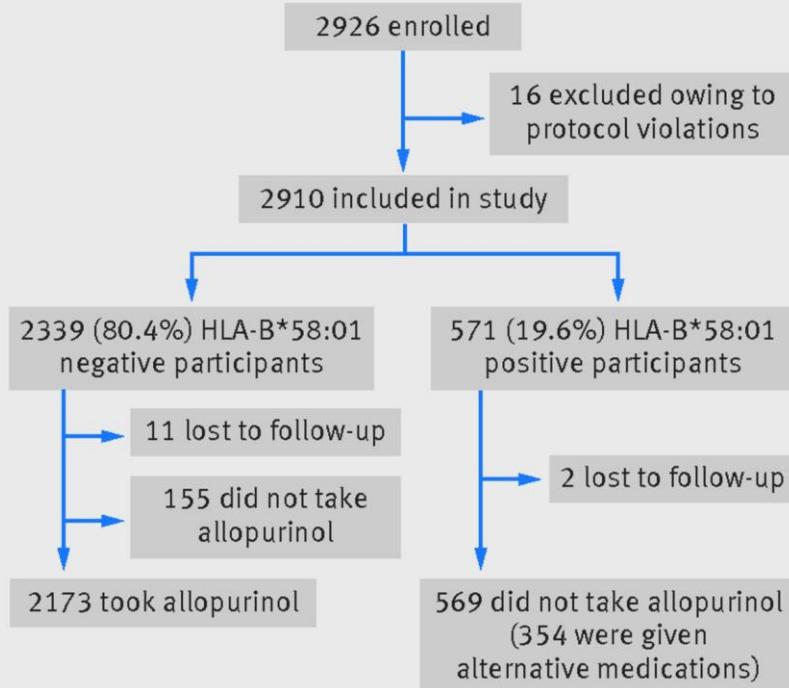
BMJ



Gout
Allopurinol
HLA-B*58:01



NHIRD-TWB → reduce health expenditures



Adverse event	HLA-B*58:01 positive participants receiving alternative drug treatment (n=354)	HLA-B*58:01 negative participants receiving allopurinol (n=2173)	Total (n=2910)
Mild cutaneous events			
Rash and itching	3*	94	97
Blisters	0	0	0
Oral ulcers	0	2	2
Rash, itching, oral ulcers, and fever	0	1	1
Rash, itching, and other adverse events	0	22	22

Records from the **National Health Insurance research database**
Incidence of SCARs ~0.3%

frequency distribution of pharmacogenetic phenotypes predicted by genotypes of TWB cohort

Gene	Drug	Rx ^a /year	EM	IM	PM	ADR ^b carrier rate
CYP2B6	Efavirenz	1,662,525	66.0%	30.5%	3.6%	
CYP2C19	Clopidogrel	63,664,076	39.8%	56.4%	3.8%	
CYP2C9	Celecoxib	65,058,810	93.6%	6.3%	0.1%	
CYP3A5	Tacrolimus	10,272,406	8.1%	40.6%	51.2%	
IL28	Peginterferon	40,941	88.6%	11.1%	0.3%	
NAT2	Isoniazid	7,885,251	28.8%	59.2%	12.0%	
SLCO1B1	Simvastatin	50,695,934	78.9%	19.9%	1.3%	
TPMT	Azathioprine	7,435,217	97.0%	2.9%	0.02%	
UGT1A1	Atazanavir	719,793	53.2%	39.8%	7.0%	
VKORC1	Warfarin	16,121,944	1.1%	19.2%	79.7%	
HLA-A*3101	Carbamazepine	17,078,849				2.0%
HLA-B*1502	Carbamazepine	17,078,849				4.1%
HLA-B*5701	Abacavir	3,049,217				0.2%
HLA-B*5801	Allopurinol	23,888,472				10.5%
MT-RNR1	Amikacin	321,561				4.7%

^aRx = prescriptions.

^bADR = adverse drug reactions.

NOTCH3 cysteine-altering variant is an important risk factor for stroke in the Taiwanese population

We queried the Taiwan Biobank database for cysteine-altering mutations in exons 2–24 of NOTCH3 within these genomes. The reference coding sequence of NOTCH3, NM_000435.3, was used for annotating the variants. (**p.R544C** (c.1630G>A), **p.C853Y** (c.2558G>A), and **p.C884Y** (c.2651G>A))

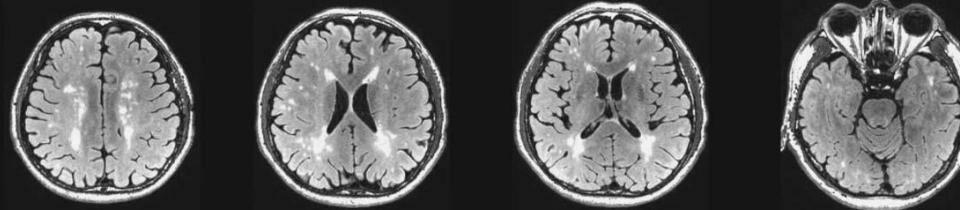
The cysteine-altering NOTCH3 variants identified from the Taiwan Biobank database were genotyped in the control participants and patients with stroke using the TaqMan genotyping assay

Only the NOTCH3 p.R544C variant was found in 4 individuals (TP-VGH (n =550))

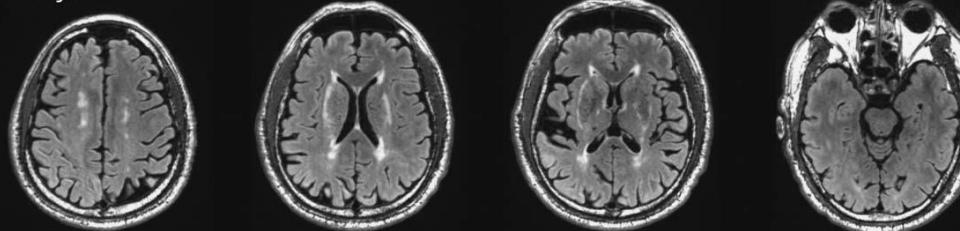
	Controls			Patients with stroke		
	Taiwan biobank (n = 6,488)	TP-VGH (n = 550)	Biobank + TP-VGH (n = 7,038)	TP-VGH (n = 350)	TC-VGH (n = 450)	TP-VGH + TC-VGH (n = 800)
Male	2,293 (35.3)	230 (41.8)	2,523 (35.8)	248 (70.9)	327 (72.7)	575 (71.9)
Age, y	48.4 ± 10.9	56.7 ± 15.0	49.1 ± 11.5	64.4 ± 13.6	67.5 ± 13.2	66.2 ± 13.5
Hypertension	682 (10.6)	186 (33.8)	868 (12.4)	248 (70.9)	329 (73.1)	577 (72.1)
Diabetes	300 (4.6)	72 (13.1)	372 (5.3)	130 (37.1)	168 (37.3)	298 (37.3)
Hyperlipidemia	388 (6.0)	138 (25.1)	526 (7.5)	129 (36.9)	181 (40.2)	310 (38.8)
Smoking habit	1,228 (18.9)	98 (17.8)	1,326 (18.8)	122 (34.9)	136 (30.4)	258 (32.4)
Alcohol consumption	387 (6.0)	108 (19.6)	495 (7.0)	56 (16.0)	87 (23.2)	143 (19.7)
Family history of stroke	1,146 (17.8)	—	—	40 (14.1)	14 (4.0)	54 (8.5)
NOTCH3 p.R544C mutation (+)	56 (0.9)	4 (0.7)	60 (0.9)	8 (2.3)	9 (2.0)	17 (2.1)

Physical examination revealed that they were free of neurologic deficits. Three of them received brain MRI scans, and all had a variable degree of leukoencephalopathy.

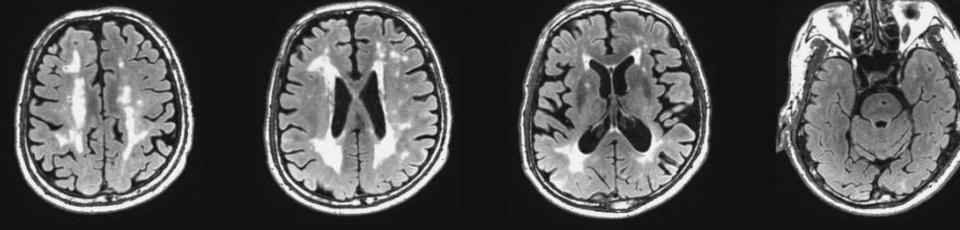
C-I, 59 years male



C-II, 66 years male



C-III, 67 years male



multi-gene

GWAS study

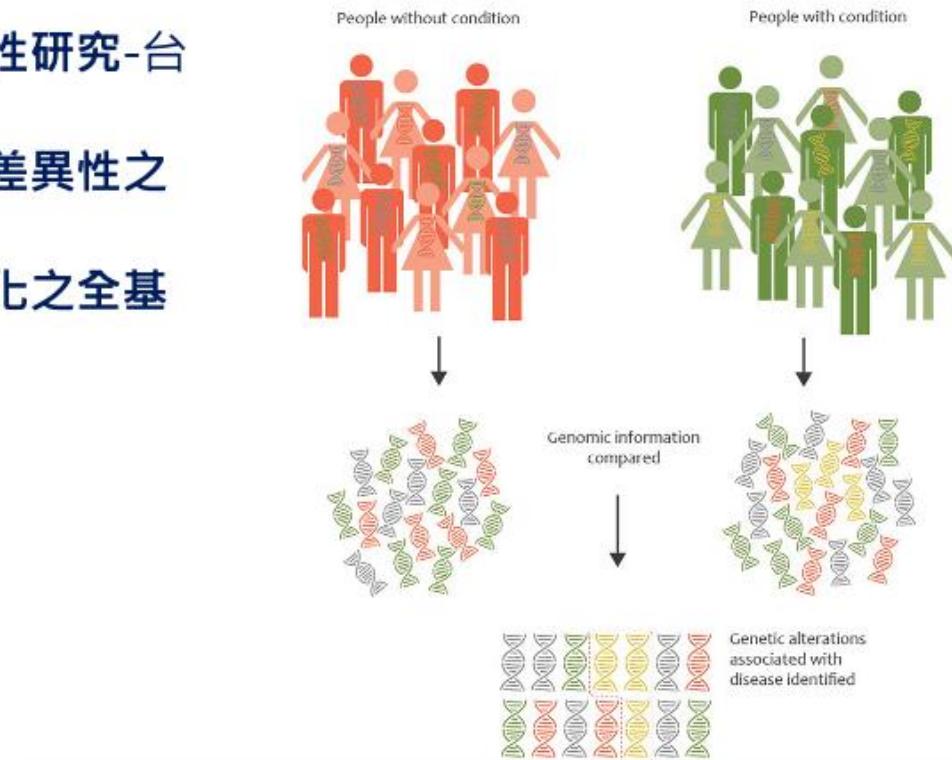
- 偏頭痛及阿茲海默氏症之全基因體關聯性研究-台北榮總
- 利用全基因關聯性研究於影響人類身高差異性之基因鑑定與功能性探討-中國醫藥大學
- 利用台灣生物資料庫探討成人肺功能變化之全基因體關聯研究-中央研究院
 - Calculate polygenic risk score (PRS) for individual j using m SNPs

$$PRS_j = \frac{\sum_{i=1}^m \ln(OR_i) \times SNP_{ij}}{m}$$

where

- $\ln(OR_i)$ = effect size for SNP i from discovery sample
- SNP_{ij} = number of risk alleles (0,1,2) for SNP i, individual j in target sample
- m = number of SNPs considered in test set

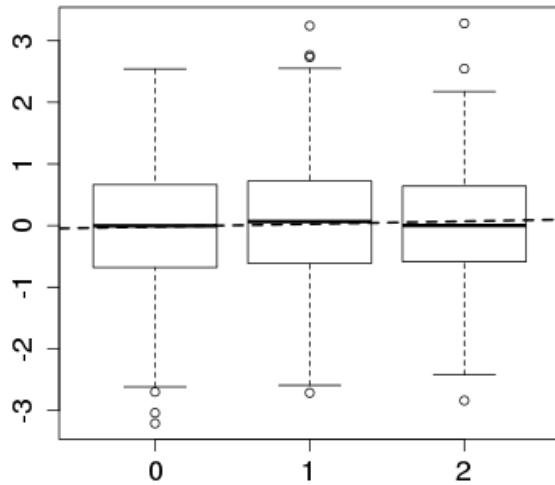
Purcell / ISC et al. Common polygenic variation contributes to risk of schizophrenia and bipolar disorder Nature 2009



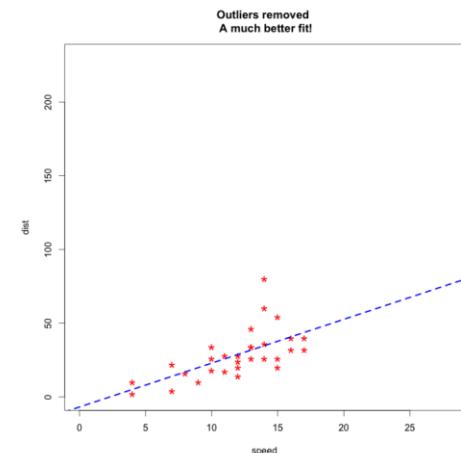
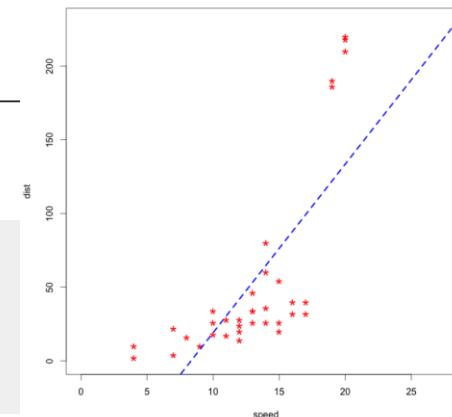
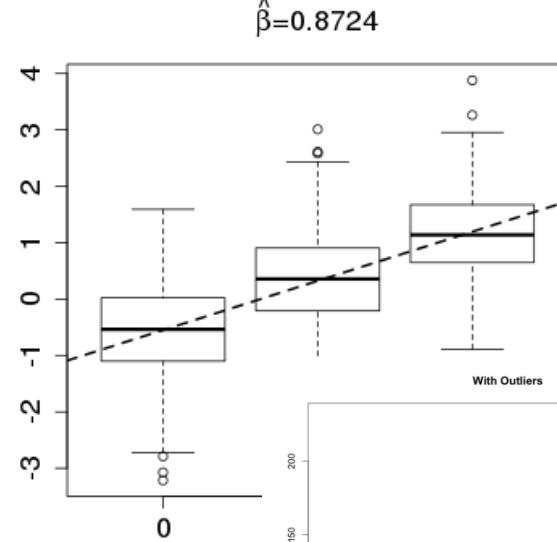
BIOBANK • 健康世代
中央研究院・臺灣人類生物資料庫

association study linearMod <- lm(glucose ~ bmi, data=twb)

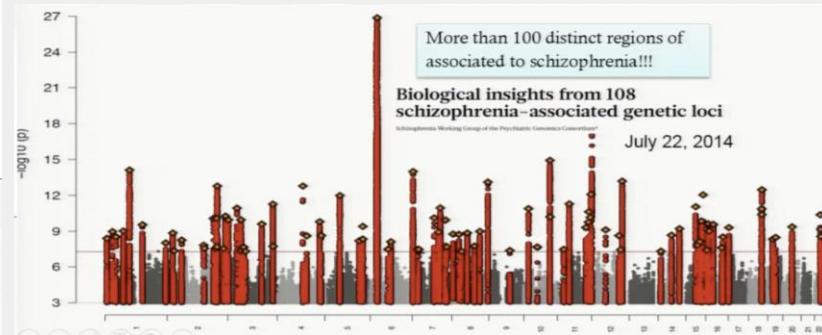
$$\hat{\beta} = 0.04424$$



$$\hat{\beta} = 0.8724$$



the power of sample size - schizophrenia | psychiatric genomics consortium



polygenic risk score

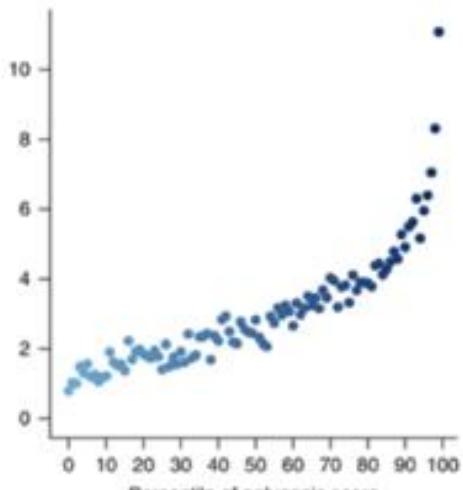
Discovery GWAS

	Weight*	Risk Allele		
SNP1	0.2	A		
SNP2	-0.3	C		
SNP3	0.1	G		
Individual	Alleles SNP1	Alleles SNP2	Alleles SNP3	
1	AT	AA	CG	
2	AA	CA	GG	
3	TT	AC	CG	
4	TT	AA	GG	
5	TA	CA	GC	
6	AT	CA	CG	
7	AA	AA	GG	
8	AA	CC	CG	
9	TA	CC	GC	
10	AT	AA	CG	

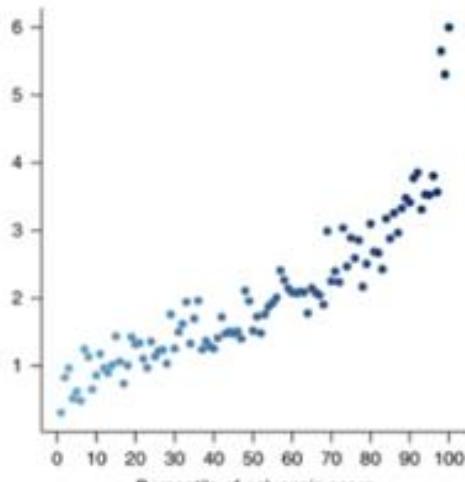
PRS:

Individual	SNP 1	SNP 2	SNP 3	PRS
1	0.2+0.0	0.0+0.0	0.0+0.1	0.3
2	0.2+0.2	-0.3+0.0	0.1+0.1	0.3
3	0.0+0.0	0.0-0.3	0.0+0.1	-0.2
4	0.0+0.0	0.0+0.0	0.1+0.1	0.2
5	0.0+0.2	-0.3+0.0	0.1+0.0	0.0
6	0.2+0.0	-0.3+0.0	0.0+0.1	0.0
7	0.2+0.2	0.0+0.0	+0.1+0.1	0.6
8	0.2+0.2	-0.3-0.3	0.0+0.1	-0.1
9	0.0+0.2	-0.3-0.3	0.1+0.0	-0.3
10	0.2+0.0	0.0+0.0	0.0+0.1	0.3

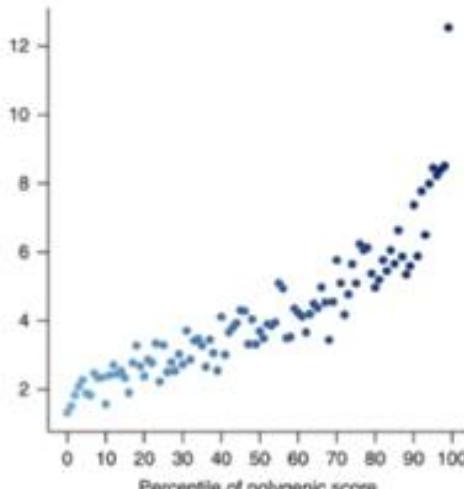
disease risk prediction



Prevalence of Coronary Artery Disease



Prevalence of Type 2 Diabetes

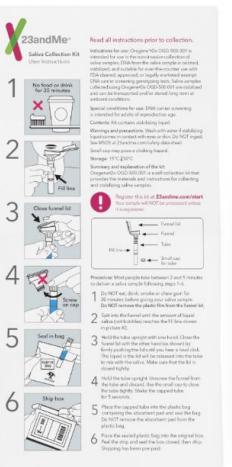


Prevalence of Breast Cancer

“...it is time to contemplate the inclusion of polygenic risk prediction in clinical care, and discuss relevant issues.”

Khera et al. *Nature Genetics* 50, 1219–1224 (2018)

Direct to consumer genetic testing (DTG)



For most health conditions (like diabetes or cancers), each person has some risk of developing the condition during their life. This diagram represents this as a bucket – a person experiences the condition when their bucket gets full up.

Most health conditions arise due to a combination of genetic and other risk factors.

● Genetic factors ■ Other factors



Everyone starts life with some genetic risk factors for the condition. Some people have very few, some people have a lot. You are born with this risk and you can't change it. Direct-to-consumer genetic tests aim to measure this risk (though their measurement is often far from perfect).



Over the course of life, people are exposed to other factors that increase the chance of them experiencing the condition.



If you had more genetic risk factors in your bucket to begin with, it takes fewer other risk factors to fill the bucket and result in the health condition.



Some of the other factors, you can't change, like your age. Some factors, you might be able to work on, like smoking, or alcohol intake.

Even if you have a 'high genetic risk' of a particular condition, for most health conditions, having a high genetic risk does not mean you'll get it.

By working on the factors you can change, you might be able to reduce the chance of developing a health condition, even if you have a high genetic risk.

Rethinking data quality!! Big data create the world!!



AT&T Wi-Fi 3:40 PM amazon echo dot 3RD GENERATION

Activity Voice

Tell me a challenge to do

Here's something I found on the web. According to ourcommunitynow.com: The challenge is simple: plug in a phone charger about halfway into a wall outlet, then touch a penny to the exposed prongs.

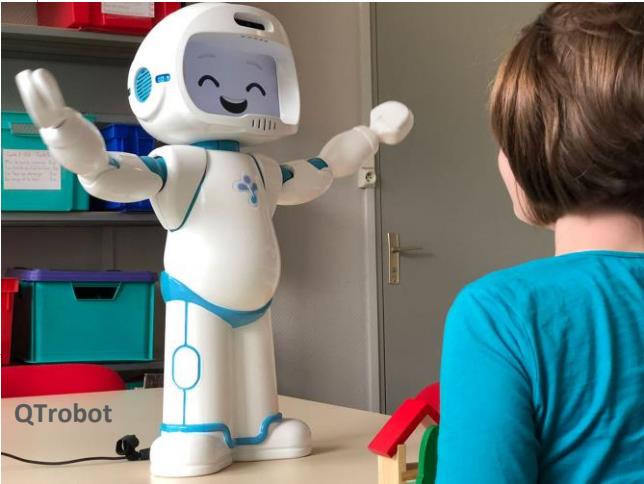
LEARN MORE ON OURCOMMUNITYNOW.COM



.....firukulal.....



Therapy Robot Teaches **Social Skills** to Children With Autism.



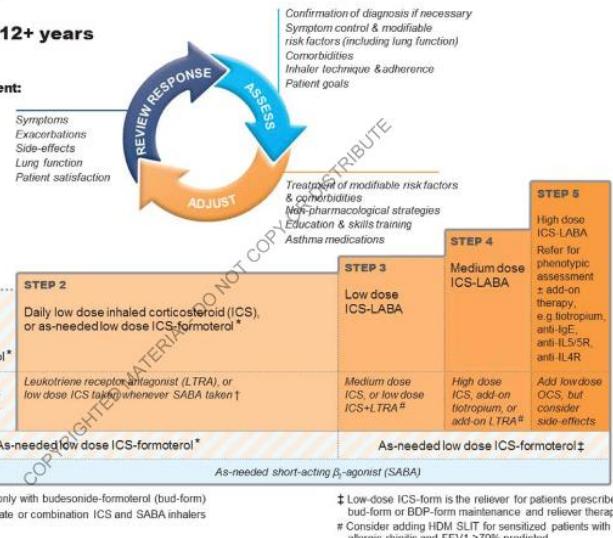
Precision medicine

Box 7. The GINA asthma treatment strategy

Adults & adolescents 12+ years

Personalized asthma management:

Assess, Adjust, Review response

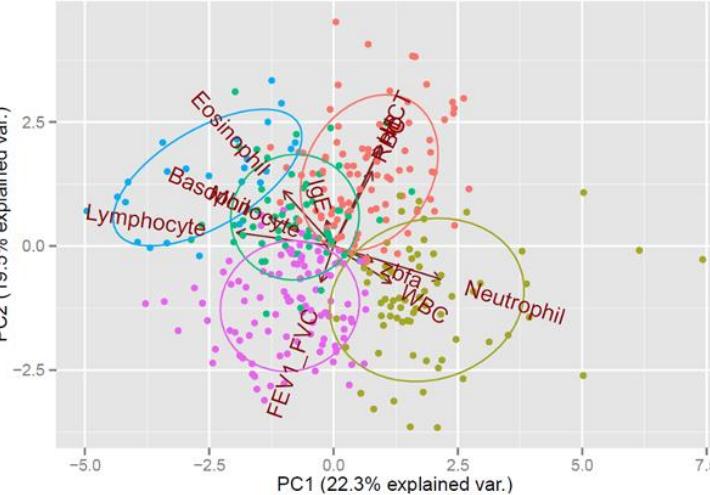


6. ADVAIR DISKUS (fluticasone propionate)

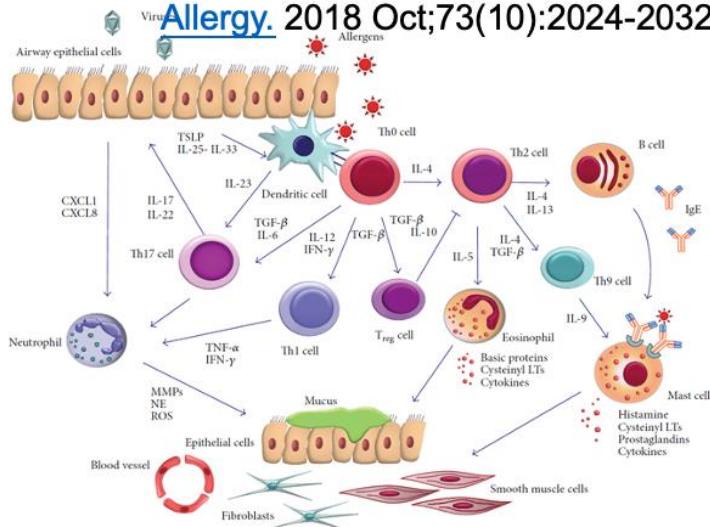
Asthma



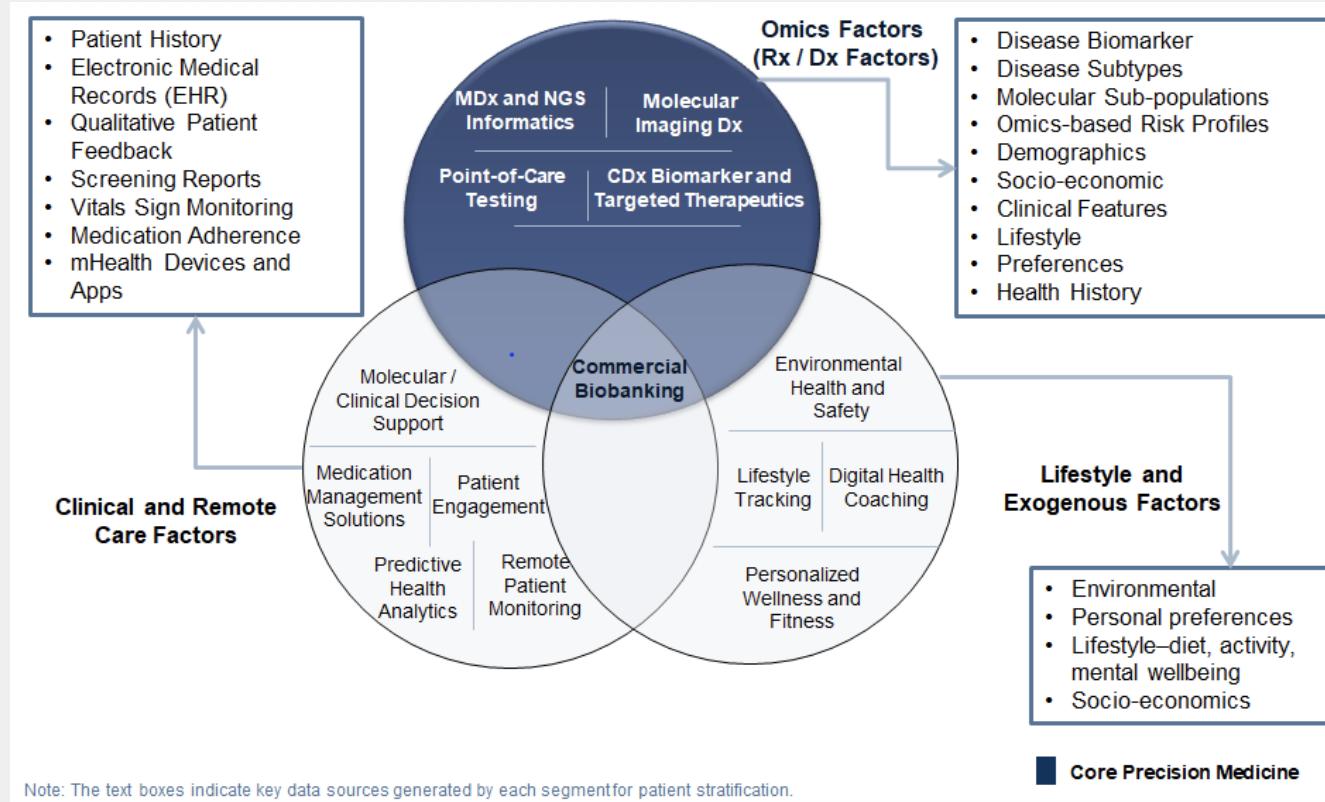
PC2 (19.5% explained var.)



Allergy. 2018 Oct;73(10):2024-2032.



Biobank - provide clinical research support that translates into bedside diagnostics and treatments, and advances research technologies into clinical applications



Lion man 35,000~40,000 years old

精準醫療並非只是醫學領域的轉變
而是人看待自己與形塑自己方式的轉變
是一個重新認識自己的過程

