HURDLE

Epigenetics and the science behind biological age clocks - InflammAge as a case study

Lisa J. Schmunk, PhD Research & Development Manager

Visit us at stand B38

Today's agenda:

~20 min presentation ~10 min Q&A

- 1. Introduction to the world of Science & Epigenetics
- 2. Deep dive into Epigenetics and Ageing
- 3. What epigenetic clocks can tell us about our health
- 4. InflammAge as a case study
- 5. The role of epigenetics clocks in the diagnostic journey
- 6. Summary
- 7. Q&A

Biology in a nutshell - Nature vs Nurture

Our bodies are made up of **cells**, each with the same **DNA** inside that we inherit from our parents.

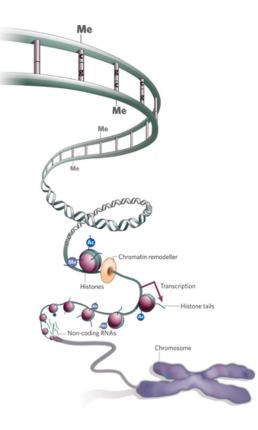
Our genetic makeup is fixed at birth

• DNA code ATCG, 3 billion letters per copy, 23 x 2 chromosomes

Central dogma of Biology:

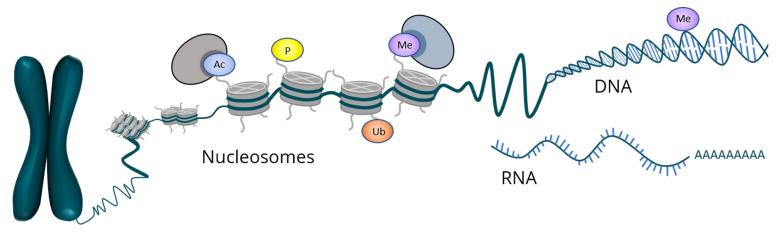
- DNA -> RNA -> Protein
- **Gene** = stretch of DNA that can be "expressed" to create a functional product (e.g. an enzyme)

Epigenetics refers to the layer of non-genetic influences on gene expression and can change over time.





What is epigenetics?



Chromosome

Image: BPS Bioscience 2023



What is epigenetics?

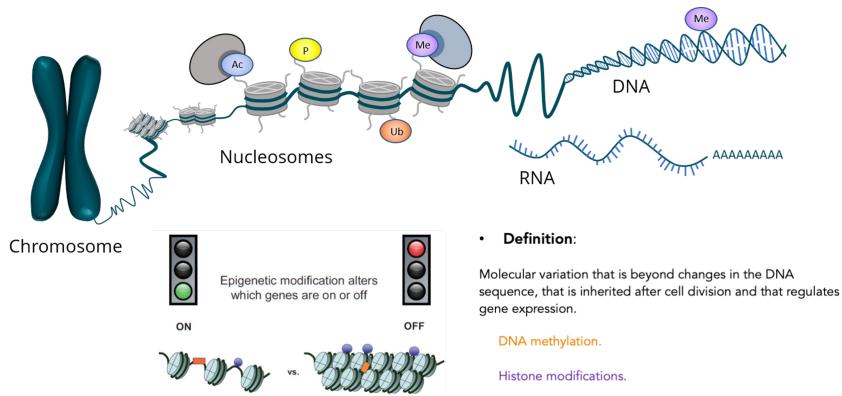
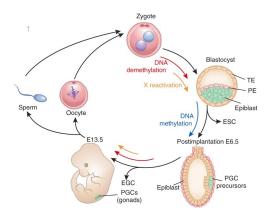


Image: BPS Bioscience 2023

Others (non-coding RNAs?).

Epigenetics and physiology

Early development

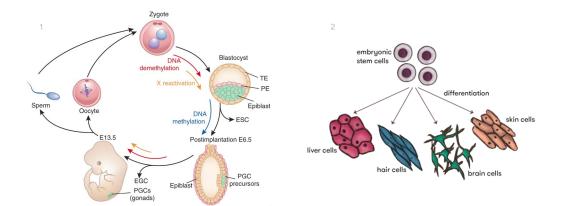




Epigenetics and physiology

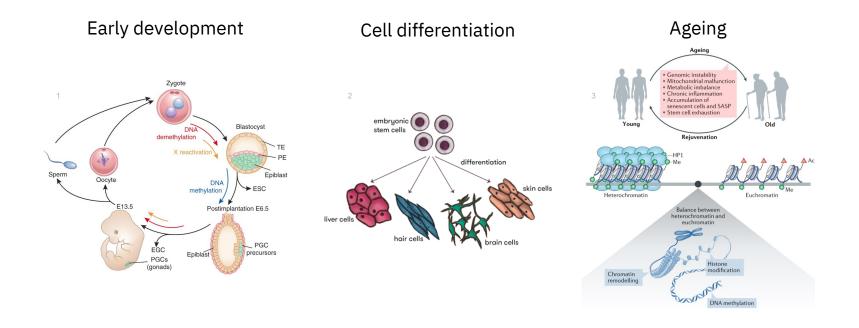
Early development

Cell differentiation





Epigenetics and physiology



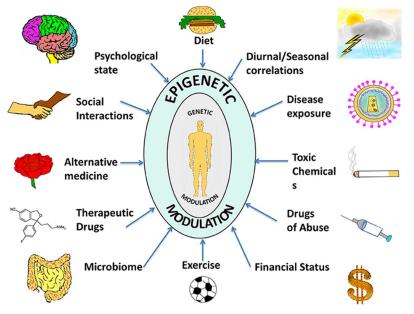
Epigenetics integrates genetics x environment

Identical twins

Mark and Scott Kelly

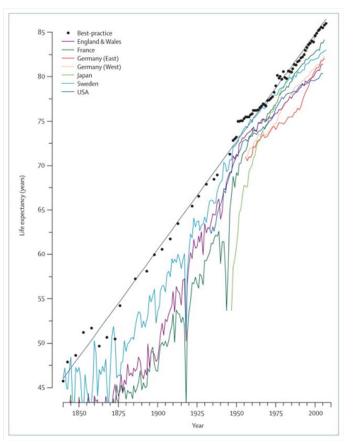


Source: https://www.nasa.gov/feature/nasa-twins-studyconfirms-preliminary-findings



Kankerhan et al. Front. Cell Dev. Biol., 2014

Modern Ageing - Lifespan vs healthspan



We are living longer:

Almost 2X lifespan since 200 years ago.

Yet sicker: rise of NCDs:

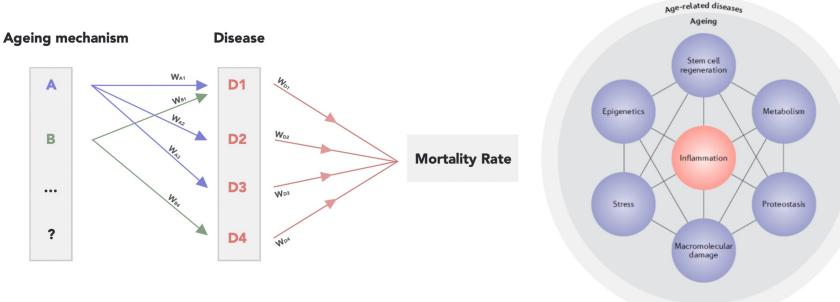
Cardiovascular, cancer, diabetes, neurodegenerative, ... Largely preventable through lifestyle interventions.

Focus \rightarrow extend healthspan.

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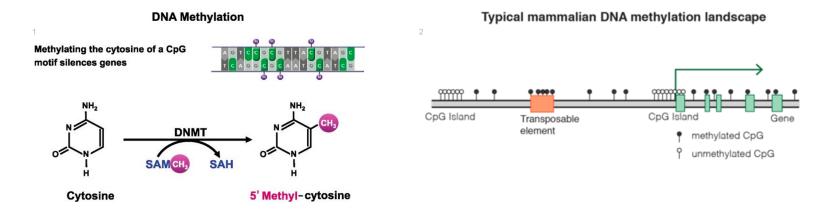
The Lancet, vol. 374, no. 9696, pp. 1196-1208, Oct. 2009

Ageing is composed of many molecular mechanisms (hallmarks)



How can we measure biological ageing?

DNA methylation - the archetypal epigenetic modification



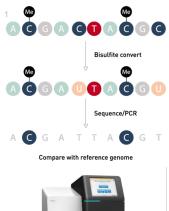
- The first molecular epigenetic mechanism discovered (early as 1948)
- DNA methyltransferase (DNMT) enzymes attach methyl group to carbon 5 of cytosine on CpG motifs
- Most common cytosine modifications in mammals are 5-methylcytosine (5-mc) and 5-hydroxymethylcytosine (5-hmc)

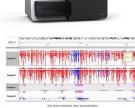
- There are *circa* 30 million CpG sites across the human genome
- Methylation of CpG sites can promote or repress gene expression

Images: 1. Diagenode 2023; 2. Biostars 2023; 3. Li et al. 2023, PNAS; 4. Slieker et al. 2018, Epi & Chrom;



Measuring methylation patterns

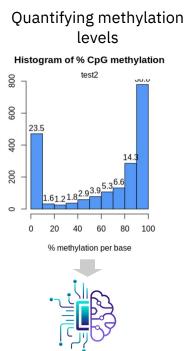




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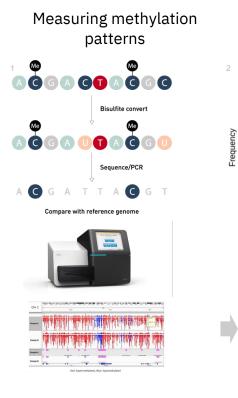


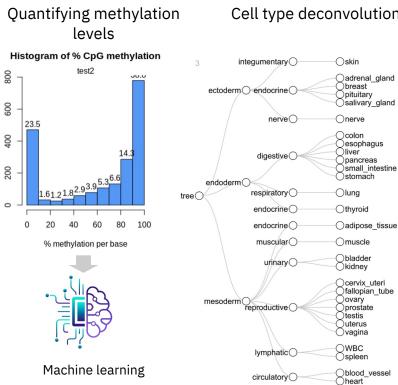




Machine learning







Cell type deconvolution

⊖skin

∋pituitary Osalivary gland

nerve

∋colon

Desophagus Dliver

Dpancreas

stomach

Omuscle

Dbladder

kidnev Cervix uteri)fallopian tube

Dovarv

Oprostate) testis ⊖uterus Dvagina WBC

Spleen

Oheart

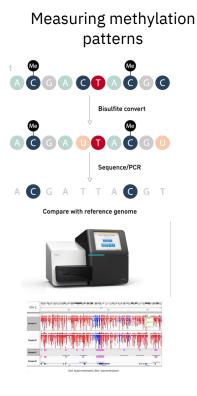
Oblood vessel

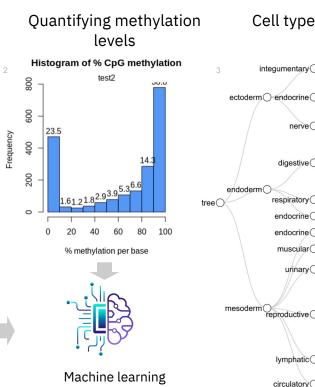
Small intestine

adrenal gland Dbreast



Images: 1. Diagenode 2023; 2. Biostars 2023; 3. Li et al. 2023, PNAS; 4. Slieker et al. 2018, Epi & Chrom;





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prostate

Cervix uteri

)fallopian tube

Small intestine

Oadipose tissue

integumentary C

nerve

digestive (

respiratory

endocrine

endocrine ()

muscular

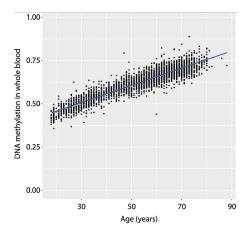
urinary(

reproductive

lymphatic(

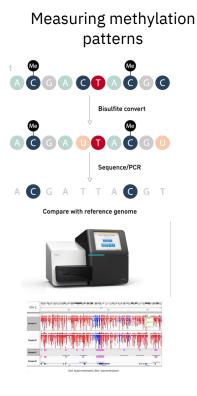
circulatory(

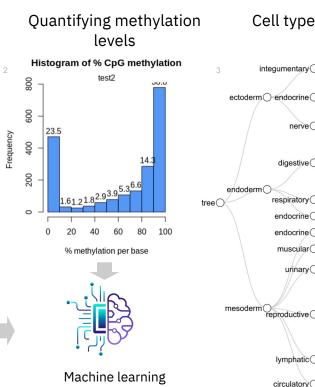
Tracking methylation changes



ELOVL2 promoter methylation changes with age in blood

Images: 1. Diagenode 2023; 2. Biostars 2023; 3. Li et al. 2023, PNAS; 4. Slieker et al. 2018, Epi & Chrom;





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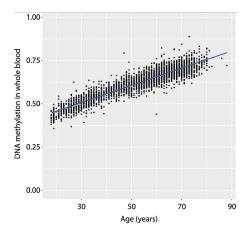
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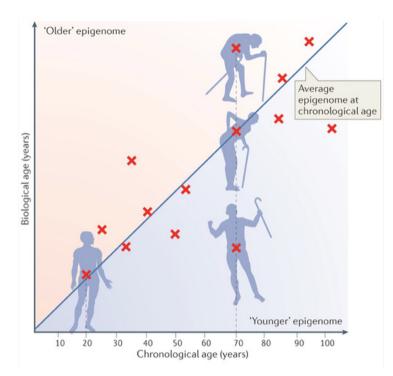
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Measuring the ageing process with epigenetics



Nature Rev. Mol. Cell Biology, vol. 16, no. 10, pp. 593-610, 2015.

Epigenetic clocks:

The most accurate biomarkers of the ageing process.

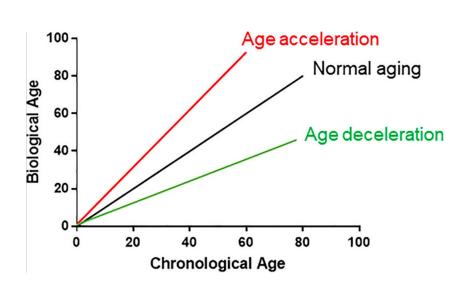
They measure your biological age.

Development of anti-ageing therapies.

Chronomics epigenetic clock \rightarrow saliva

Epigenetic clocks and their clinical relevance

• Epigenetic age acceleration (EAA) is associated with meaningful variables in humans.



Biological aging methylation 'clocks'

- <u>Clinical</u>
- All-cause mortality
- Obesity
- Cancer
- Cardiovascular disease
- Alzheimer's
- Werner's syndrome
- Huntington's disease
- Down syndrome
- Sotos syndrome
- HIV infection
- ...

Nat. Review Genetics, vol. 19, pp. 371-384, 2018.

Epigenetic clocks and their clinical relevance

• Epigenetic age acceleration (EAA) is associated with meaningful variables in humans.

Extrinsic Intrinsic **Epigenetic Age Epigenetic Age** 1 Insulin & glucose C-reactive protein BMI & Waist-to-hip ratio Triglycerides Systolic blood pressure HDL cholesterol Fish Poultry Fruits & vegetables Moderate alcohol Education & income L Exercise

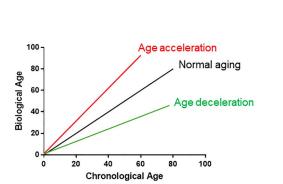
Pre-clinical / lifestyle factors

Clinical

- All-cause mortality
- Obesity
- Cancer
- Cardiovascular disease
- Alzheimer's
- Werner's syndrome
- Huntington's disease
- Down syndrome
- Sotos syndrome
- HIV infection
- ...

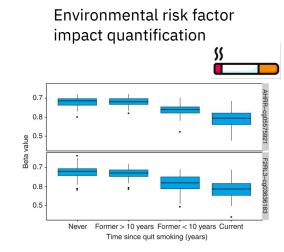
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Epigenetic clocks and their clinical relevance



Biological aging

methylation 'clocks'

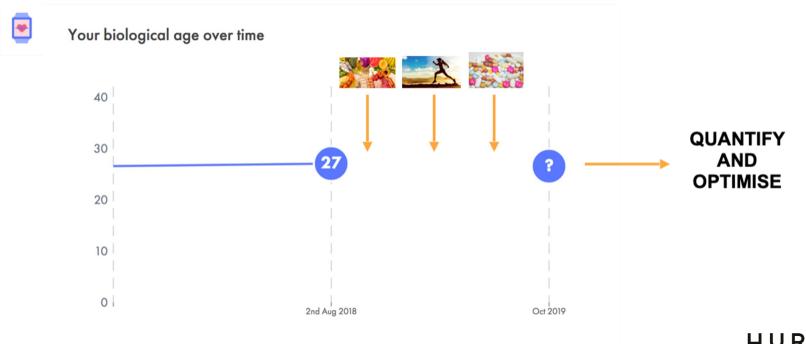


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Measuring physiological risk factors



Epigenetic clocks to track intervention success



Preventive healthcare and epigenetics - InflammAge

- At **Hurdle** we trained a novel DNA methylation aging clock using biologically informed by features related to systemic chronic inflammation. This work was supported by Bayer Consumer Health
 - First biomarker of its kind rooted in biology of chronic inflammation and epigenetic aging
 - Non-invasive and accessible saliva test
 - Easily deployable as screening self test
 - Captures long term inflammation trends (think HbA1c vs glucose)
 - Actionable measurement of a major driver of biological-age related chronic disease risk



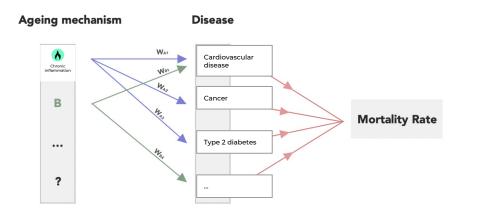


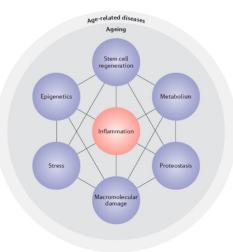






Preventive healthcare and epigenetics - InflammAge

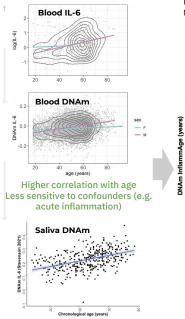






Preventive healthcare and epigenetics - InflammAge

Built saliva DNAm proxies for blood SCI markers



Trained age predictor ML model

using 42 SCI saliva DNAm proxies: novel InflammAge biomarker N=338, MAE=3.8337

100

25

50 75 Chronological age (years) 100







novel InflammAge biomarker

N=338. MAE=3.8337

25

75 Chronological age (years)

100

Infla





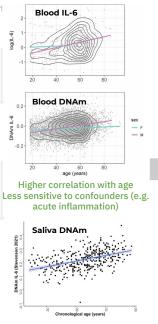


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Preventive healthcare and epigenetics - InflammAge

Built saliva DNAm proxies for blood SCI markers



Higher accessibility and scalability

Trained age predictor ML model InflammAge acceleration is associated with: using 42 SCI saliva DNAm proxies:

- Blood markers out of clinical reference ranges (N=61)
- Chronic pro- inflammatory disease (HIV,

N=46control+142HIV)

IDA

MDS

leukaemia

oth anaemi

pulm fibros sec pulm I

mycoses

oth organ

covid

peripheral arteria

- Inflammatory conditions in GS biobank (N= c.20,000)

50.0

712

61.3

72.1

72.8

611

BB P

63.6

63.1 61.9

68.4 66

63.2

0.457

0.656

0.561

0.529

0.484

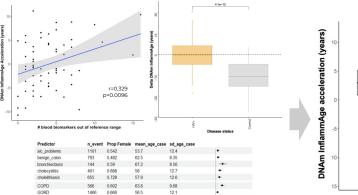
0.57

0.623

0.581

We demonstrated actionability

with InflammAge reduction in a nutraceutical interventional trial (N=18)



14.8

12.2 9.03

14.6

8.2 13.8

7.98

8.41 9.14

10

15.1

12.4

9.69

13.8

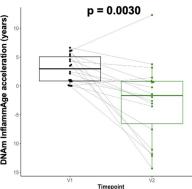
13.8

11.1

13.9

13.8

0 0.5 1 1.5 2 2.5



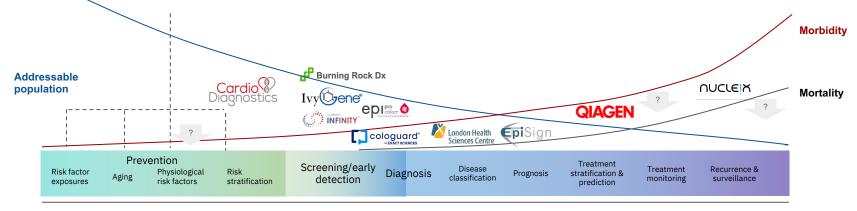
Preventive healthcare and epigenetics

Prevention/risk

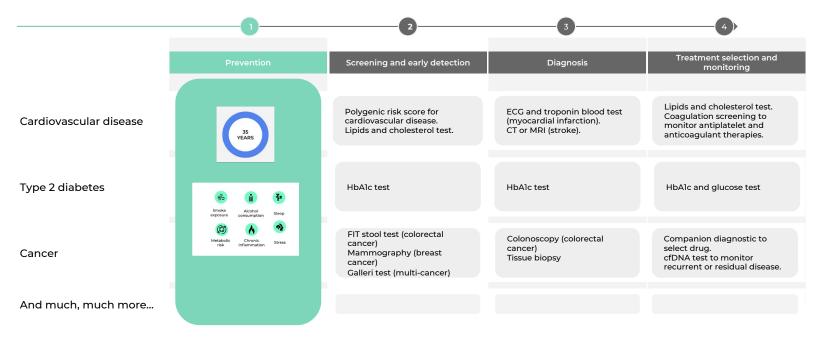
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- AI/ML models for risk factor quantification 1000s of DNAm sites
- Integrate environmental risk exposures, aging, physiological stress with genetics
- Classified as wellness test by FDA faster to market + wider reach
- Validate as risk stratification biomarkers against clinical endpoints
 - Risk factors become actionable focus earlier pre-clinical intervention prevention of morbidity



Deconvoluting epigenetic biological age for preventative healthcare



Summary

- 1. Epigenetics can **integrate** genetics and environment to quantify complex traits like aging and disease risk
- 2. DNA methylation is an **accessible, dynamic data source** for next gen AI/ML built biomarkers
- 3. Biological age biomarkers such as InflammAge can track the effect of interventions
- 4. DNA methylation biomarkers could link **prevention, risk stratification, and early detection** for tomorrow's population-health screening strategies



Acknowledgments

InflammAge biomarker development:



Daniel Martin-Herranz, PhD Toby Call, PhD



Dr Waylon J. Hastings



Prof Riccardo Marioni Dr Daniel Mccartney



Dr Kirsty McGee Dr Jack Sullivan Dr Thomas Jackson Prof Janet Lord



This work was financially supported by Bayer Consumer Health



Hira Javaid, PhD Epigenetic Scientist



Lisa Schmunk, PhD R&D Manager



Scan to learn more

Get in touch at lisa.schmunk@hurdle.bio



Come and find us at our stand B38 (Britten Room) for an exclusive discount code on our Biological Age test!

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Disclaimer

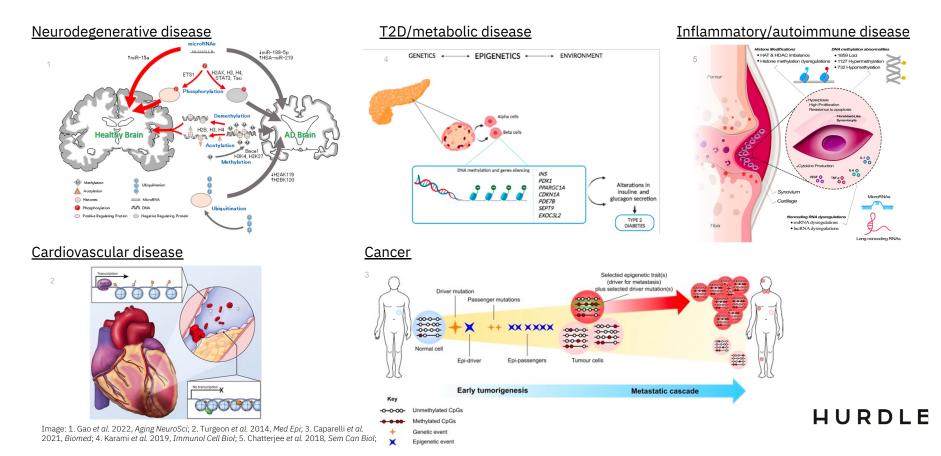
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Epigenetic drivers and fingerprints of disease



Deploying the biomarker in Hurdle's DaaS platform for global scale

