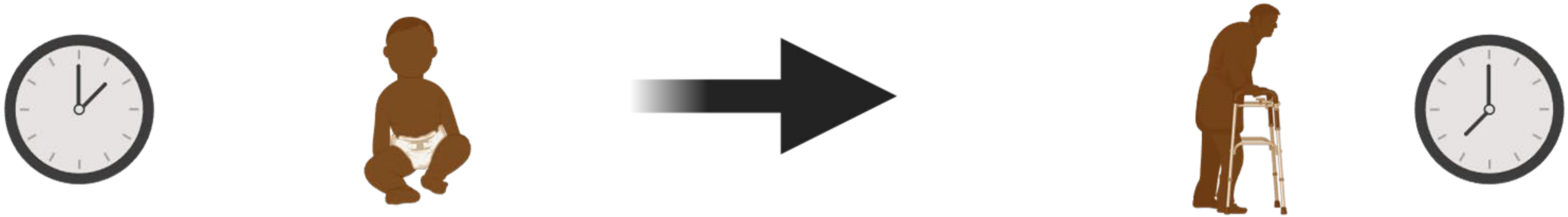
Aging at a Glance:
Enabling Age Estimation of Bats

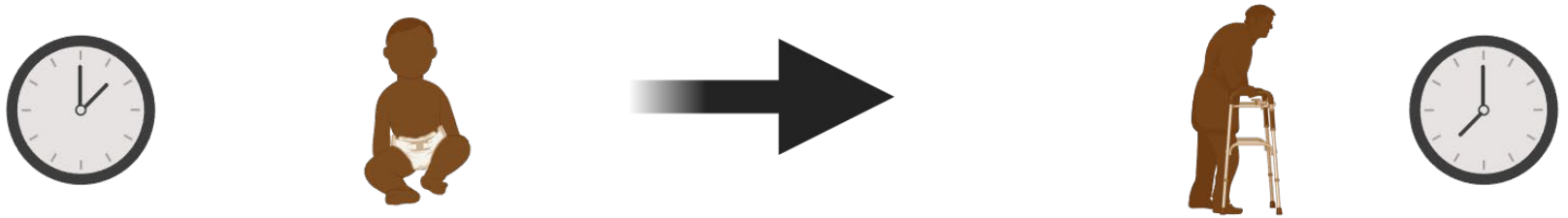
GBatNet

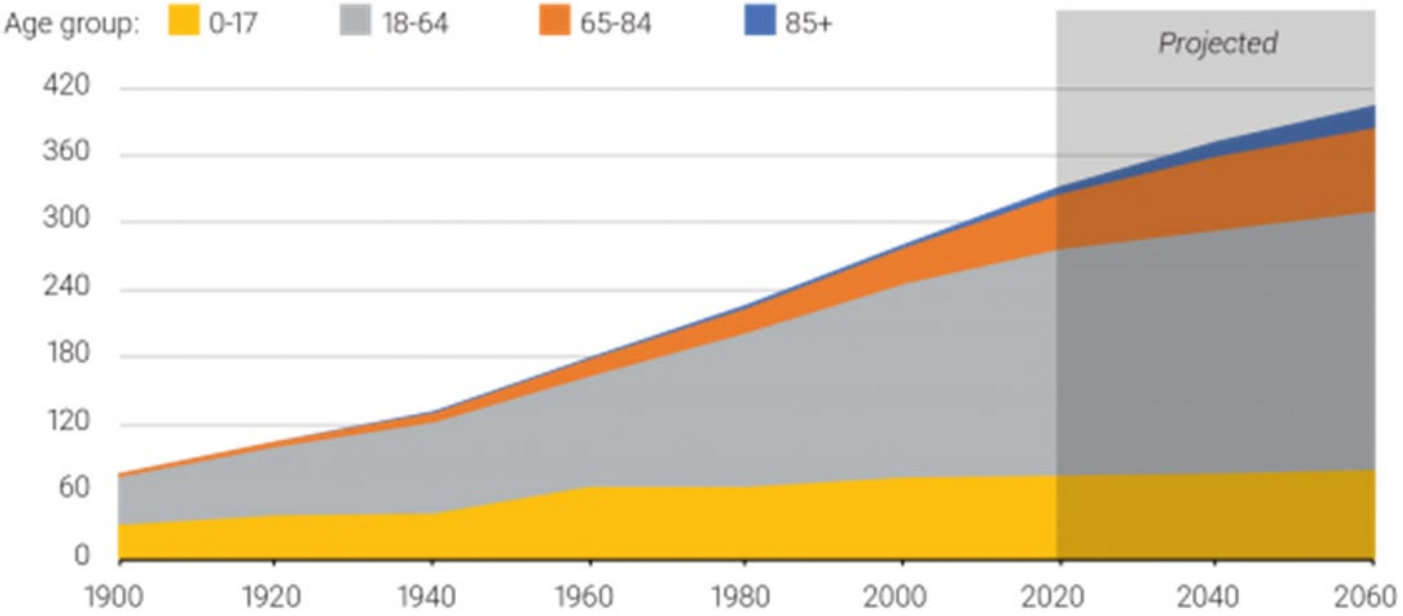
Everyone ages – but why?



Society is Growing Older, Fast

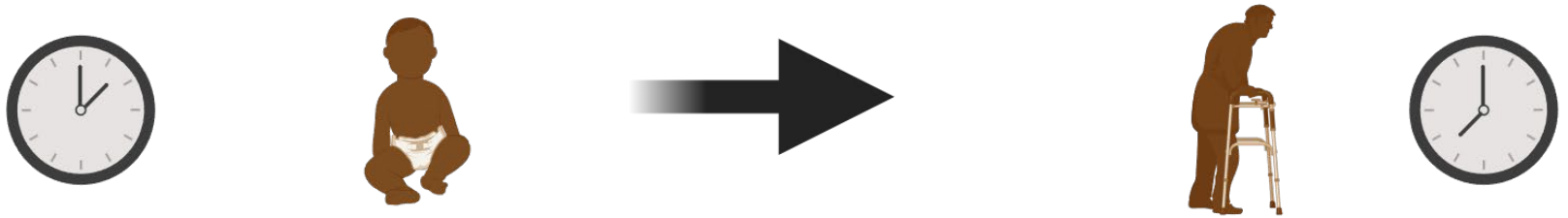
CDC, U.S. Census Bureau

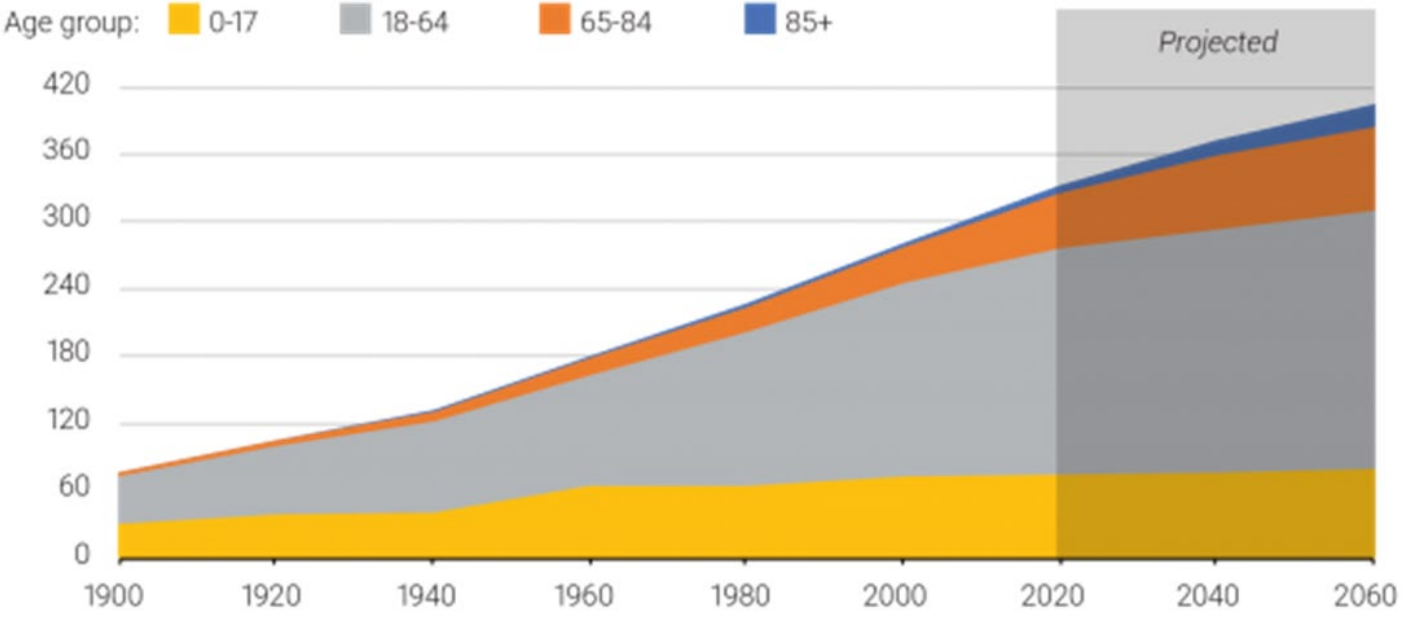


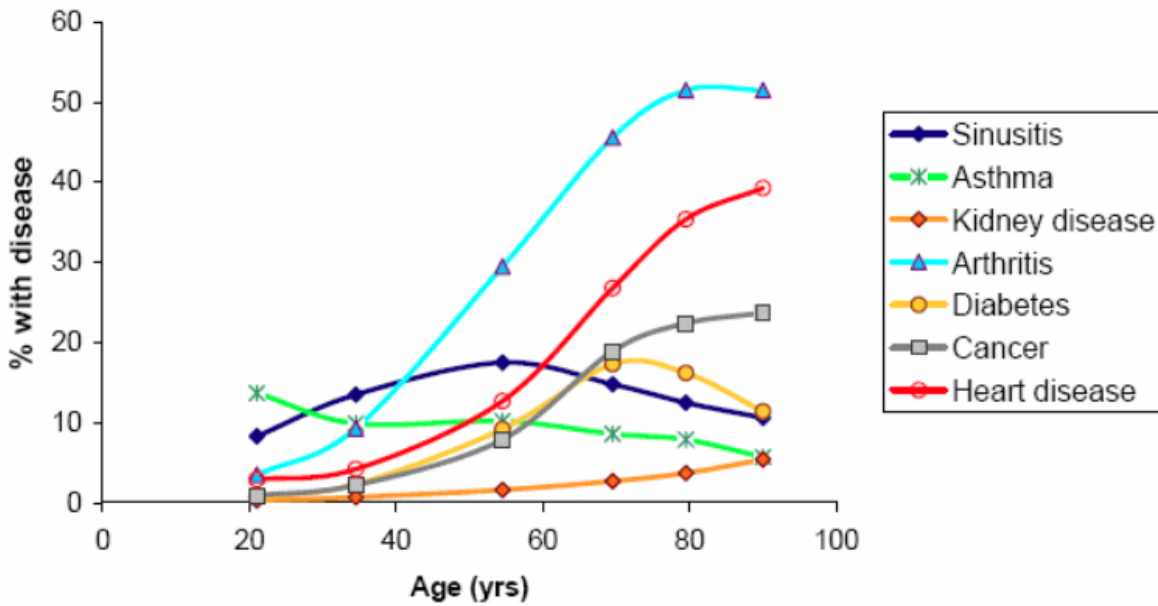


A Rising Age Group Lifts All Causes of Mortality

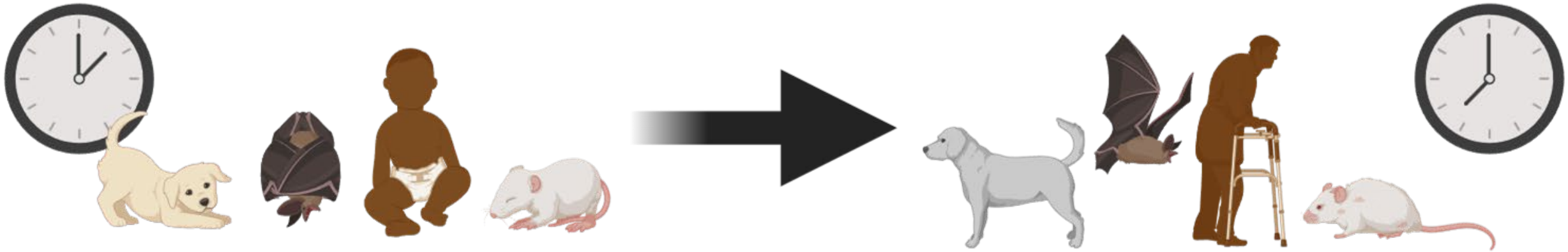
CDC, U.S. Census Bureau







Aging is a **Fundamental Part** of all Life



All animals age, but some animals age faster than others

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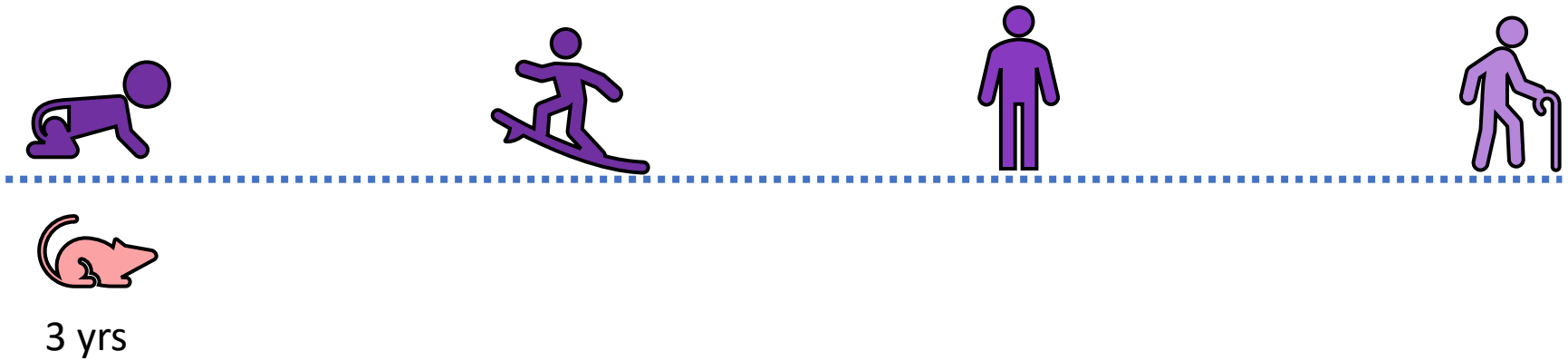

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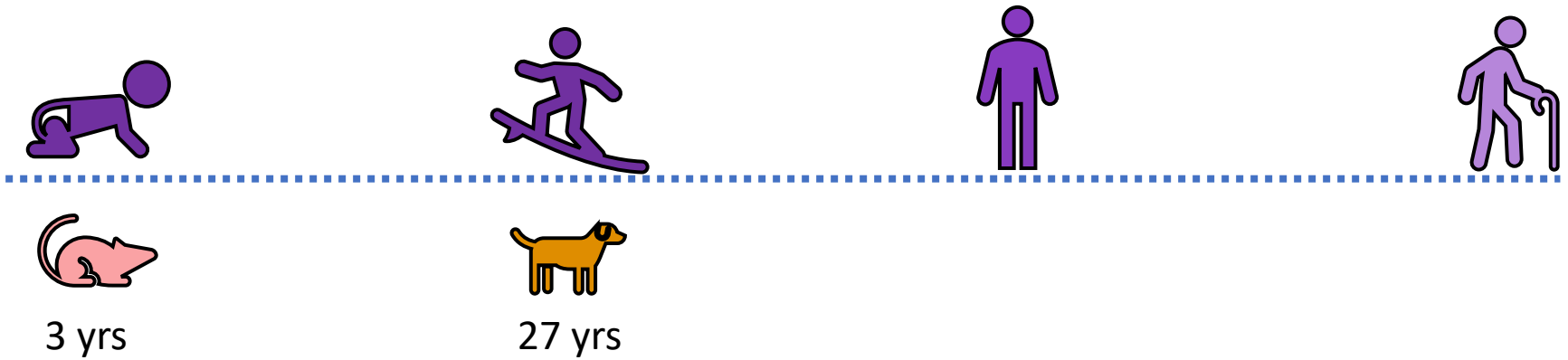

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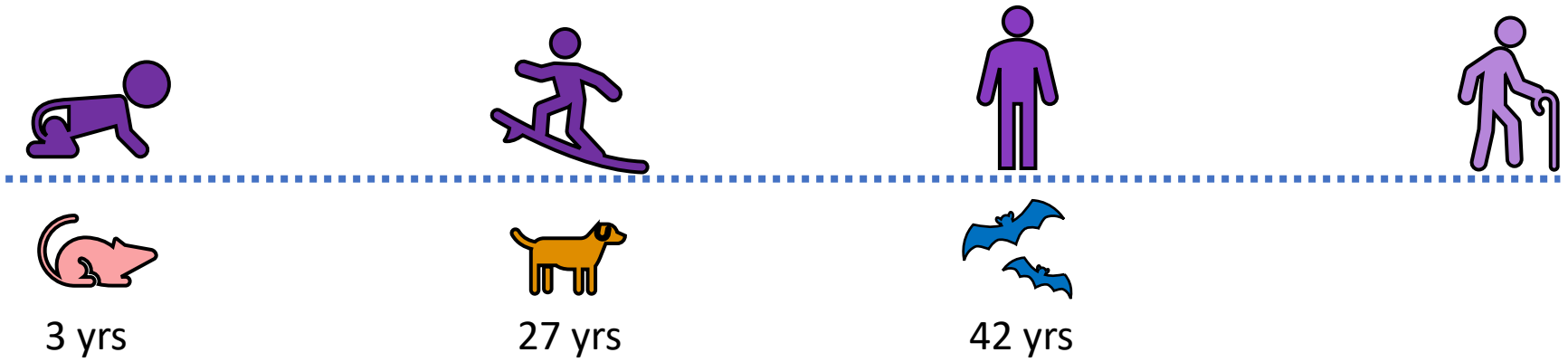

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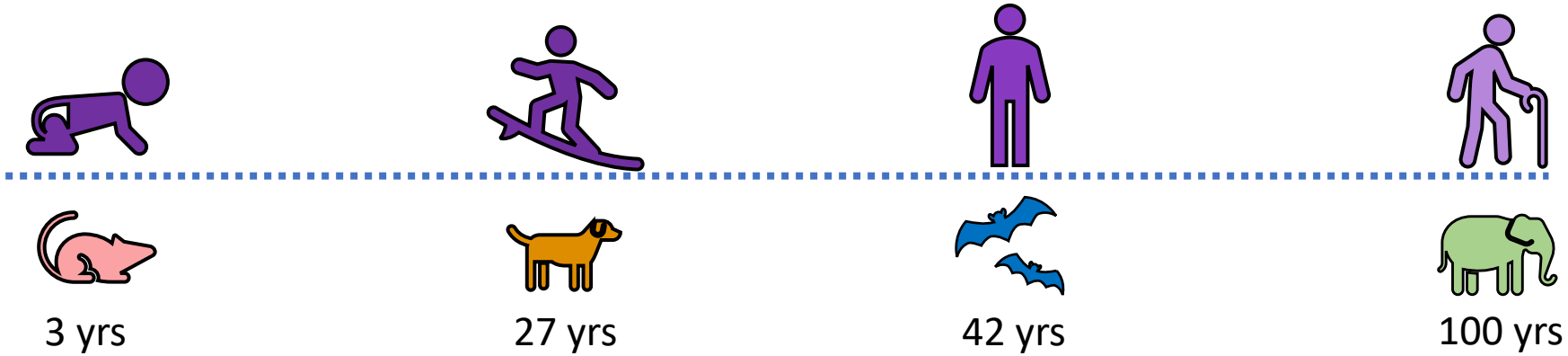

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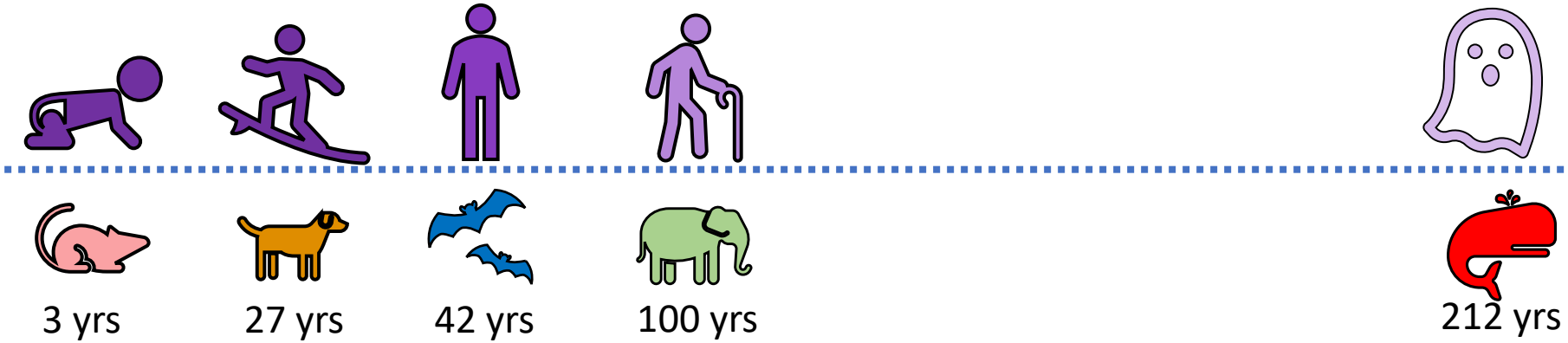
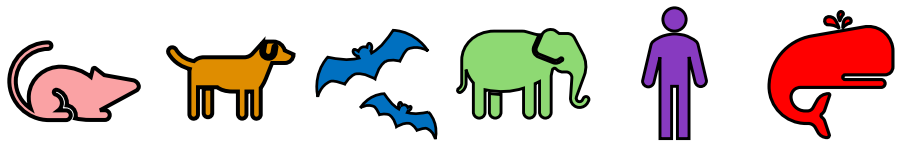
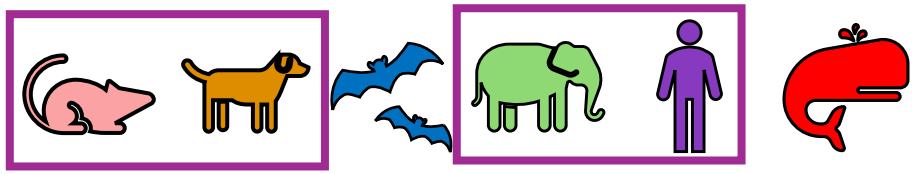




How do we know how long they live?



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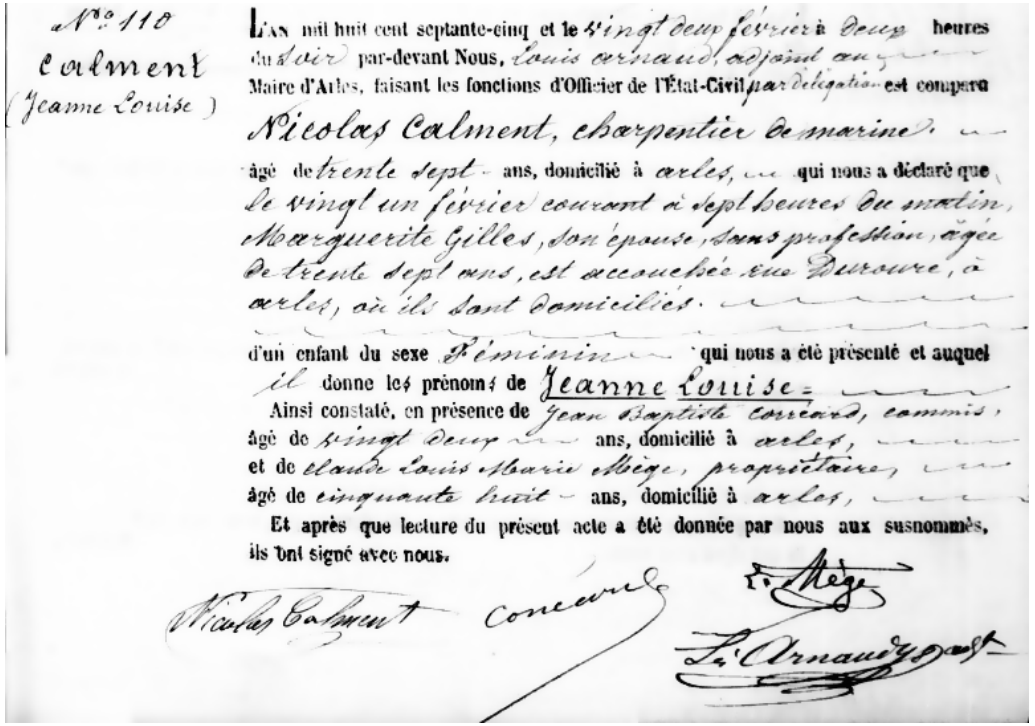


N° 110
Calment
(Jeanne Louise)

L'An mil huit cent septante-cinq et le vingt deux février à Deux heures du soir par-devant Nous, Louis arnaud, adjoint au Maire d'Arles, faisant les fonctions d'Officier de l'État-Civil par délégation est comparu Nicolas Calment, charpentier de marine âgé de trente sept ans, domicilié à arles, qui nous a déclaré que le vingt un février courant à sept heures du matin, Marguerite Gilles, son épouse, sans profession, âgée de trente sept ans, est accouchée une Demoure, à arles, où ils sont domiciliés.

d'un enfant du sexe Féminin qui nous a été présenté et auquel il donne les prénoms de Jeanne Louise.

Ainsi constaté, en présence de Jean Baptiste carreard, commis, âgé de vingt deux ans, domicilié à arles, et de Claude Louis Marie Mège, propriétaire, âgé de cinquante huit ans, domicilié à arles,

Et après que lecture du présent acte a été donnée par nous aux susnommés, ils ont signé avec nous.

Nicolas Calment — Carreard — Mège — L. Arnaud

Accurate birth and death records are the **gold standard** for aging research

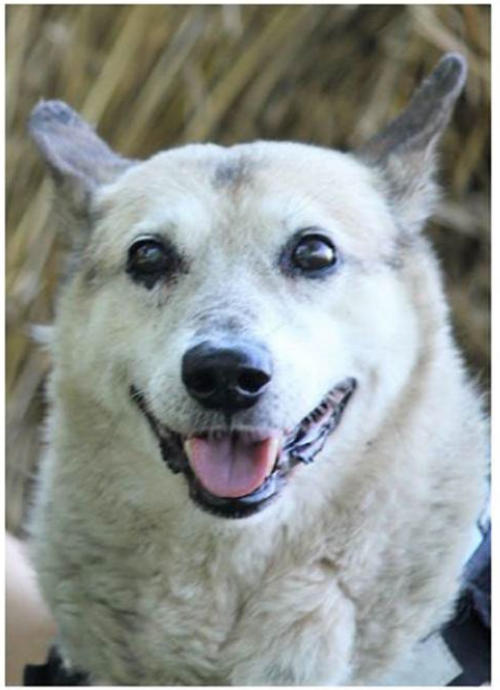
Jeanne Louise Calment, 122 yrs

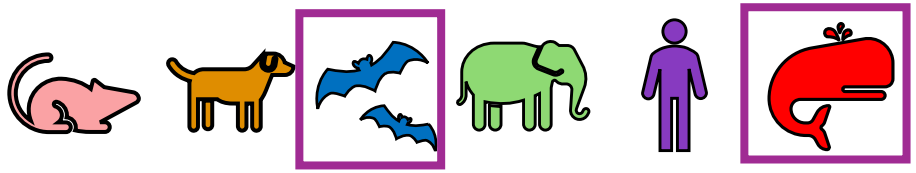
21 February 1875 – 4 August 1997

Captive populations similarly provide a gold standard for lifespan

Vatsala, ~105 yrs

Buksi (27 yrs) & Kedves (22 yrs)





How do we know how long they live?

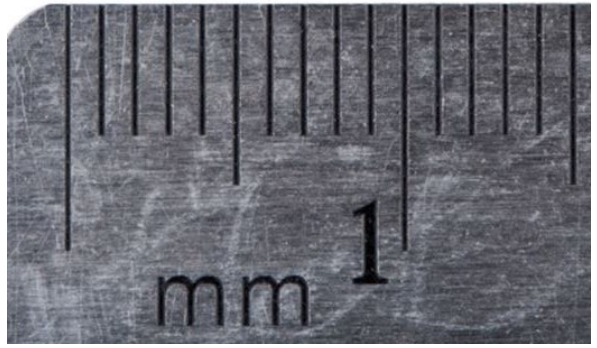
The problem: its hard to keep captive bats

Statler (~34 yrs)

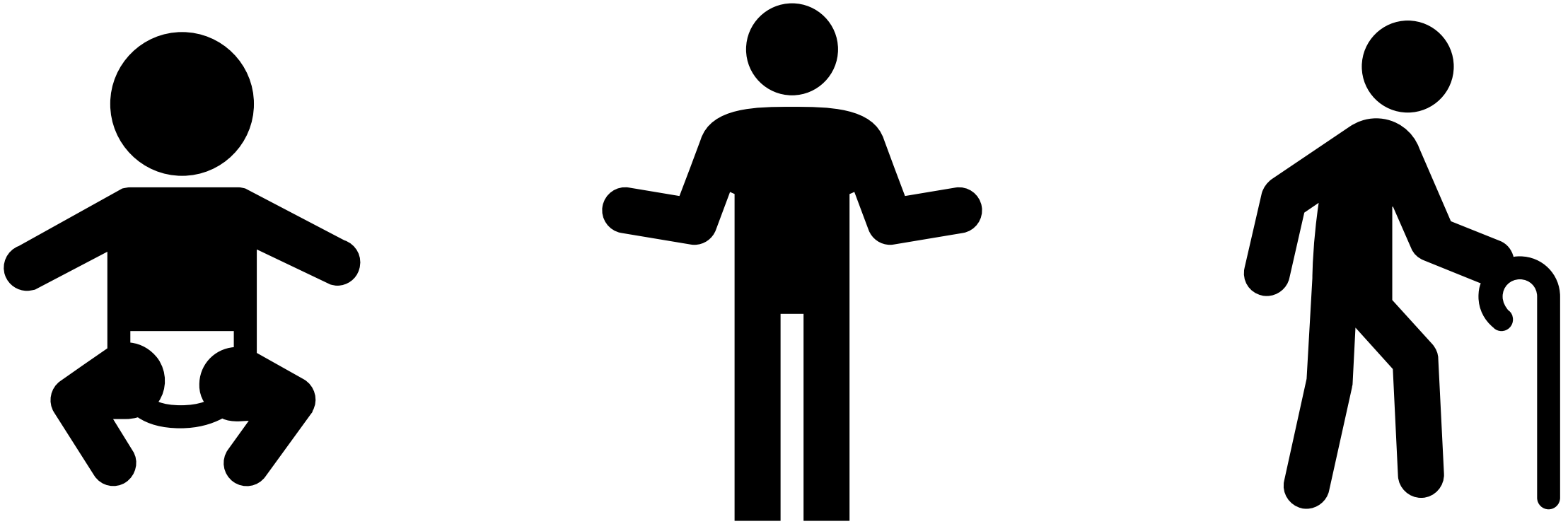
- Only a small number of species can be successfully kept in captivity
- Of those, most are large, fruitivorous bats like Statler
- **They aren’t the longest-lived bats**

Most lifespan records of bats are based on capture-recapture

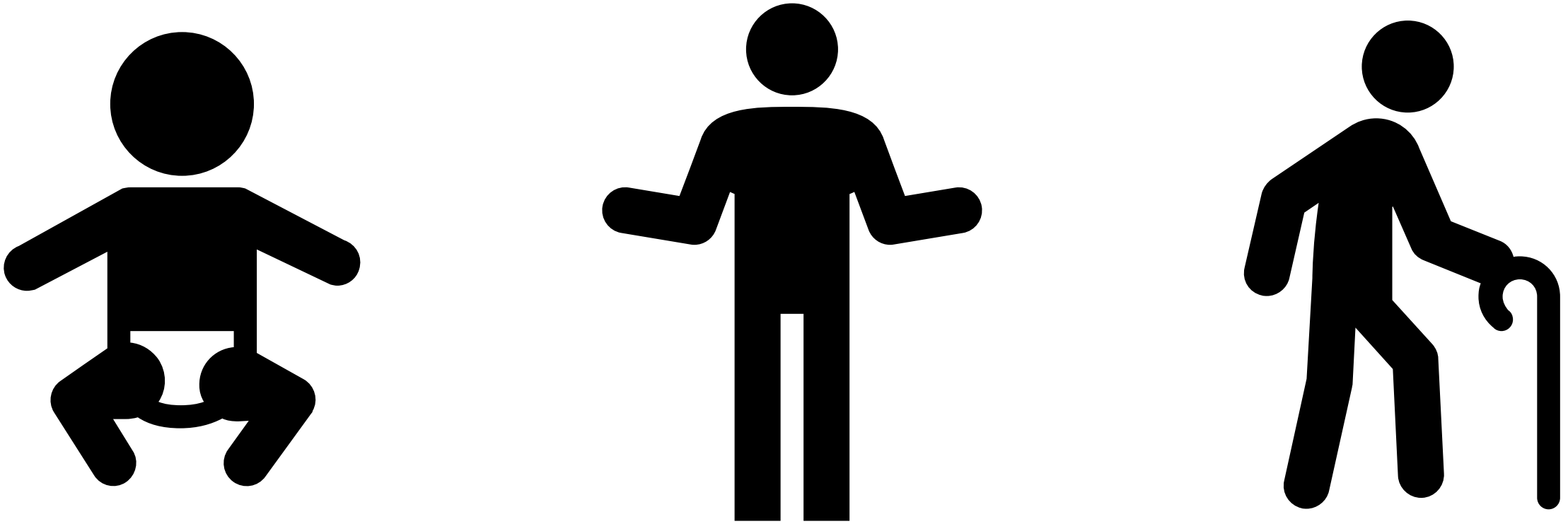
1. Catch bats
2. Mark bats
3. Release bats
4. Hope nothing happens to mark
5. Hope nothing happens to bat
6. Hope the marking method doesn't hurt the bat
7. Come back every year or few years and hope you catch the same bat



Why do we even care about aging bats?



Aging affects everything!



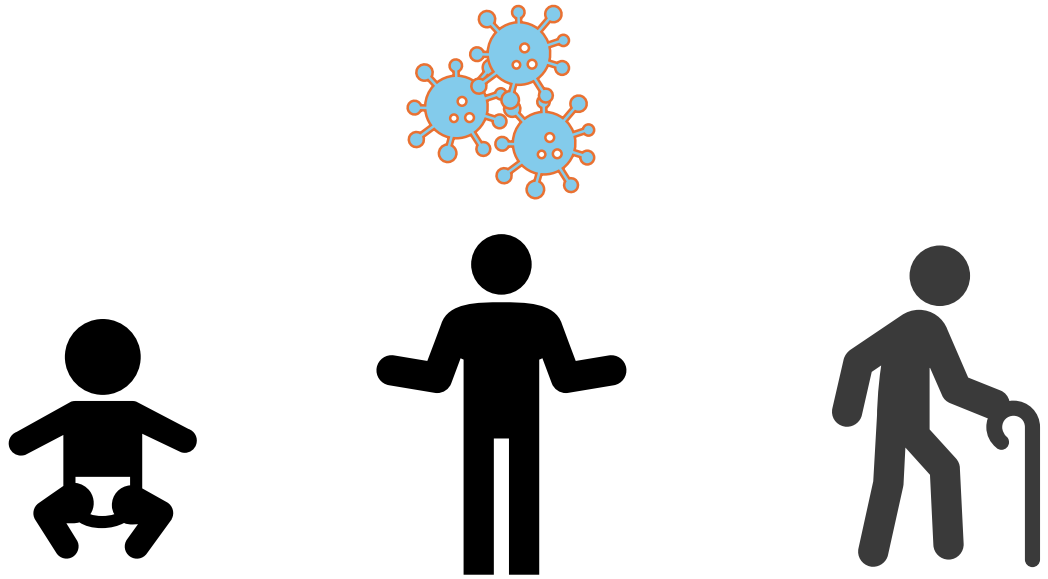
Aging affects everything!

Stress ◆ Immunity ◆ Disease ◆ Behavior

&

More!

Age affects disease transmission



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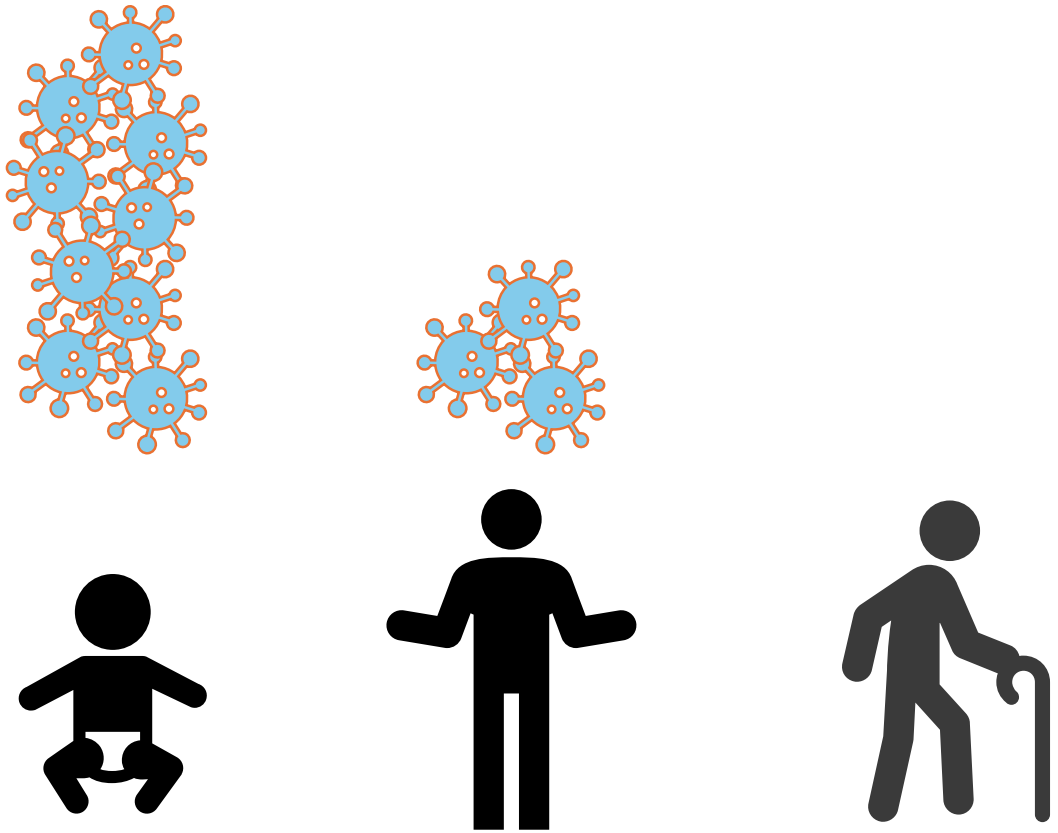

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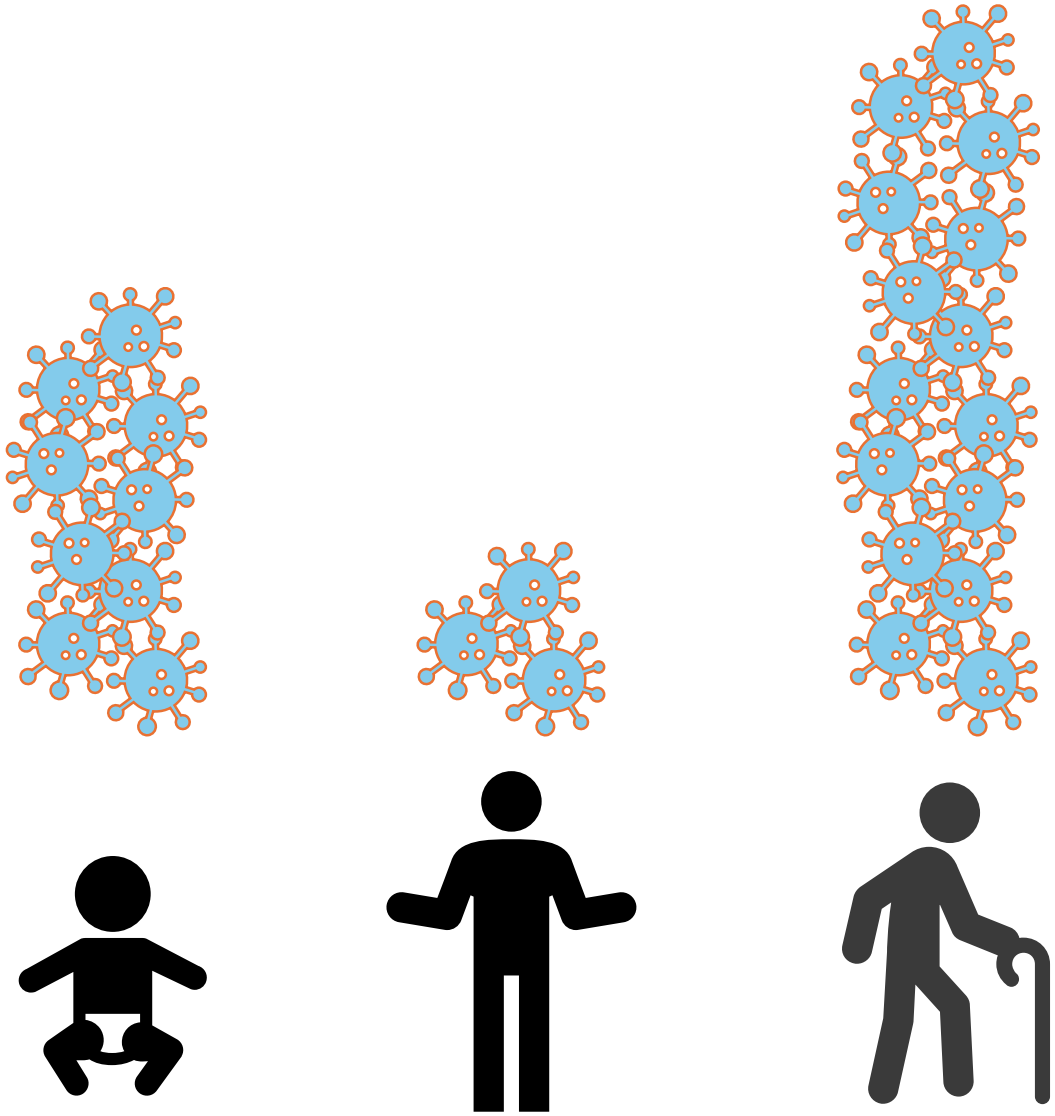

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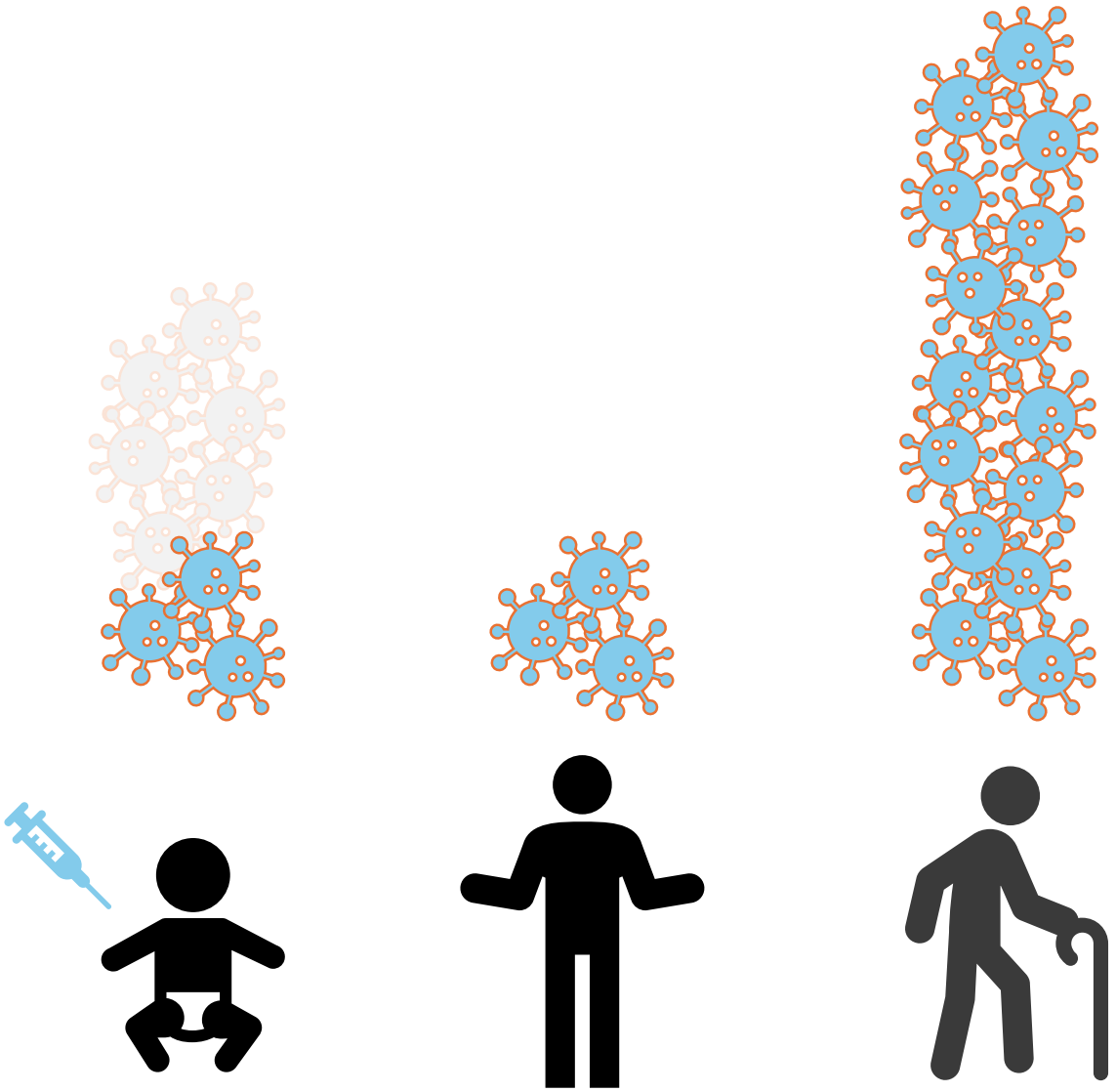

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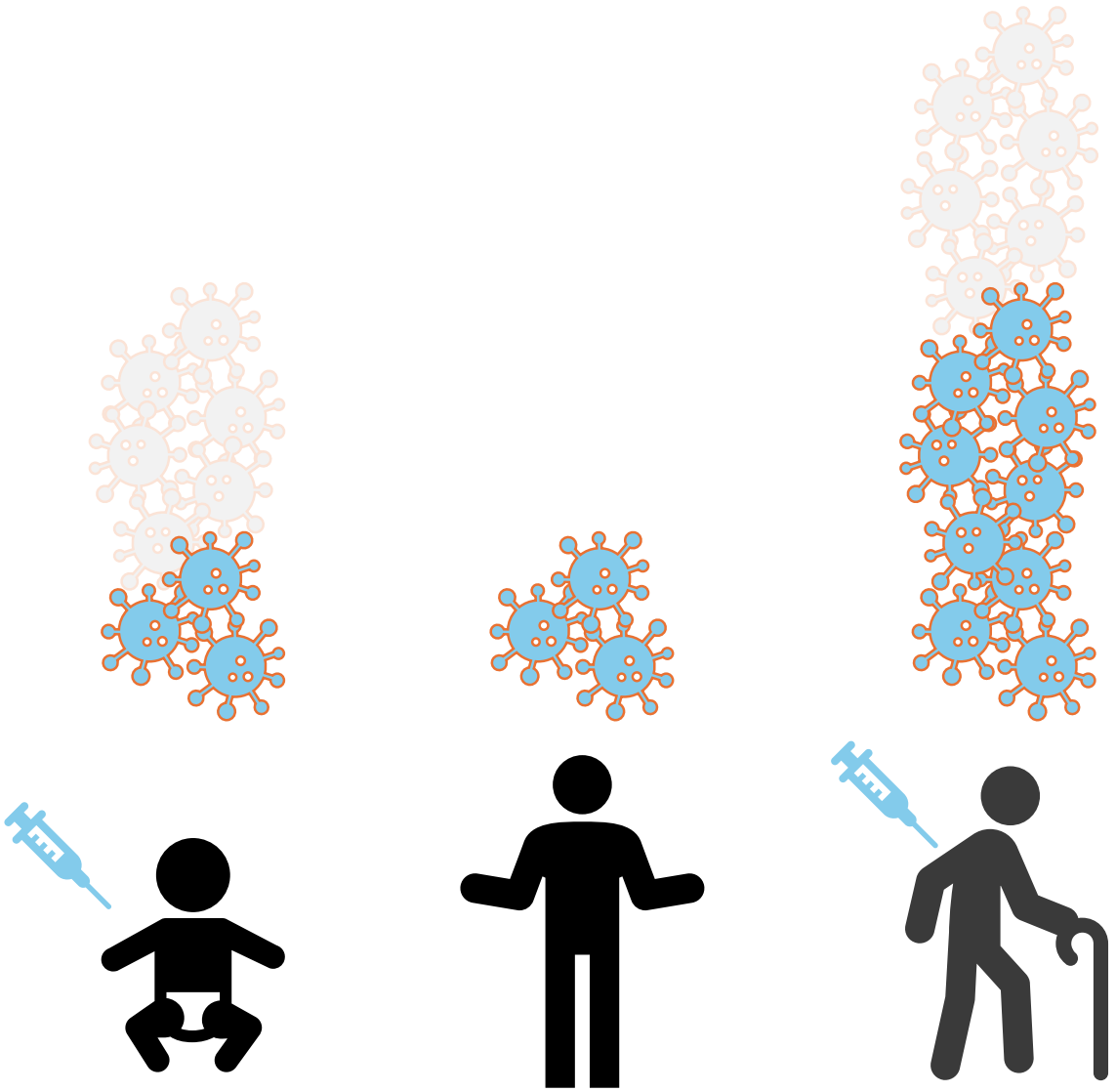

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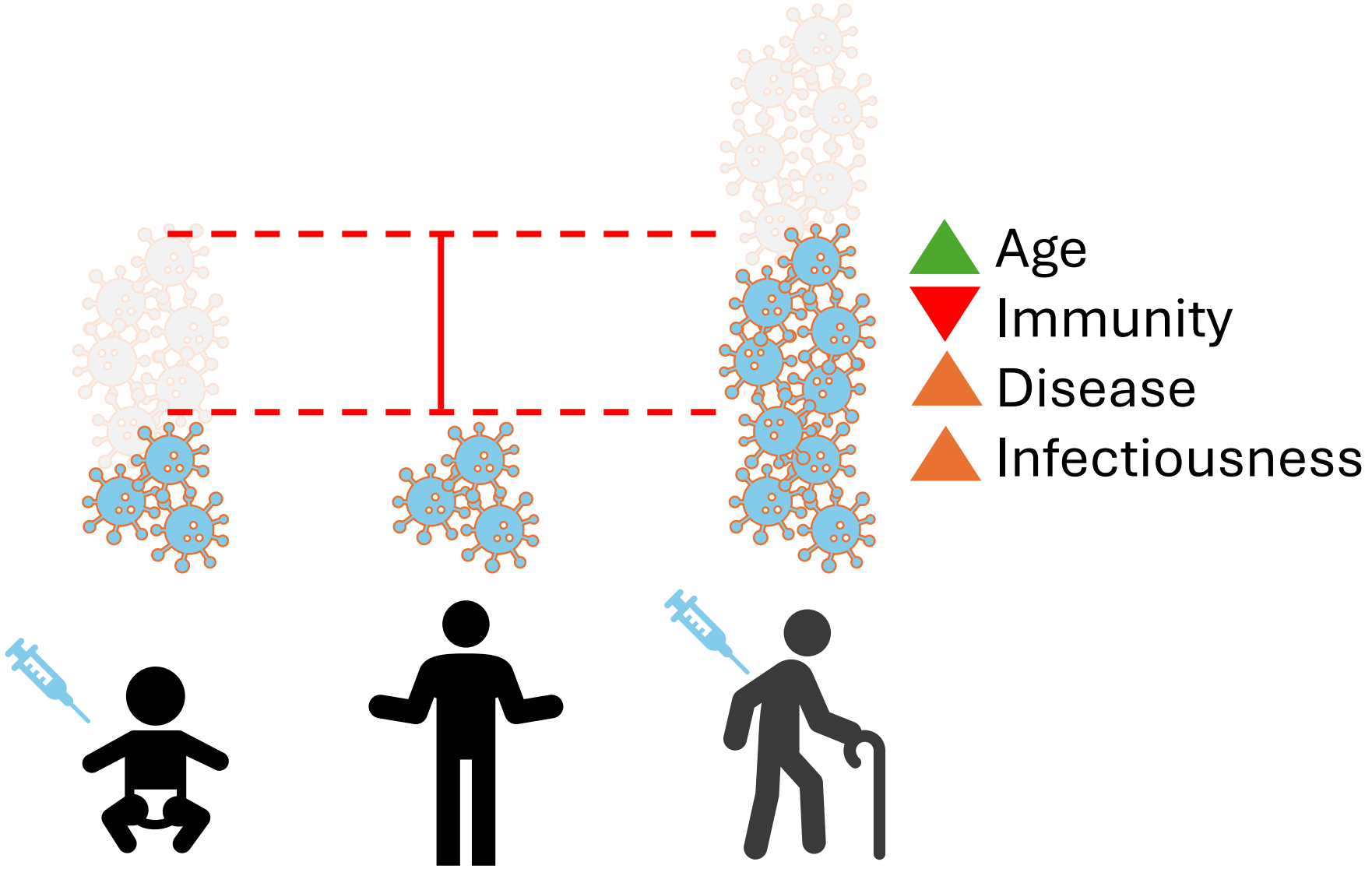

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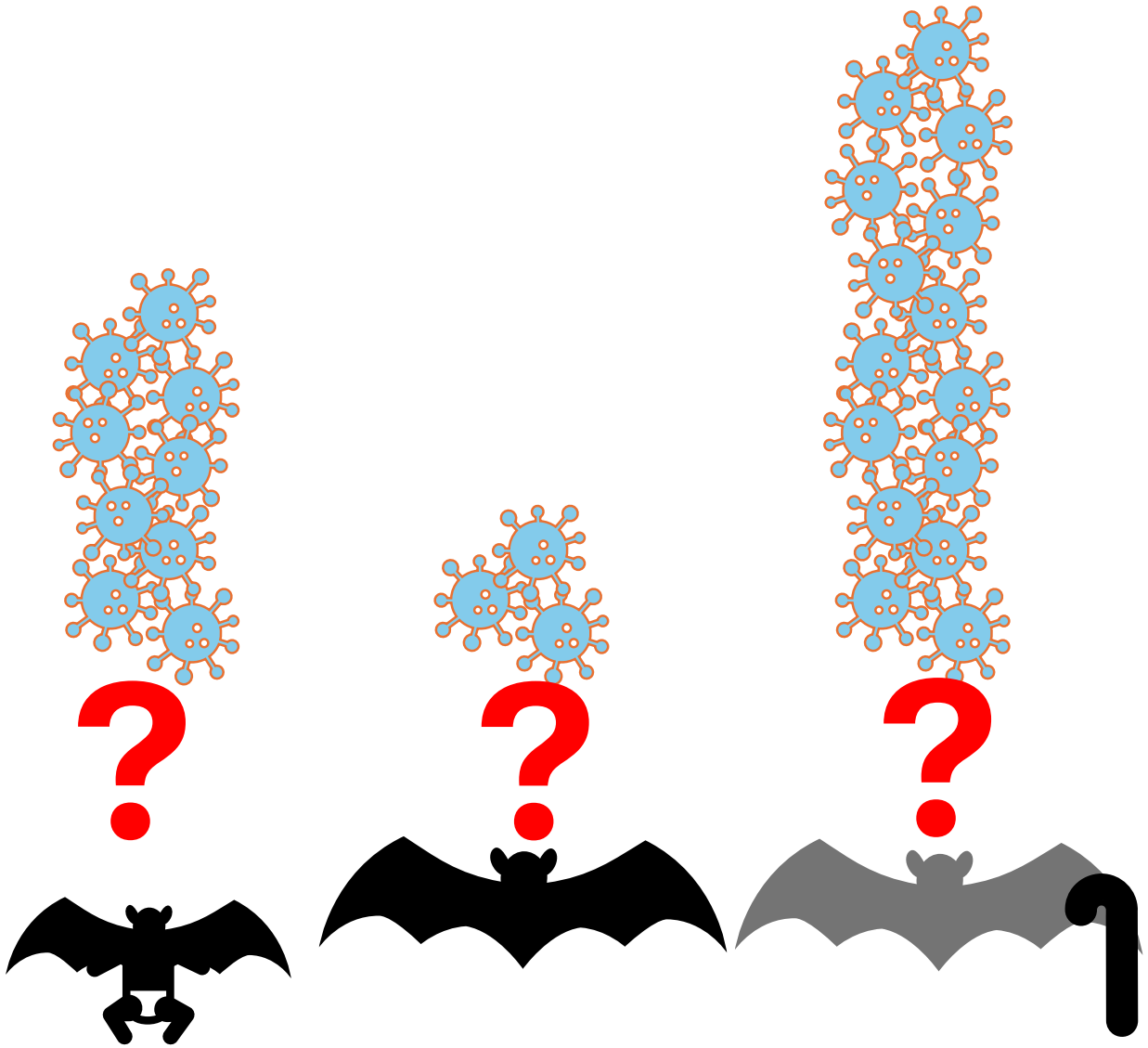
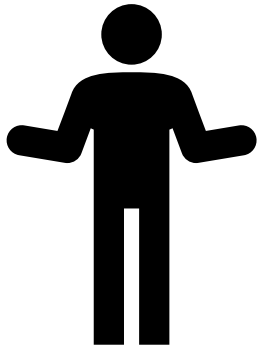


Age affects senses and behavior



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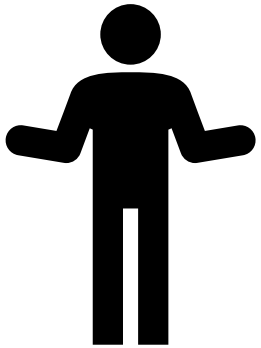
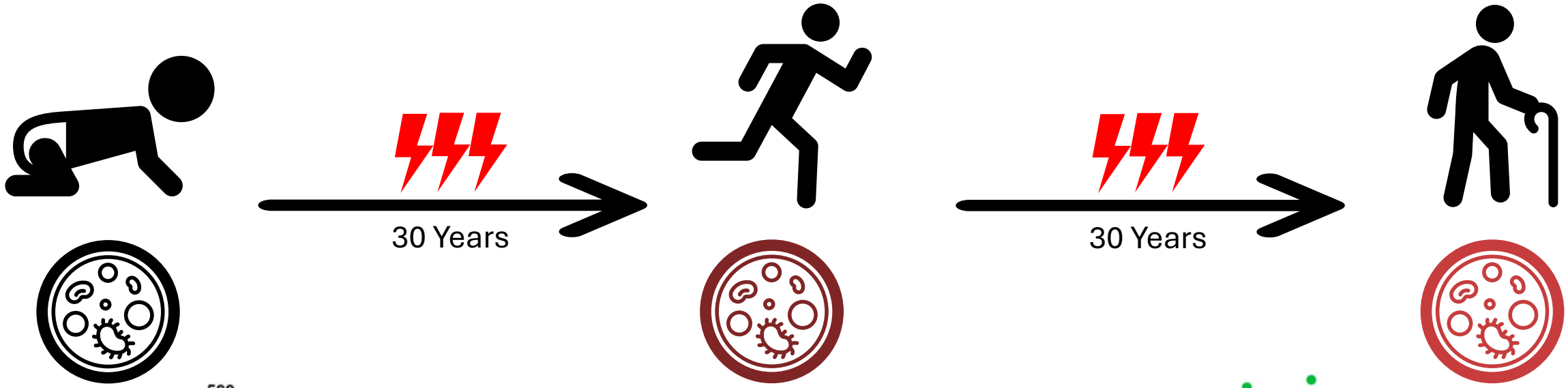
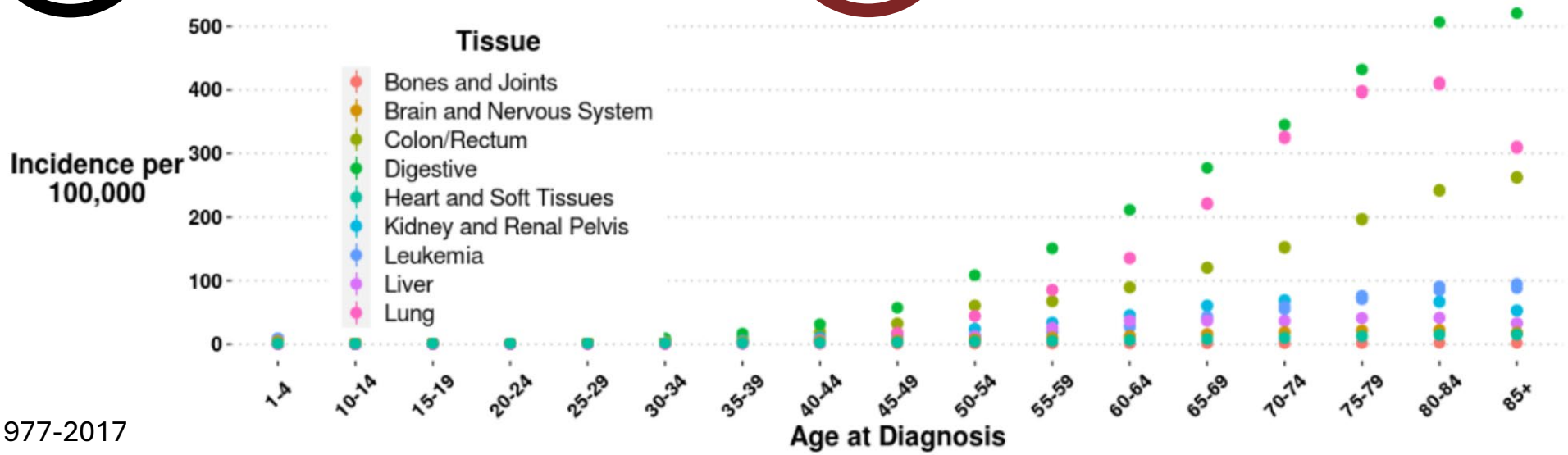


Age affects senses and behavior

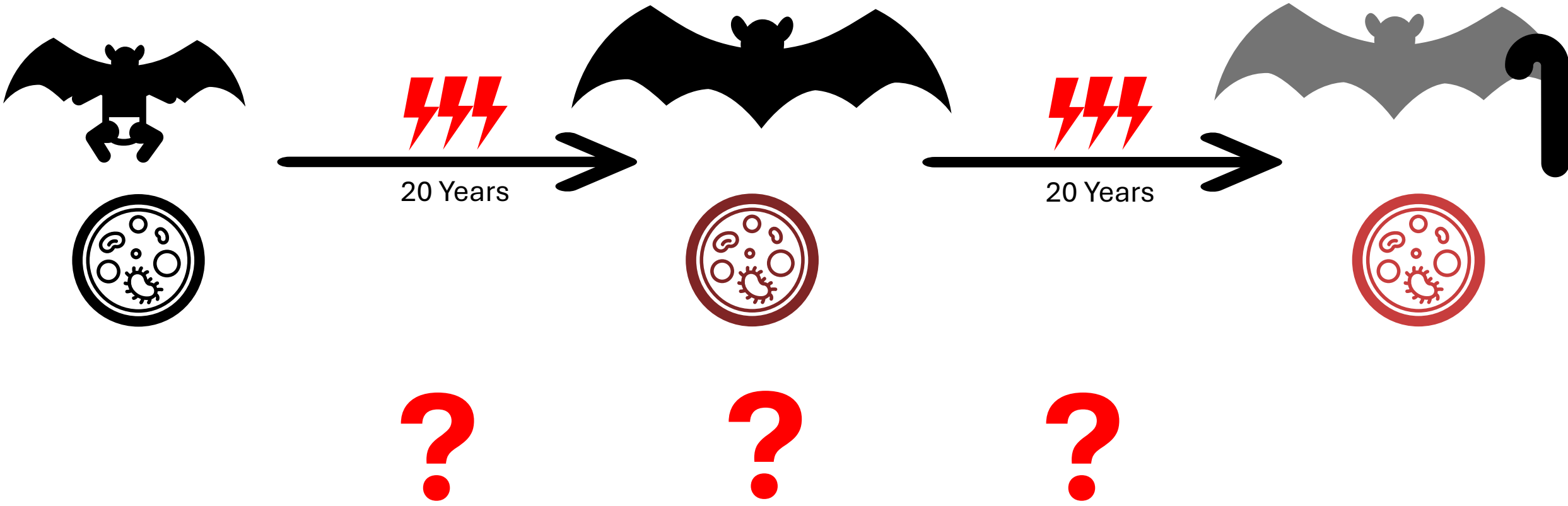
Longer Lifespan → More mutations → More Cancer





NCI SEER, 1977-2017

Longer Lifespan → More mutations → More Cancer



Our Dilemma

Age is important:

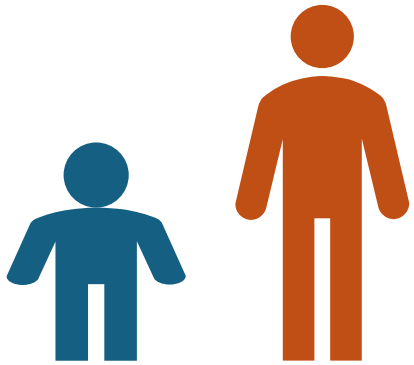
- All animals age
- Animals age quite differently
- Age affects everything

Age is hard to find out:

- Banding: dangerous and low throughput
- Captivity: challenging and limited

What if there was some other marker for age?

Biomarkers provide a proxy for traits and disease



Height

Biomarkers provide a proxy for traits and disease

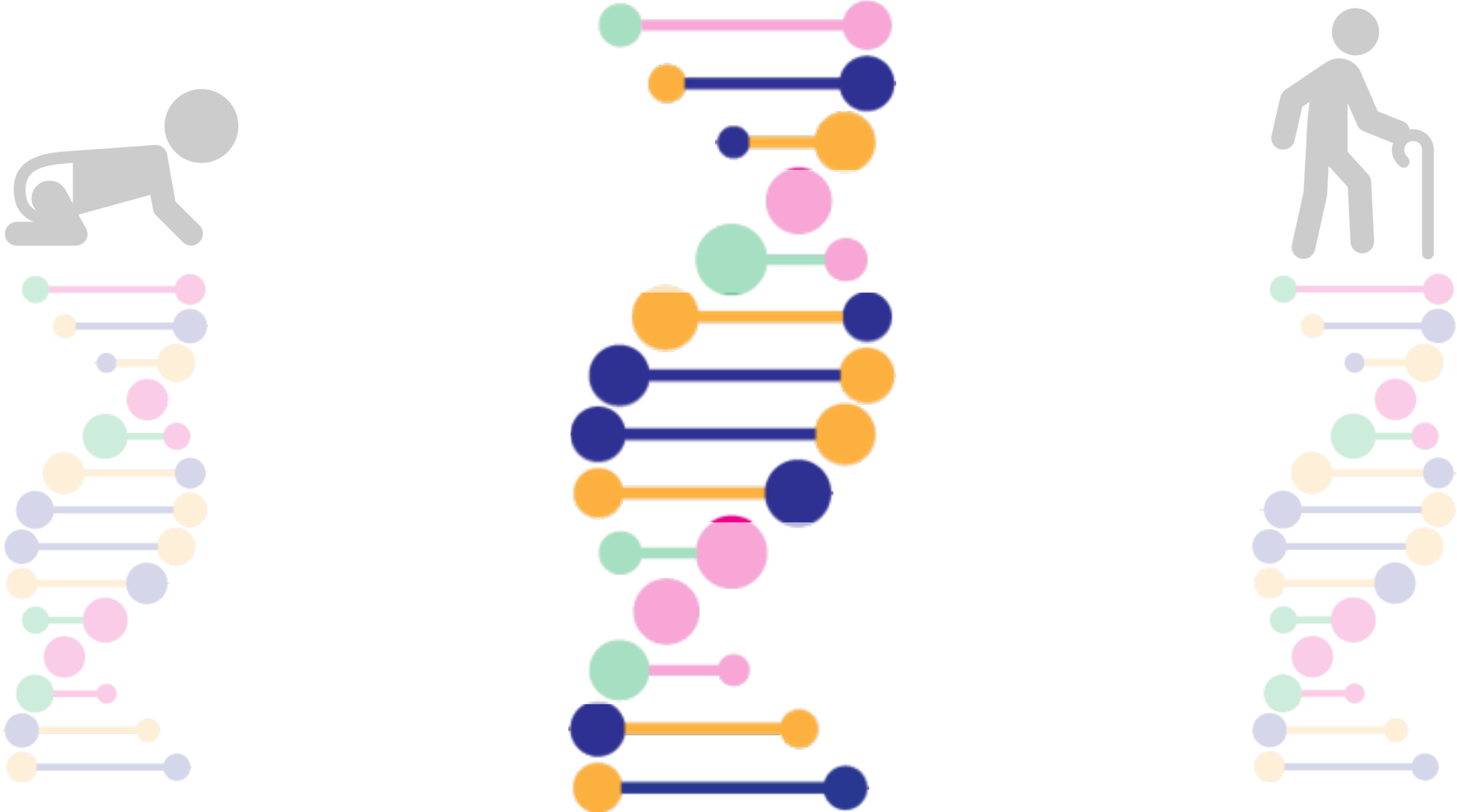
Sickness

We all have an internal clock, conveniently on our DNA

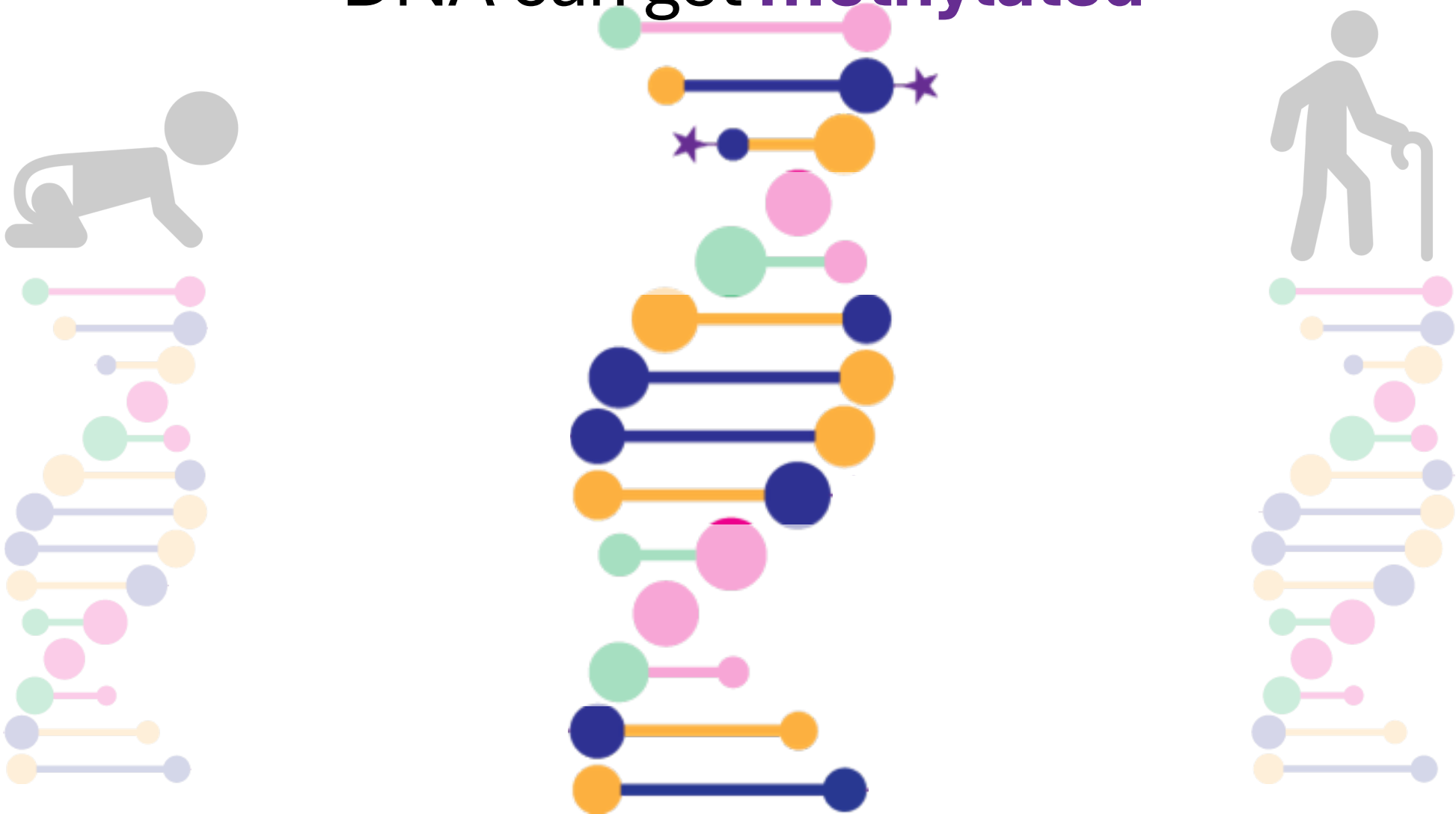
DNA has 4 letters:

A, C, G, & T

CpG sites are special



CpG sites are special
DNA can get **methylated**



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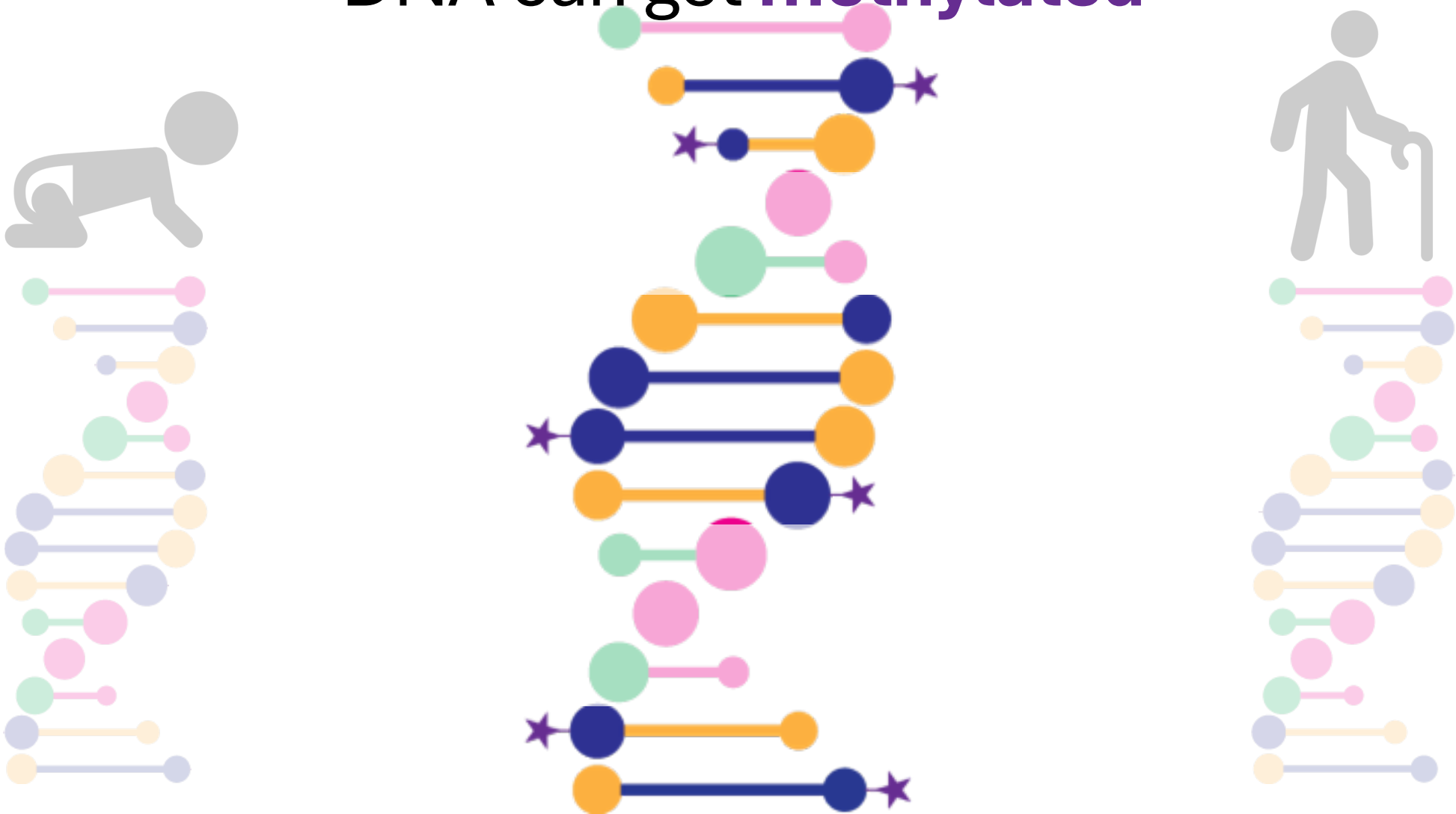
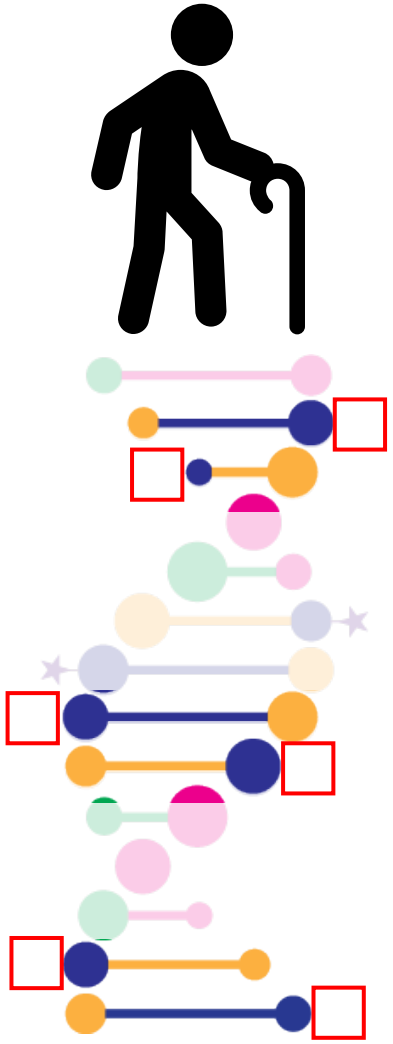
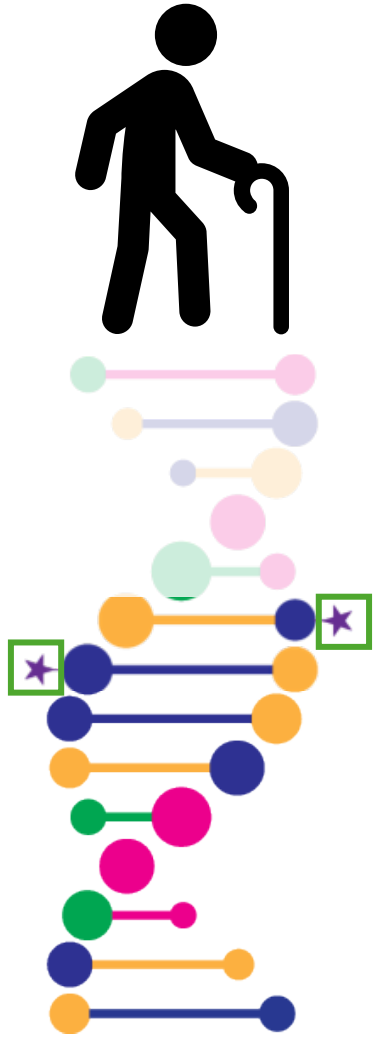


At birth, we all have a common set of mCpG patterns

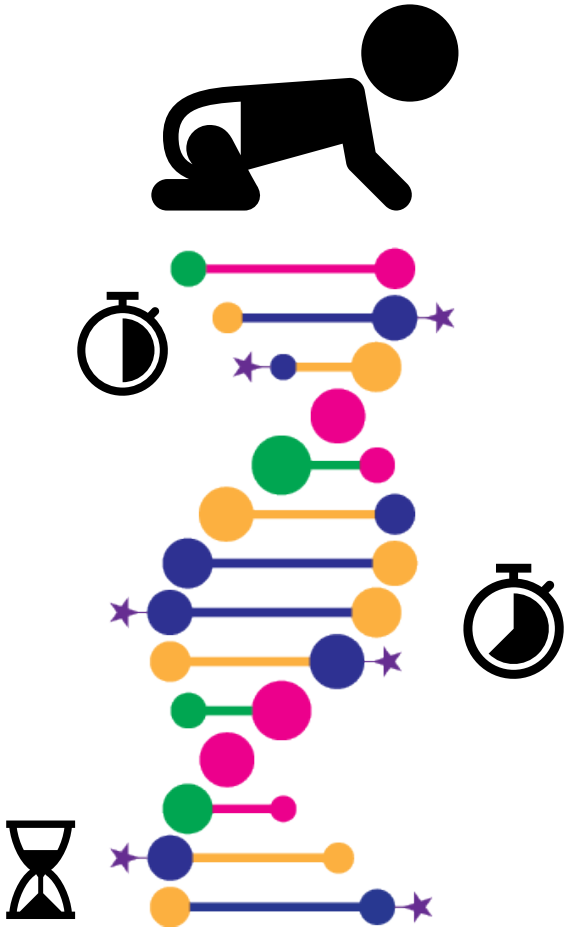
Some of these mCpG's are lost over time

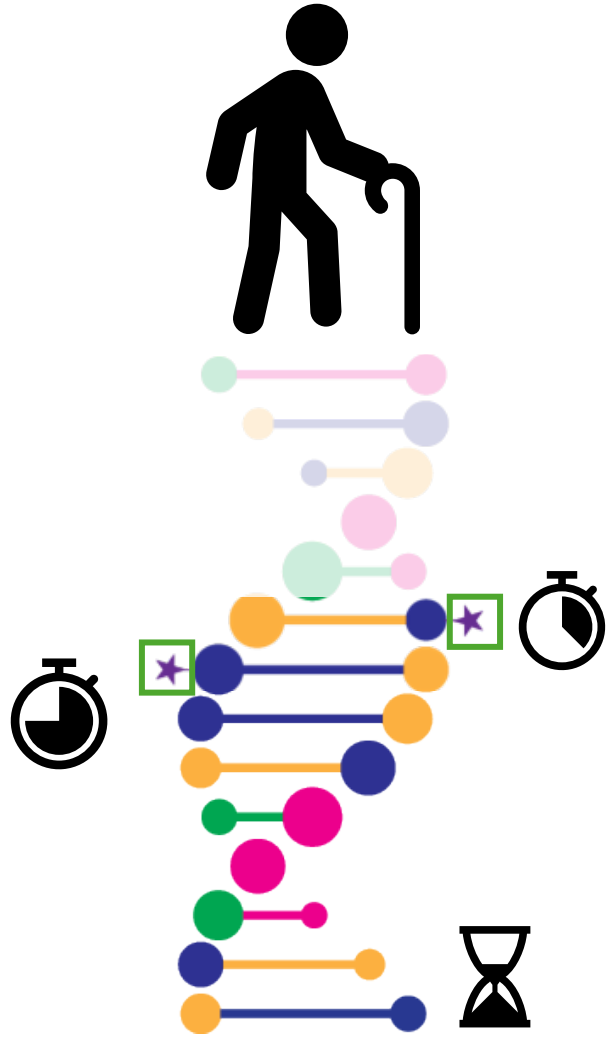


Other mCpG's are gained over time

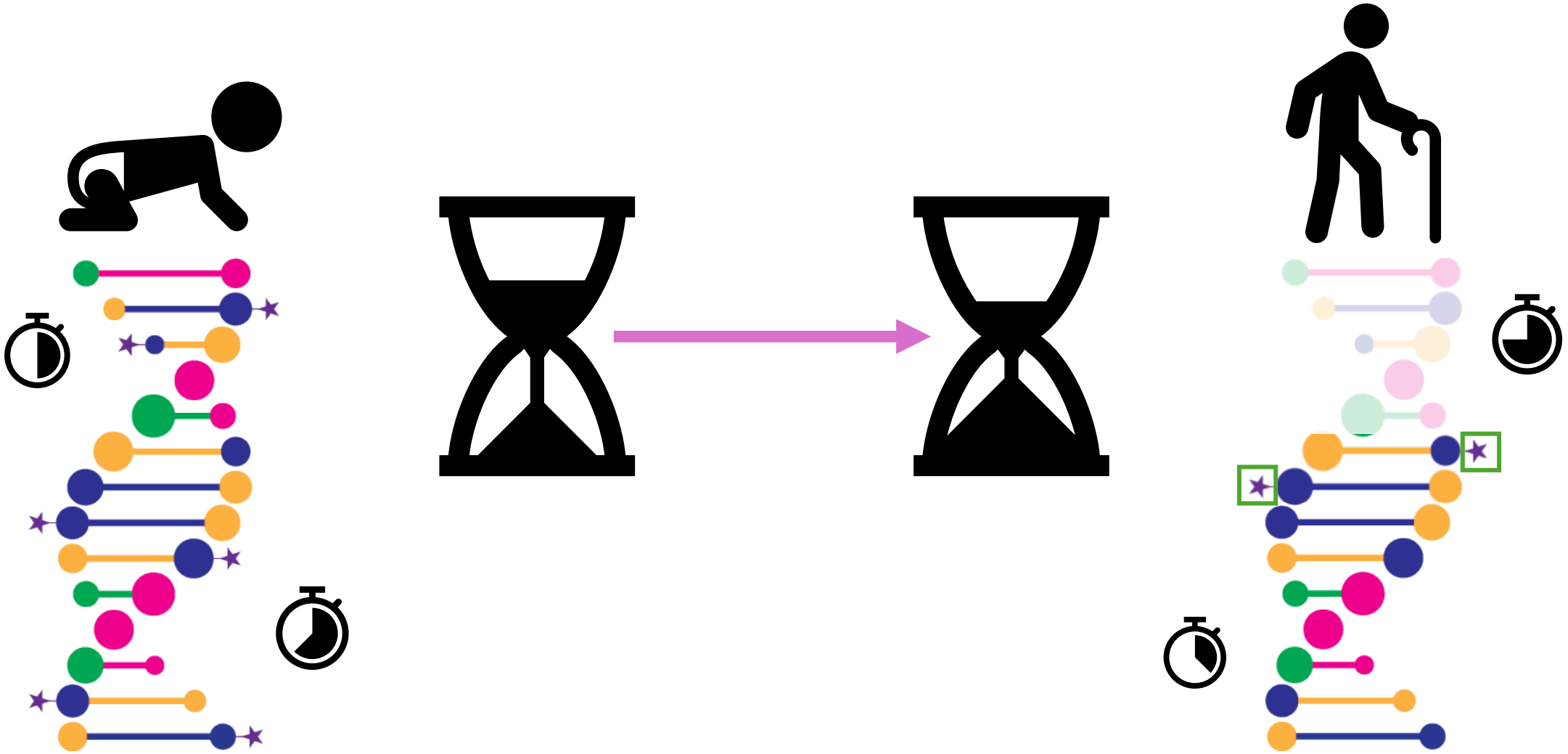


Each of these changes has its own pace

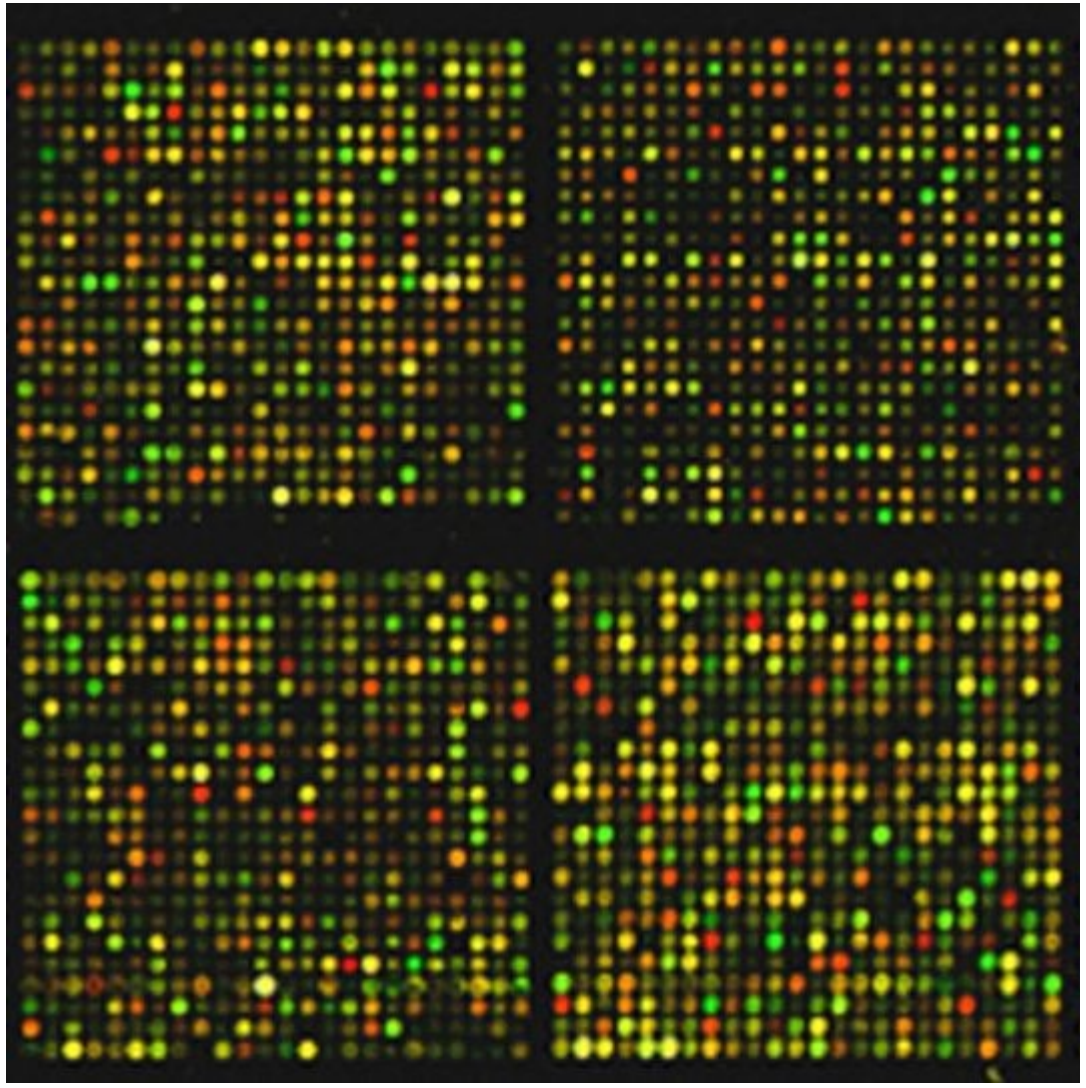




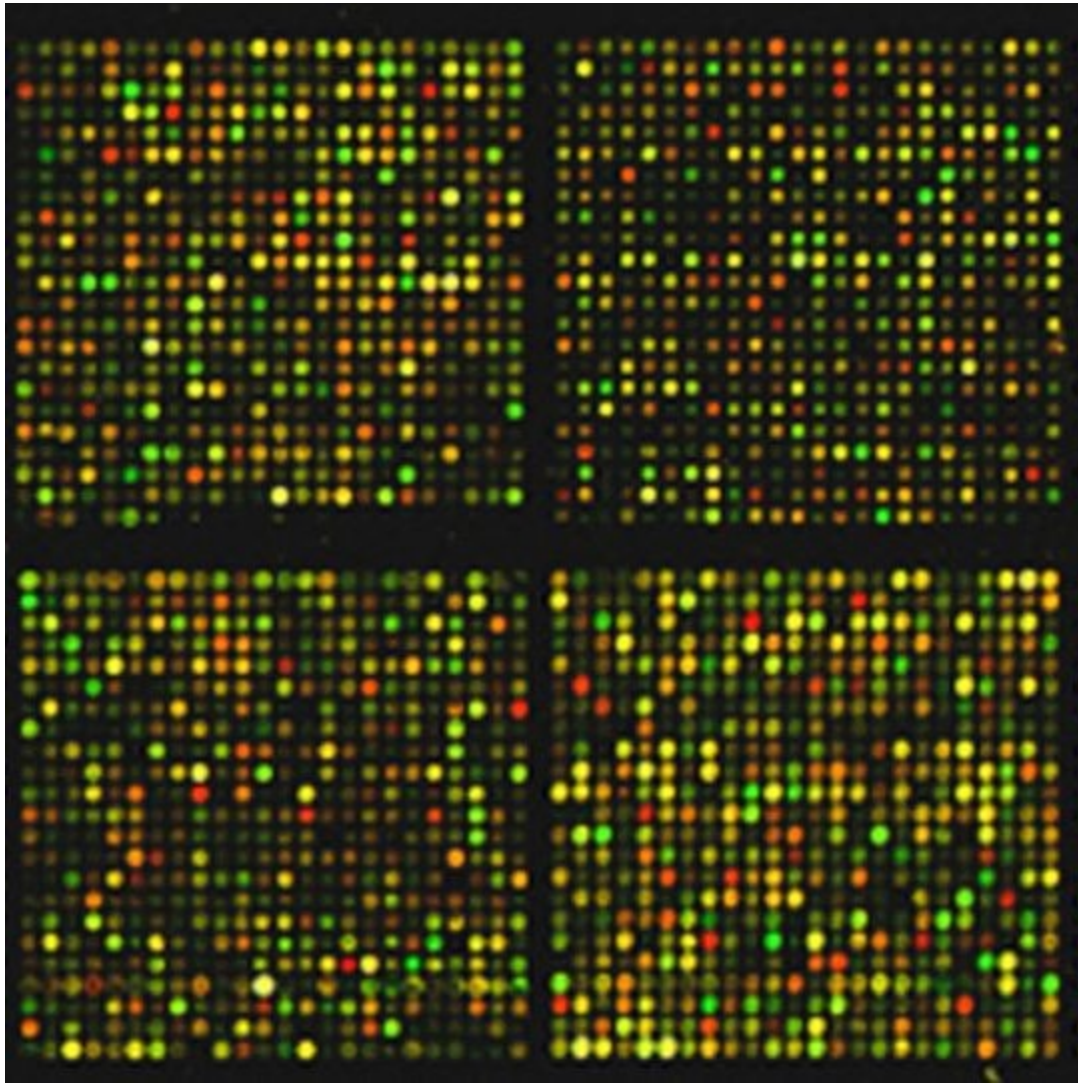
Together, you can make an aging clock

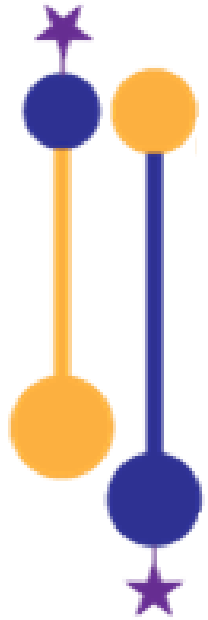


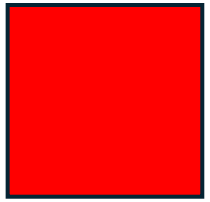
Microarrays: one of the earliest sequencing technologies



Microarrays can tell you if a known sequence is methylated or not







Red

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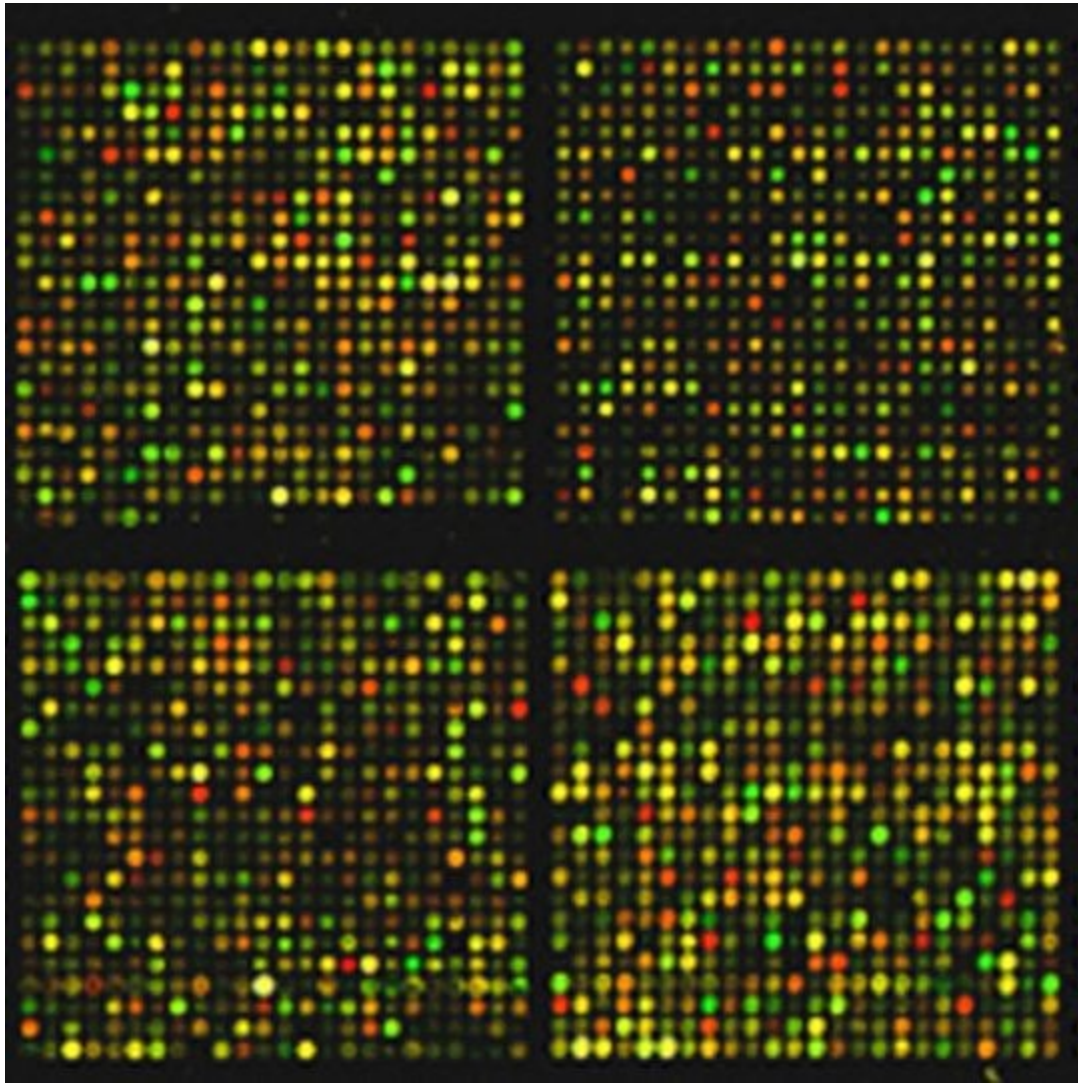

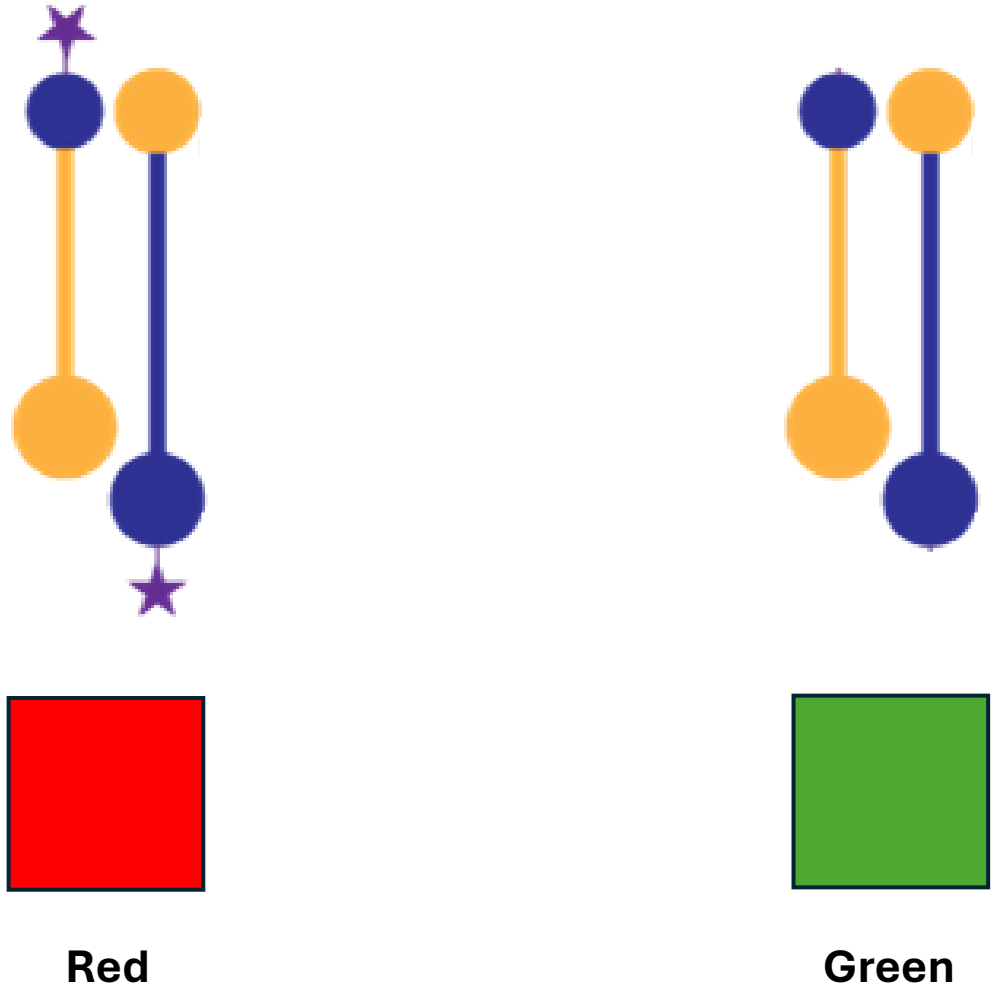

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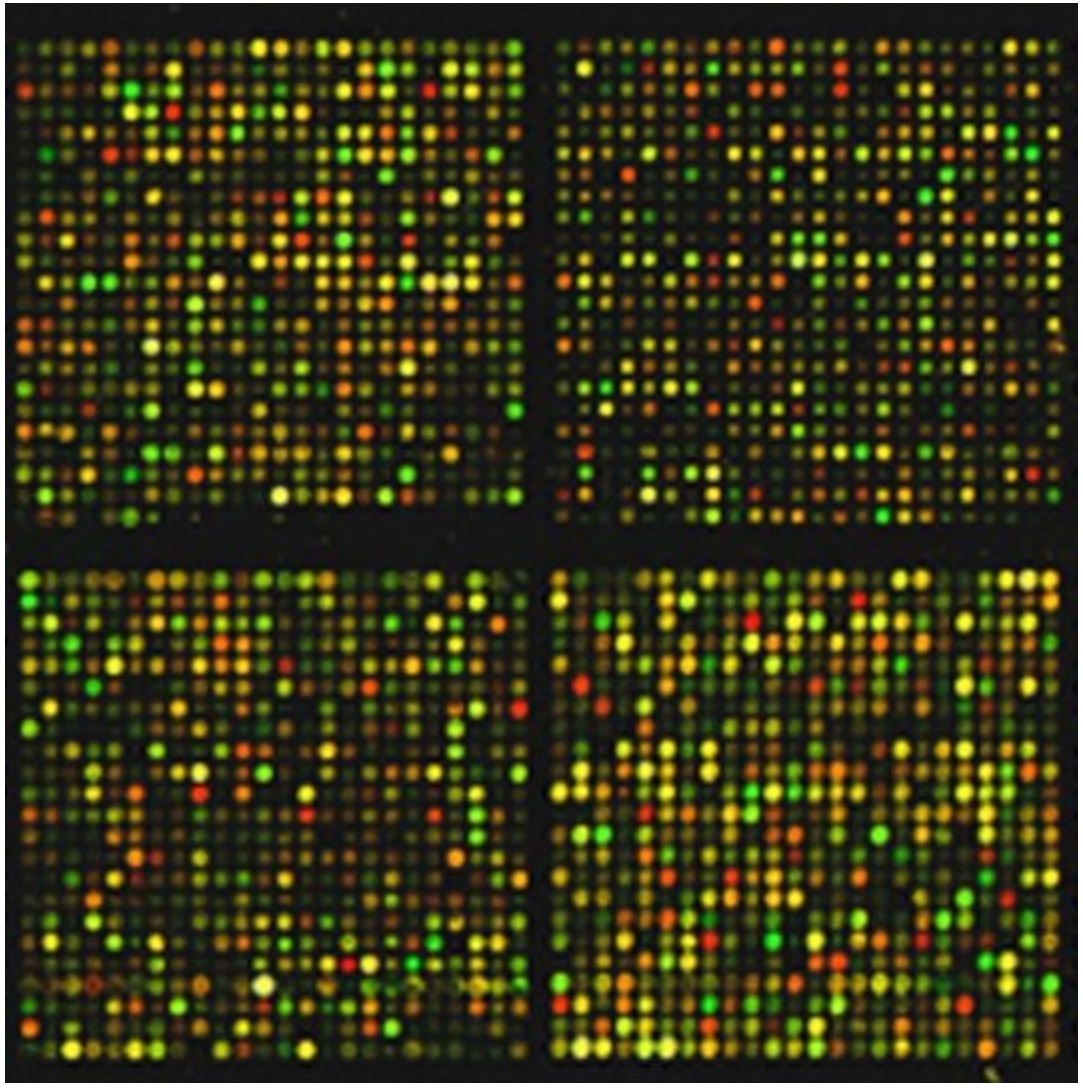
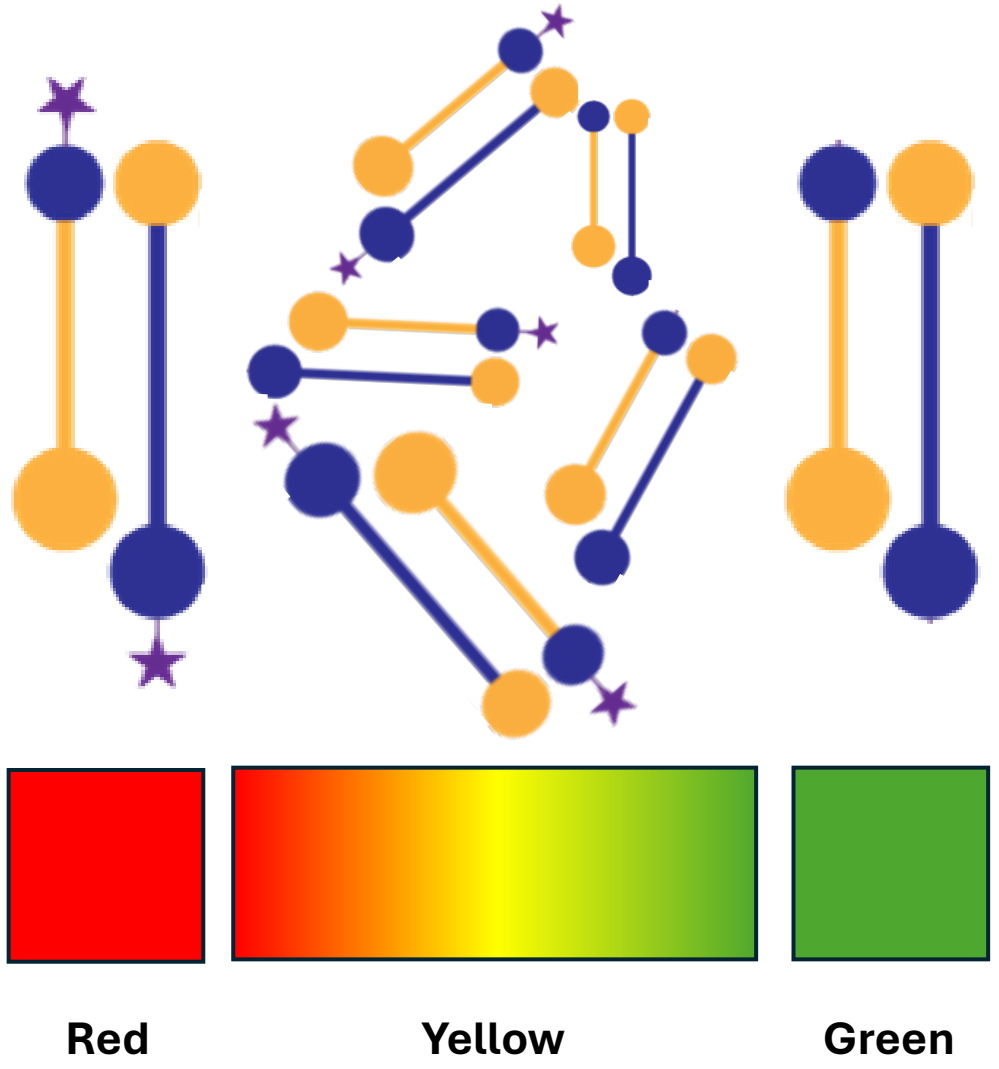
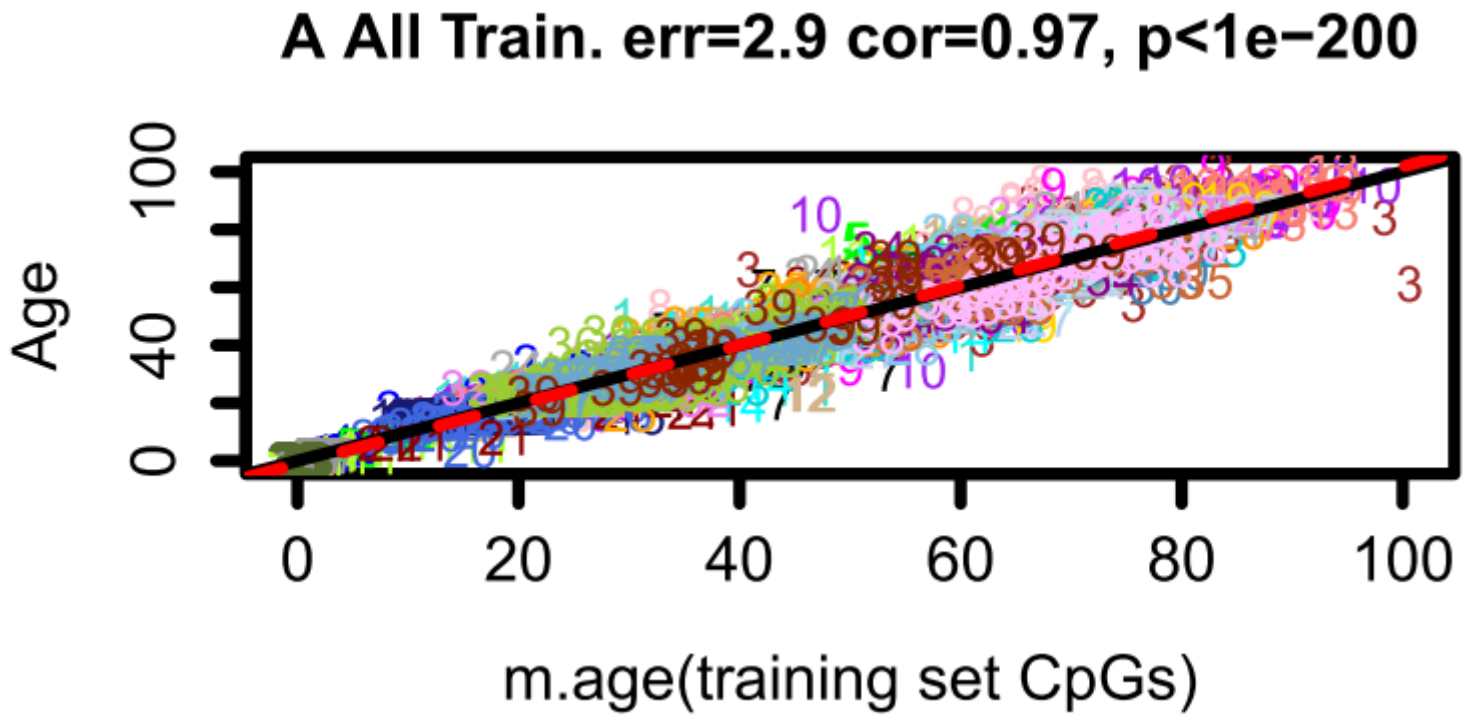


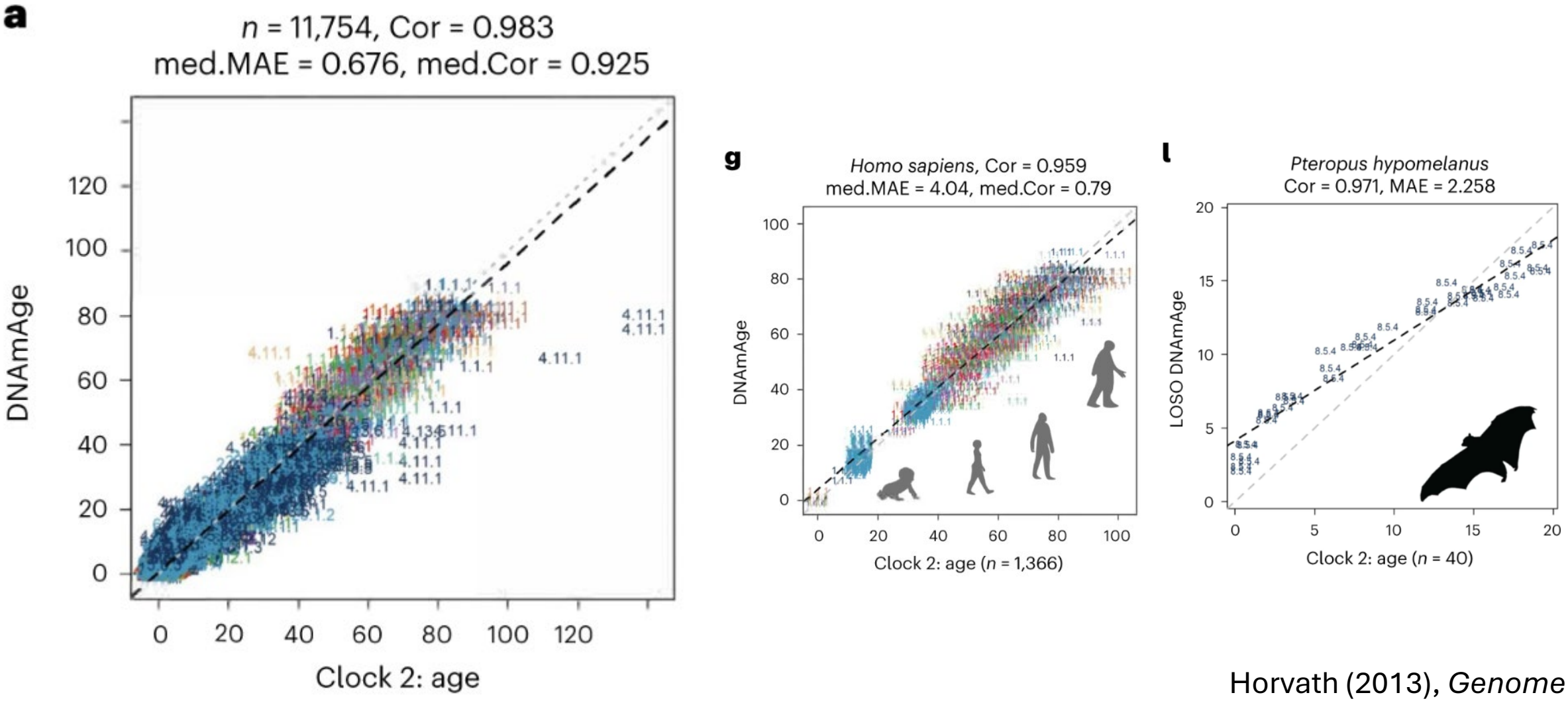


This actually works quite well – in humans



Horvath (2013), *Genome Biology*

It also works really well across mammals – including bats!

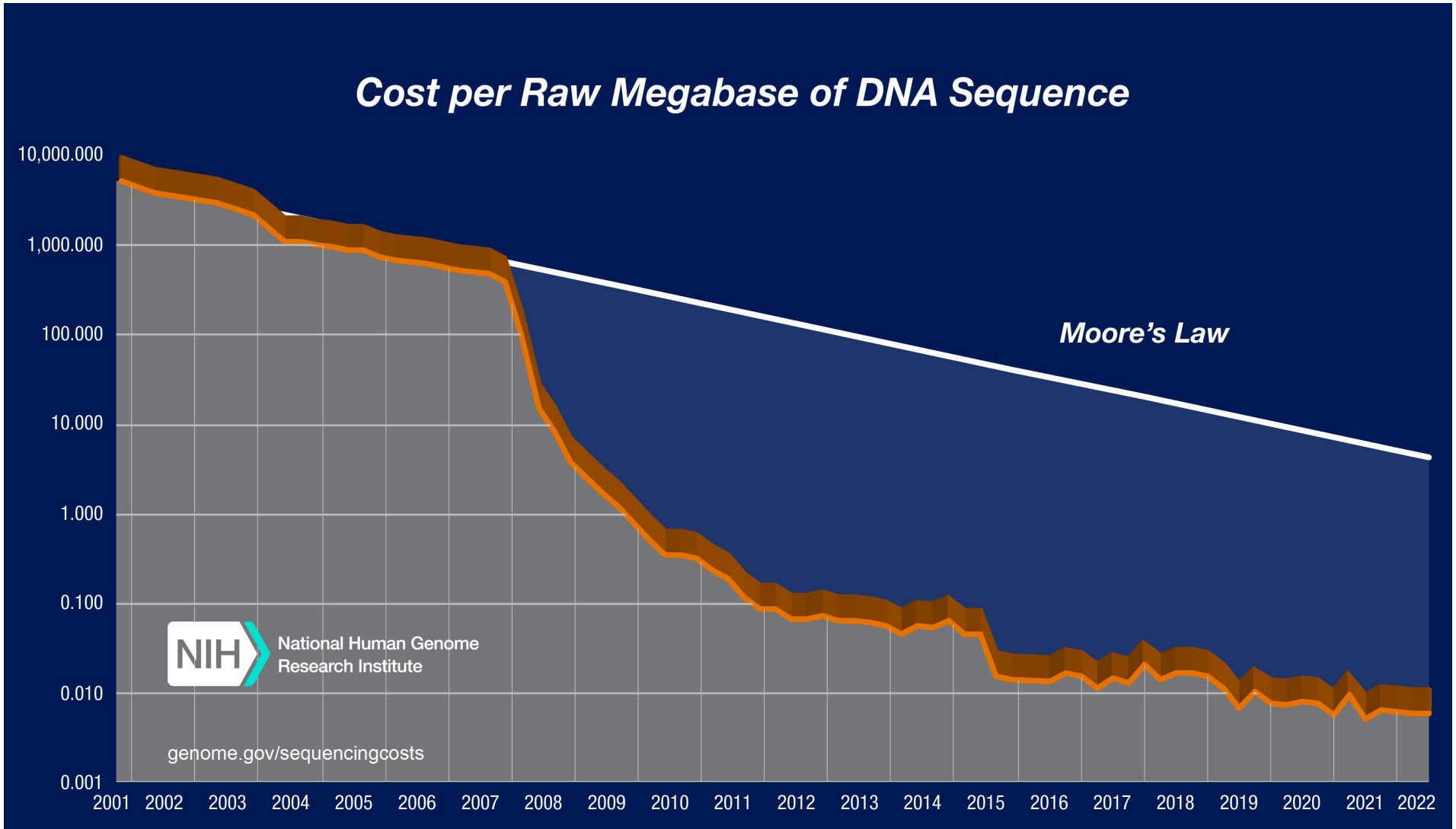


Horvath (2013), *Genome Biology*

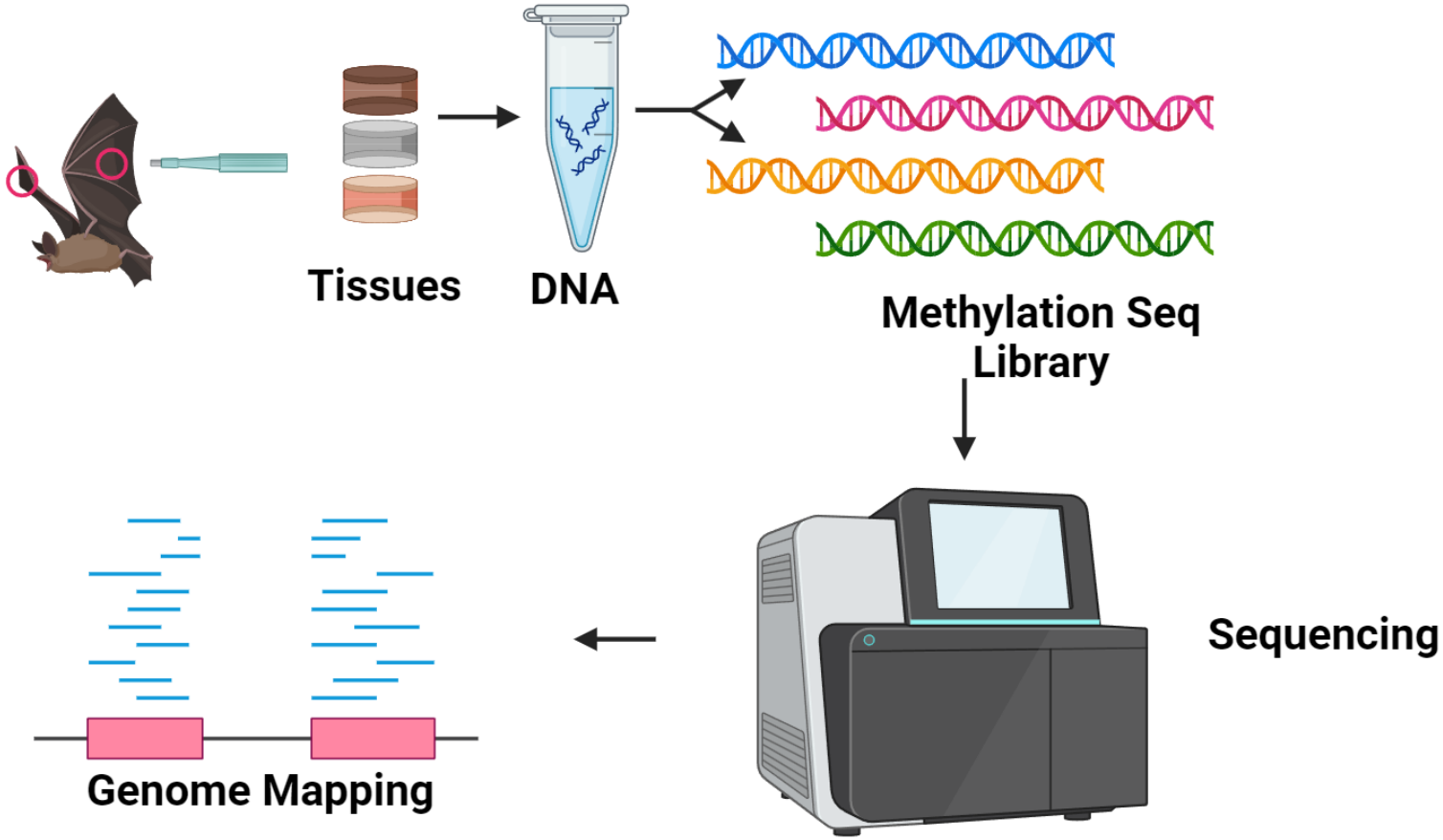
The only problem?


The only problem

Microarrays don’t scale well – but new sequencing technologies do



The new process in a nutshell



Our goals:

Short Term:

- Generate **new training data** using next-generation sequencing

Our goals:

Short Term:

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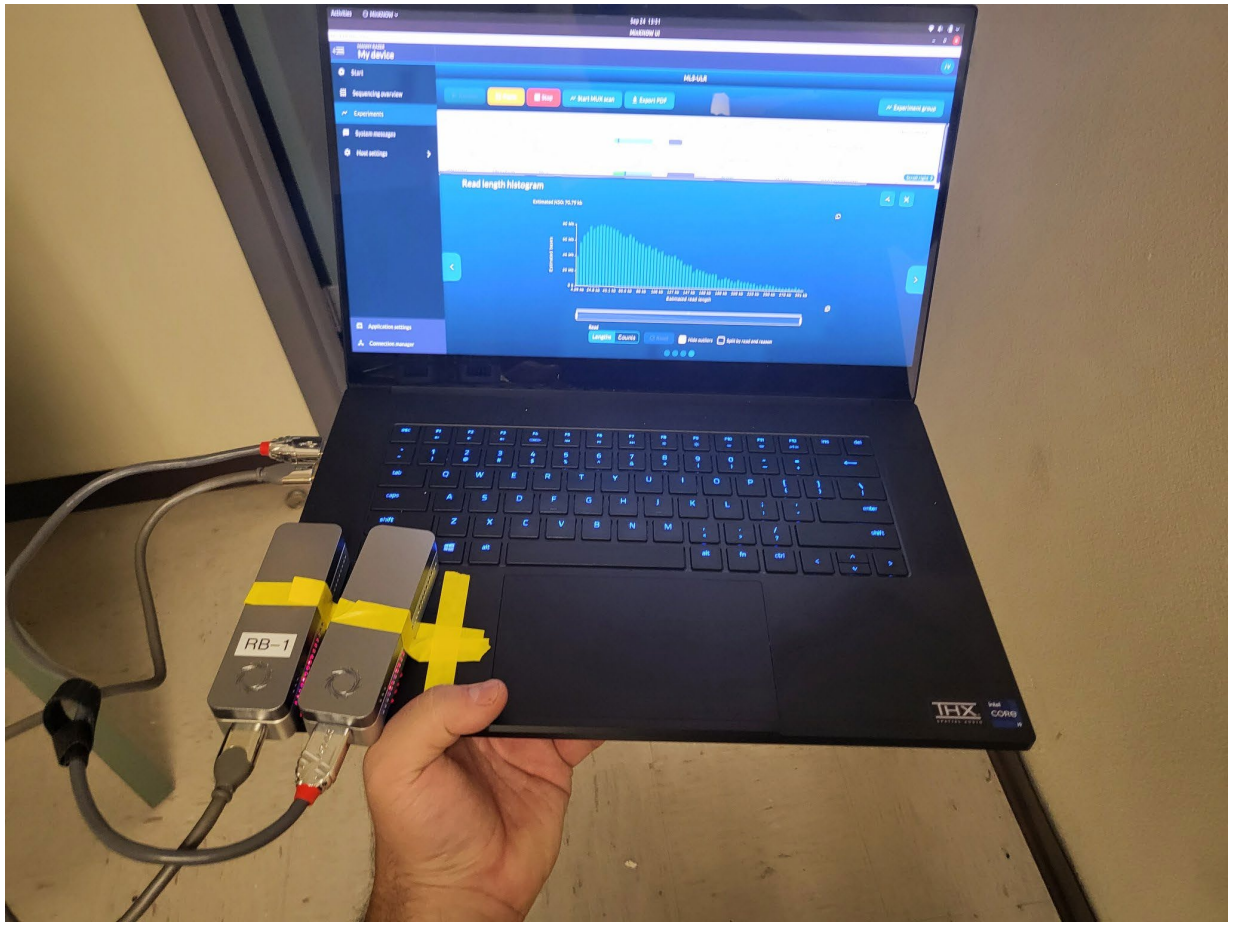

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