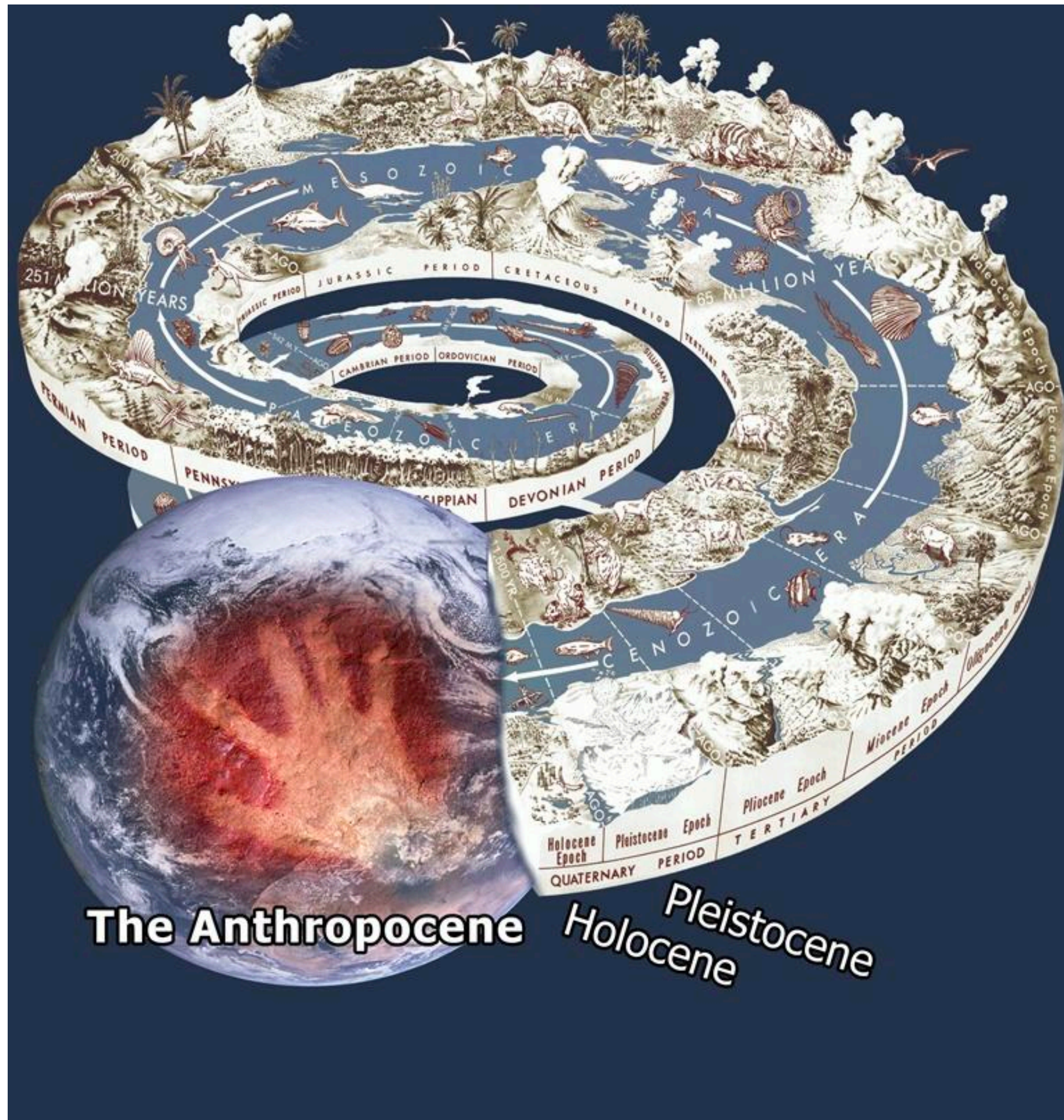


Conservation genomics



We're now in the Anthropocene



One in four species are at risk of extinction

Species assessed by the IUCN Red List



Amphibians
40%



Conifers
34%



Reef corals
33%



Sharks & Rays
31%



Selected crustaceans*
27%



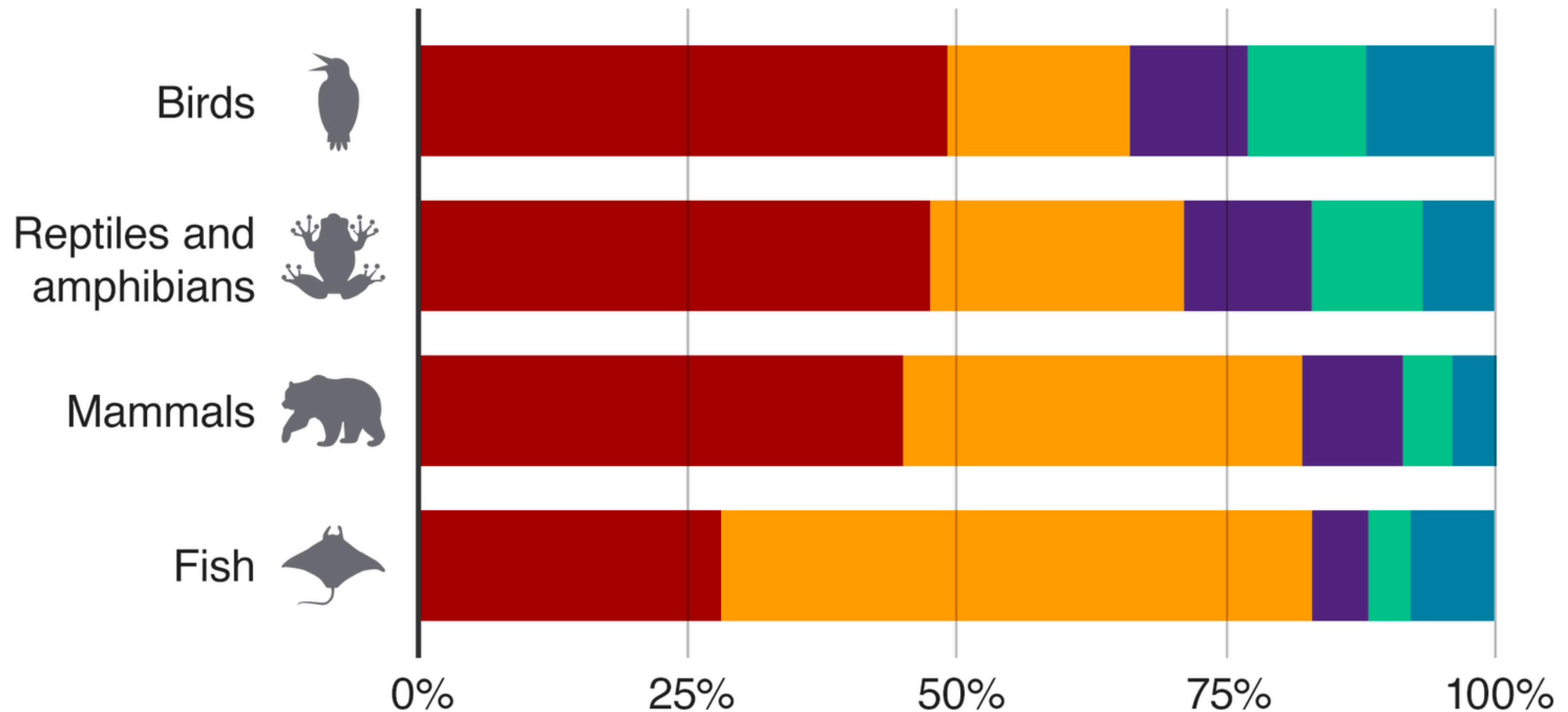
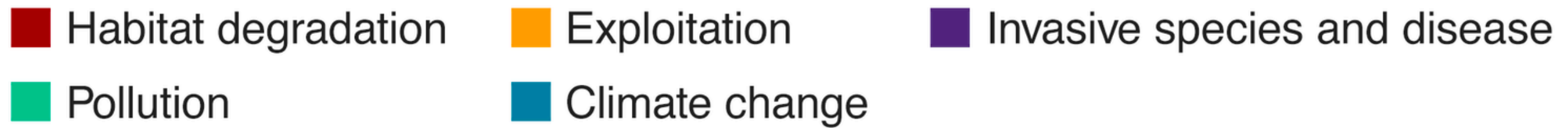
Mammals
35%



Birds
14%

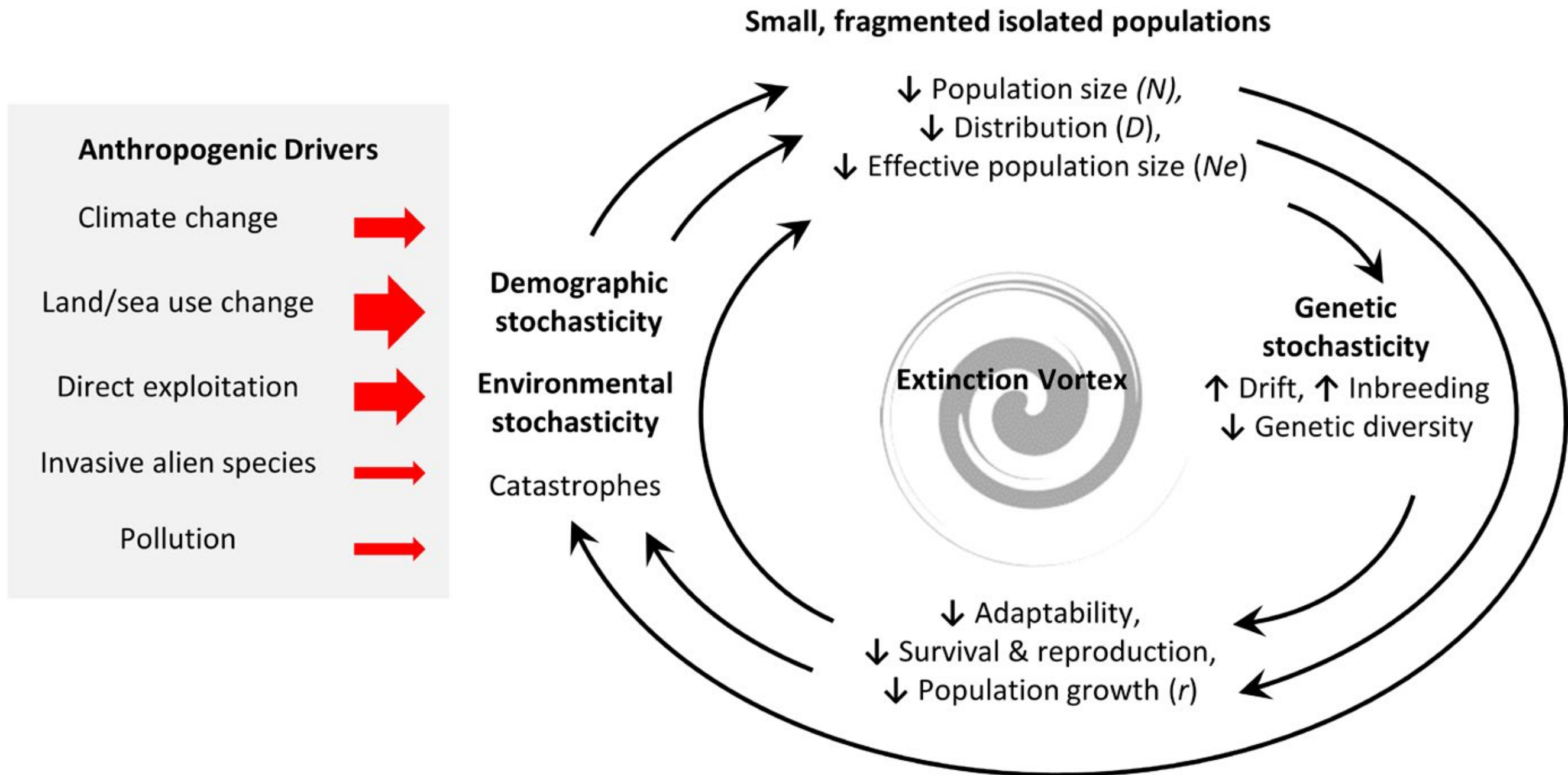
Habitat loss is a major threat to biodiversity

The Living Planet Report assesses key drivers of species decline

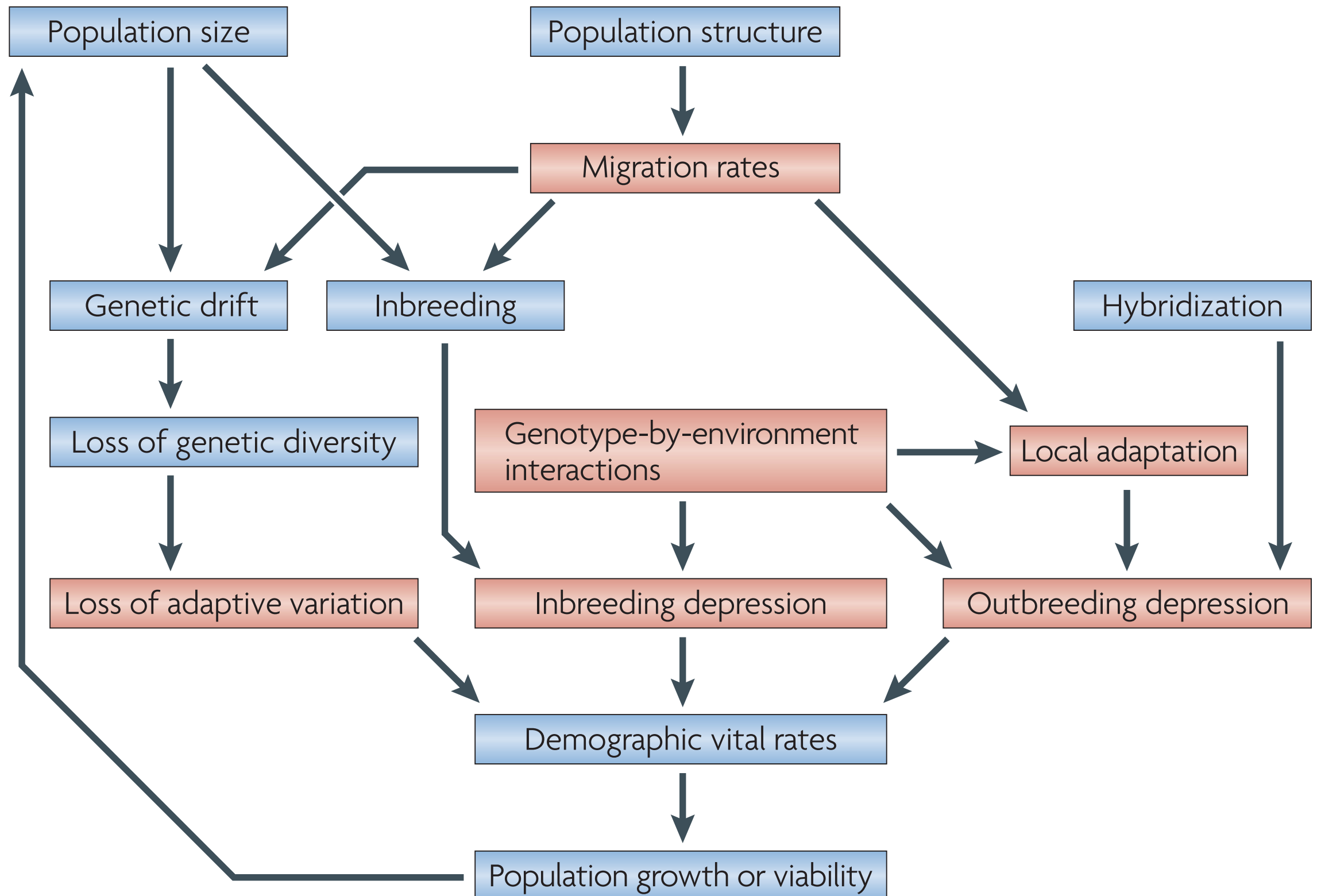


Note: A sample of 3,789 populations evaluated by the Living Planet Index

The extinction vortex



Conservation genetics & genomics



Conservation genetics & genomics

- Inferring population demography
- Identifying adaptive genetic variation
- Informing genetic rescue efforts

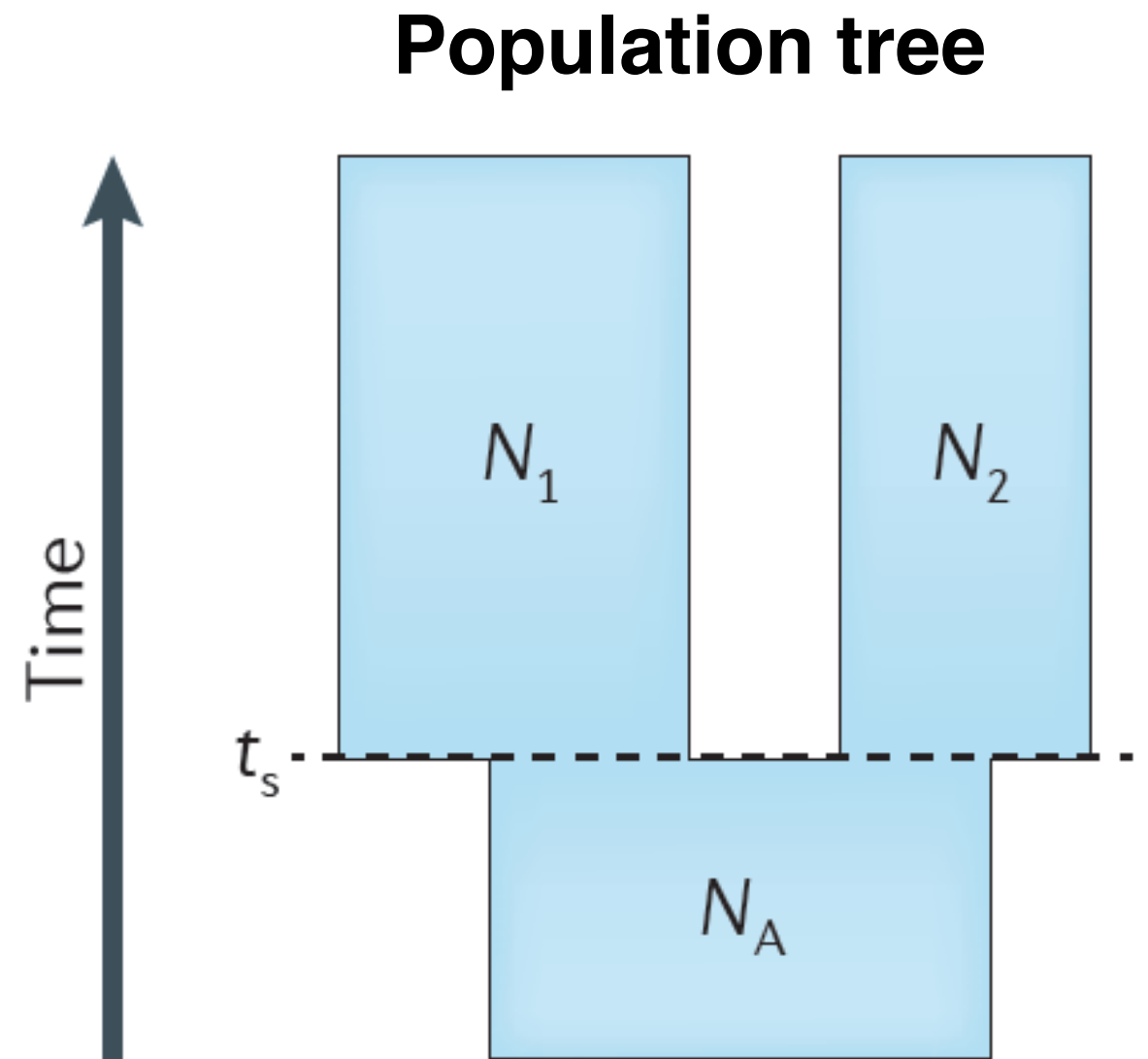
Conservation genetics & genomics

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What is population demography?

Effective population sizes back in time (expansions, bottlenecks, etc.)

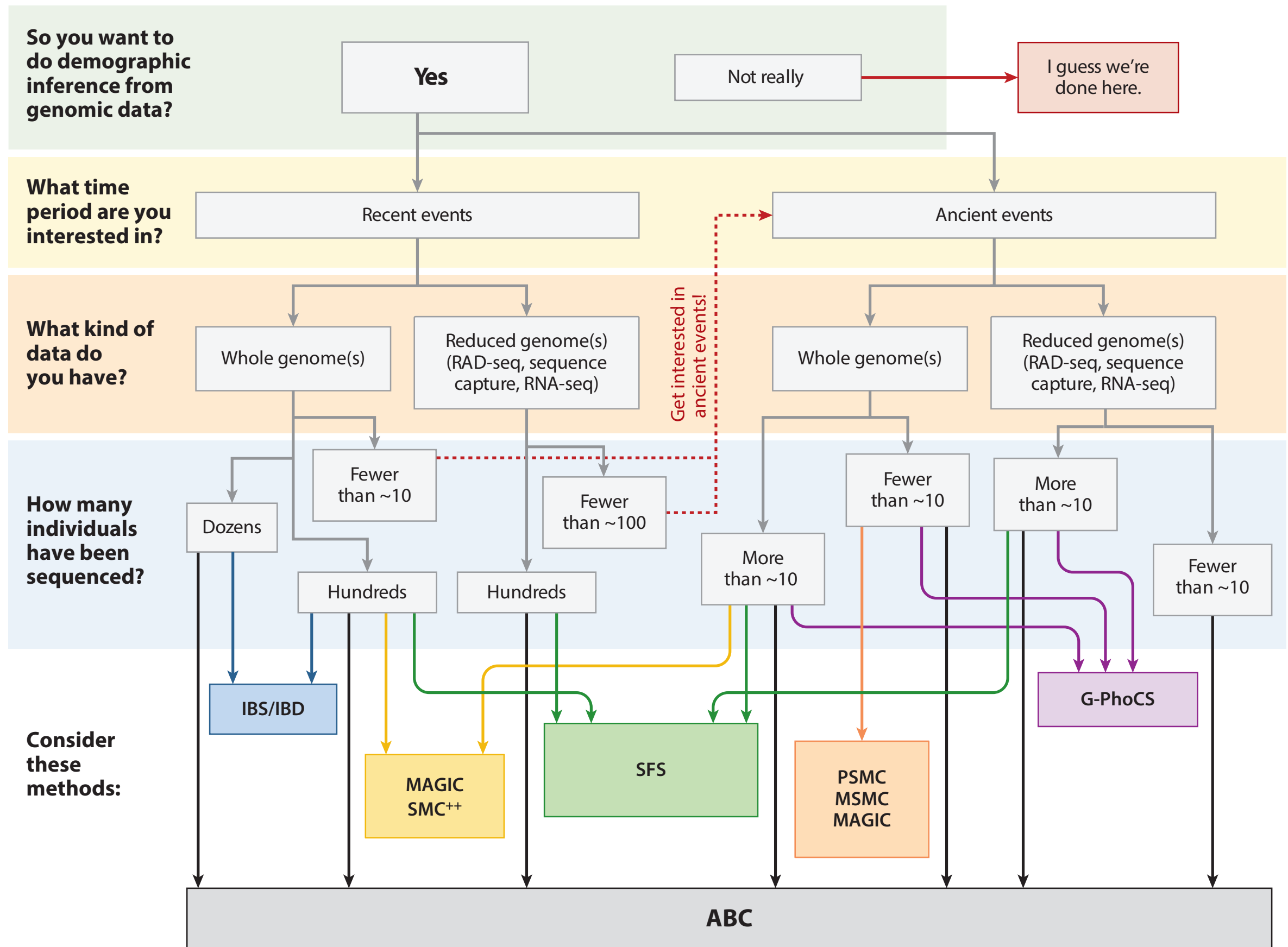
Population structure (split times) and migration rates over time



Why model demographic history?

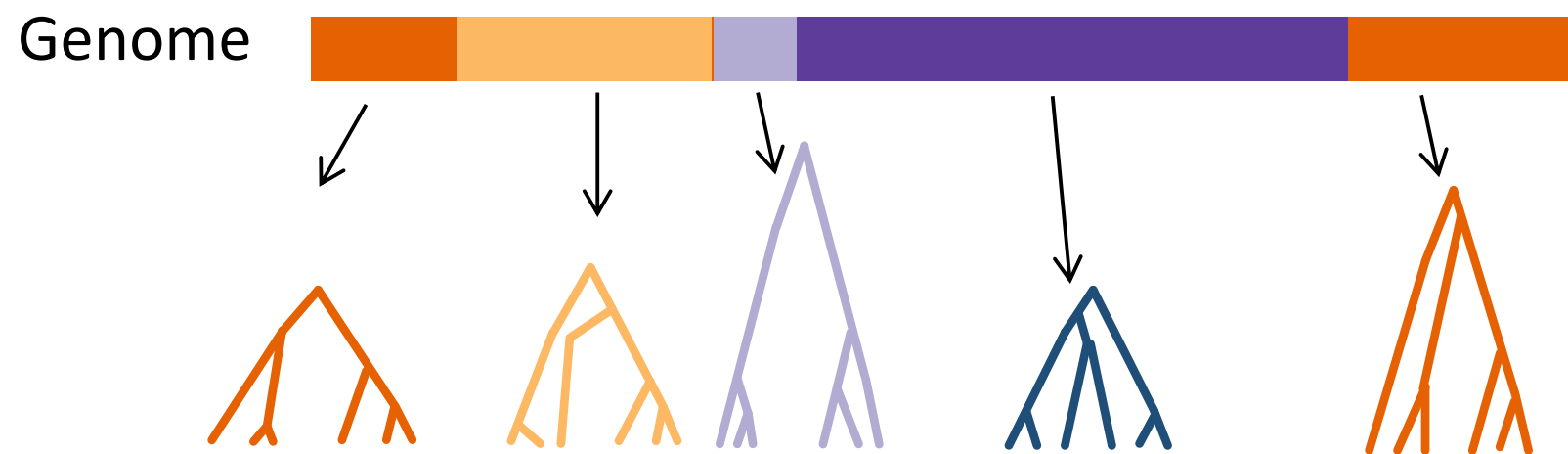
- Understand population history
- Neutral background for tests of selection
- Conservation: present vs. historical levels of genetic diversity

Many methods for demographic inference

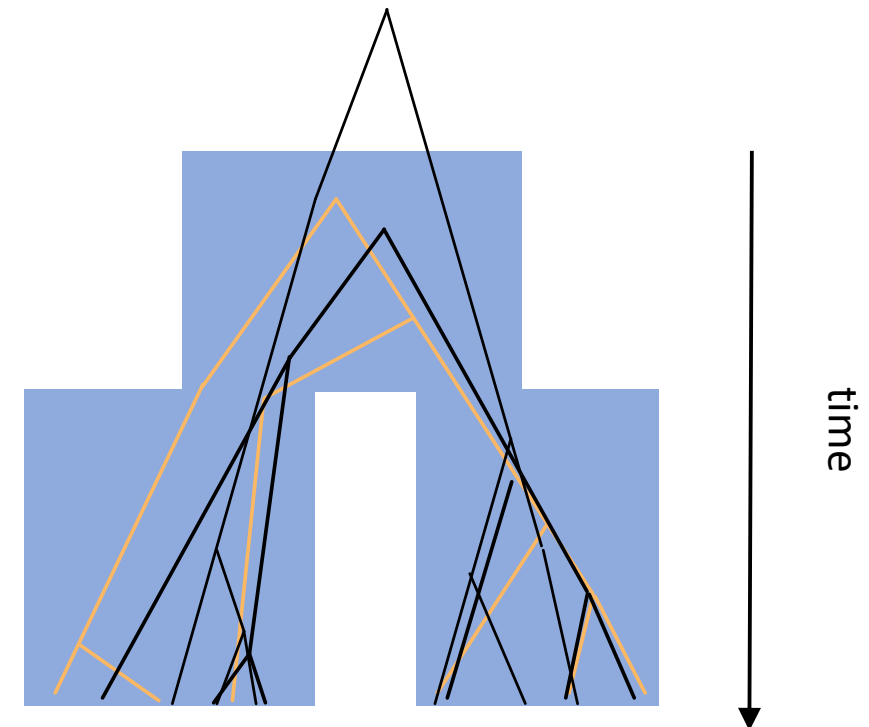


Reconstructing demographic history from genomic data

Because of recombination, different regions of the genome can have different gene trees

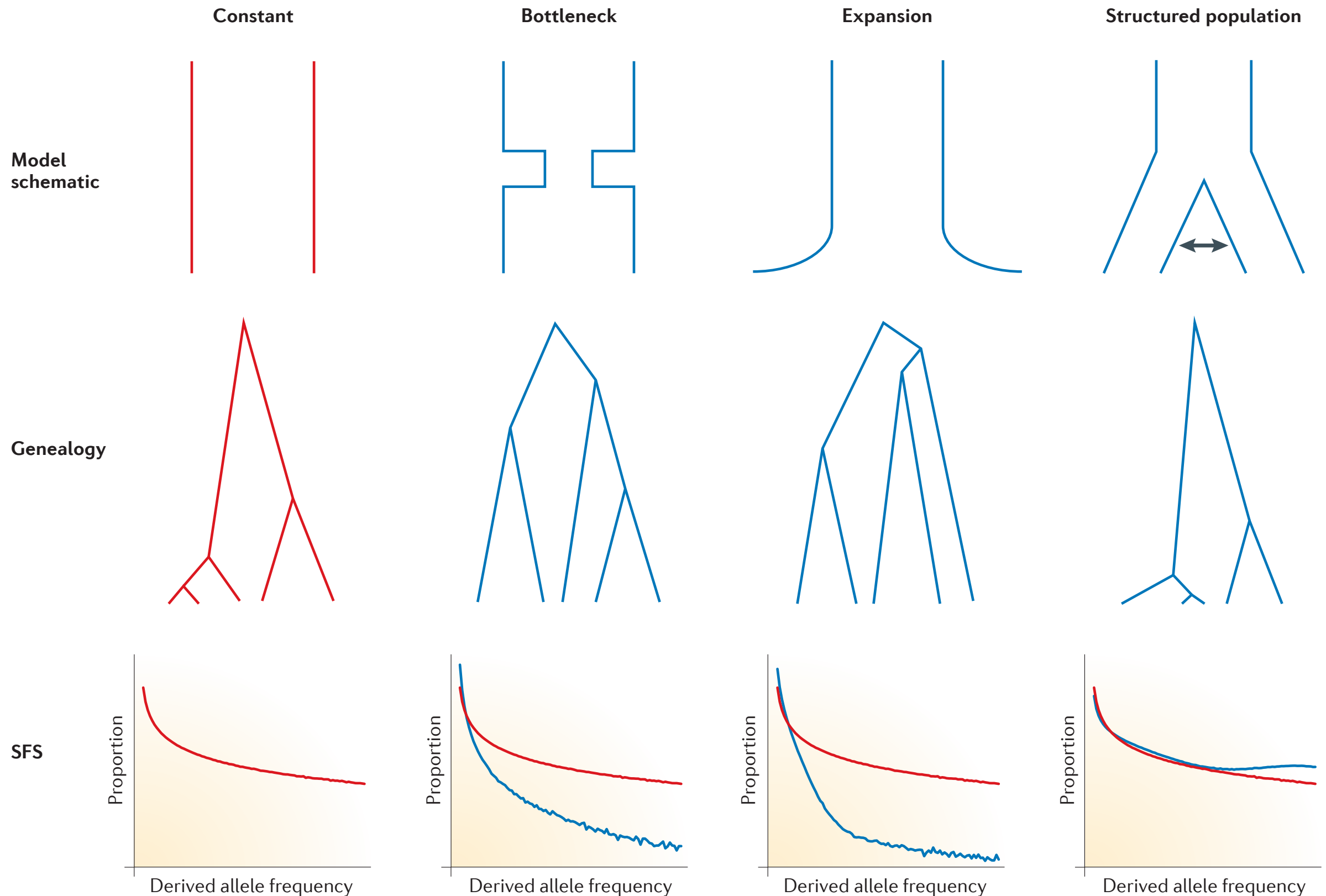


- Demography is expected to affect the entire genome
- Natural selection acts on specific functional regions



All gene trees are consistent with the population tree. Independent gene trees can be seen as independent replicates of the same population tree.

Demography influences coalescent genealogies & the site frequency spectrum (SFS)

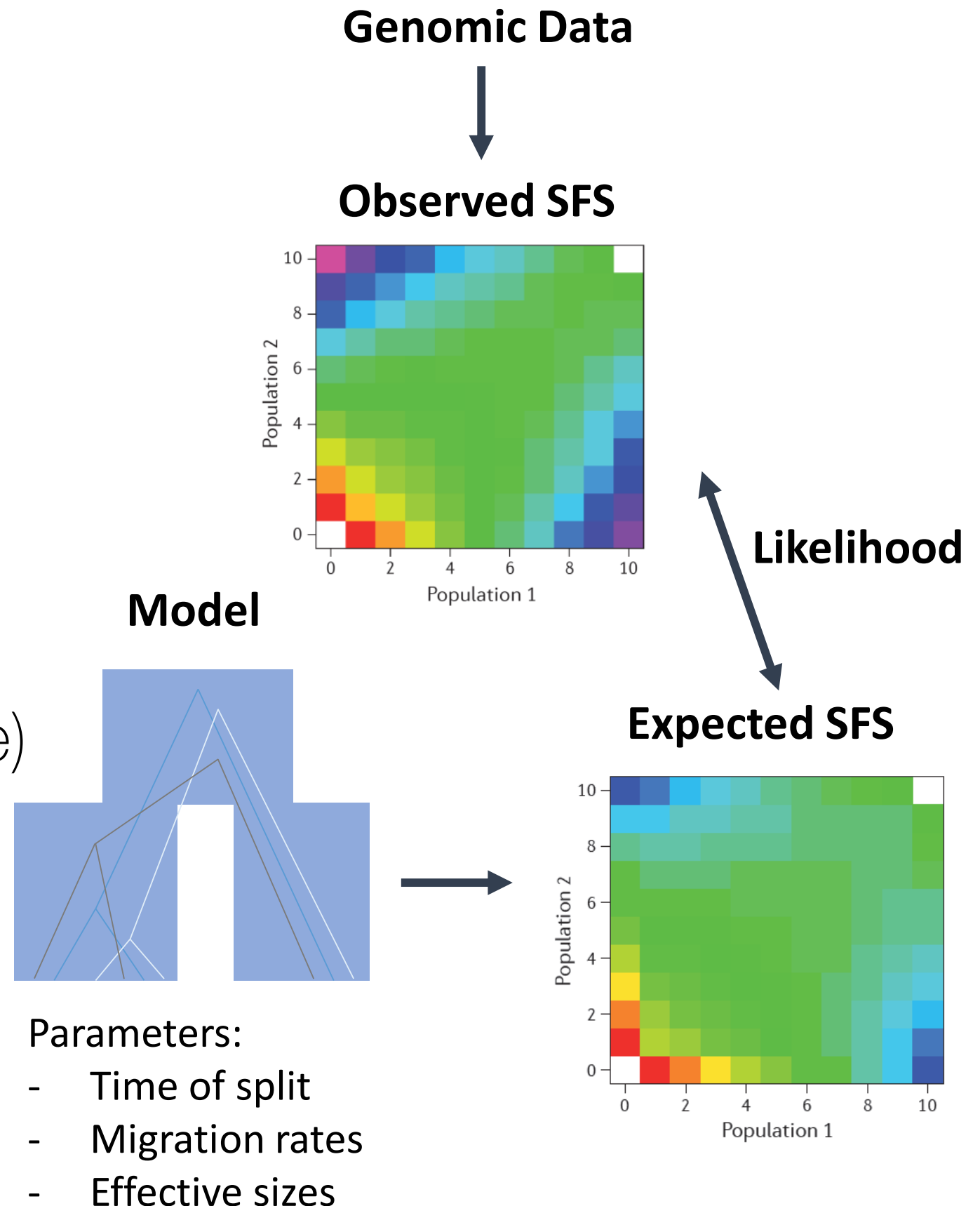


Inferring demographic history from the SFS

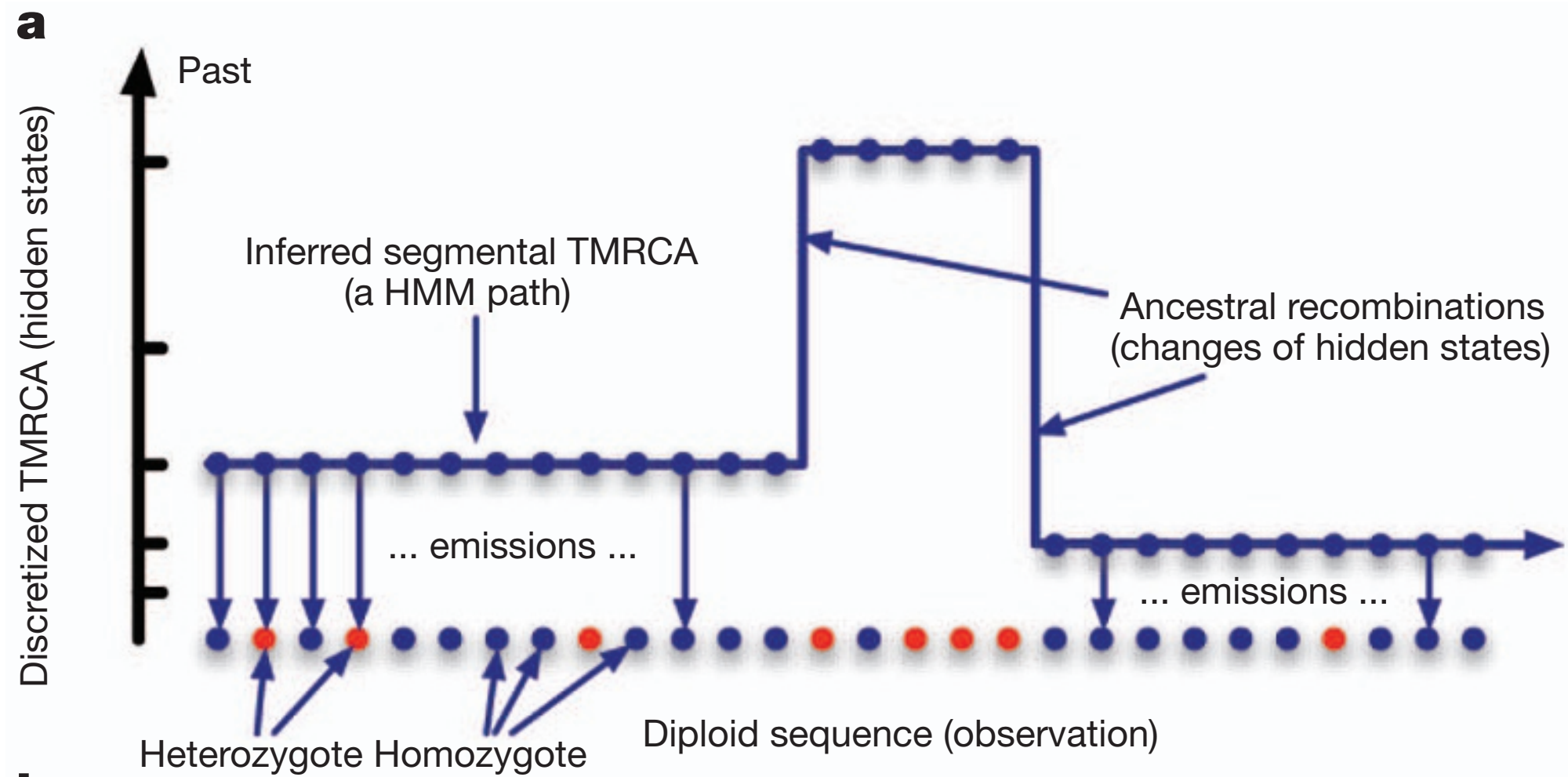
Compute likelihood of data based on the expected SFS under a given model.

Different ways of obtaining the expected SFS:

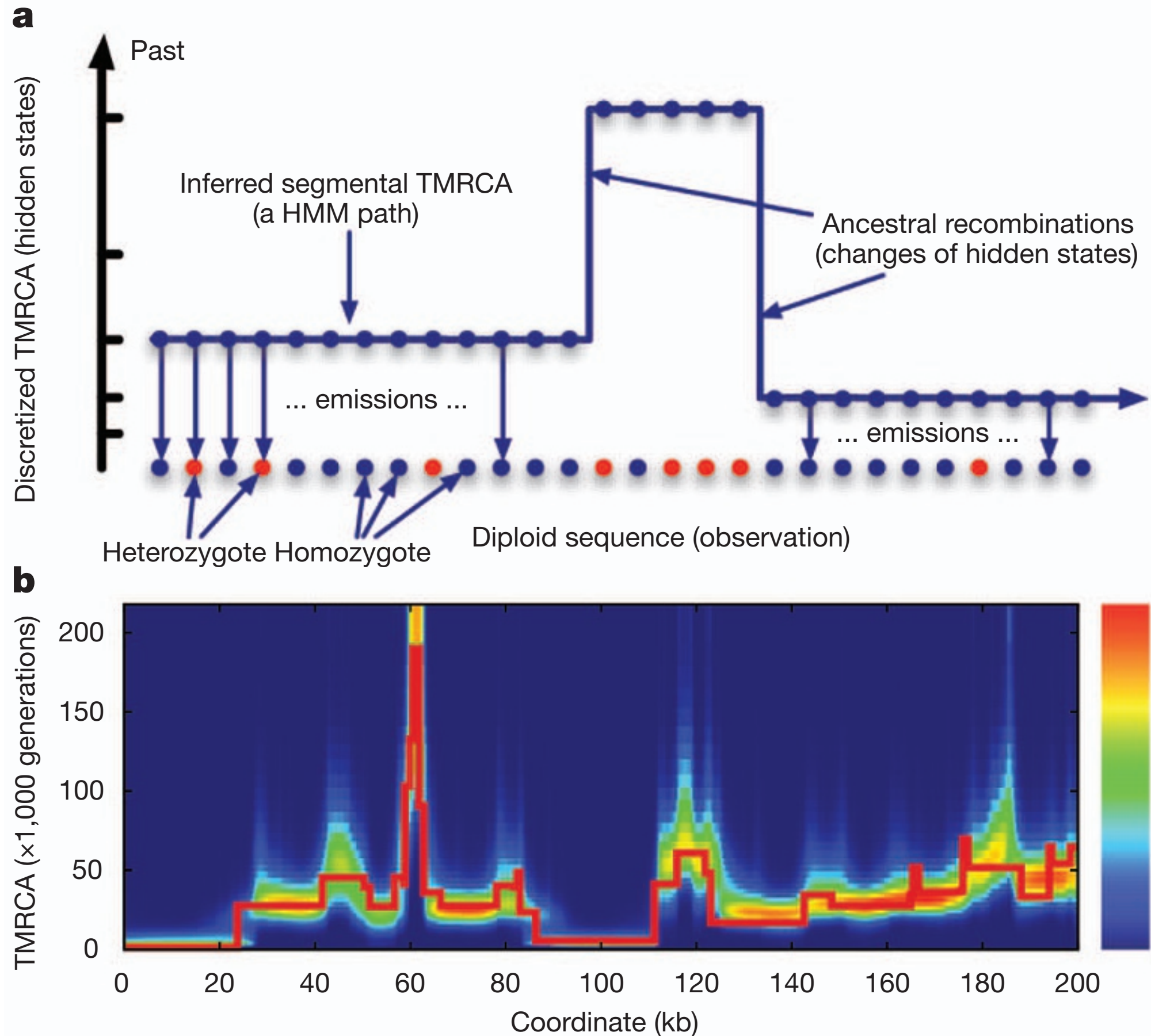
- Diffusion (forward in time)
- Coalescent (backward in time)



Pairwise Sequentially Markovian Coalescent

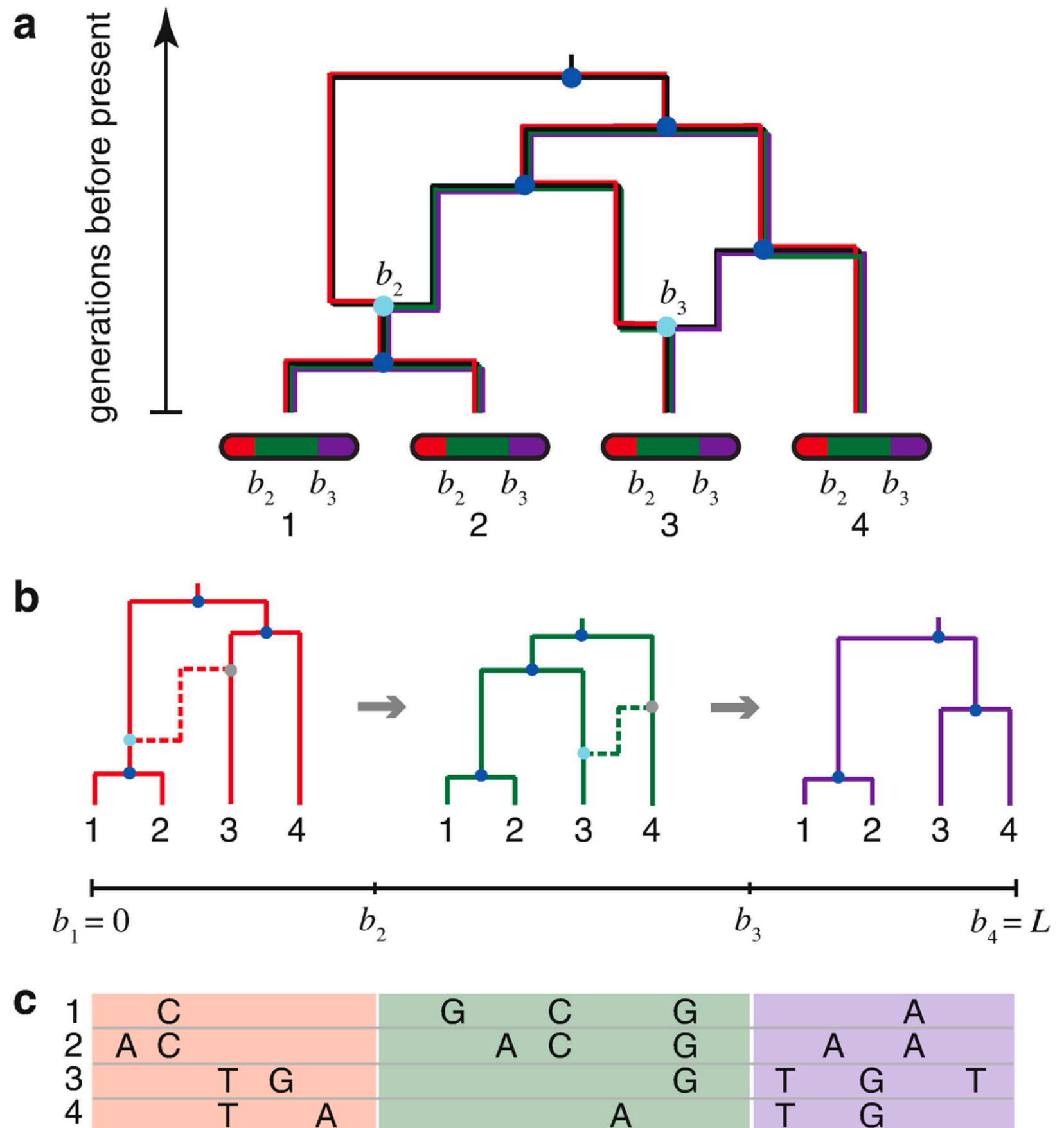


Pairwise Sequentially Markovian Coalescent

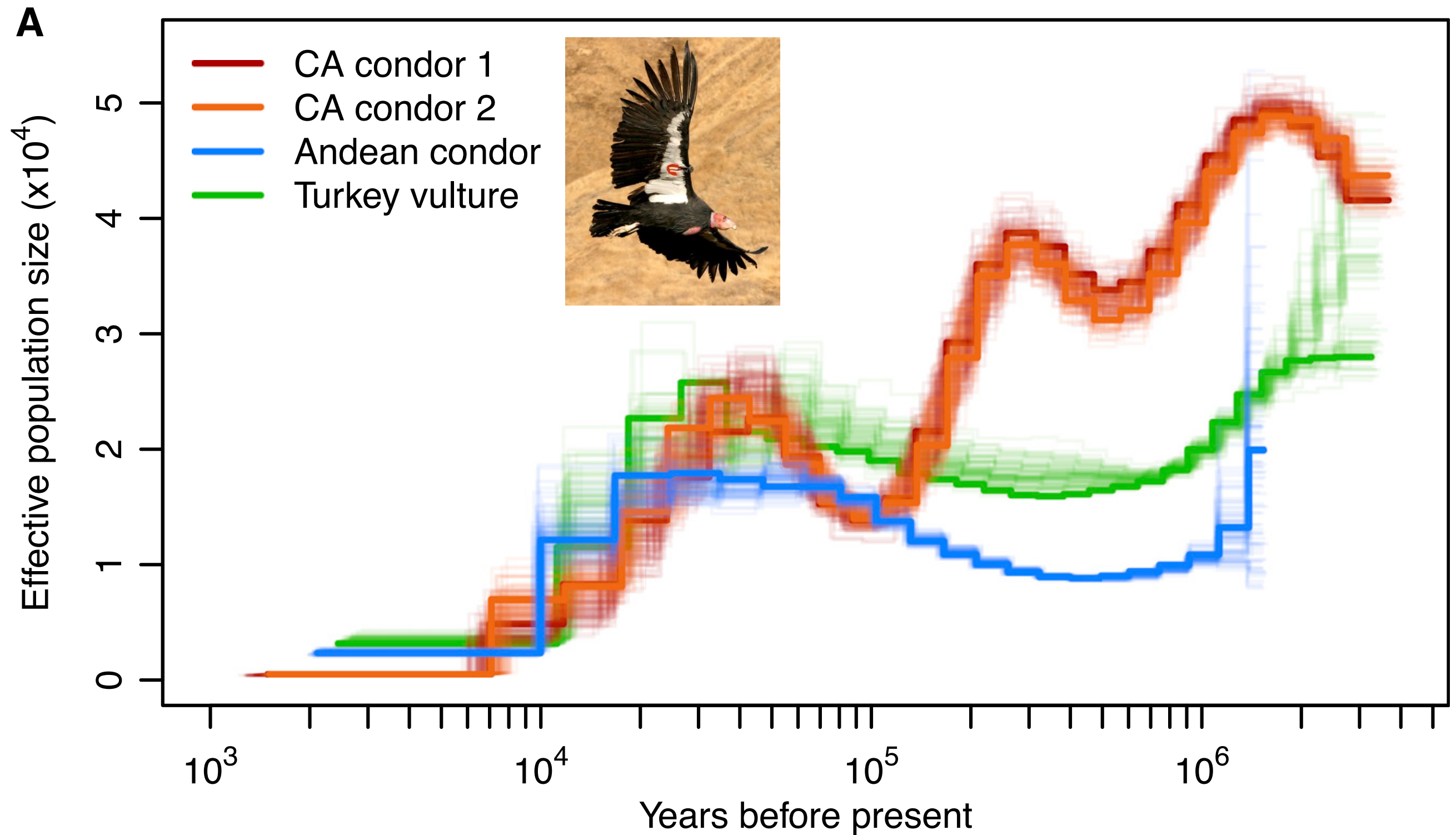


Ancestral recombination graph (ARG)

The ARG describes how individual sequences in a population are related, and provides the combined history of recombination, mutation, and coalescence.



Demographic inference of the CA condor



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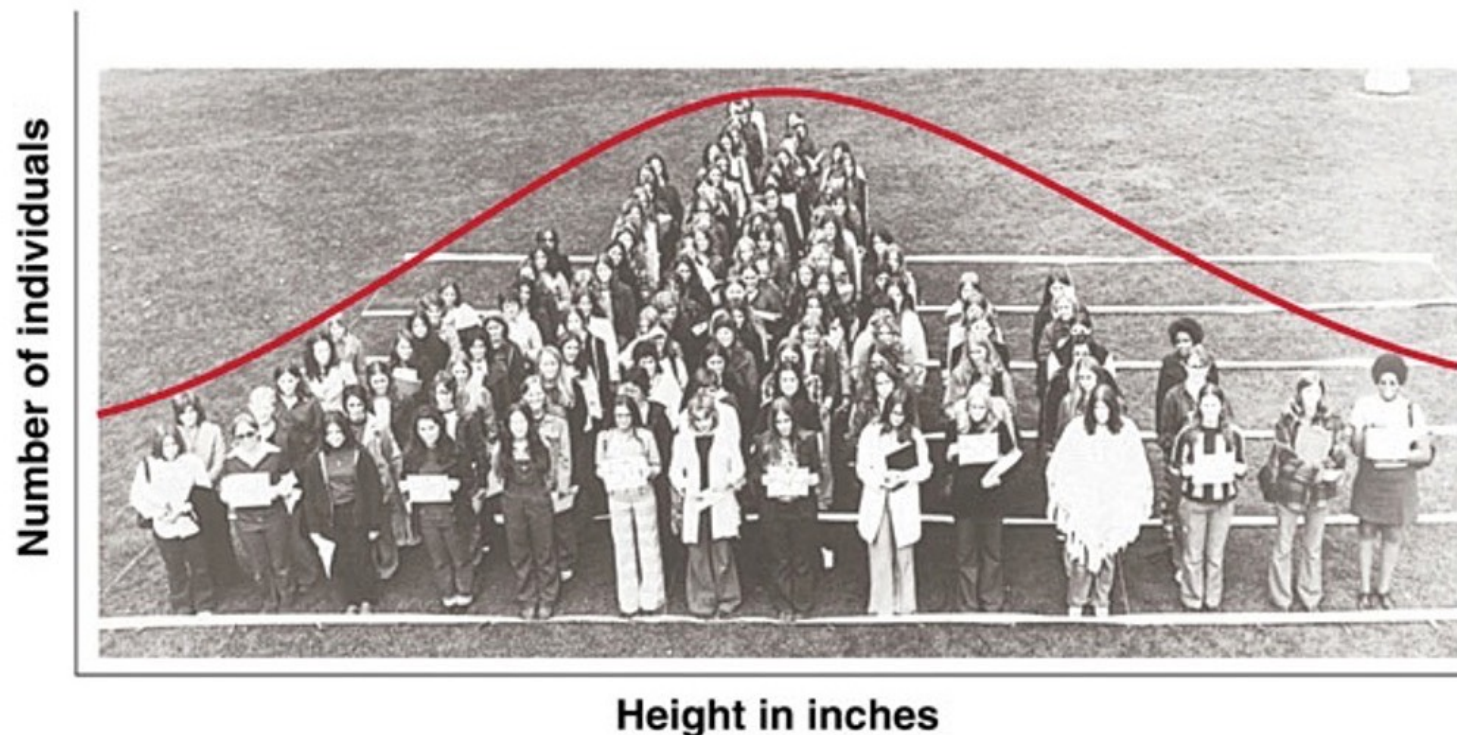
Phenotypes are determined by genetic and environmental factors

$$P = G + E$$

Phenotypes are determined by genetic and environmental factors

$$P = G + E$$

Many traits are **polygenic**, or controlled by multiple genes.



Phenotypic variation among individuals

Phenotypic variance V_P is composed of genetic variance V_G & environmental variance V_E

$$V_P = V_G + V_E$$

We can further partition V_G

$$V_G = V_A + V_D + V_I$$

Where V_A = additive genetic variance

V_D = dominance variance

V_I = epistatic variance

Heritability is the genetic contribution to phenotypic variance

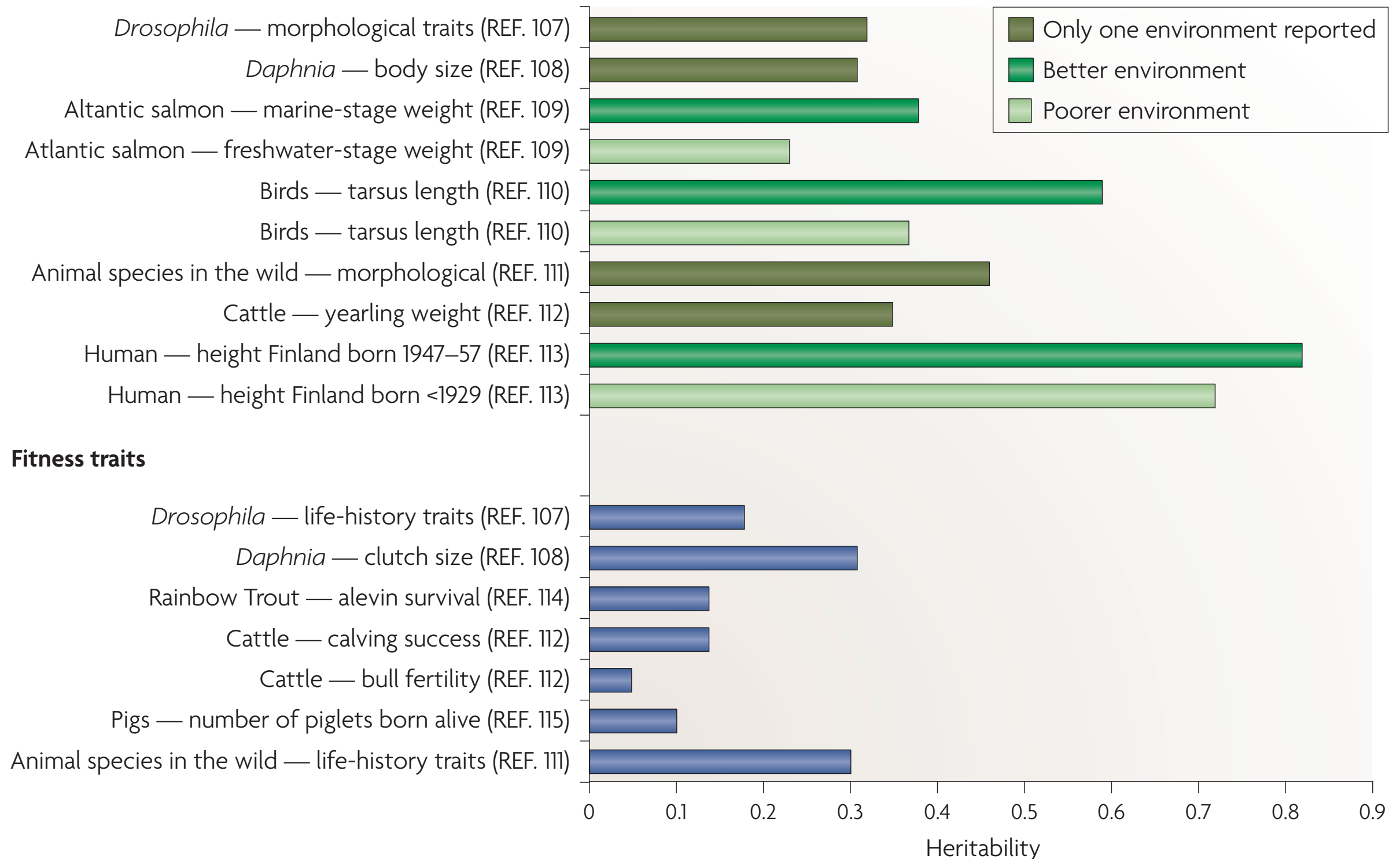
Narrow sense heritability

$$h^2 = V_A / V_P$$

Heritability underlies the predicted response to selection and is a population-specific measure

Many traits have h^2 between 0.1 & 0.9

Morphological traits



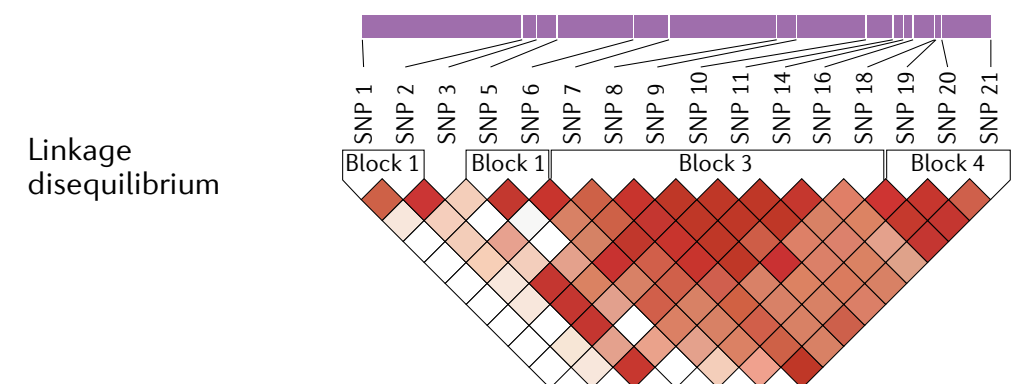
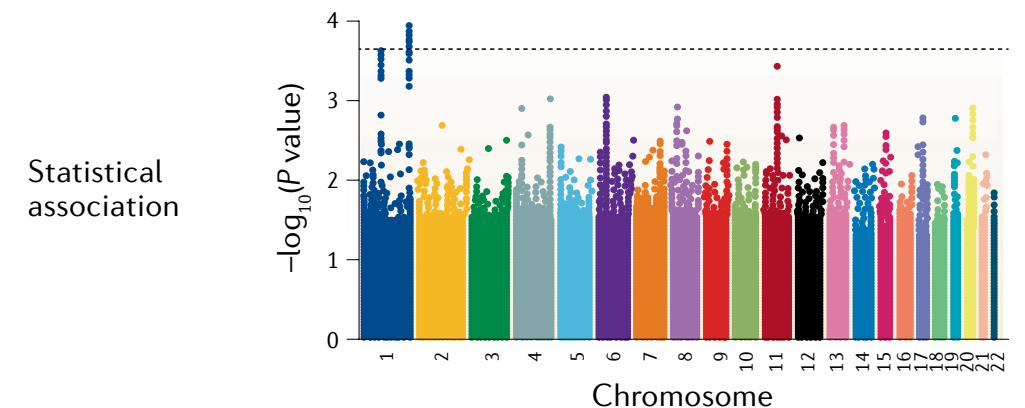
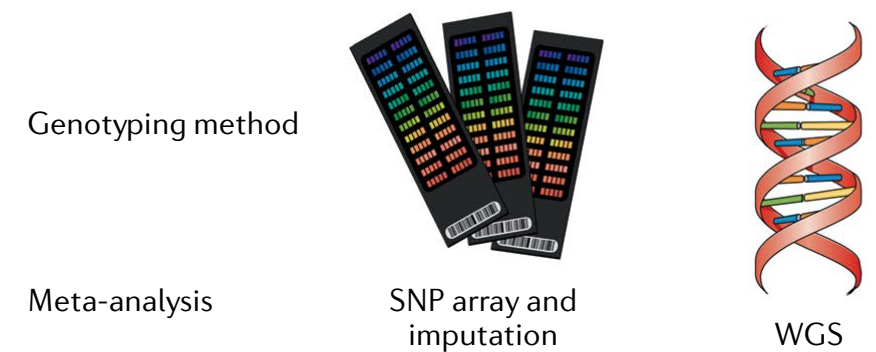
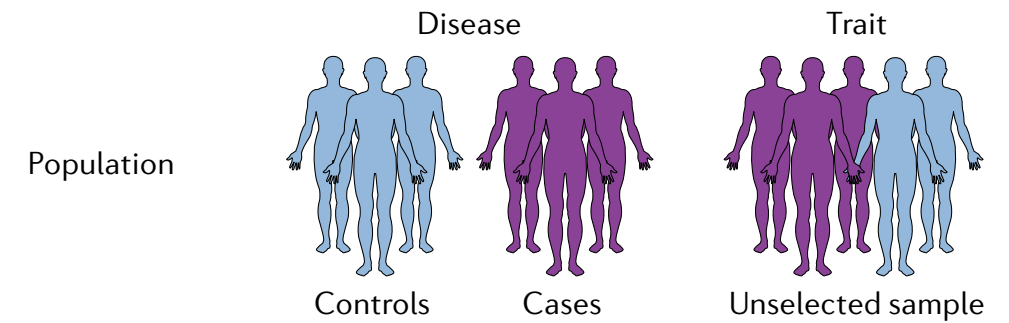
Genome-wide association study

GWAS test for associations between allele frequency at each marker and trait value

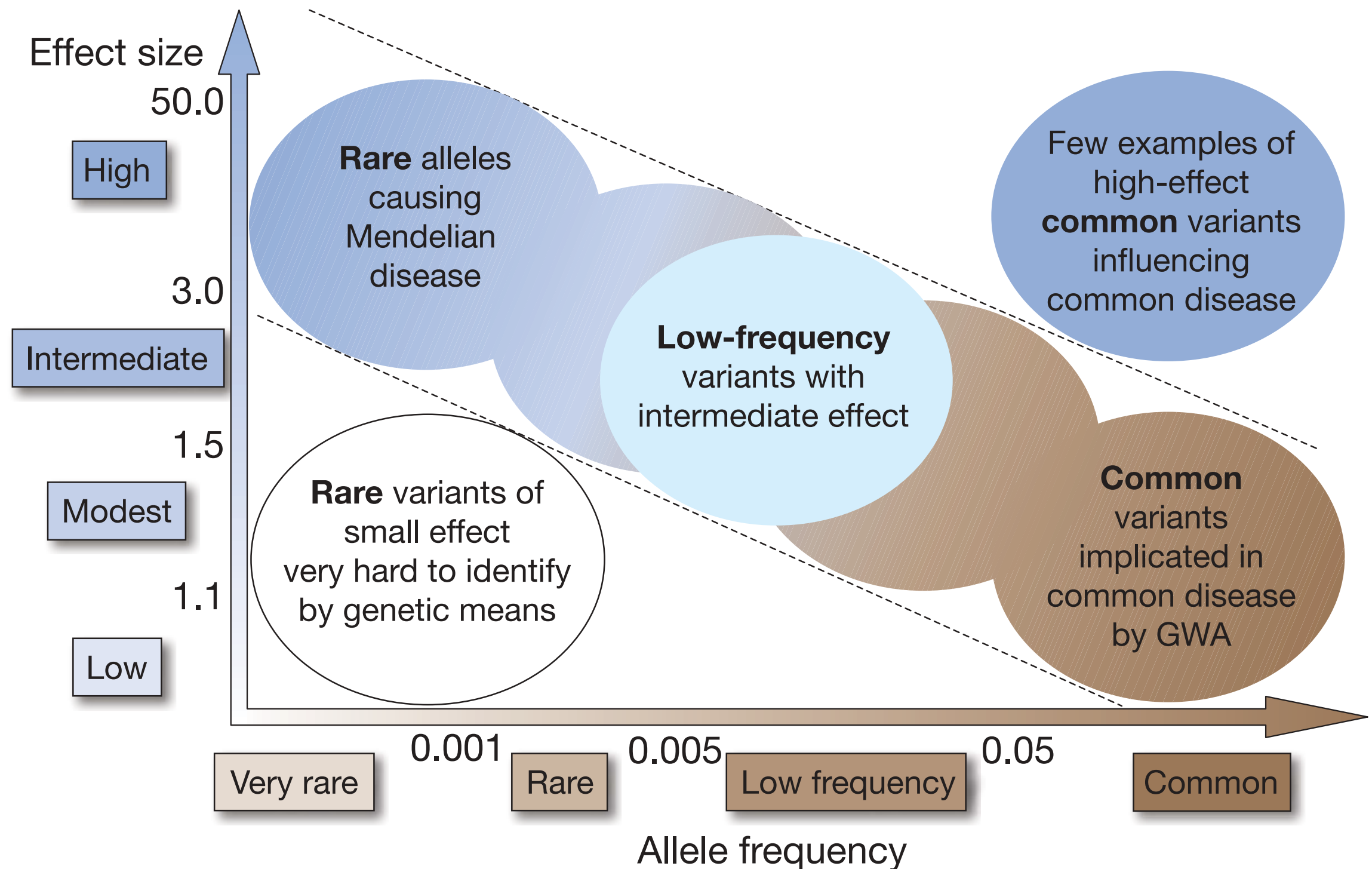
Phenotype Genotype

$$y = \alpha_l g_l + e$$

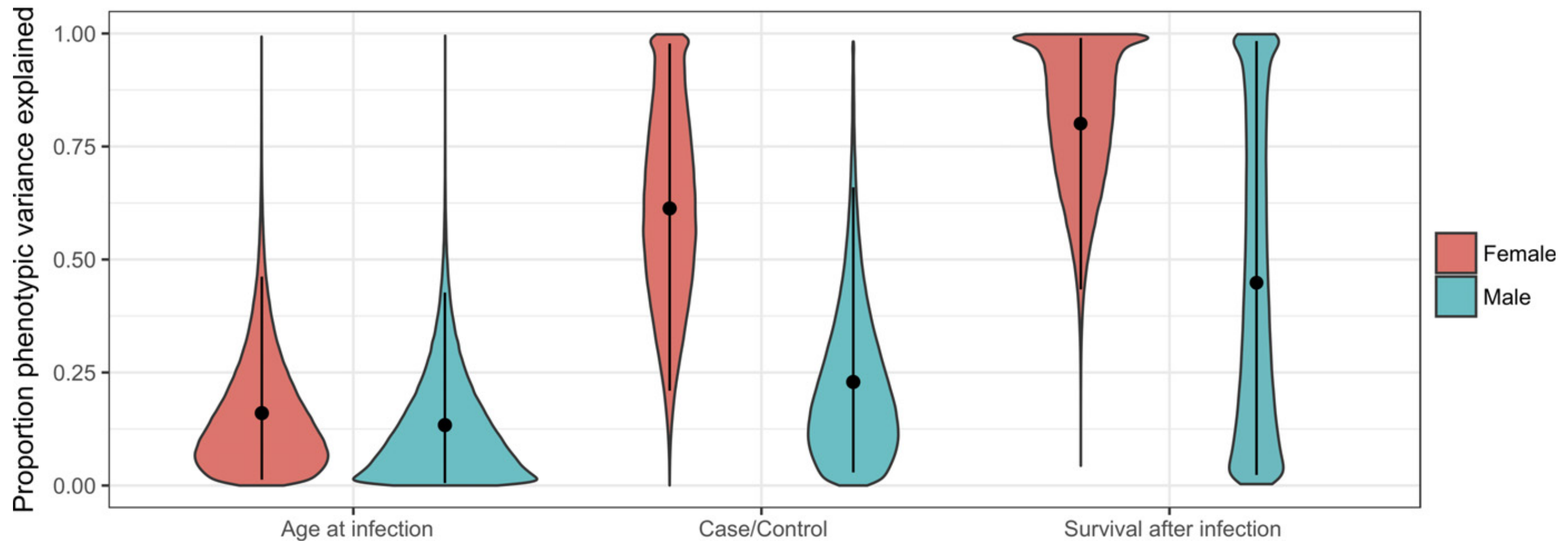
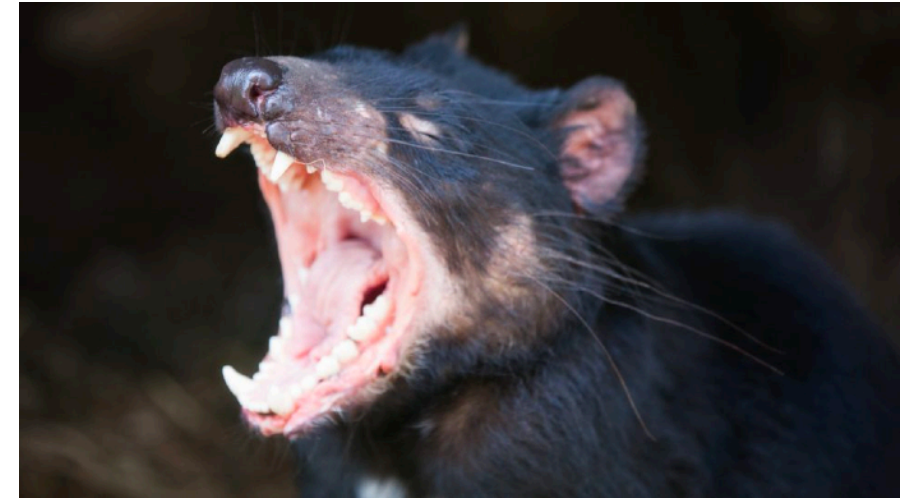
Additive effect size estimate Residual



Genetic architecture of trait determines power of detection



Heritability of cancer-related traits in Tasmanian devils



The inflated significance of neutral genetic diversity in conservation genetics

João C. Teixeira^{a,b,1}  and Christian D. Huber^{a,1} 

The crucial role of genome-wide genetic variation in conservation

Marty Kardos^{a,1} , Ellie E. Armstrong^b , Sarah W. Fitzpatrick^{c,d,e} , Samantha Hauser^f, Philip W. Hedrick^g, Joshua M. Miller^{h,i,j} , David A. Tallmon^k, and W. Chris Funk^l 

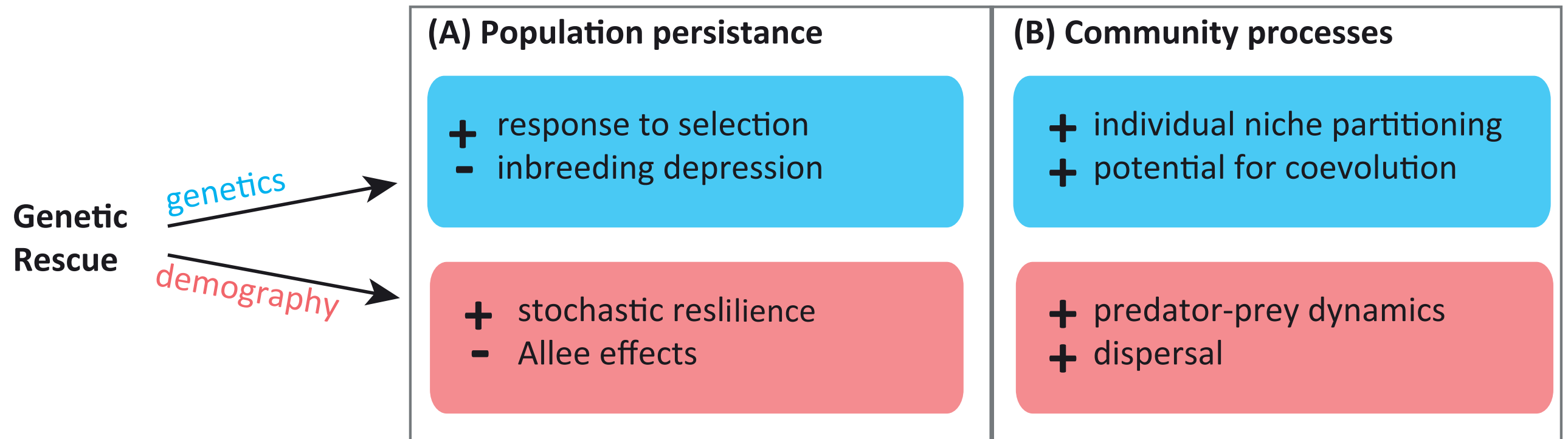
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Gene flow can rescue populations

Demographic rescue: a decrease in population extinction probability owing to the simple addition of immigrants.

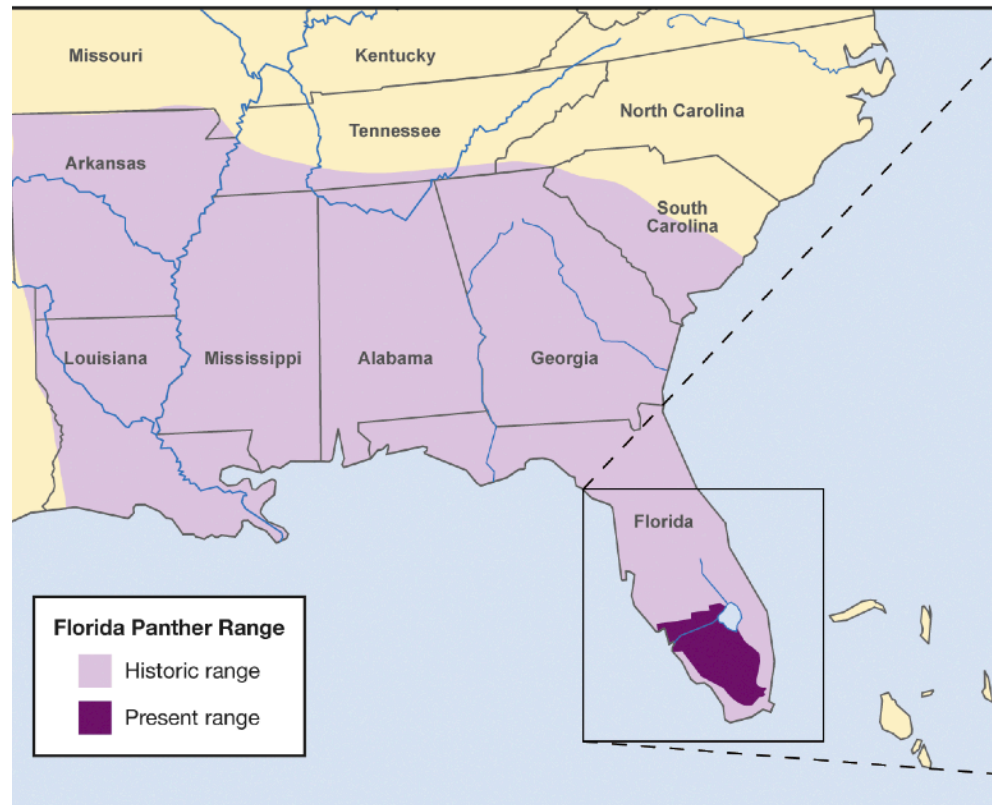
Genetic rescue: an increase in population fitness (growth) owing to the influx of genetic variation from immigrants.



Genetic rescue of the Florida Panther

Florida panthers (*Puma concolor coryi*): ~80 individuals left, listed as Federally Endangered in 1967

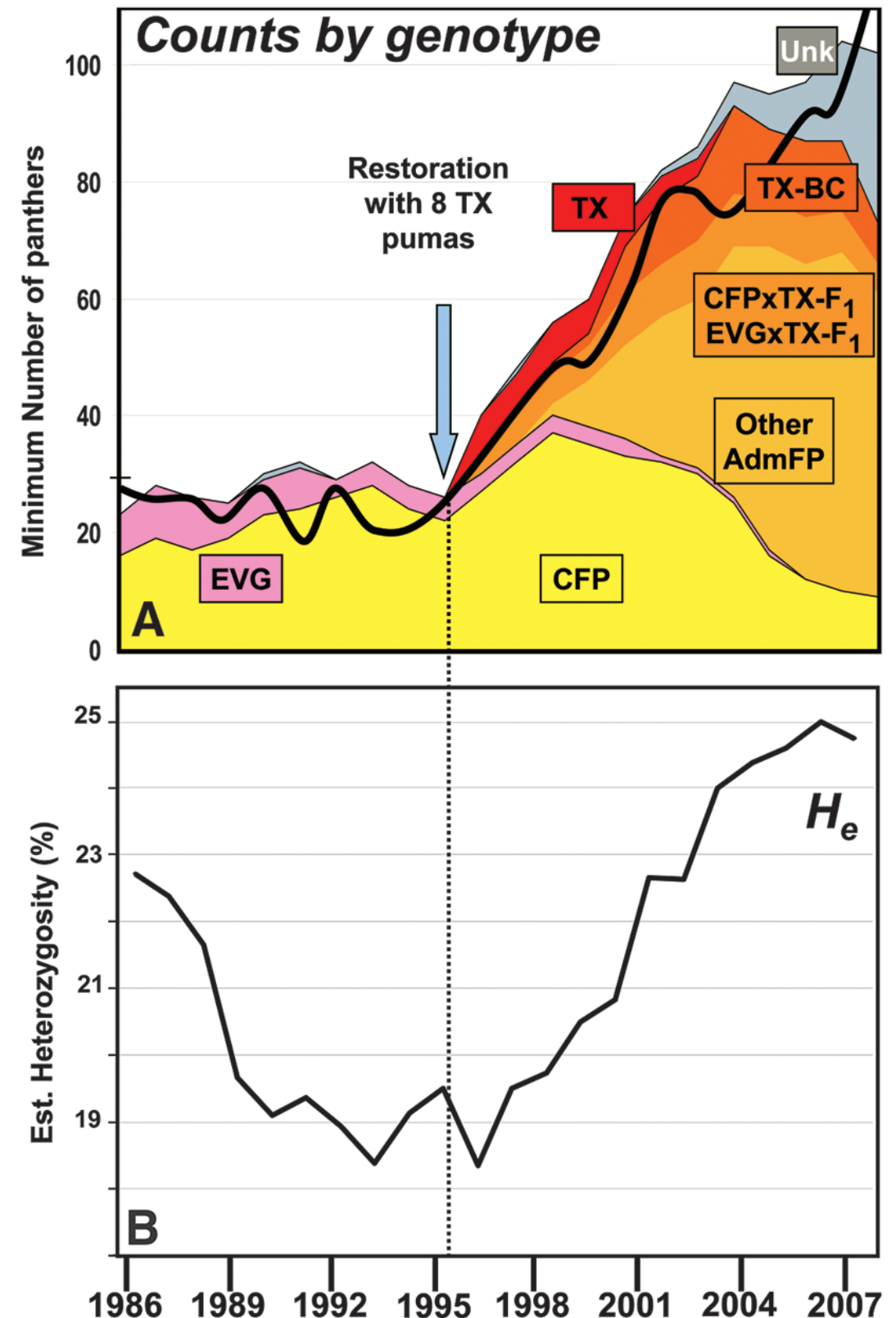
Many individuals with morphological/physiological defects: kinked tail, cowlick, sperm defects, heart defects (evidence of inbreeding depression)



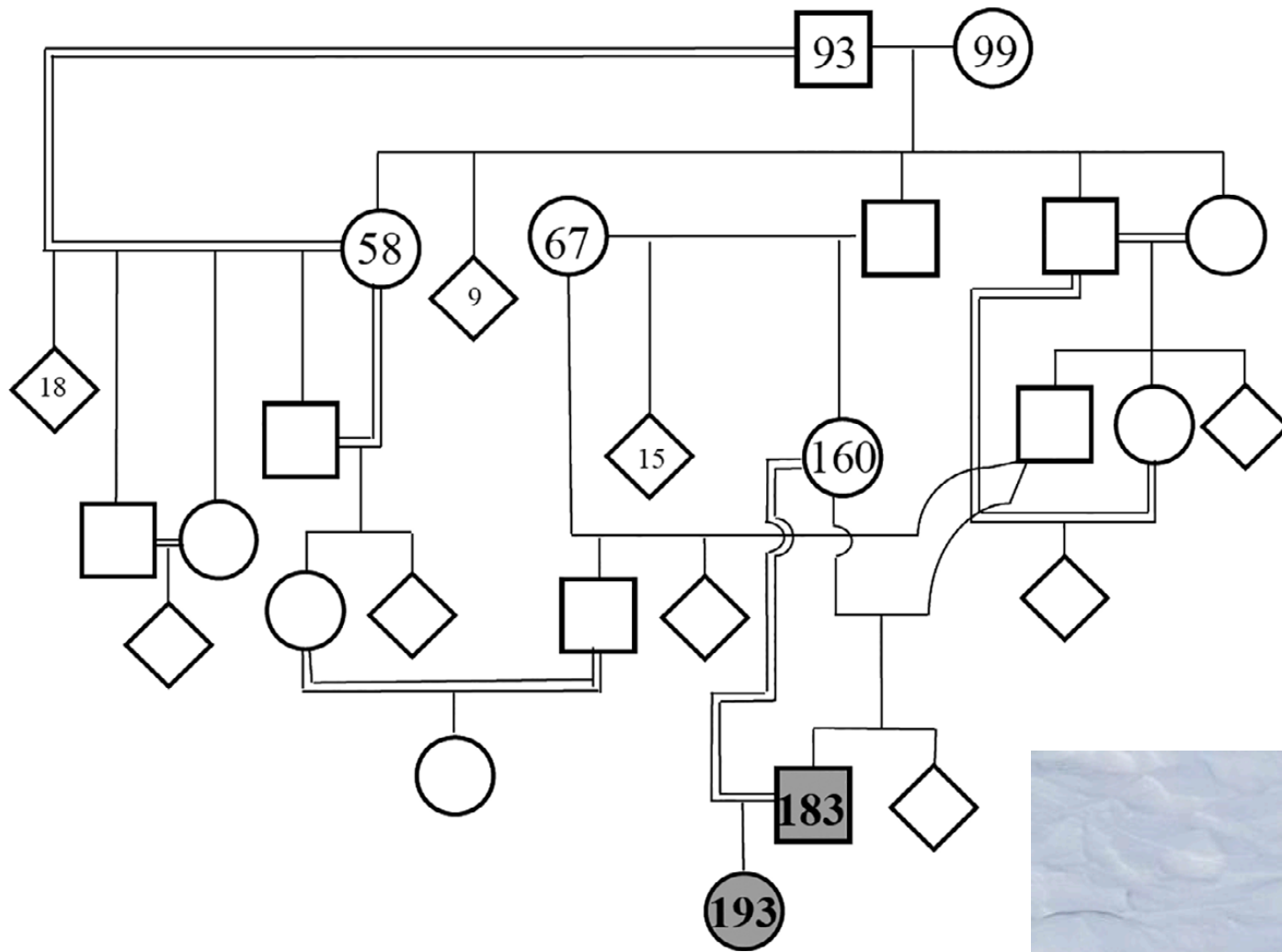
Genetic rescue of the Florida Panther

Introduction of 8 females from Texas in 1995 led to:

- increased abundance
- increased heterozygosity
- higher survival of hybrid individuals
- reduced prevalence of phenotypic characters associated with inbreeding depression



Temporary rescue of Isle Royale wolves



Potential problems with genetic rescue

Outbreeding depression: reduced fitness of hybrids due to maladaptation to local environmental conditions or genetic incompatibilities.

- More of a concern if populations are very divergent (greater chance of local adaptation)

Potential problems with genetic rescue

Outbreeding depression: reduced fitness of hybrids due to maladaptation to local environmental conditions or genetic incompatibilities.

- More of a concern if populations are very divergent (greater chance of local adaptation)

Genetic swamping: Loss of evolutionary lineages / locally adapted alleles due to gene flow.

- Gene flow increases genetic similarity of populations (genetic homogenization), which can reduce species-level genetic diversity

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Conservation genetics & genomics

