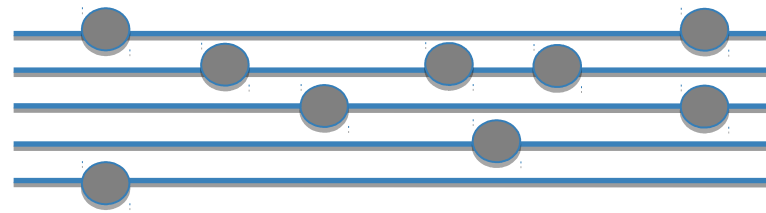


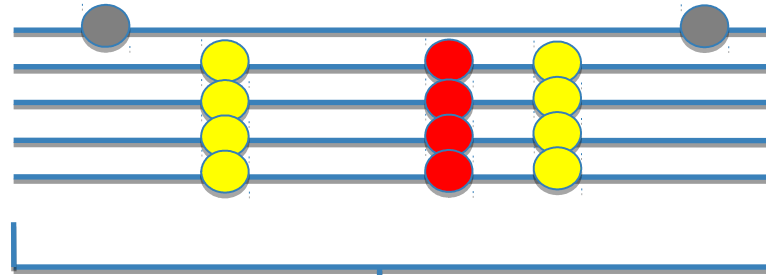
Supplementary material

Positive selection



$t < T_{sel}$

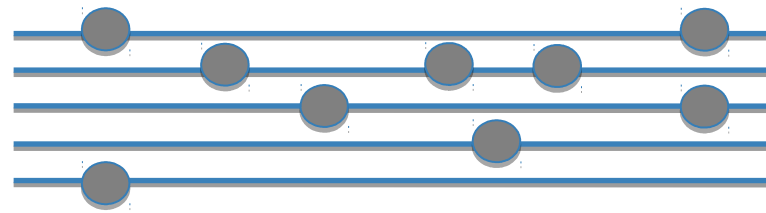
...



$t \gg T_{sel}$

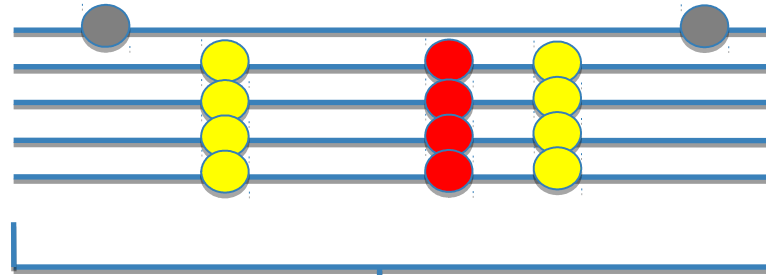
?

Positive selection



$t < T_{sel}$

...



$t \gg T_{sel}$

?

Extended Haplotype Homozygosity



$t \gg T_{\text{sel}}$

...



$t \gg \gg T_{\text{sel}}$

...

Extended Haplotype Homozygosity



$t \gg T_{\text{sel}}$

...



$t \gg \gg T_{\text{sel}}$

...

Extended Haplotype Homozygosity



$t \gg T_{\text{sel}}$

...



$t \gg \gg T_{\text{sel}}$

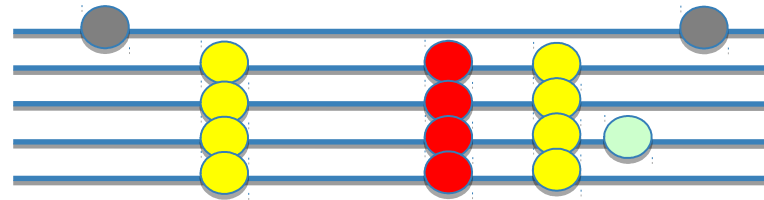
...

Extended Haplotype Homozygosity



$t \gg T_{\text{sel}}$

...



$t \gg \gg T_{\text{sel}}$

...

Extended Haplotype Homozygosity



$t \gg T_{\text{sel}}$

...



$t \gg \gg T_{\text{sel}}$

...

Extended Haplotype Homozygosity



$t \gg T_{\text{sel}}$

...



$t \gg \gg T_{\text{sel}}$

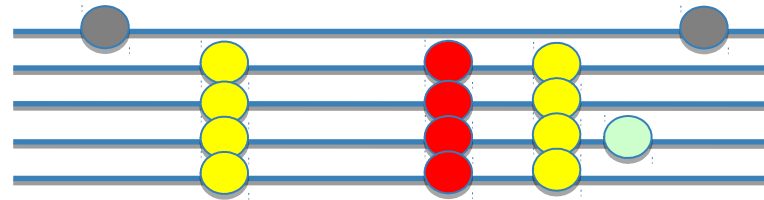
...

Extended Haplotype Homozygosity



$t \gg T_{\text{sel}}$

...



$t \gg \gg T_{\text{sel}}$

...

Extended Haplotype Homozygosity



$t \gg T_{\text{sel}}$

...



$t \gg \gg T_{\text{sel}}$

...

Extended Haplotype Homozygosity



$t \gg T_{\text{sel}}$

...



$t \gg \gg T_{\text{sel}}$

...

Extended Haplotype Homozygosity



$t \gg T_{\text{sel}}$

...



$t \gg \gg T_{\text{sel}}$

...

Extended Haplotype Homozygosity



$t \gg T_{\text{sel}}$

...



$t \gg \gg T_{\text{sel}}$

...

Extended Haplotype Homozygosity



$t \gg T_{\text{sel}}$

...



$t \gg \gg T_{\text{sel}}$

...

Extended Haplotype Homozygosity



$t \gg T_{\text{sel}}$

...



$t \gg \gg T_{\text{sel}}$

...

Extended Haplotype Homozygosity



$t \gg T_{\text{sel}}$

...



$t \gg \gg T_{\text{sel}}$

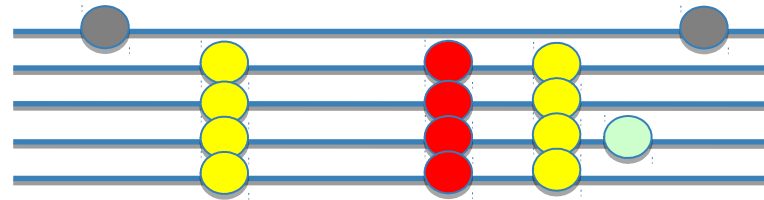
...

Extended Haplotype Homozygosity



$t \gg T_{\text{sel}}$

...



$t \gg \gg T_{\text{sel}}$

...

Extended Haplotype Homozygosity



$t \gg T_{\text{sel}}$

...



$t \gg \gg T_{\text{sel}}$

...

Extended Haplotype Homozygosity



$t \gg T_{\text{sel}}$

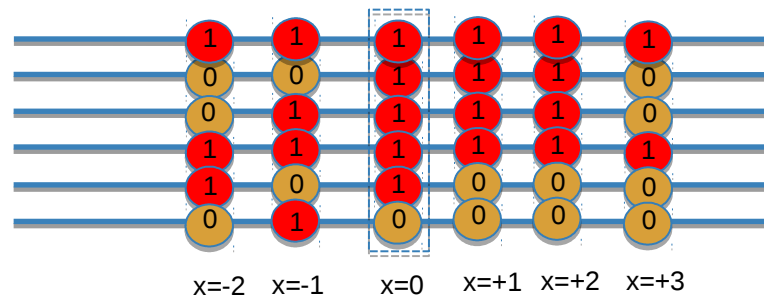
...



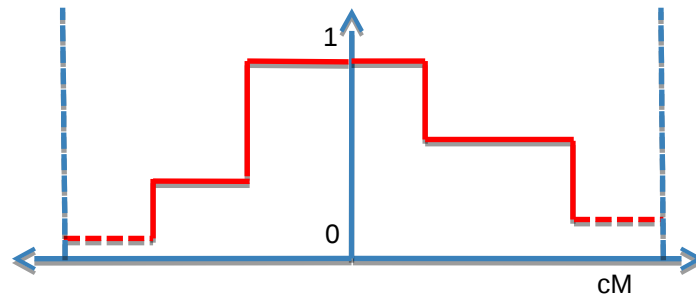
$t \gg \gg T_{\text{sel}}$

...

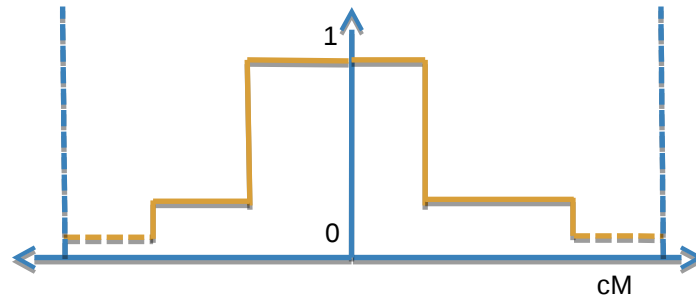
Integrated Haplotype Score



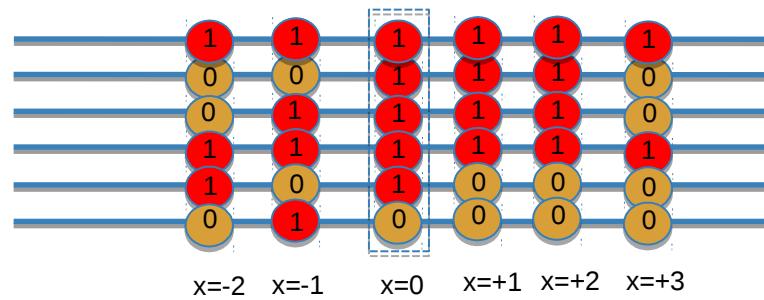
For the derived allele



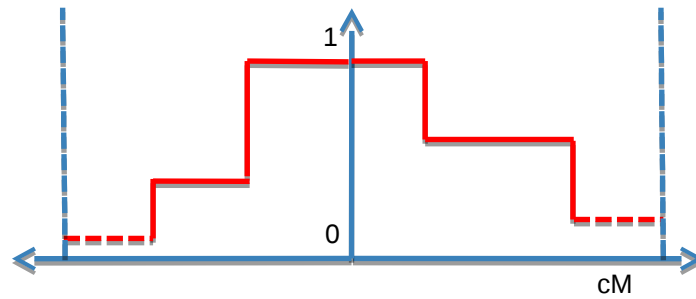
For the ancestral allele



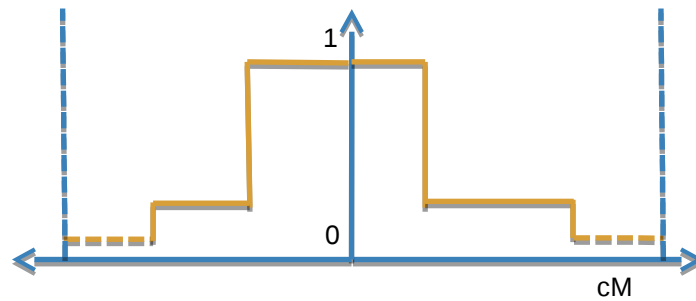
Integrated Haplotype Score



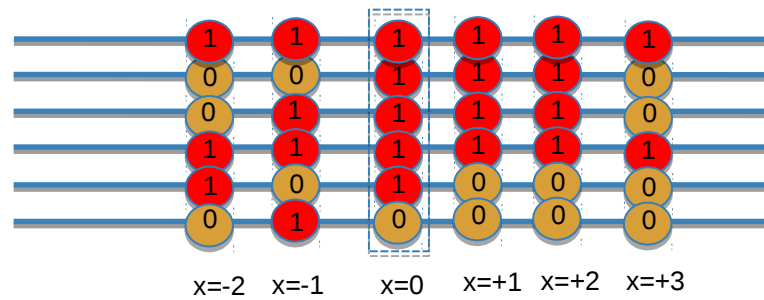
For the derived allele



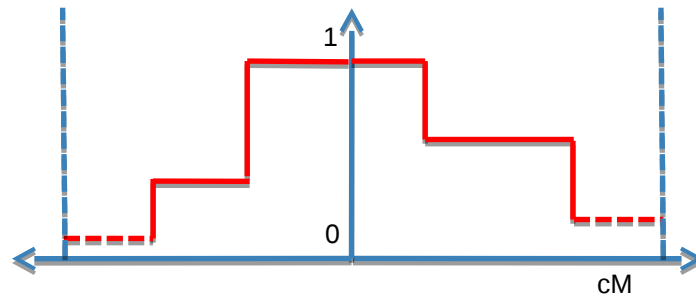
For the ancestral allele



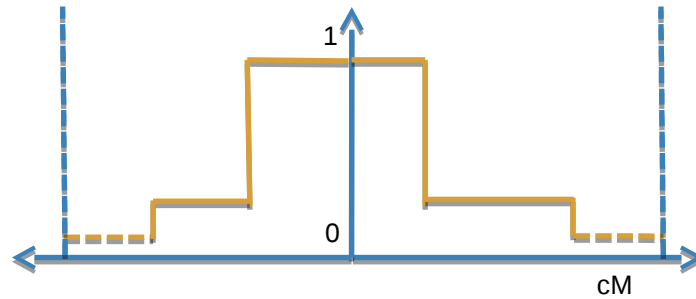
Integrated Haplotype Score



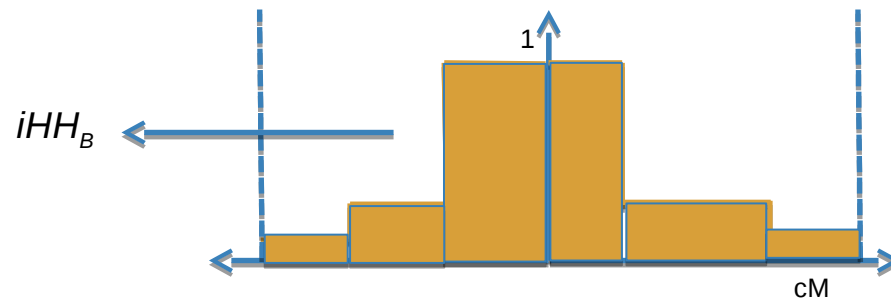
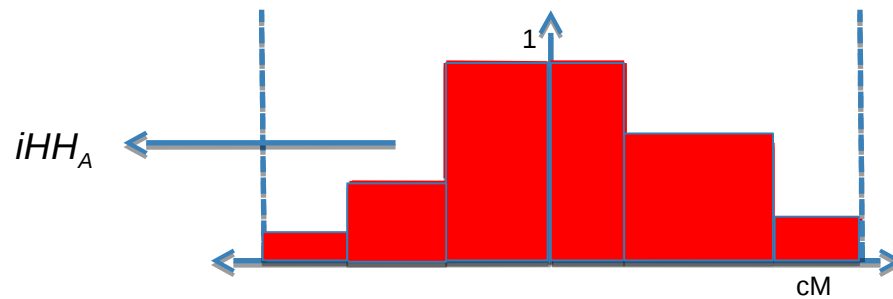
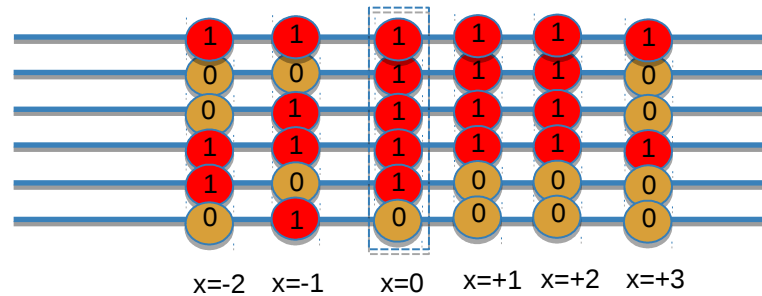
For the derived allele



For the ancestral allele



Cross-population Extended Haplotype Homozygosity



Integrated haplotype score:
 $XP-EHH = \ln(iHH_A/iHH_B)$

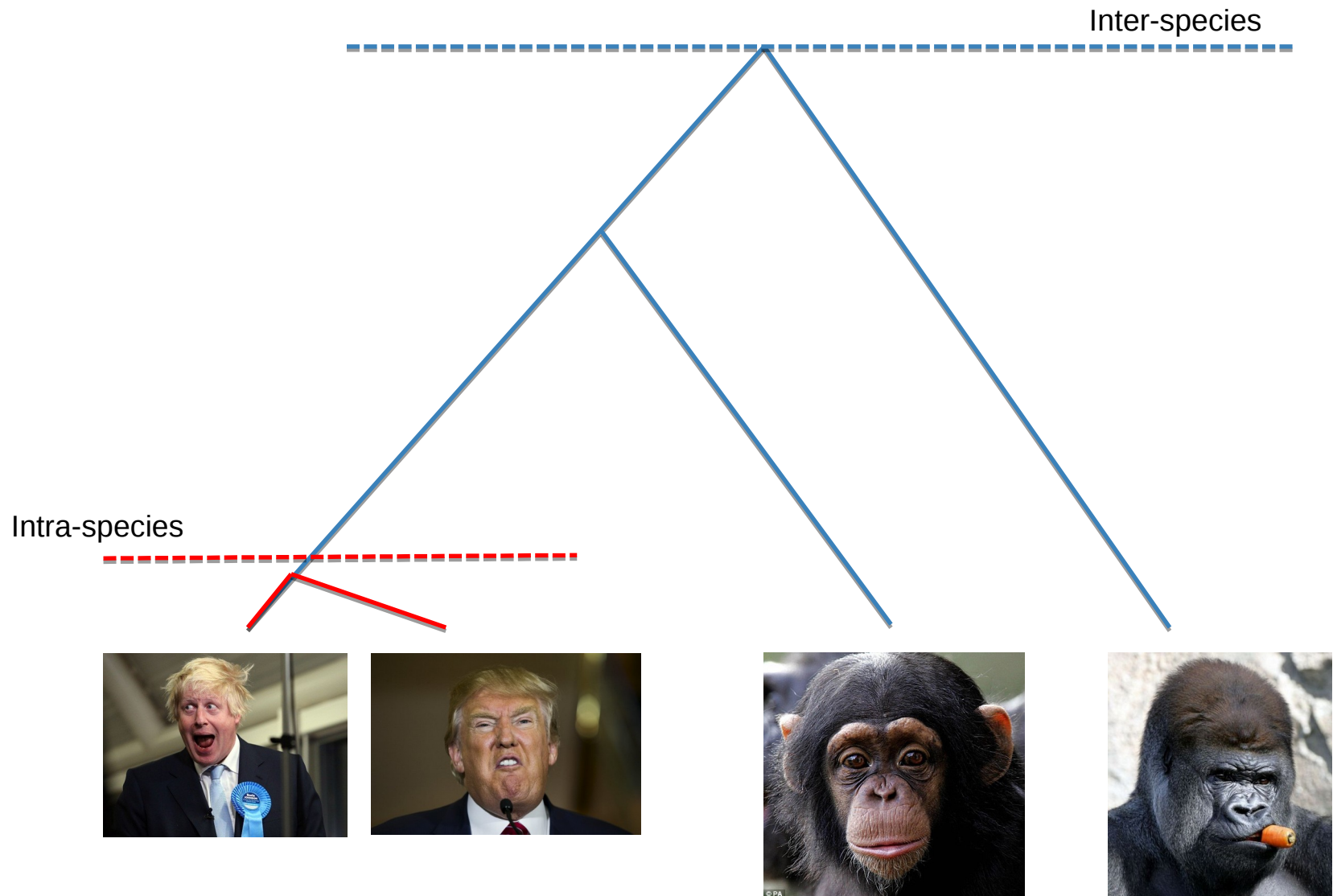


Genome-wide normalization in frequency bins
 (to mean=0 and sd=1)

Outline

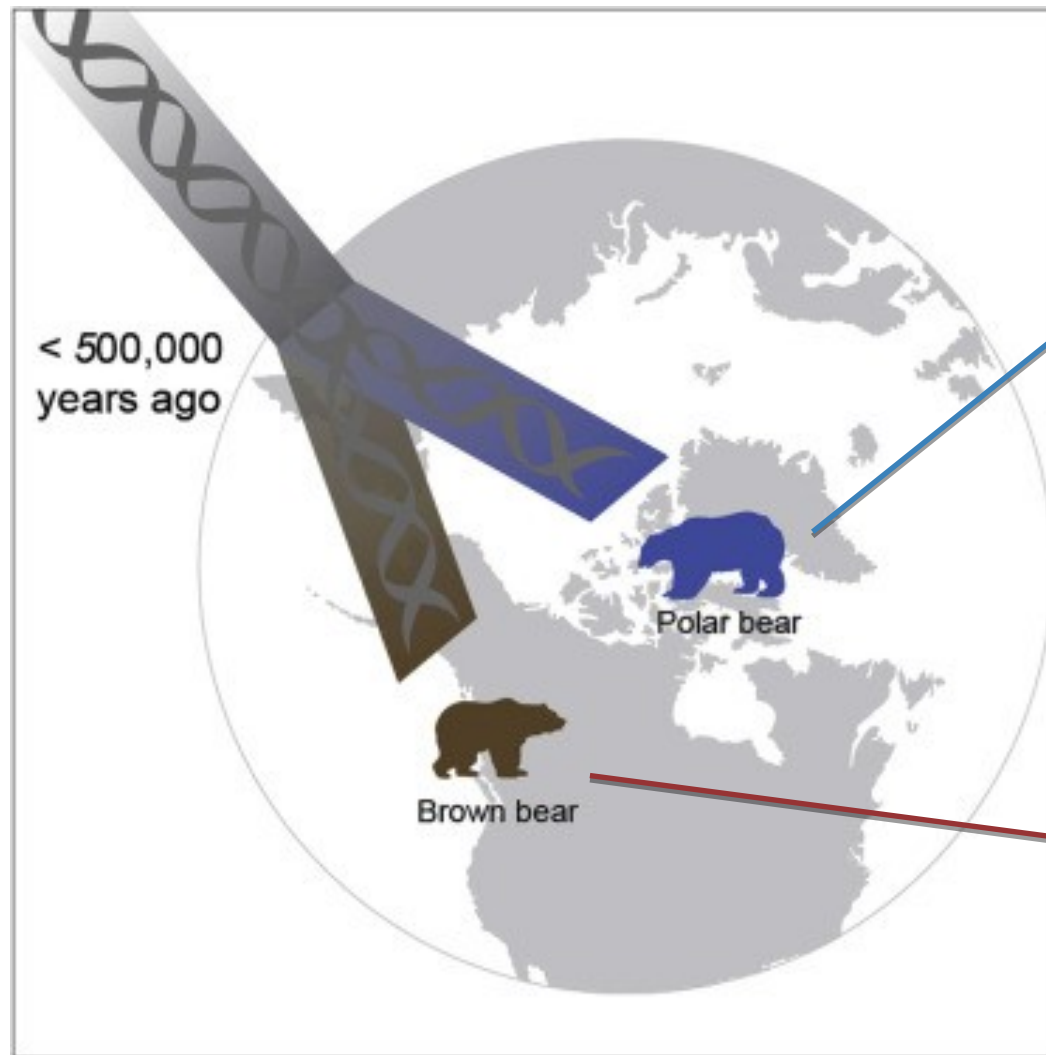
- Brief introduction to natural selection
- Inferring selection at the intra-species level using summary statistics
- PRACTICAL: detecting selection from low-depth NGS data
- The effect of demography on selection scans
- PRACTICAL: quantifying selection using ABC
- (Experimental design)

Inter-species variation



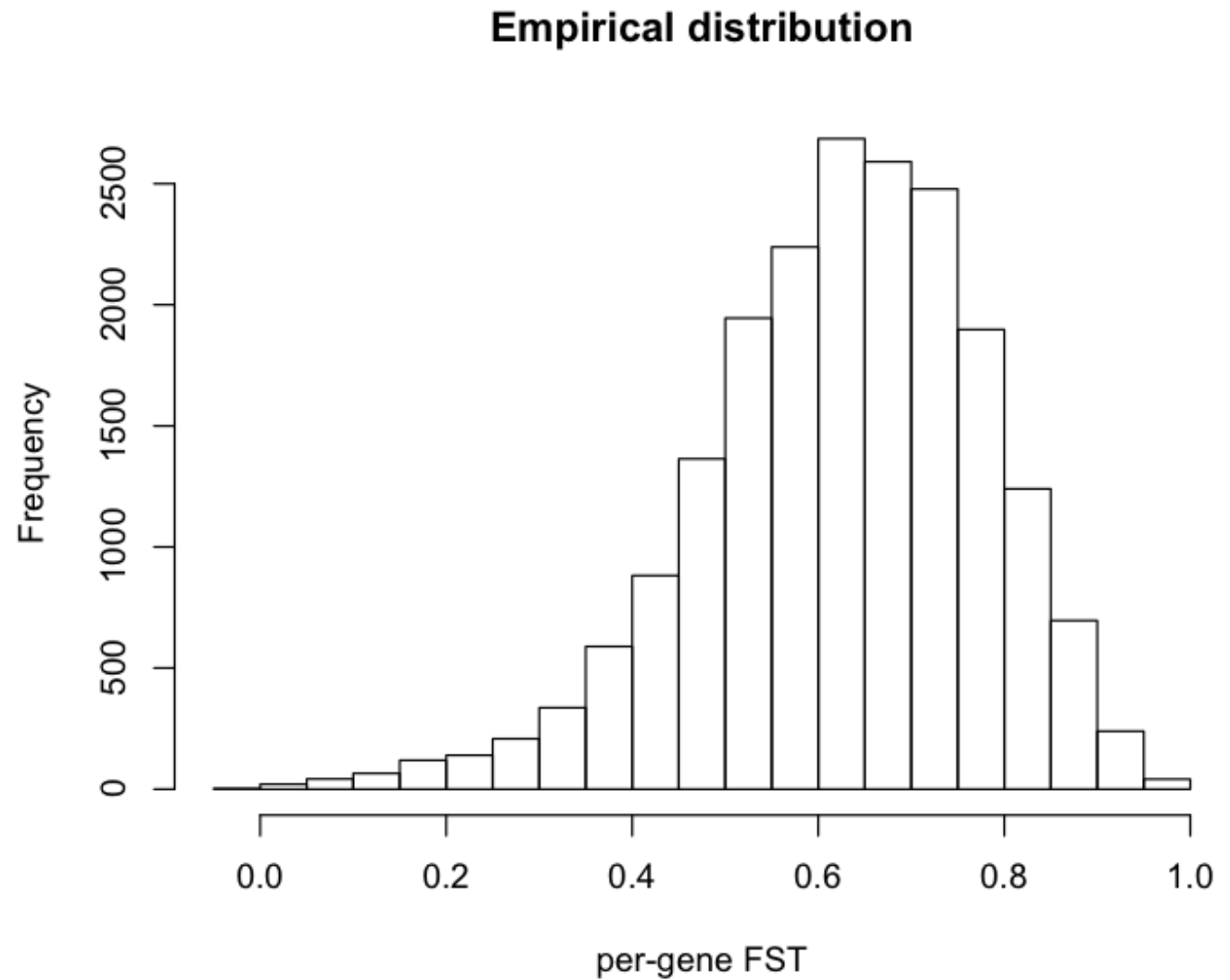
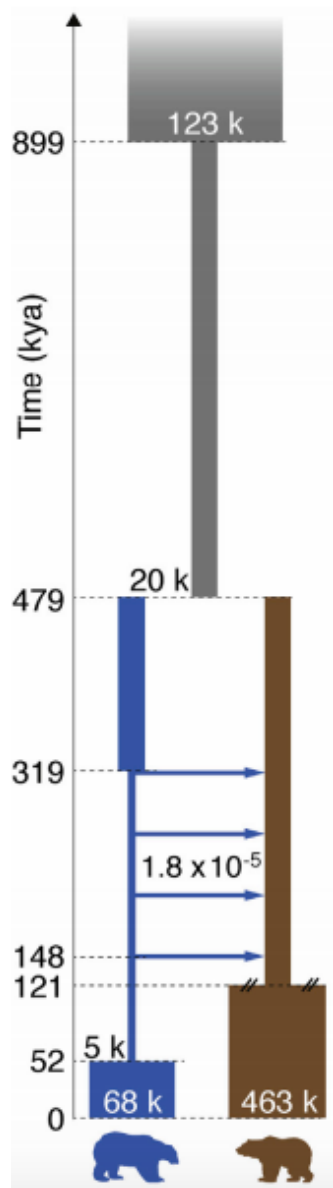
events in the deep past, macro-evolutionary trends, selection between species

Polar bears vs. Brown bears

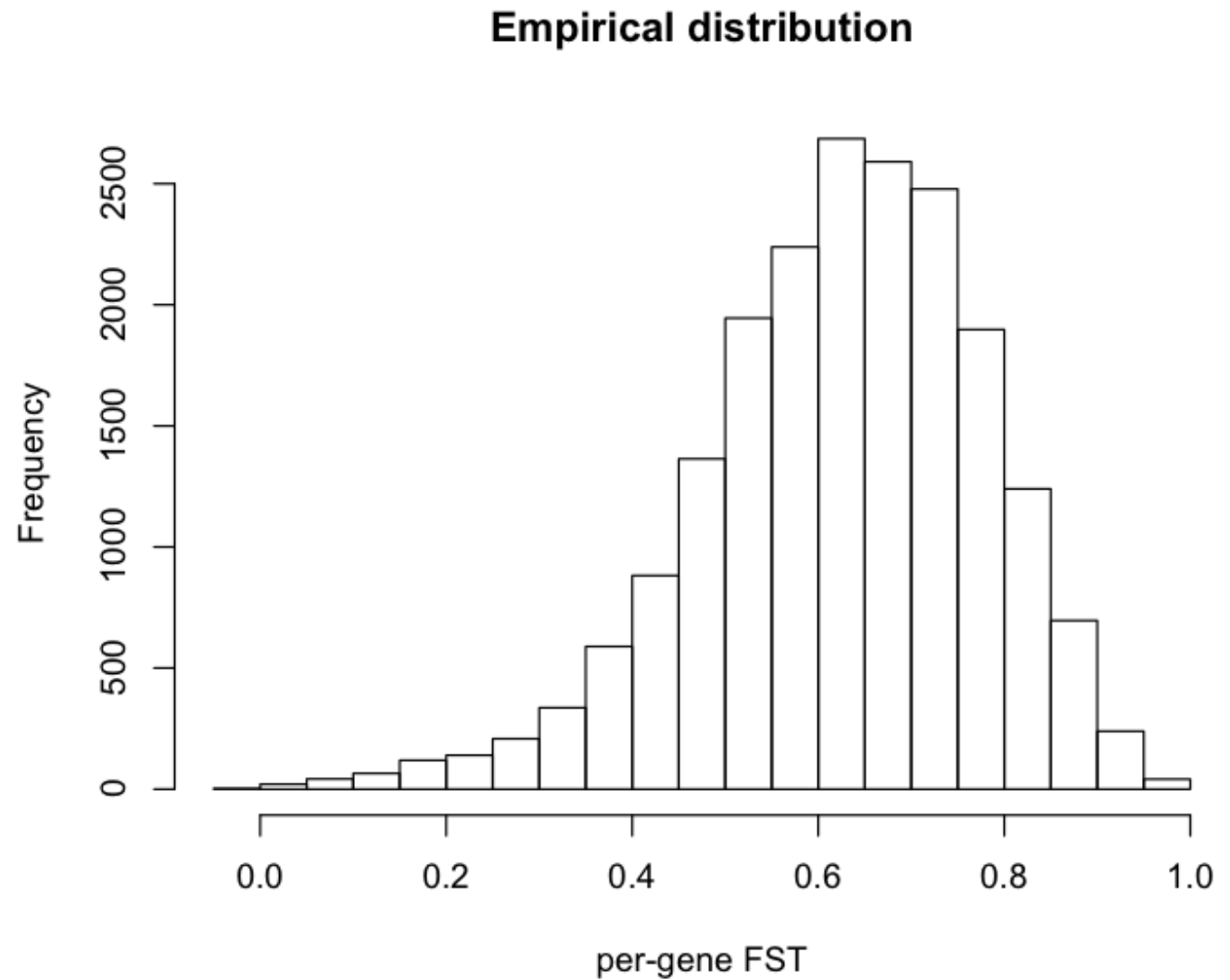
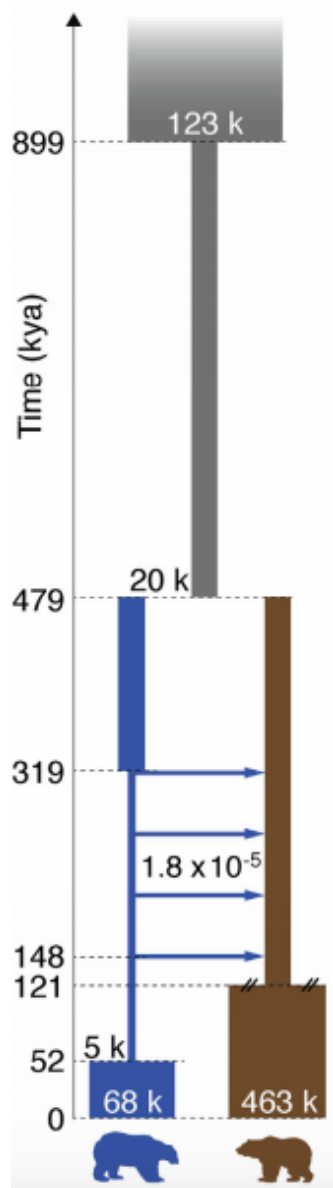


Question: what are the genetic signatures of polar bears' adaptation to the Arctic environment?

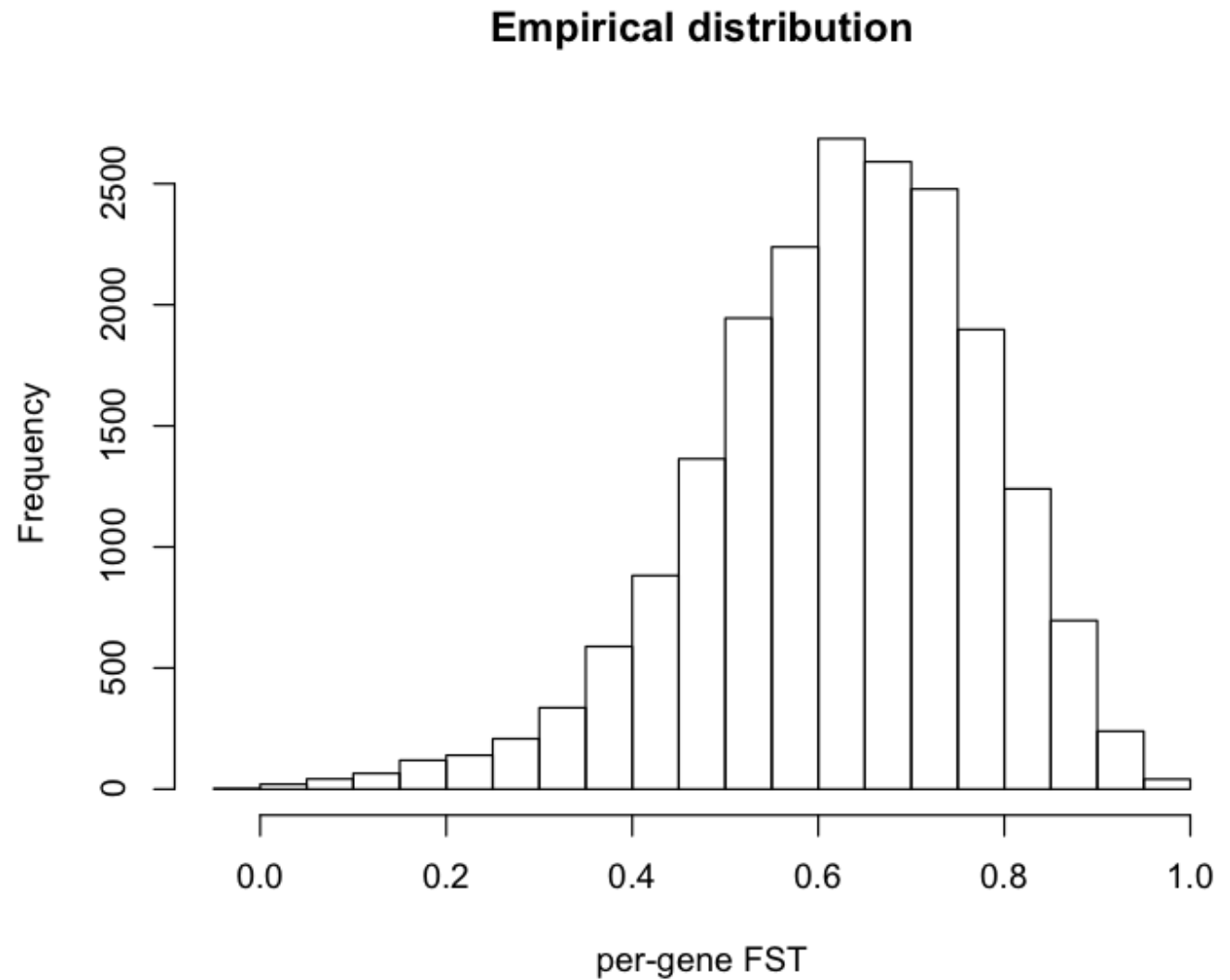
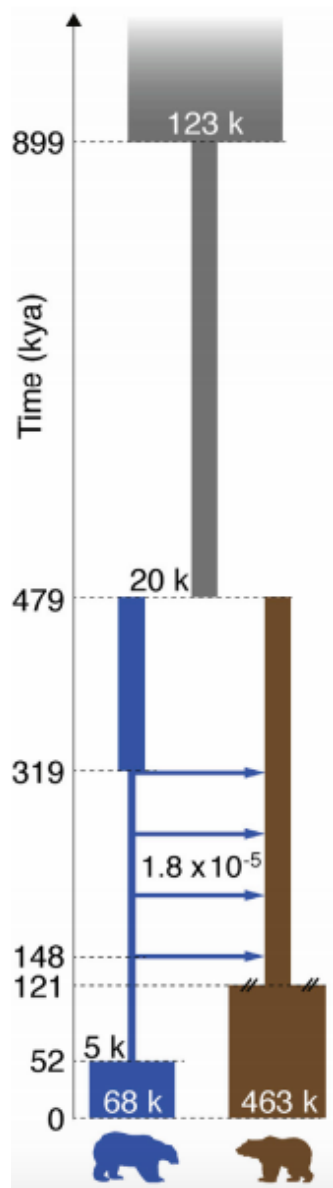
Expected genetic differentiation



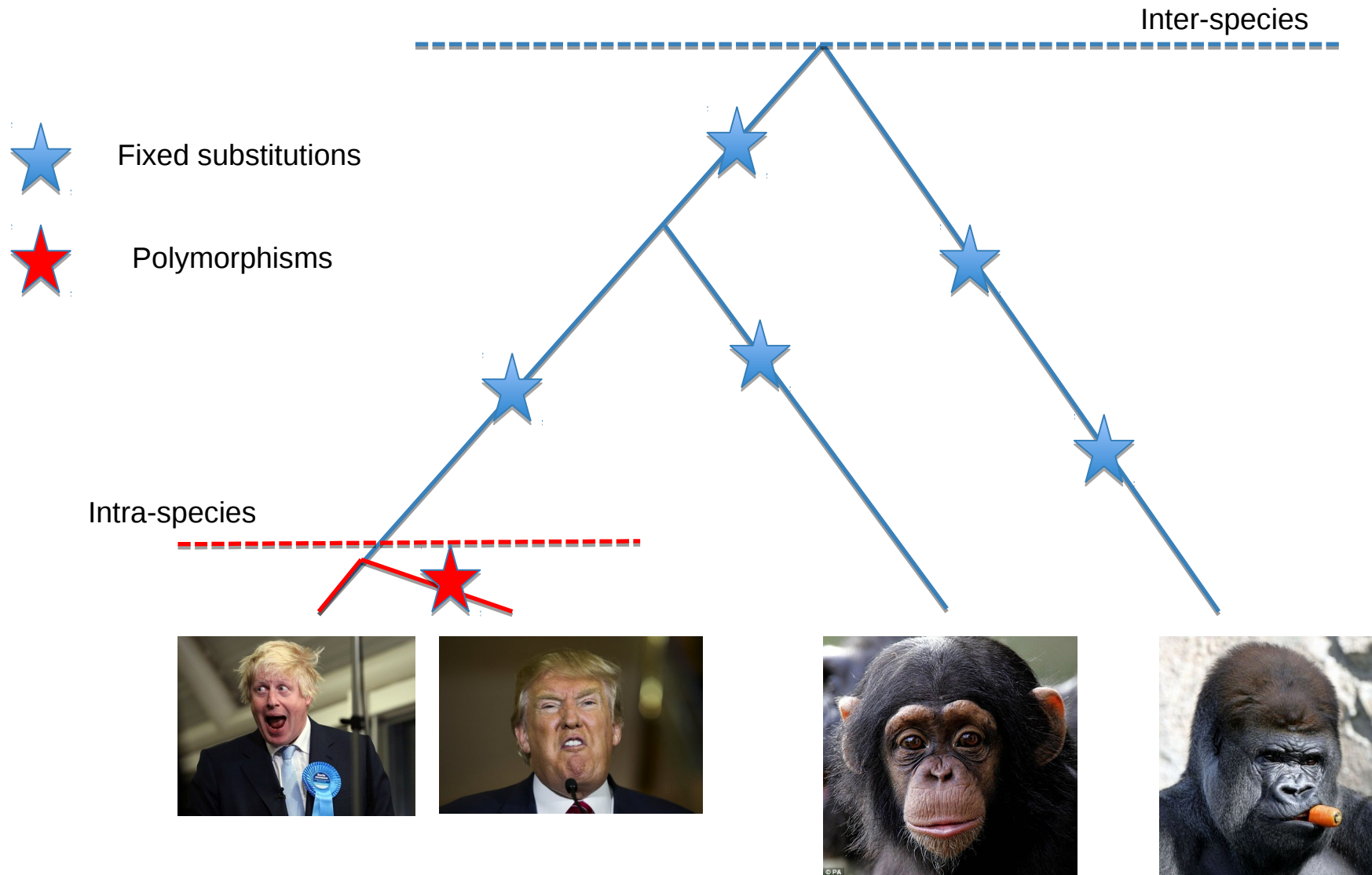
Expected genetic differentiation



Expected genetic differentiation

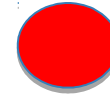


Inferring inter-species selection

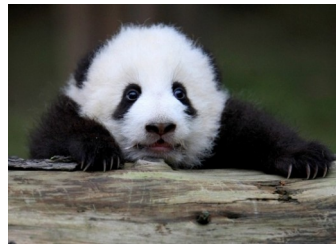
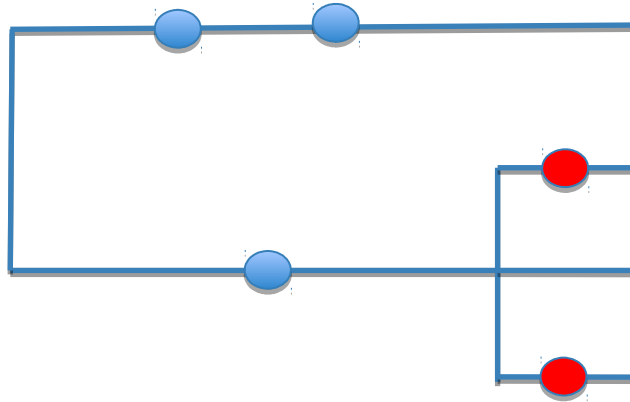


Polymorphisms and divergence

As both depend on mutation rates,
proportional.

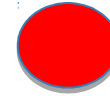


els are expected to be

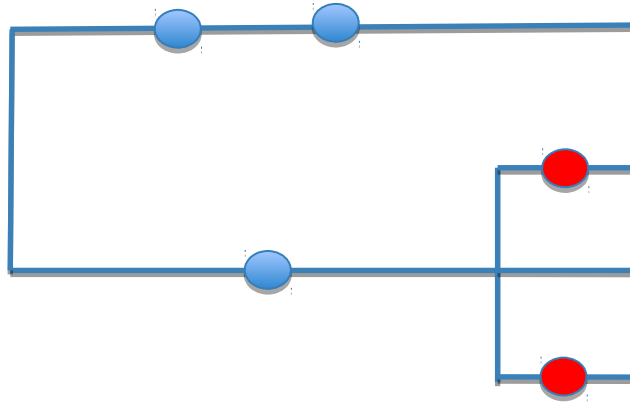


Polymorphisms and divergence

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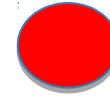


els are expected to be

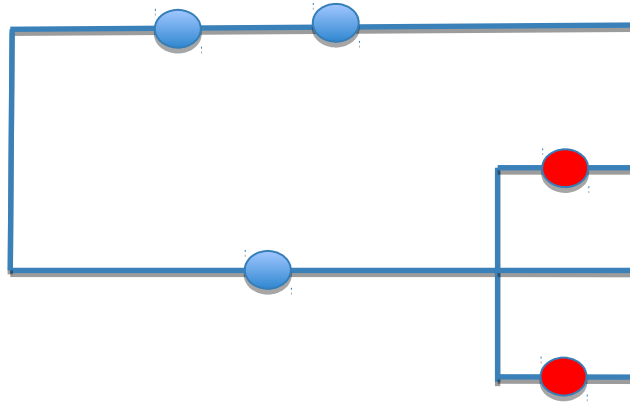


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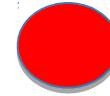


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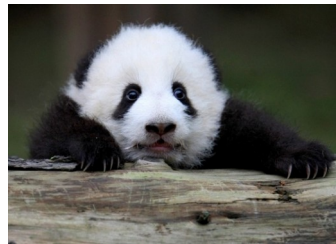
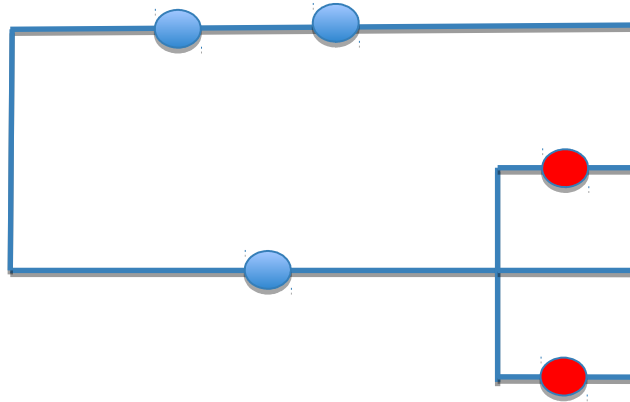


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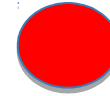


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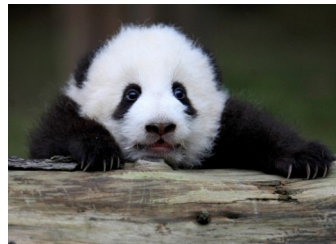
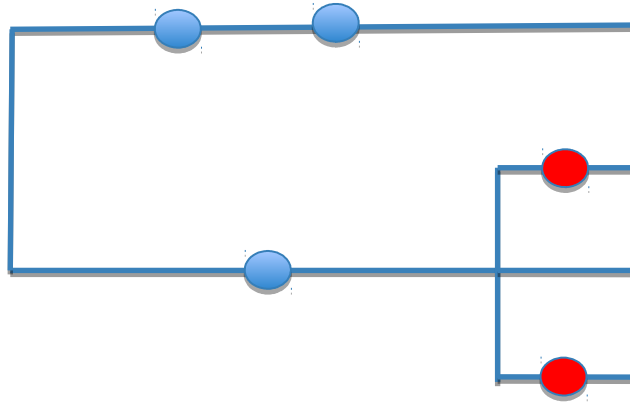


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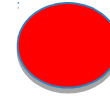


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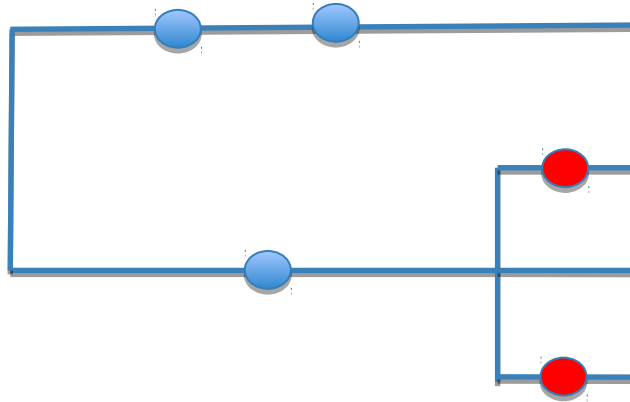


Polymorphisms and divergence

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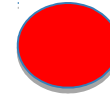


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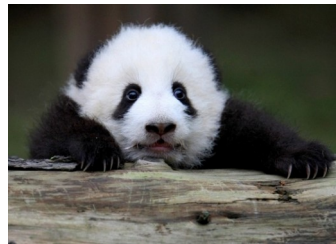
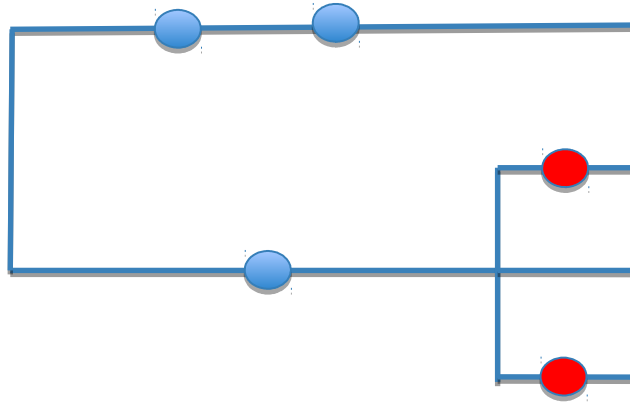


Polymorphisms and divergence

As both depend on mutation rates,
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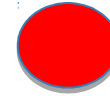


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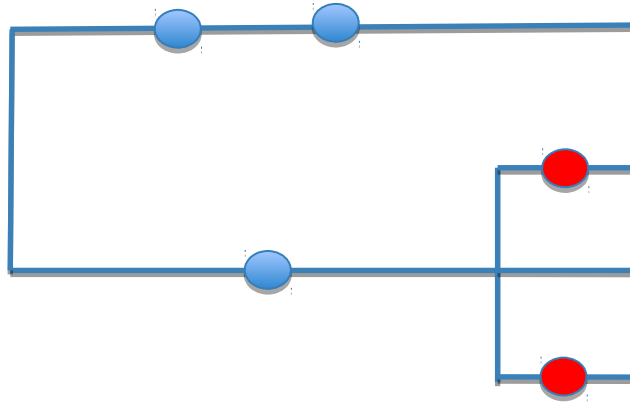


Polymorphisms and divergence

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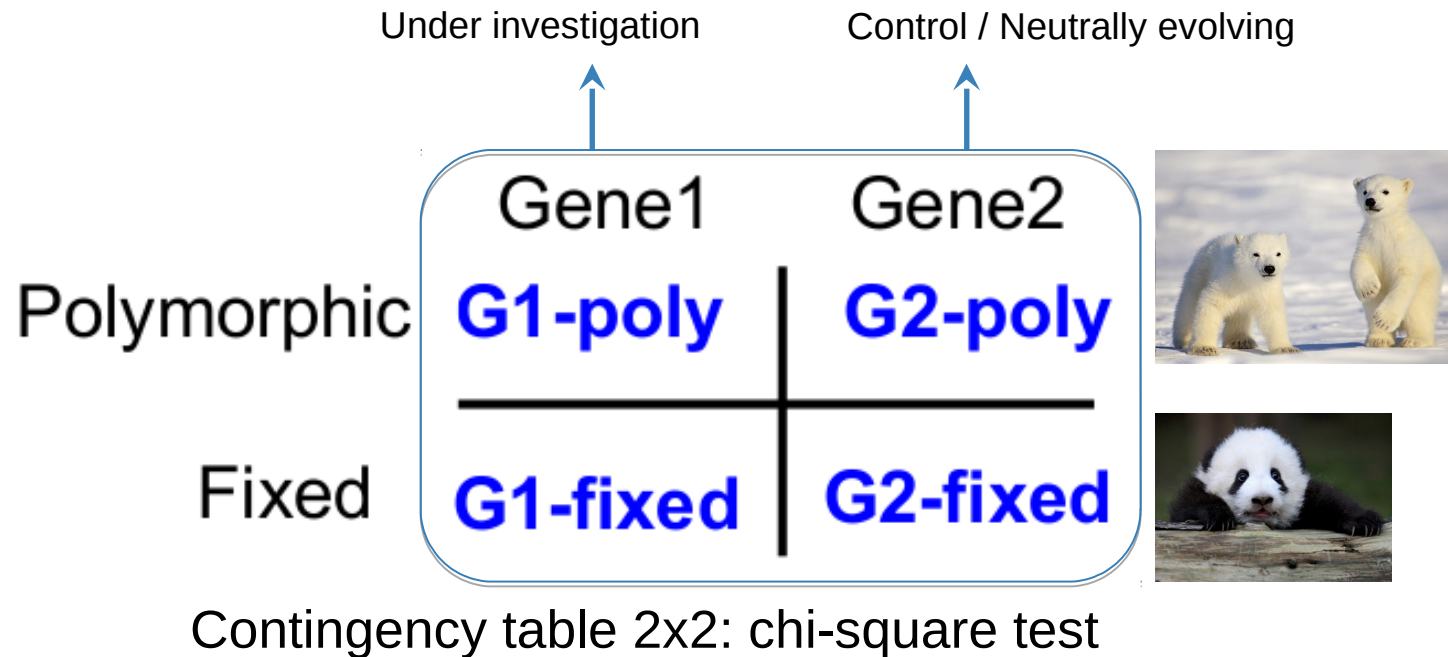


els are expected to be



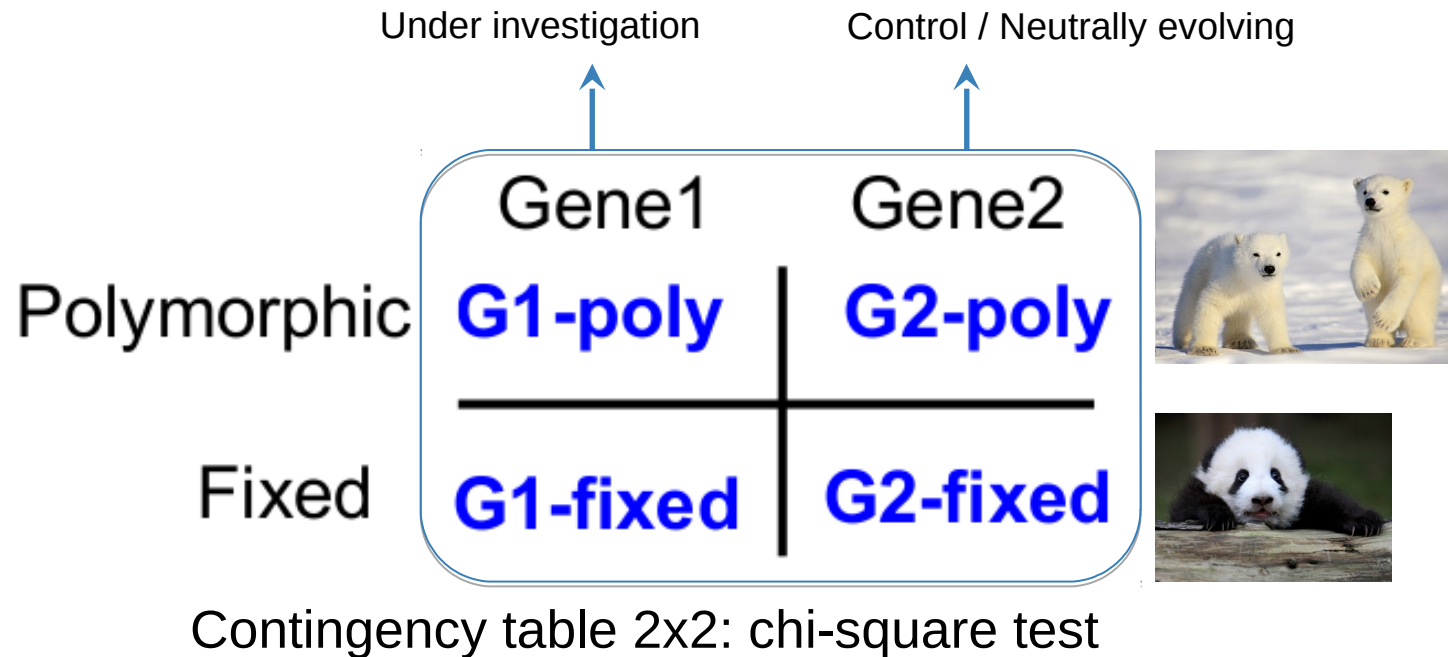
HKA test

Hudson-Kreitman-Aguadè (HKA, Hudson et al. 1987) test



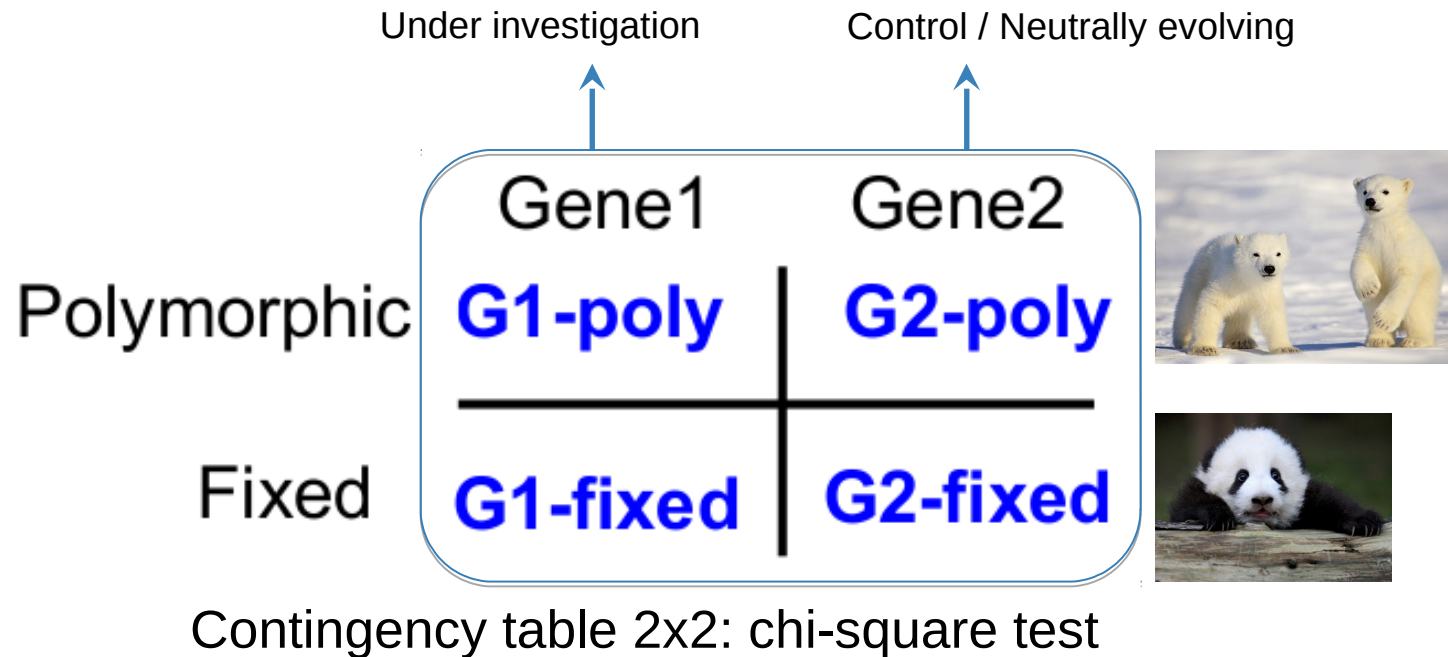
HKA test

Hudson-Kreitman-Aguadè (HKA, Hudson et al. 1987) test



HKA test

Hudson-Kreitman-Aguadè (HKA, Hudson et al. 1987) test



Coding polymorphisms

Substitutions in the coding regions may alter (non-synonymous) or not (synonymous) the protein sequence:

ATC CAA ...
I Q

Ancestral sequence



ATA GAA ...
I K

Species 1



ATG CAG ...
M Q

Species 2



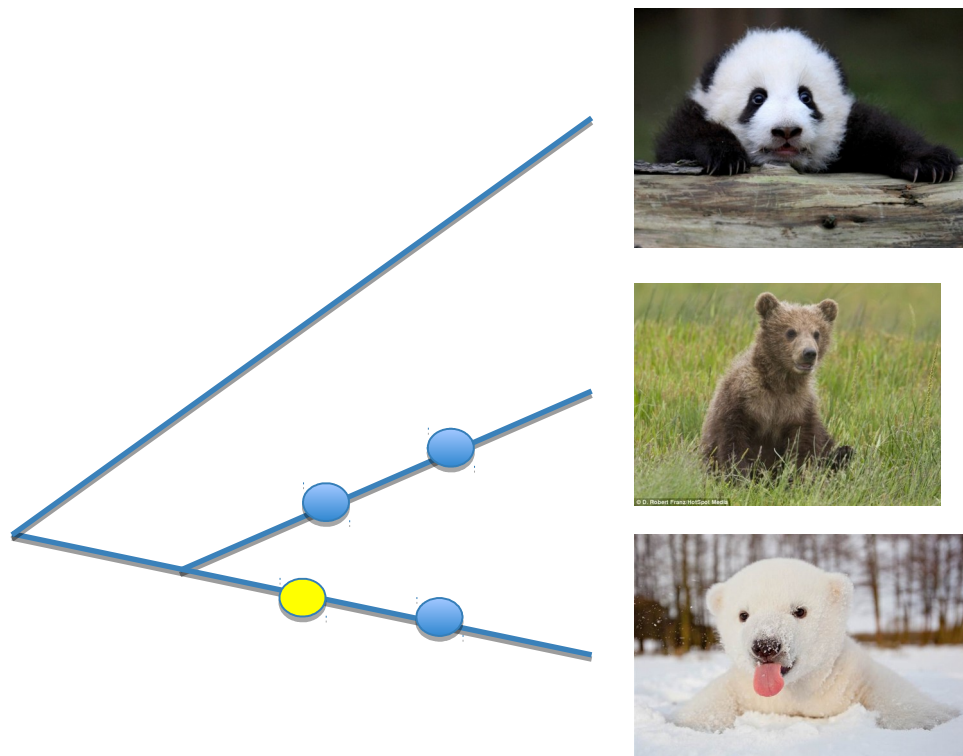
Non-synonymous



Synonymous

dN/ds

Comparison between rate of **nonsynonymous** substitutions and rate of **synonymous** substitutions (also called K_a/K_s or ω)



Non-synonymous



Synonymous

Positive selection

(novel proteins)

$$K_a/K_s > 1$$

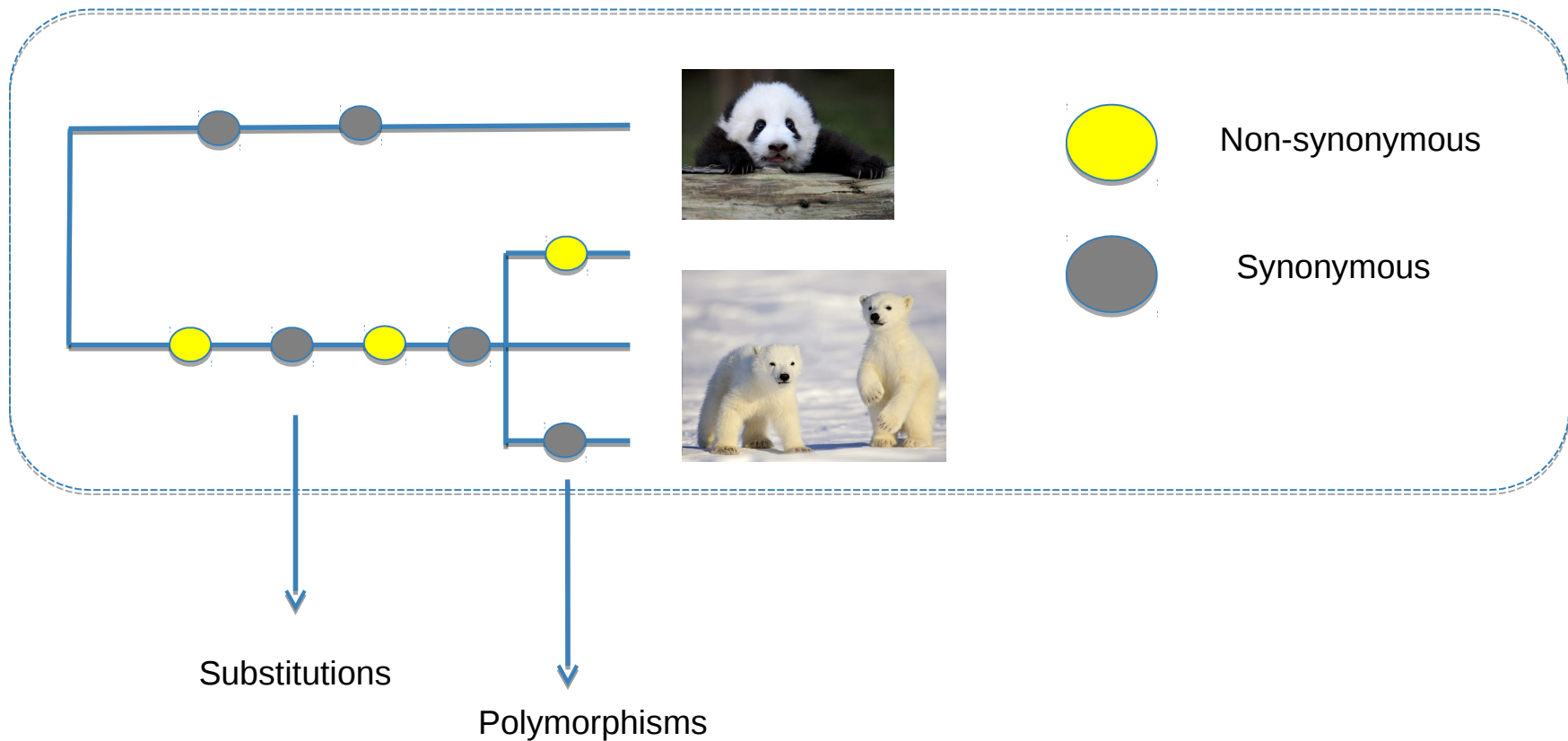
Negative selection

(against deleterious mutations)

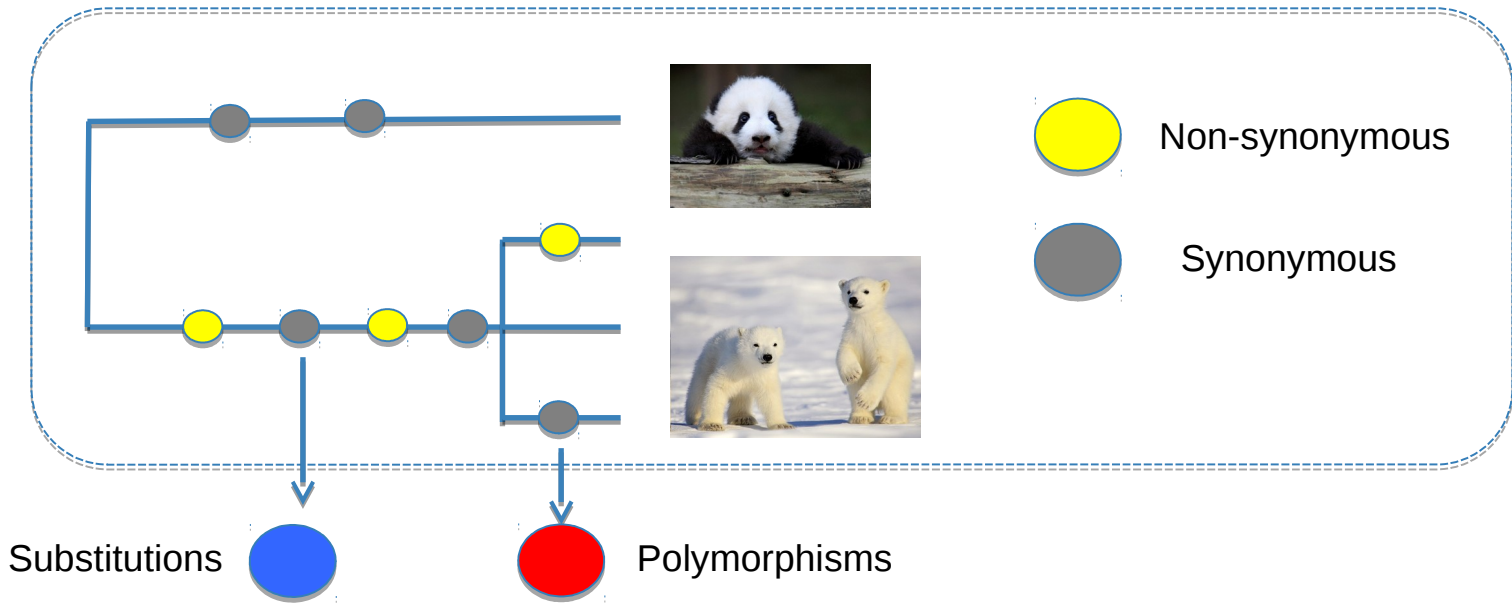
$$K_a/K_s < 1$$

Coding polymorphisms and divergence

Compare the amount of variation within a species to the divergence between species at non-synonymous and synonymous variants.

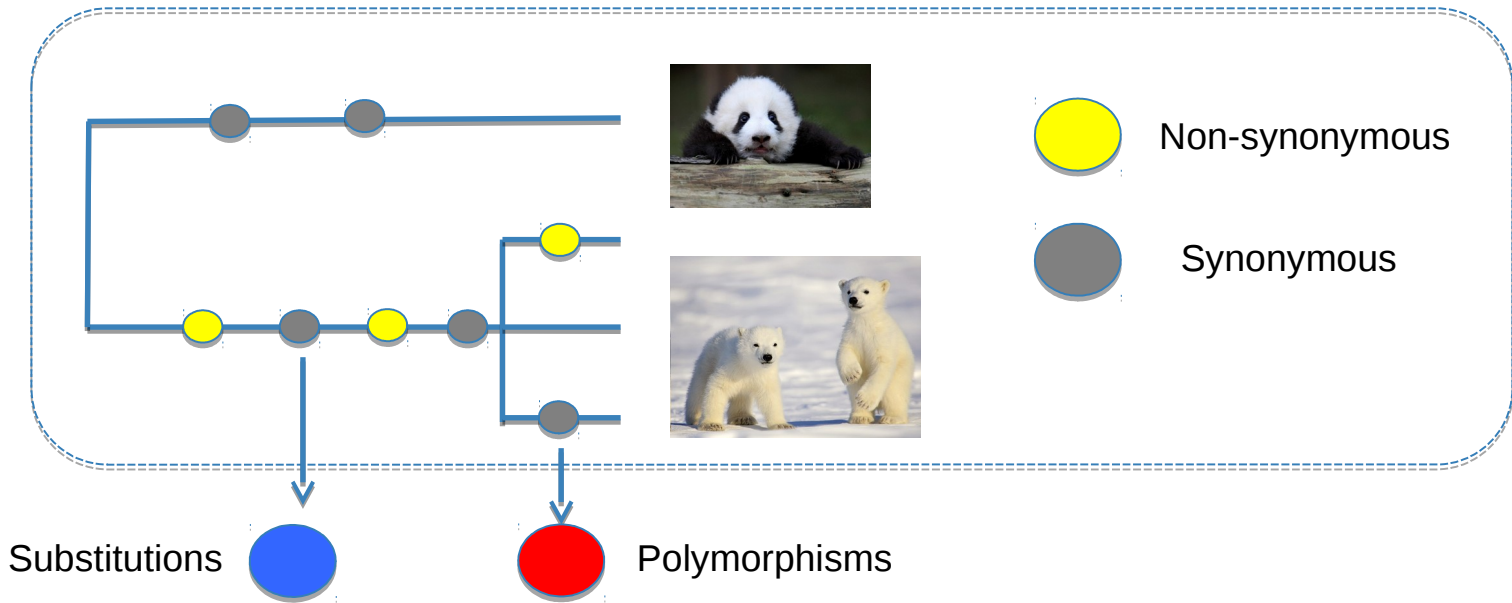


MK (McDonald–Kreitman) test



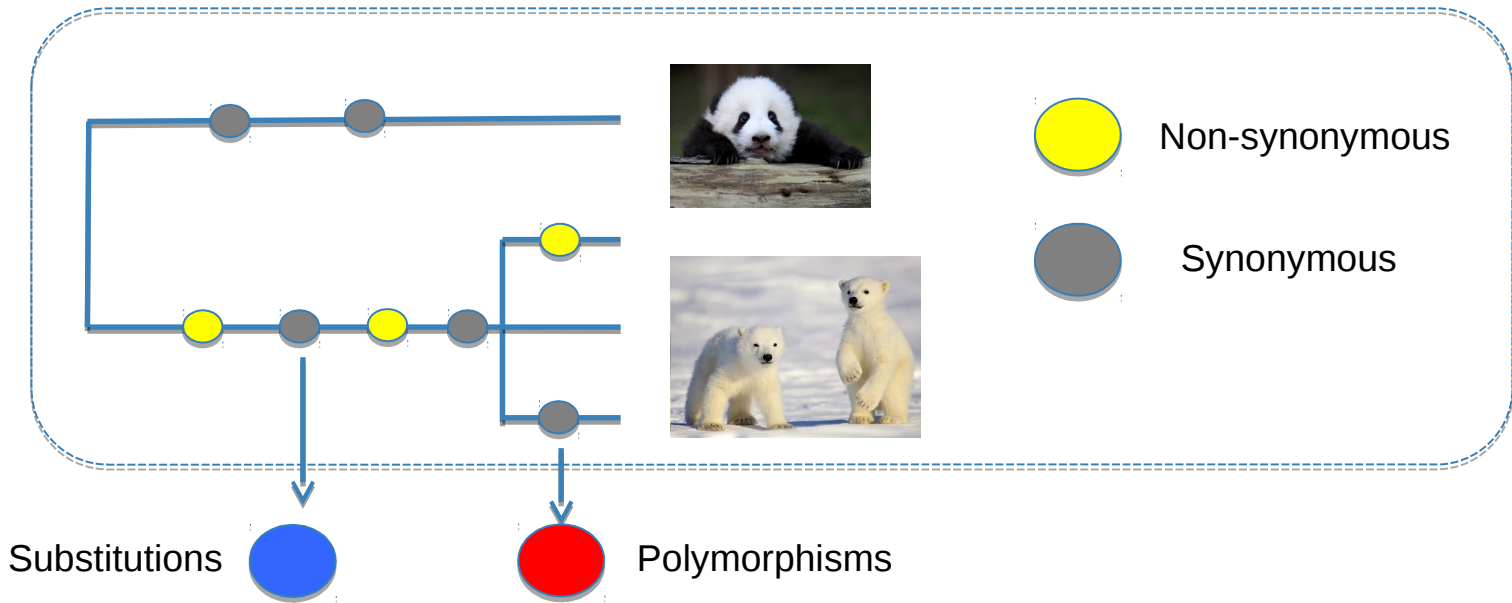
	Non-synonymous	Synonymous
Divergence		
Polymorphisms		

MK (McDonald–Kreitman) test



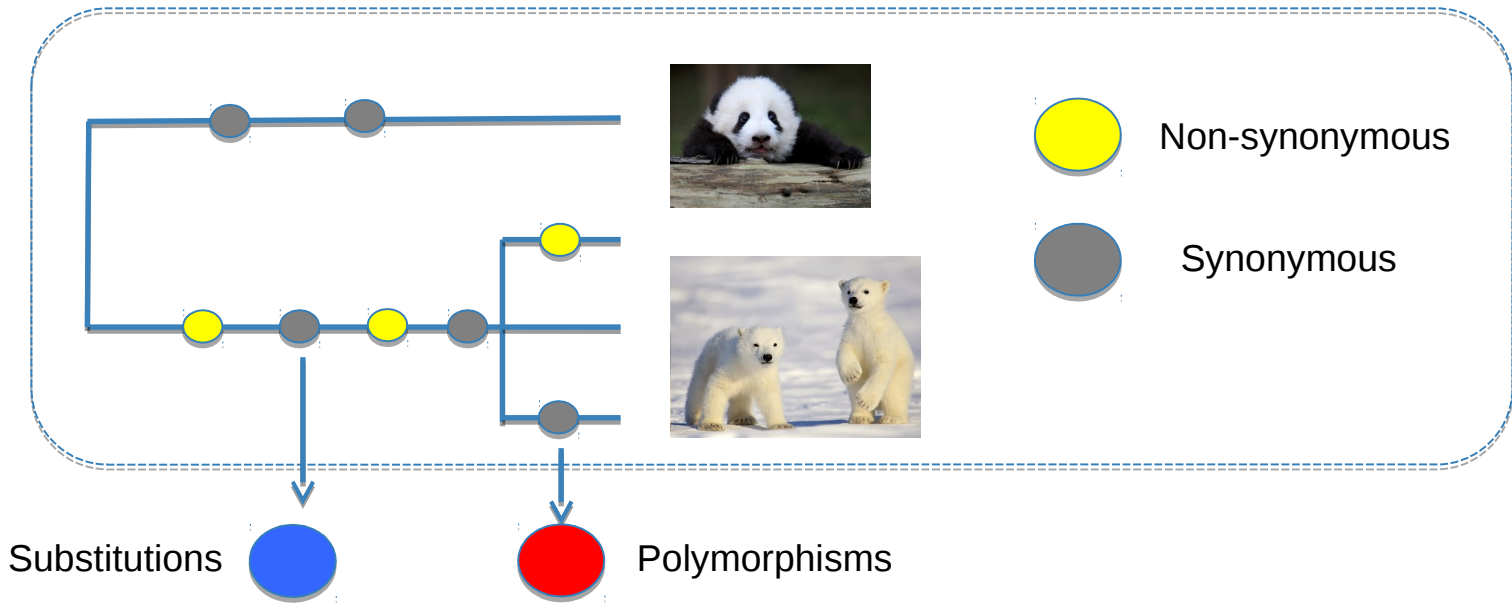
	Non-synonymous	Synonymous
Divergence		
Polymorphisms		

MK (McDonald–Kreitman) test



	Non-synonymous	Synonymous
Divergence		
Polymorphisms		

MK (McDonald–Kreitman) test



	Non-synonymous	Synonymous
Divergence		
Polymorphisms		

Summary

- Methods to detect signatures of selection are grouped based on:
 - time of selection
 - summary statistics used
- Assessing statistical significance through empirical or expected distributions
- Investigating complex models of selection and adaptation