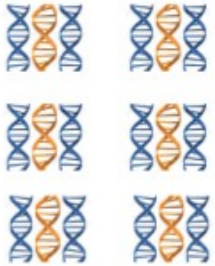
Detecting natural selection from genomic data (part 2)

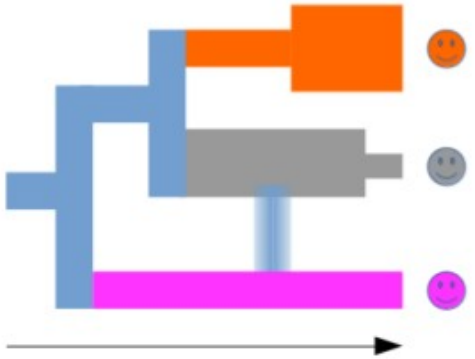
Matteo Fumagalli

Motivation

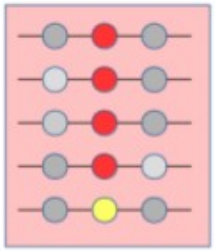
Whole genome sequencing



Demographic history



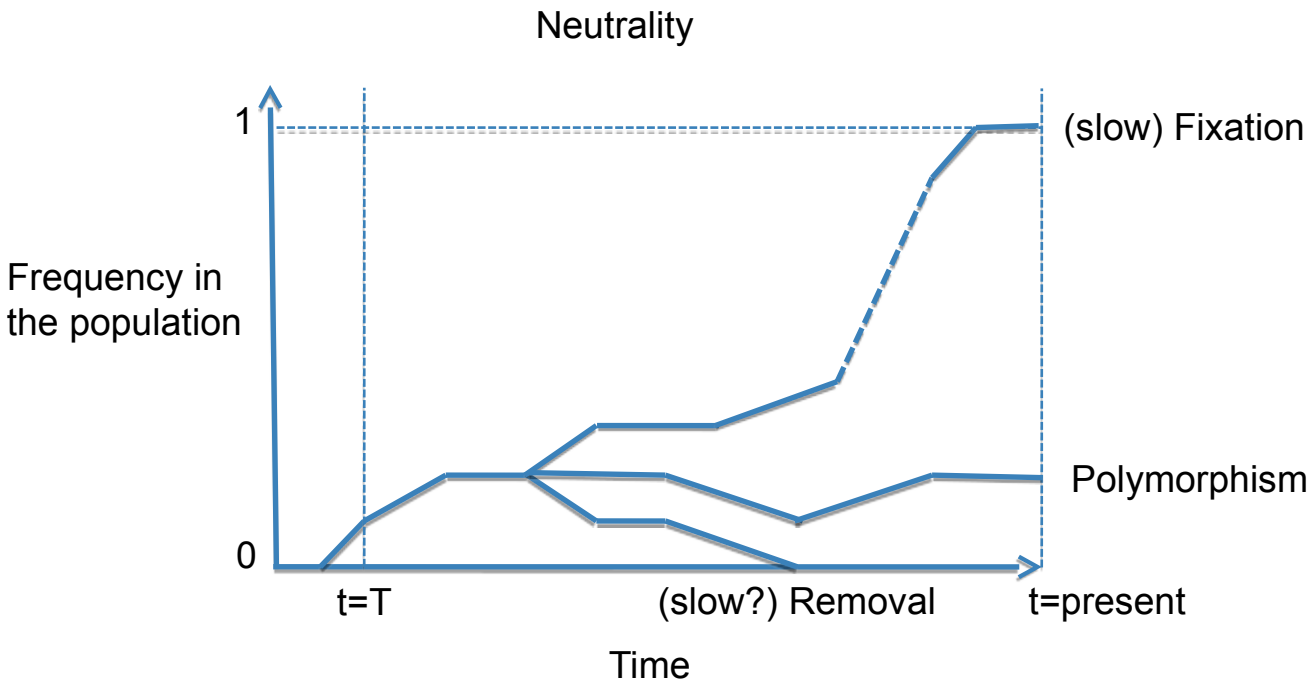
Natural selection



Natural selection

Heritable traits that increase the fitness of the become more common.

1) Mutations arise randomly and evolve according to their effect on the fitness of the carrier



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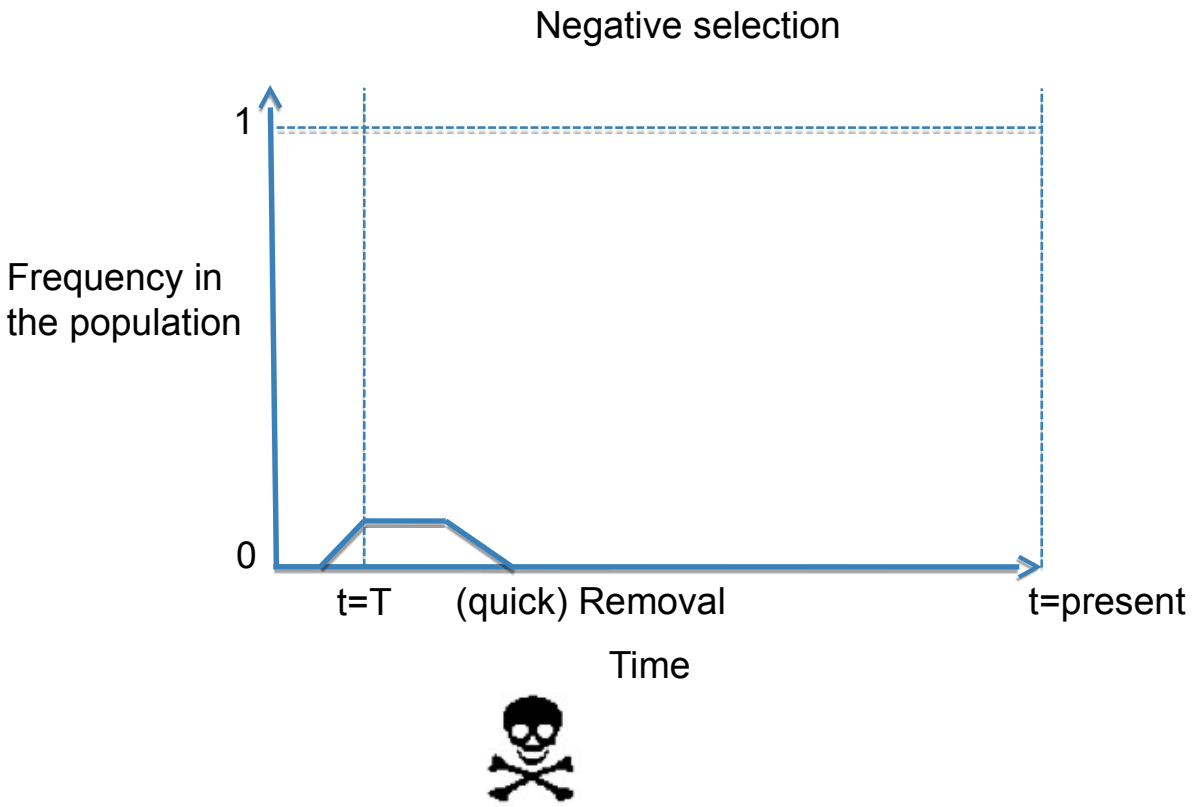

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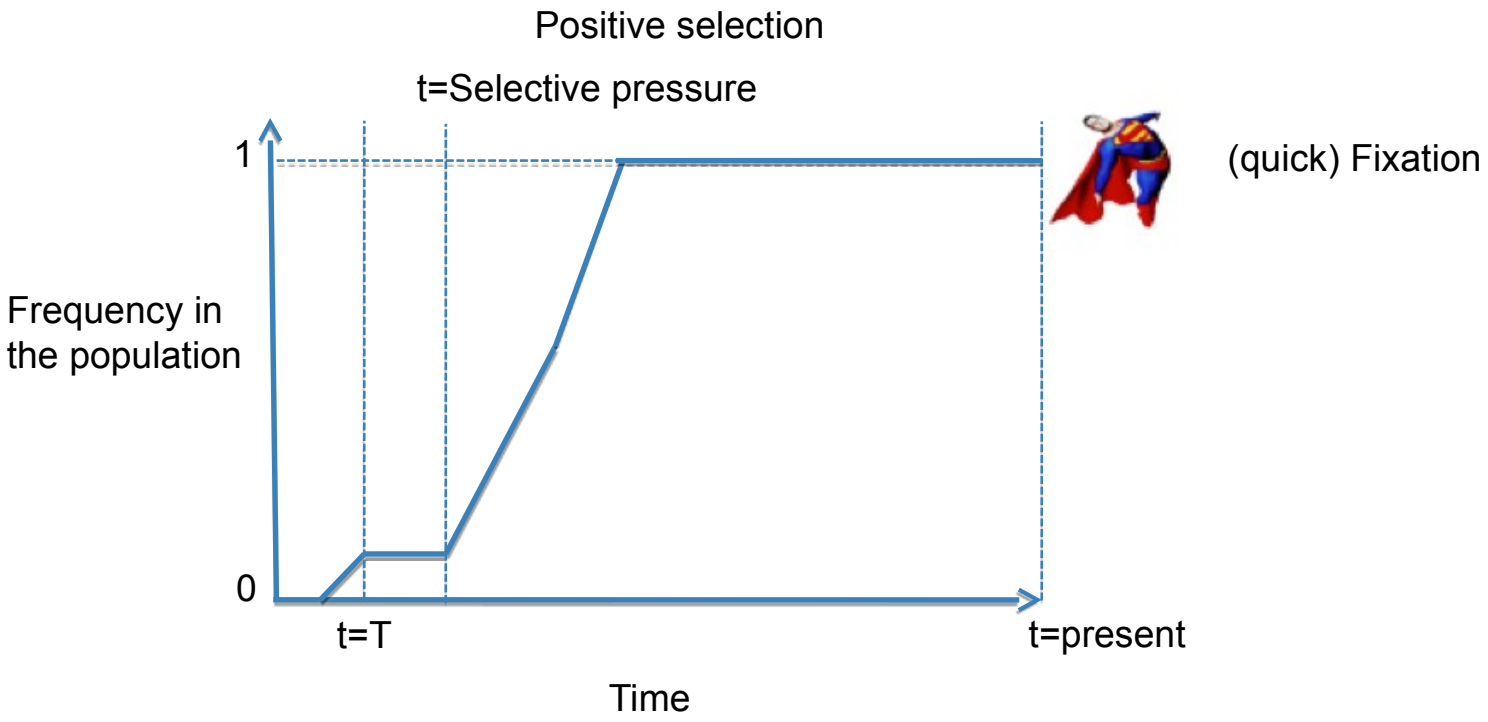

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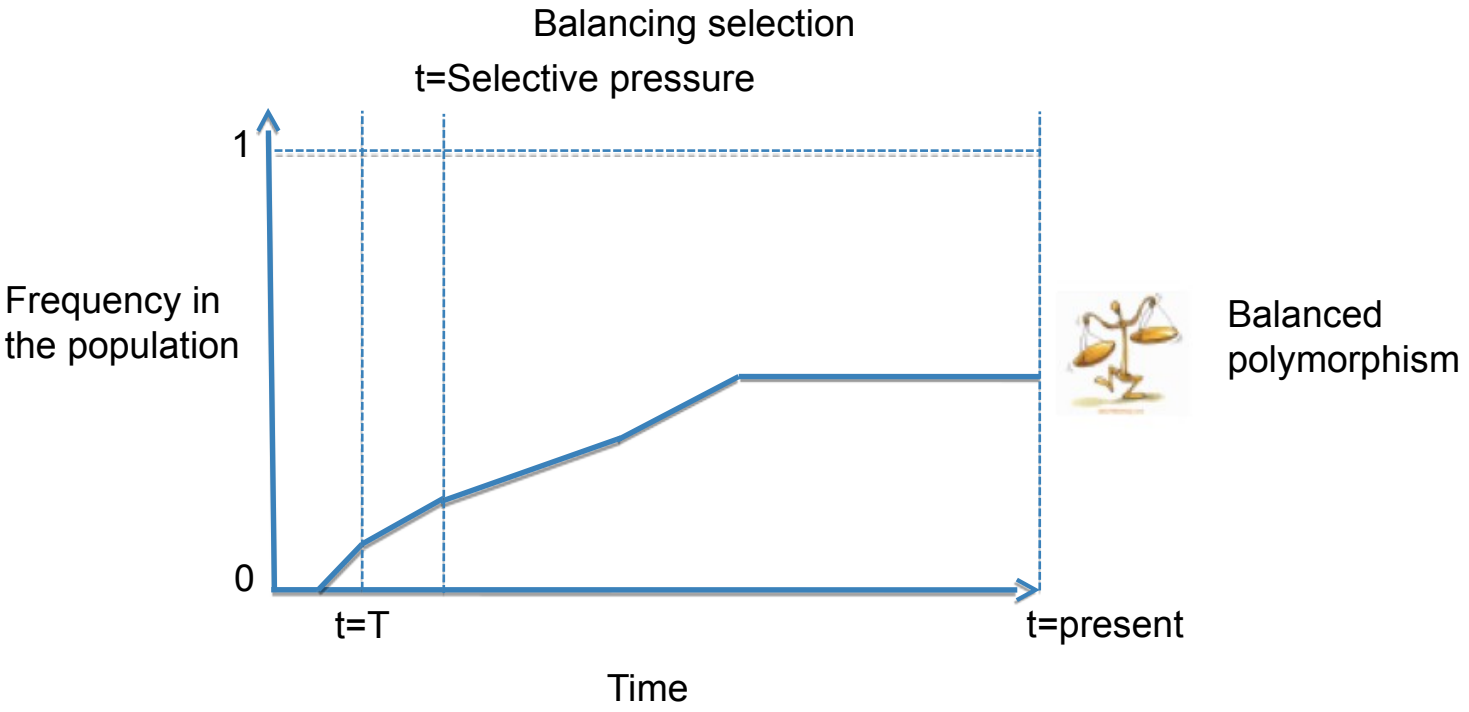

Natural selection

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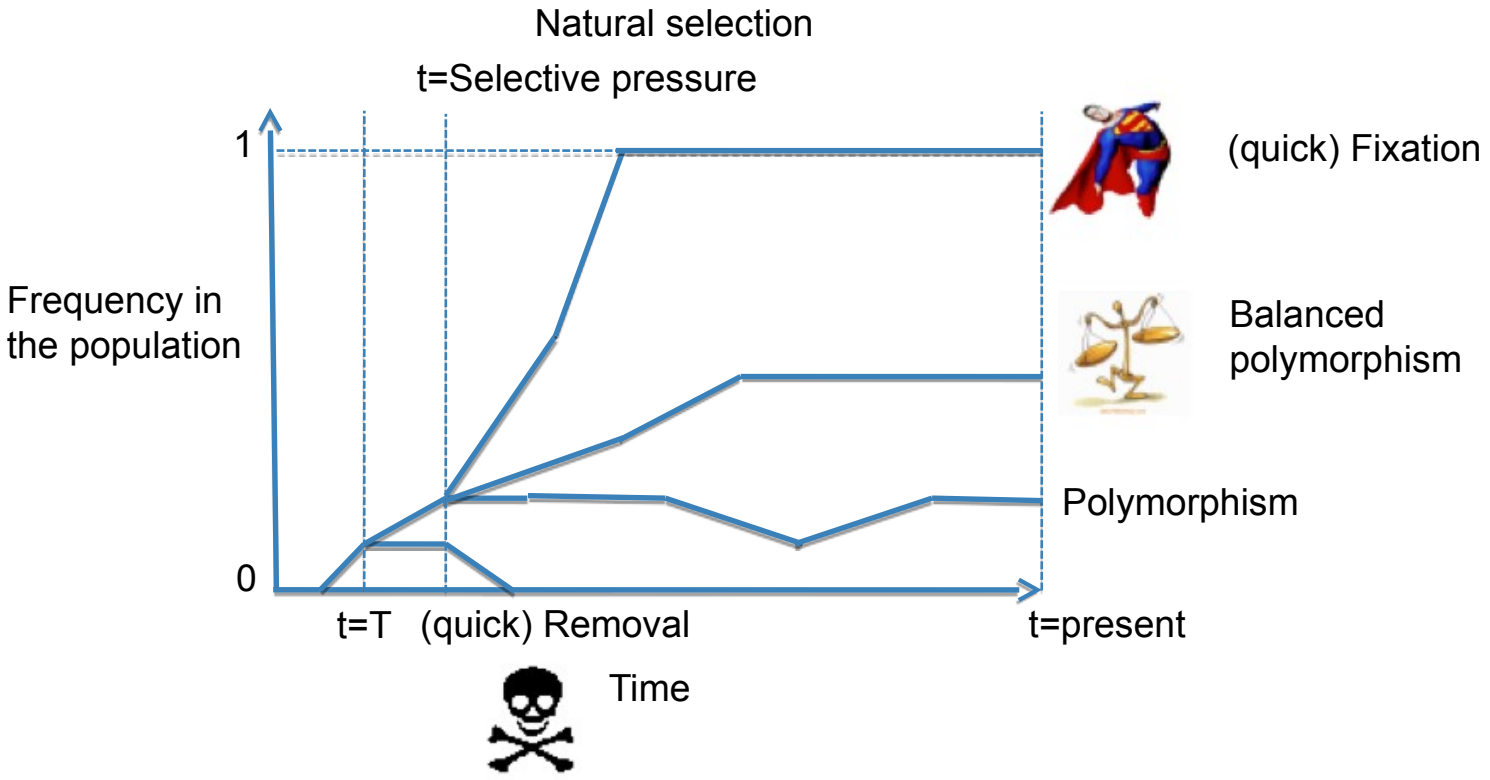
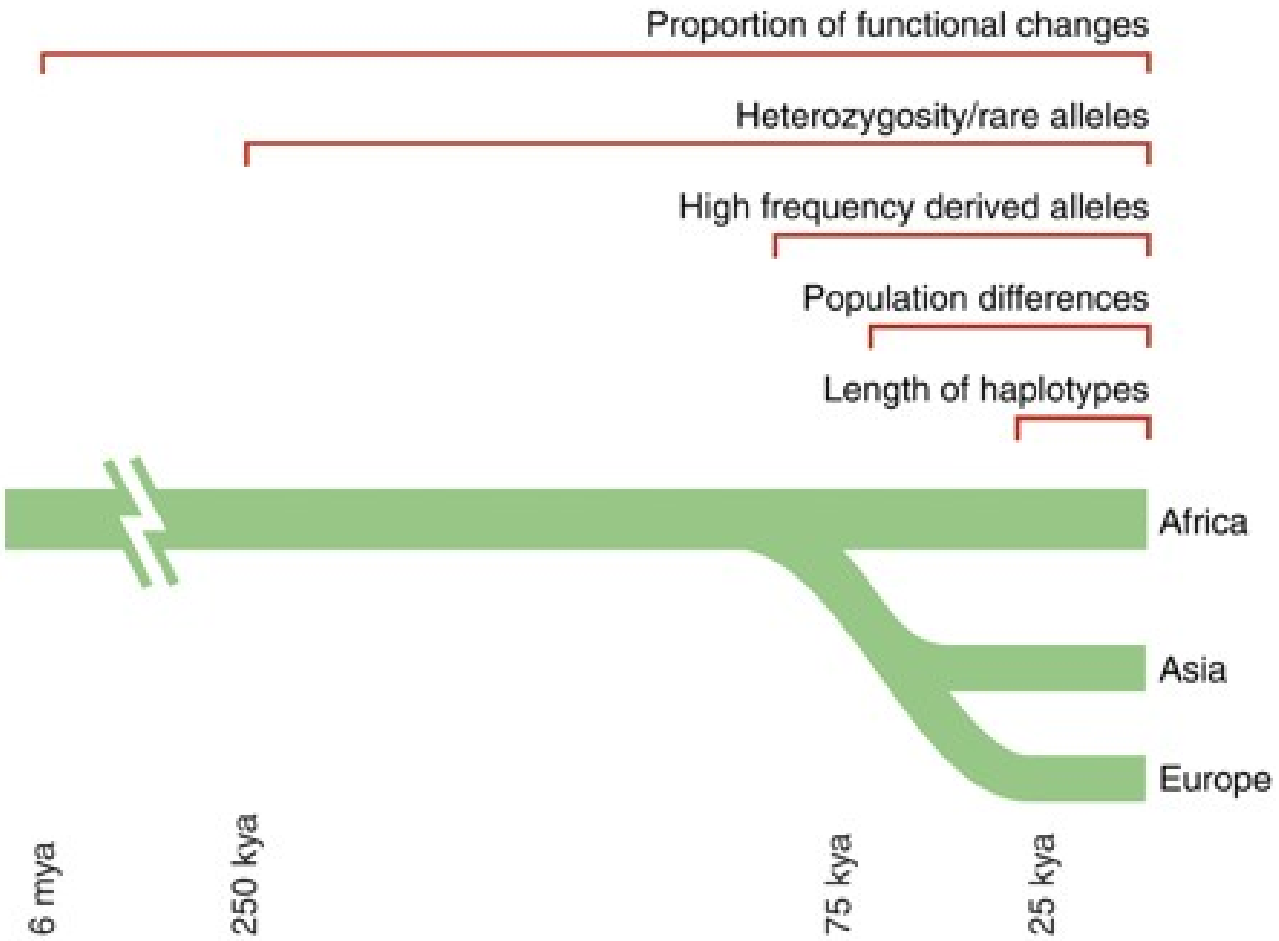


2) Sites targeted by natural selection are likely to harbour **functionality**

Methods to infer recent selection



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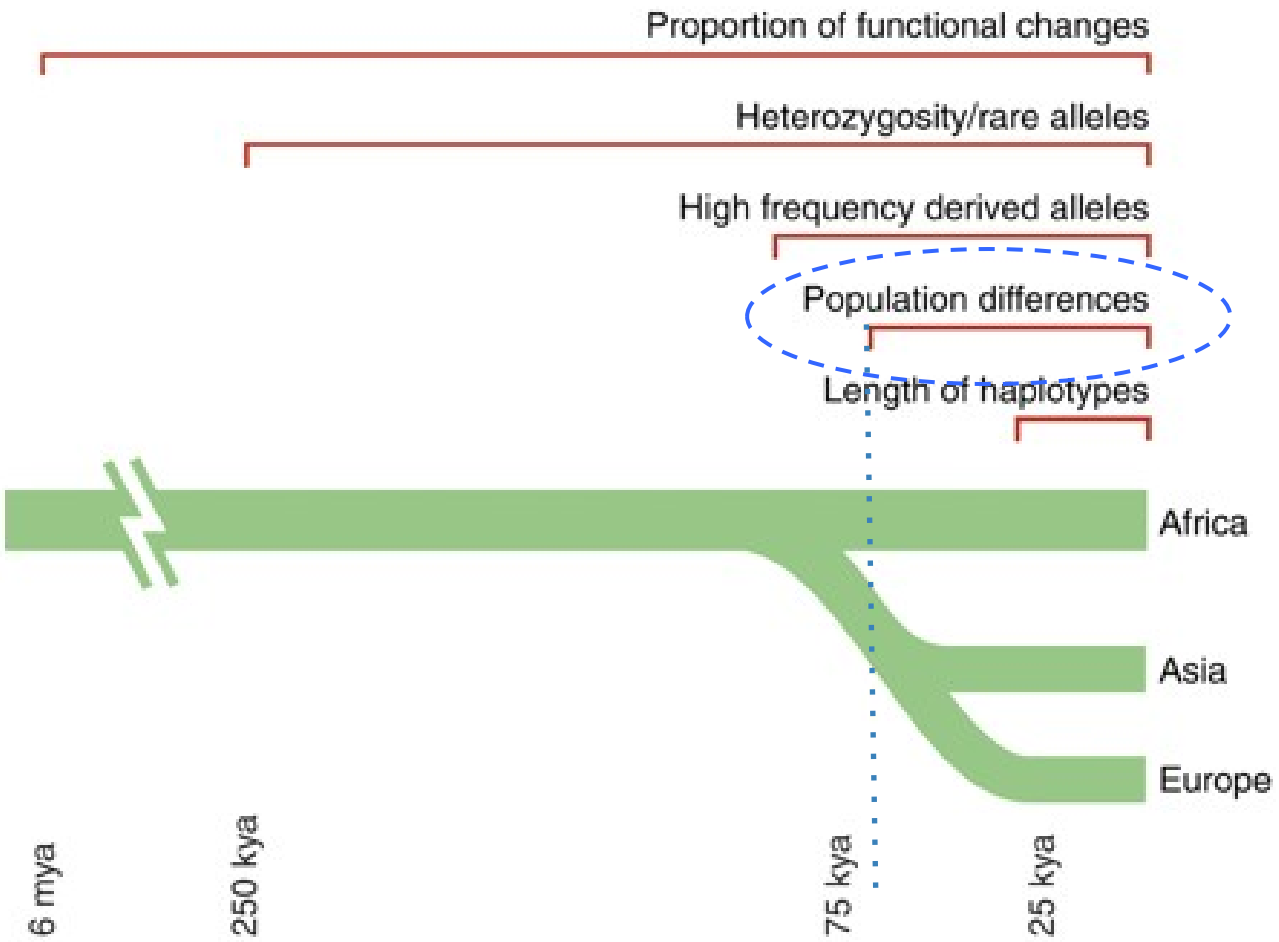
Methods to infer recent selection



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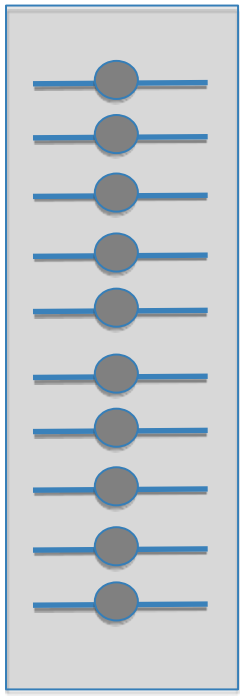
Allele frequency differentiation



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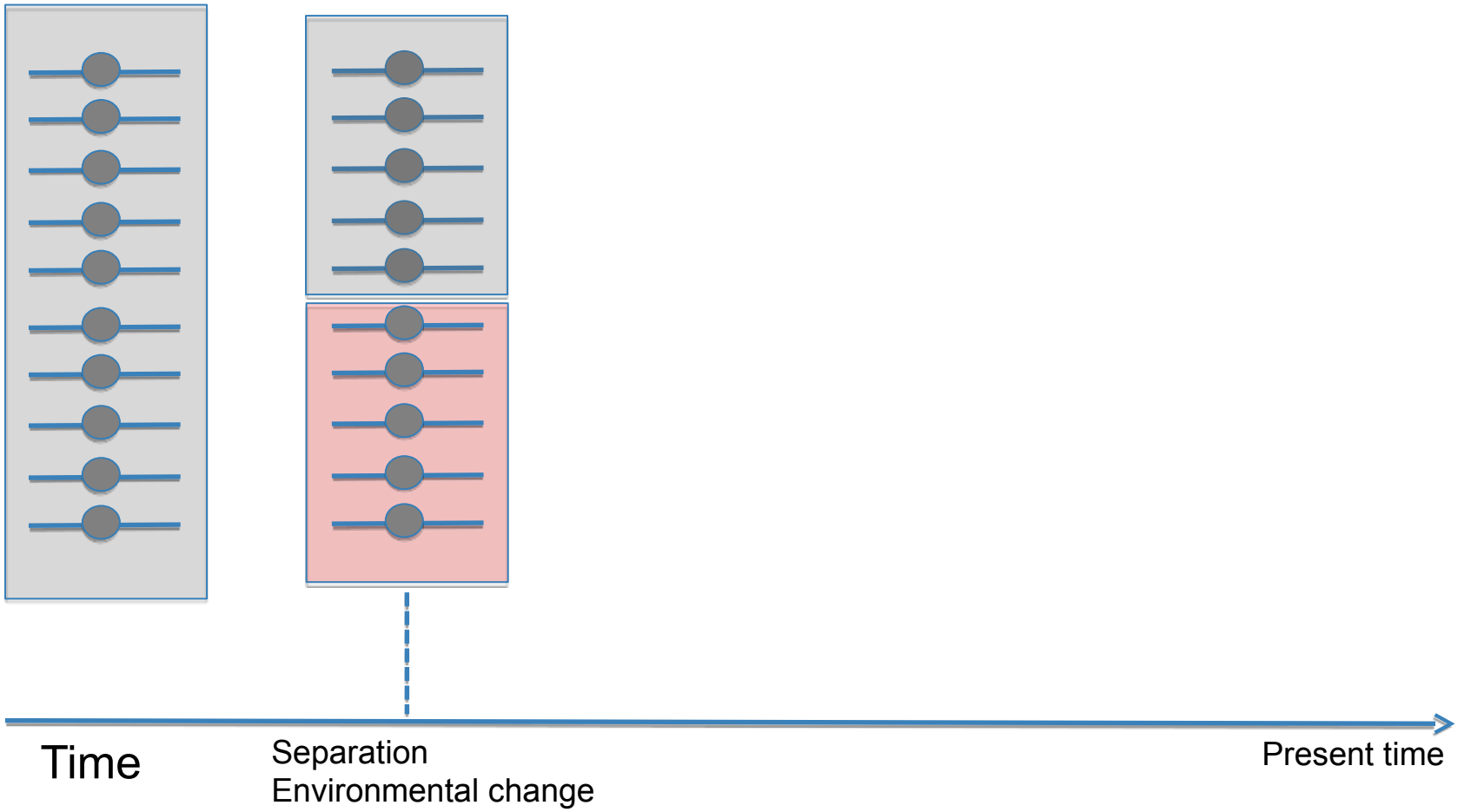

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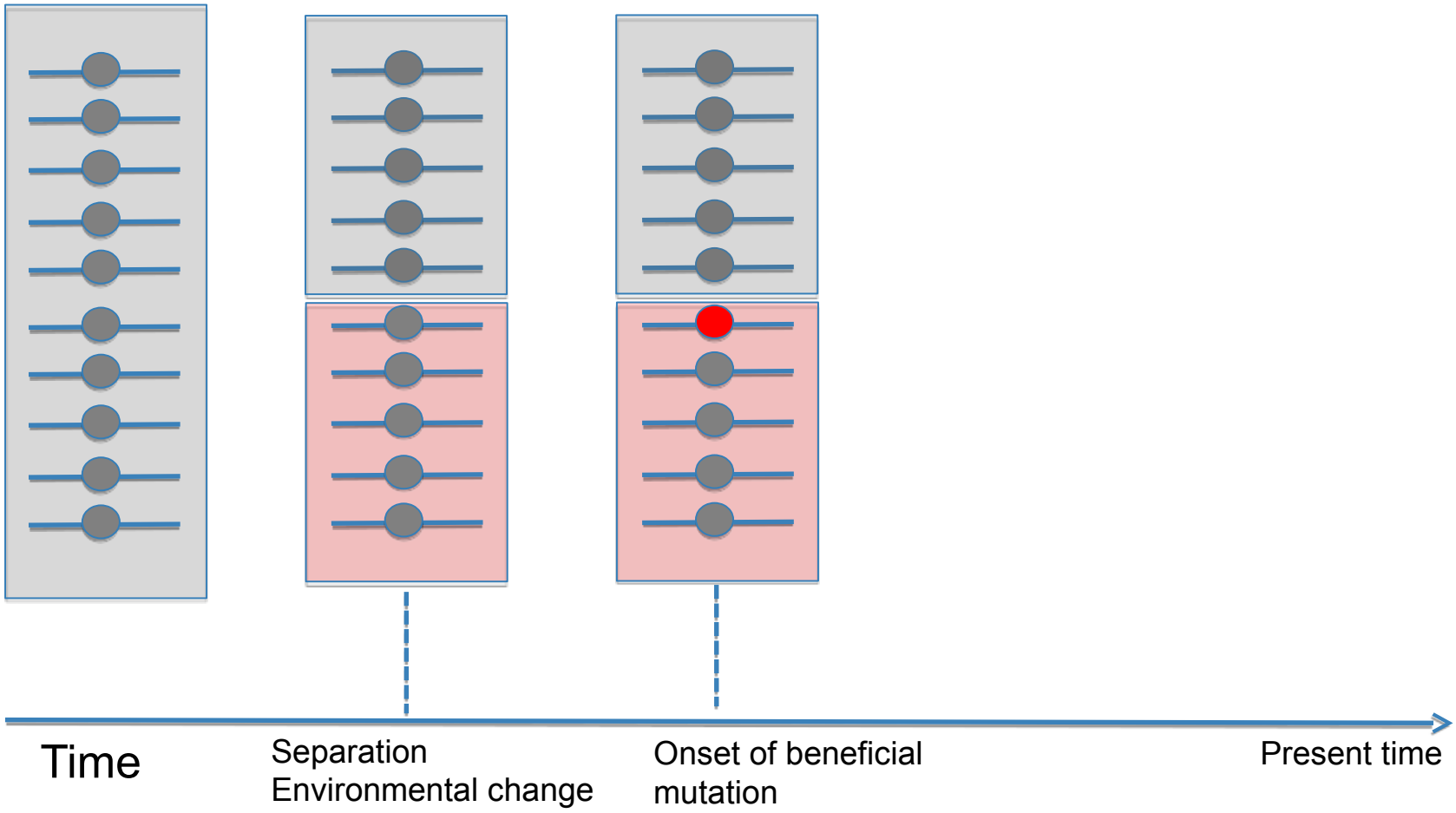

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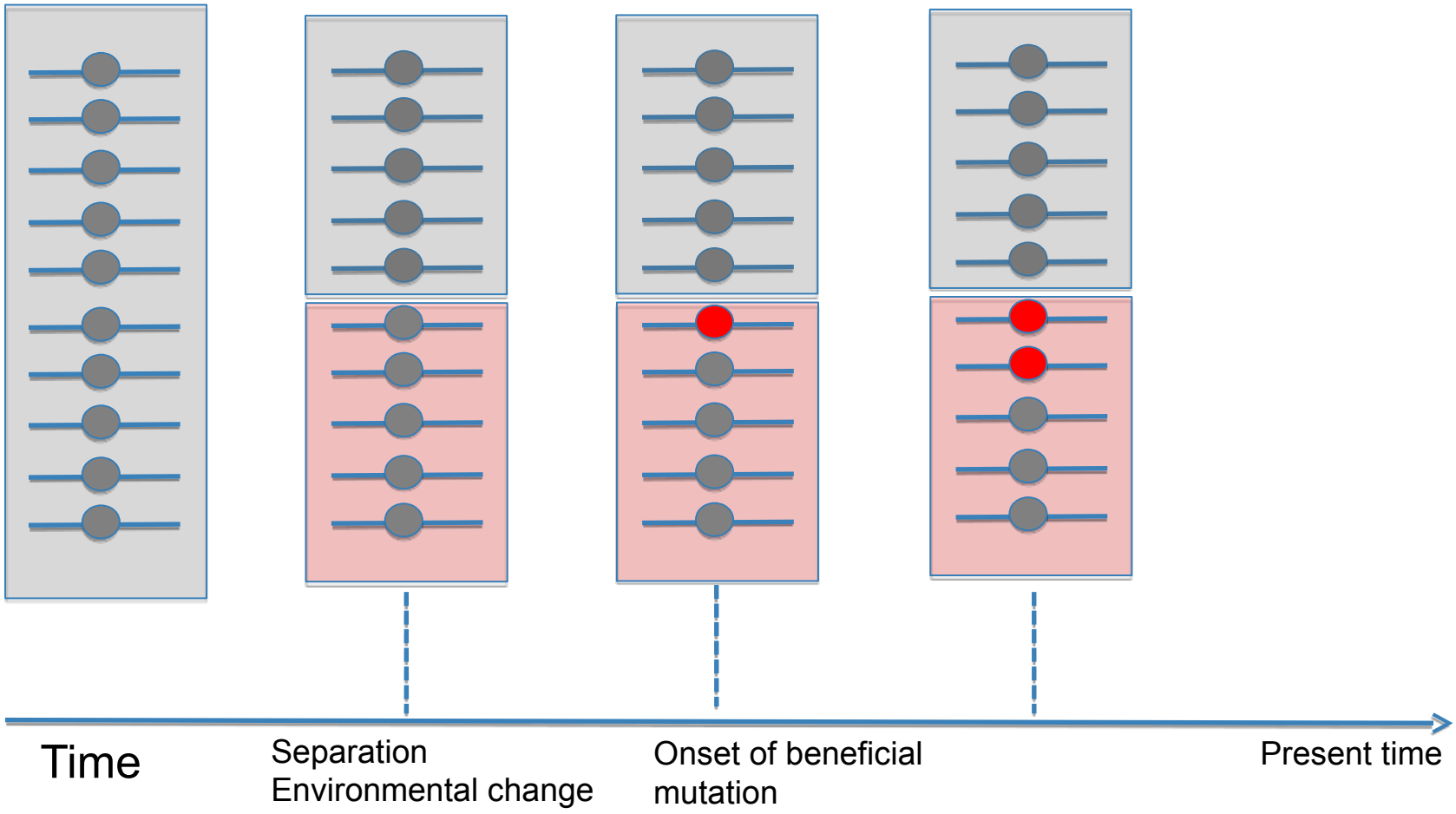

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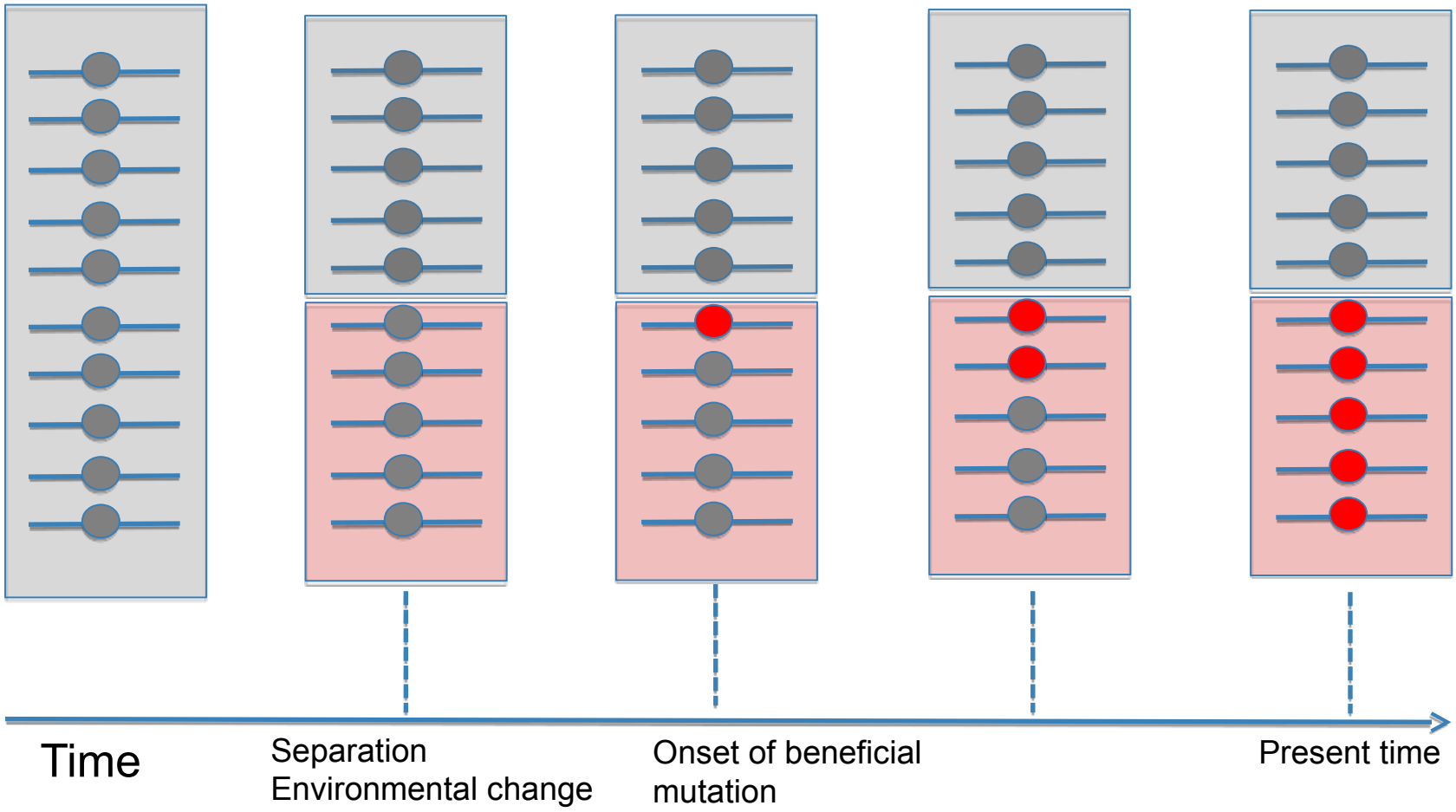


F_{ST}

Common measure for quantifying population subdivision.

$$F_{ST} = H_B / (H_W + H_B)$$

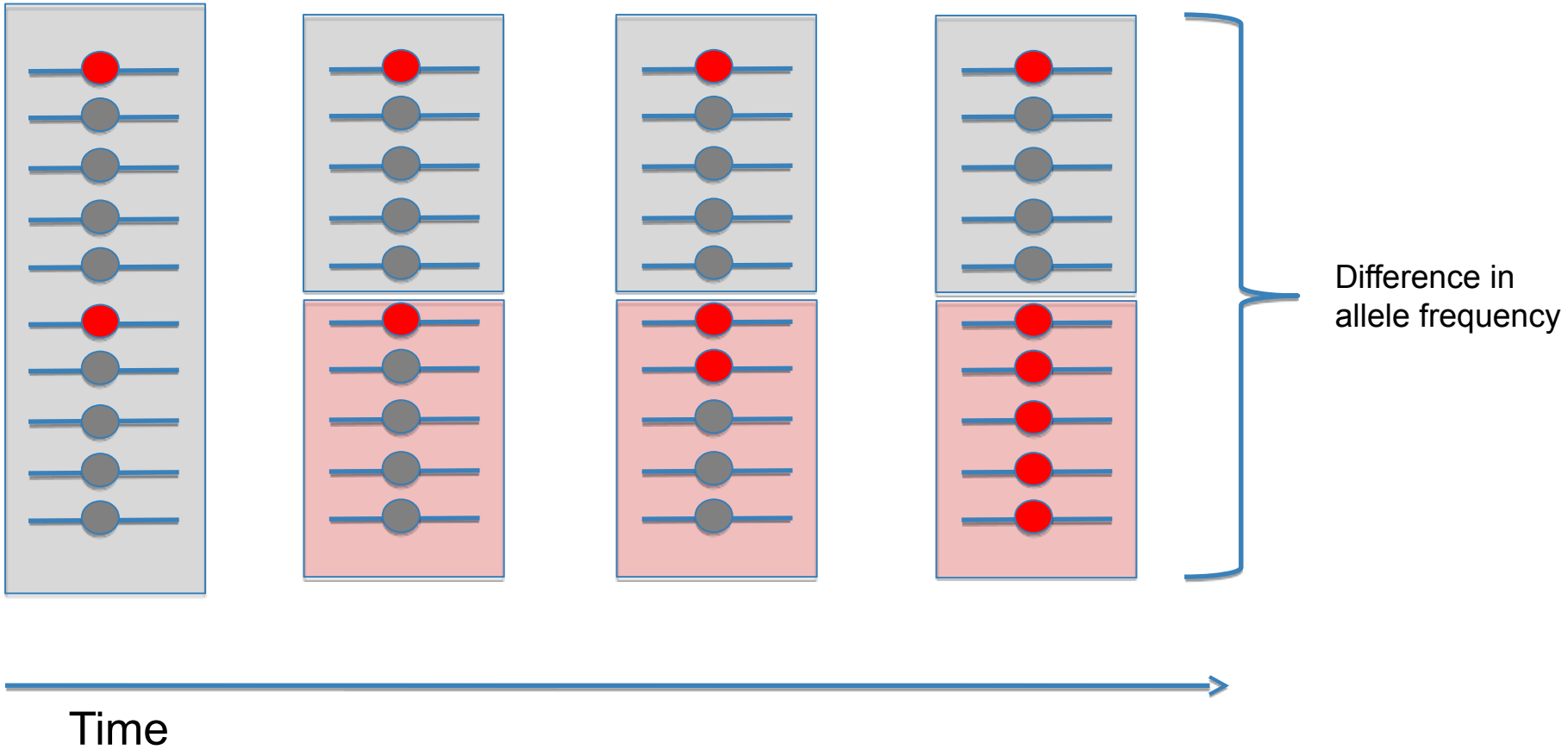
H_B: between populations

H_W: average within populations

- if $H_W << H_B 0$ then $F_{ST} \sim 1$
- if $H_B = 0$ then $F_{ST} = 0$

Allele frequency differentiation

From standing variation



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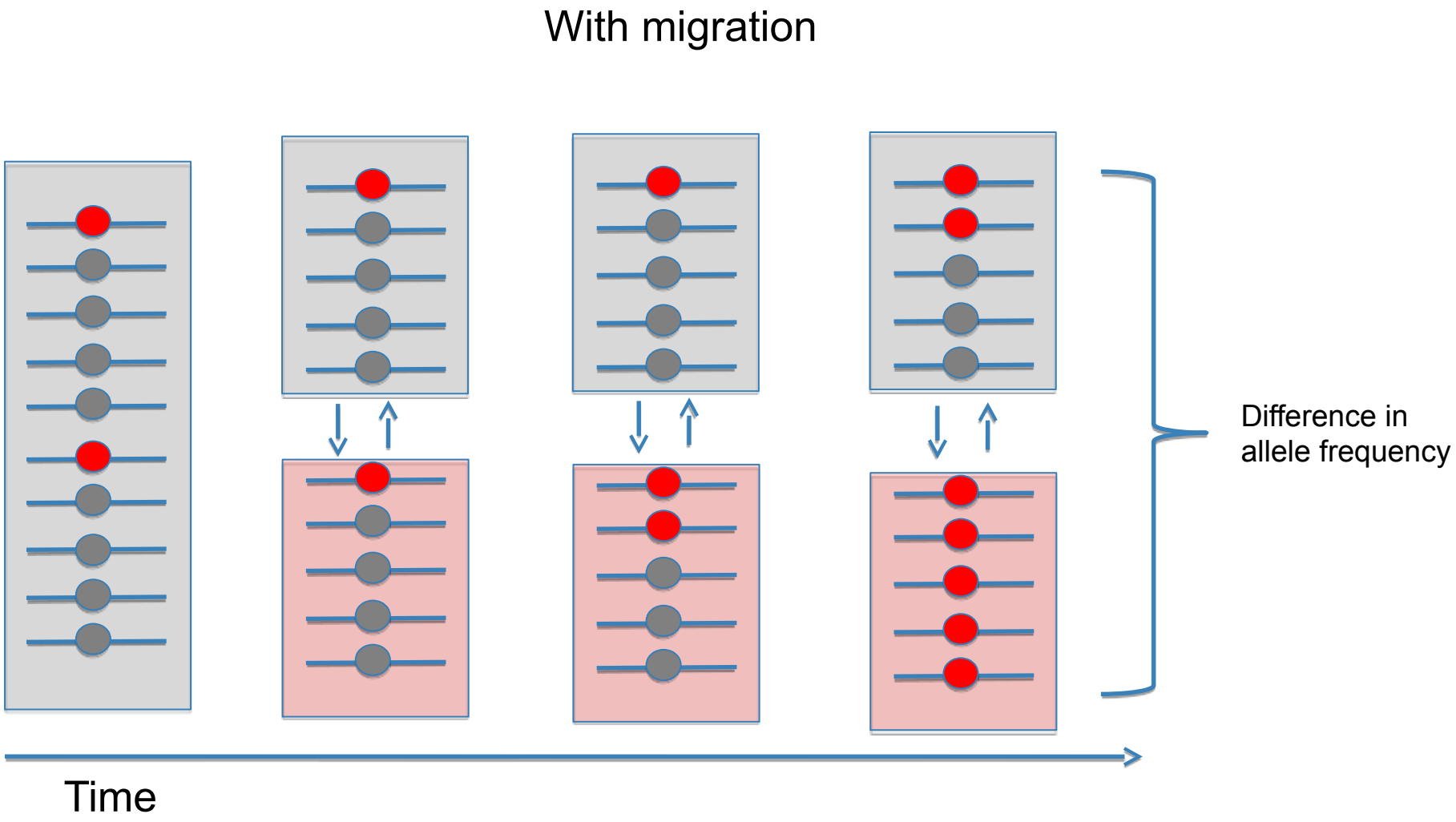
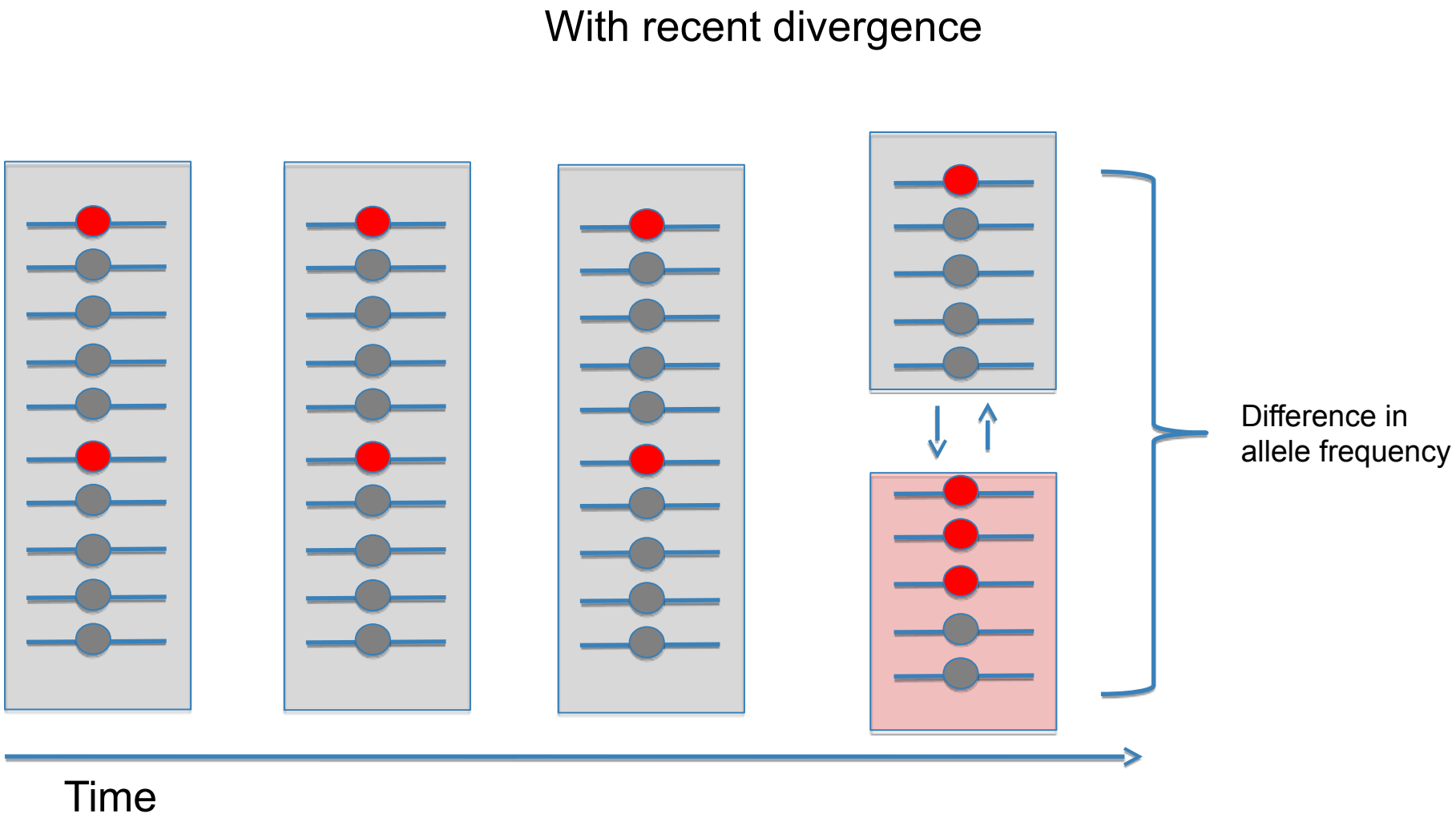
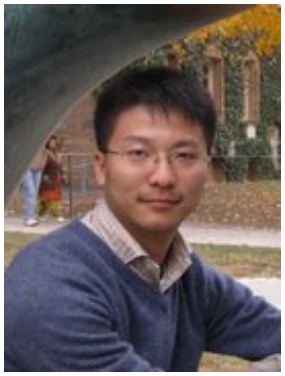


Allele frequency differentiation



Population genetic differentiation

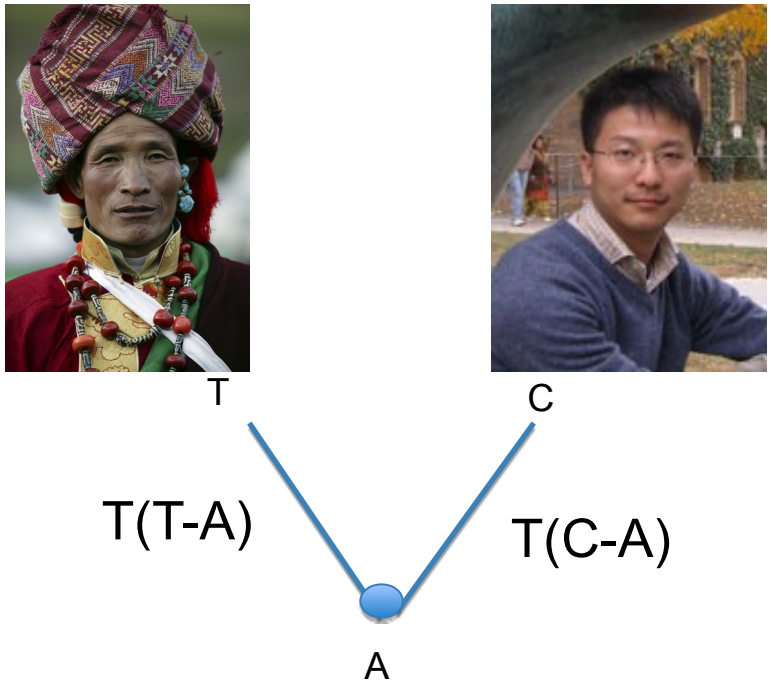
T



C

F_{ST}(T-C)

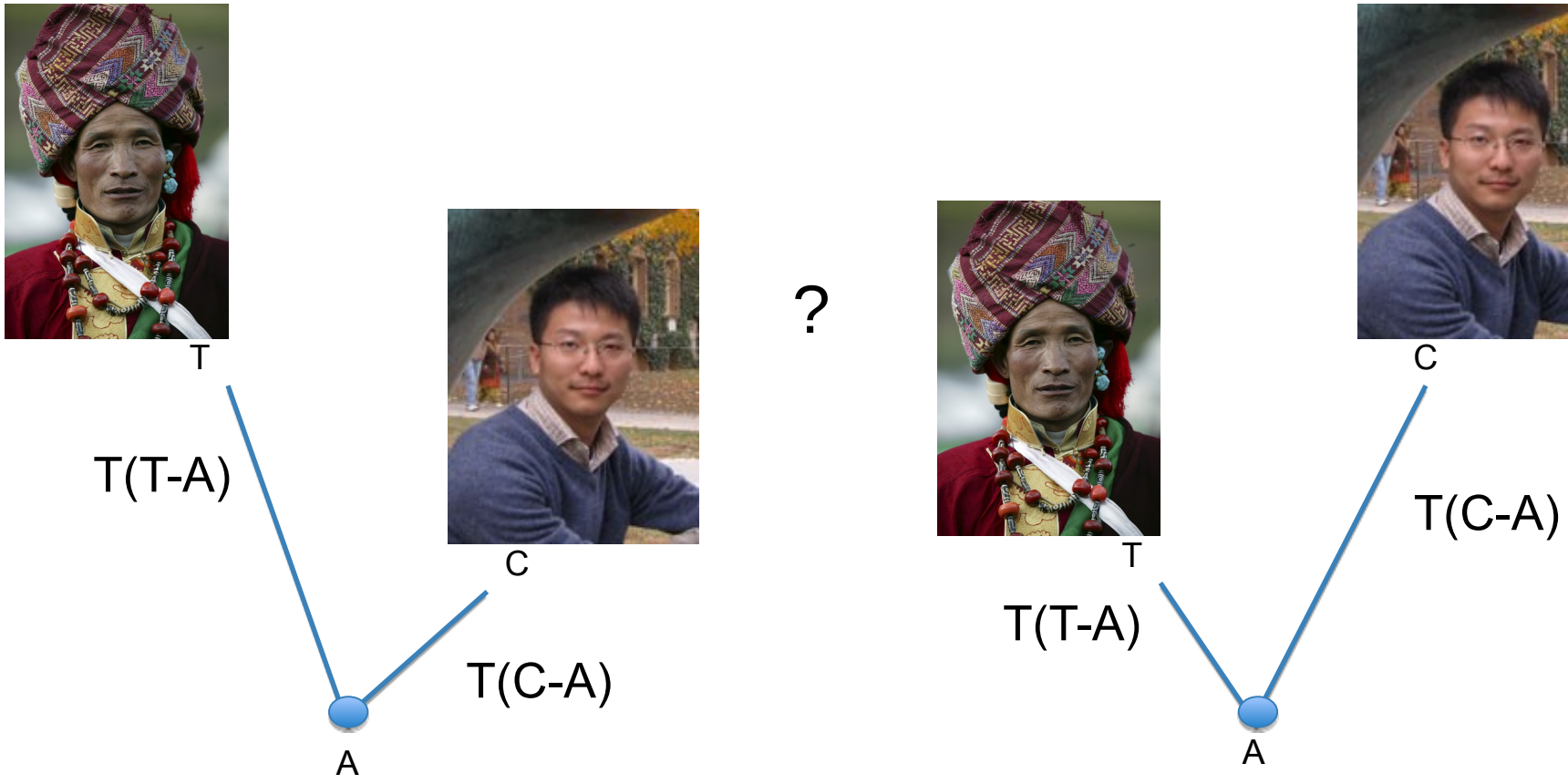
Population genetic differentiation



F_{ST}(T-C)~T(T-A-C)

Population genetic differentiation

F_{ST}(T-C)~T(T-A-C)



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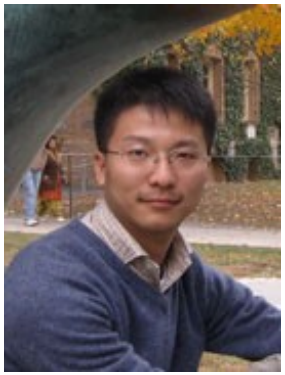

T

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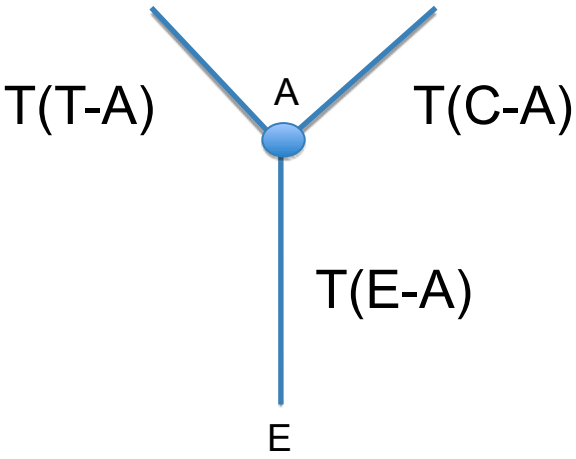
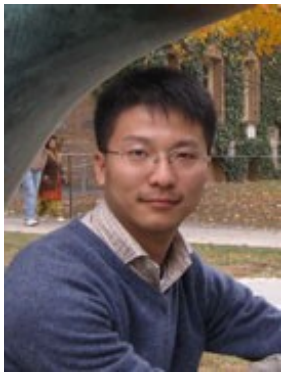
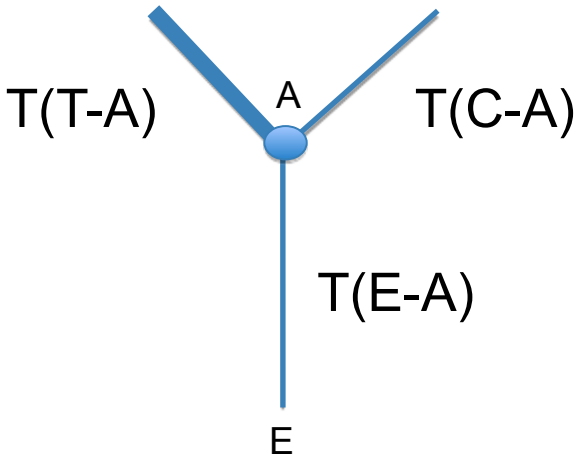


Population genetic differentiation

T



C

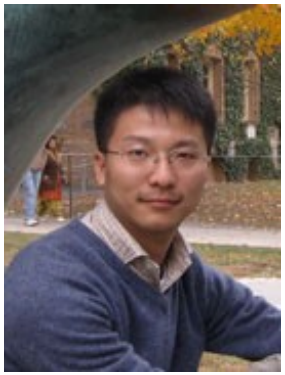


$T(T\text{-}A\text{-}C)=-\log(1-F_{ST}(T\text{-}C))$

T(T-A)?

Population genetic differentiation

T



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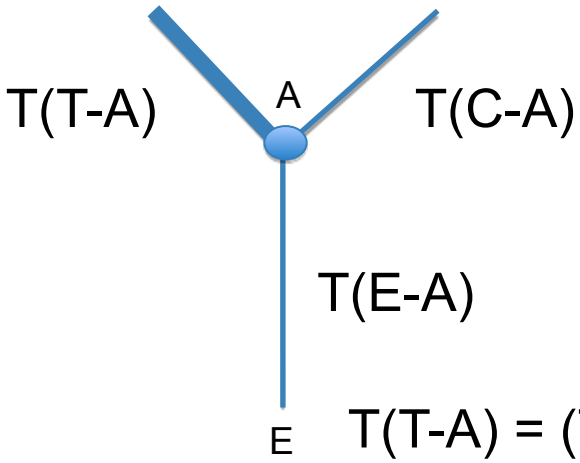
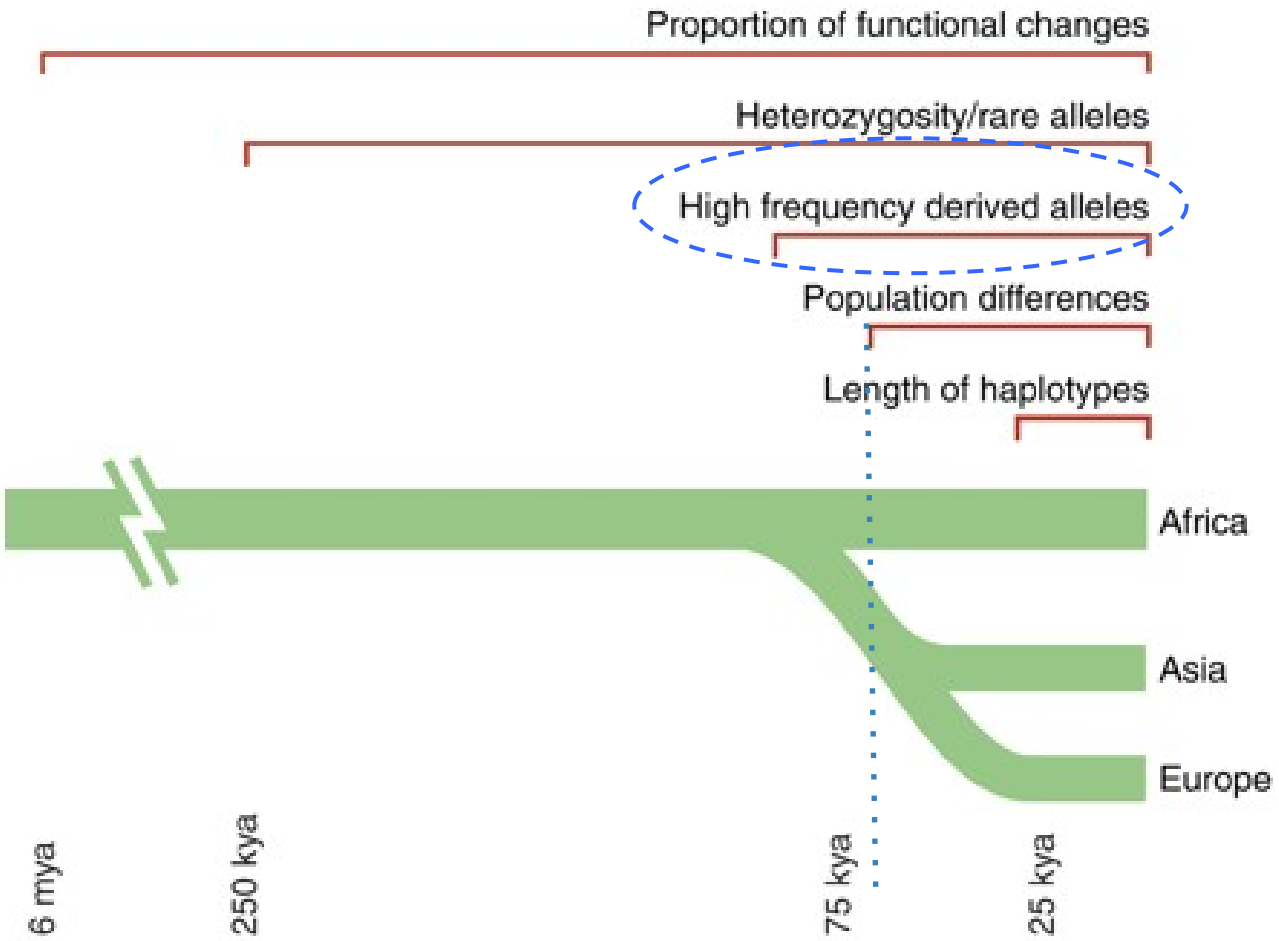


$T(T\text{-}A\text{-}C)=-\log(1-F_{ST}(T\text{-}C))$

$T(T\text{-}A) = (T(T\text{-}E)+T(C\text{-}T)-T(C\text{-}E))/2$

Methods to infer selection



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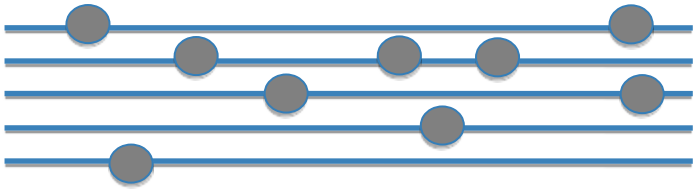
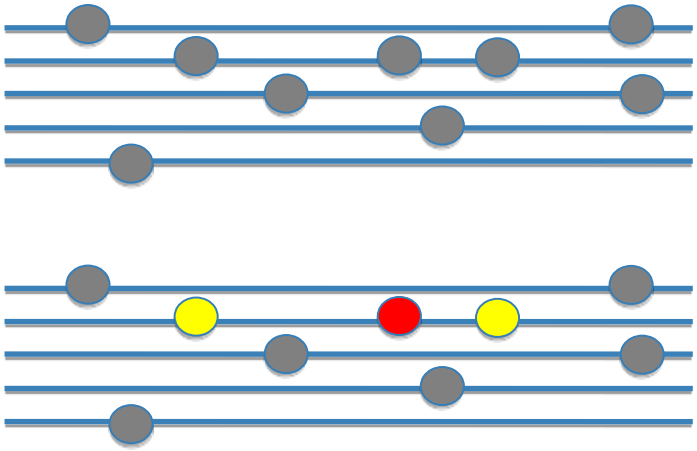
Positive selection: effect on haplotypes



$t<T_{sel}$

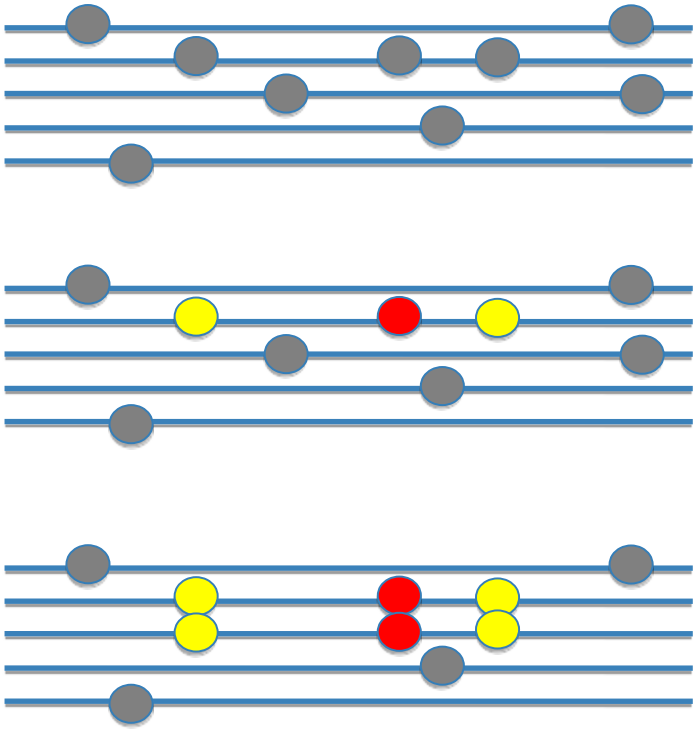
Positive selection: effect on haplotypes



$t<T_{sel}$

$t=T_{sel}$

Positive selection: effect on haplotypes



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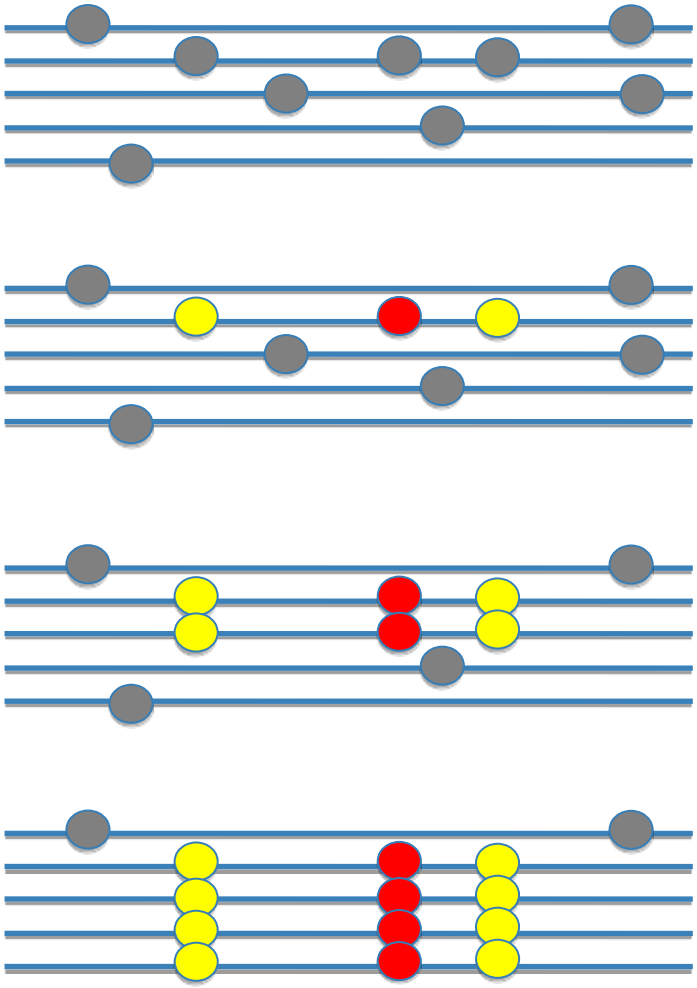
$t=T_{sel}$

$t>T_{sel}$

Positive selection: effect on haplotypes



$t<T_{sel}$

$t=T_{sel}$

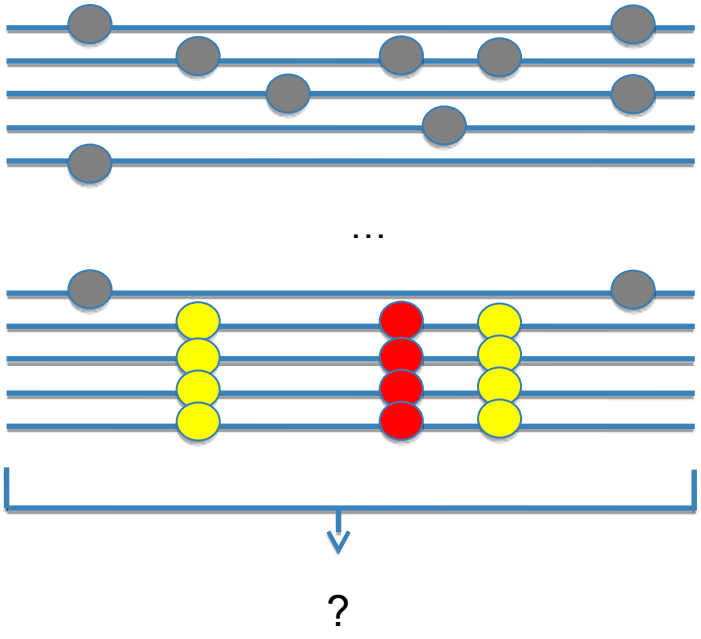
$t>T_{sel}$

$t>>T_{sel}$

Selective sweep

Genetic hitch-hiking

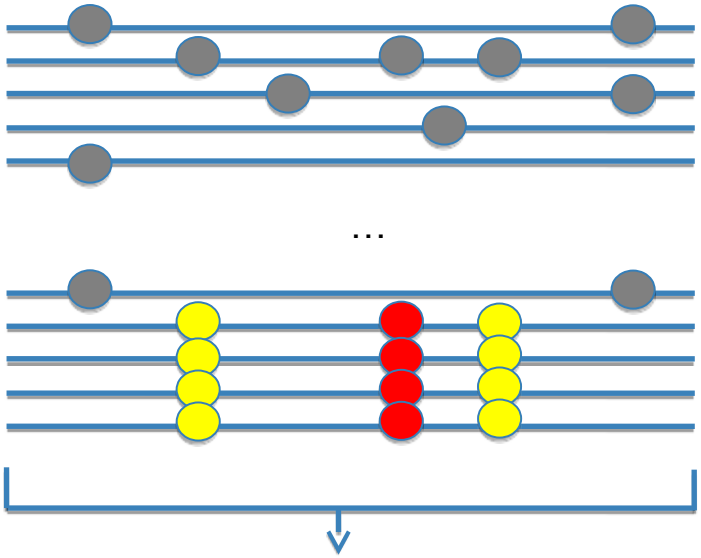
Positive selection



$t<T_{sel}$

$t>>T_{sel}$

Positive selection



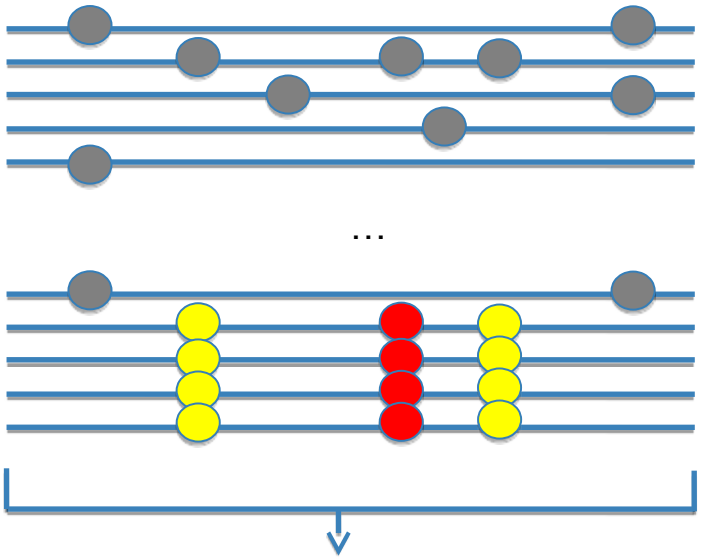
$t<T_{sel}$

…

$t>>T_{sel}$

- Reduction of polymorphisms levels (e.g. from 7 to 5 SNPs)

Positive selection



$t<T_{sel}$

$t>>T_{sel}$

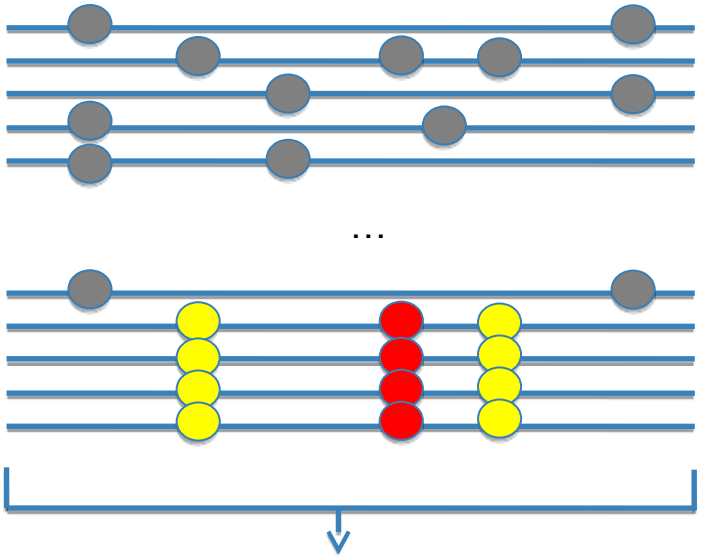
- Reduction of polymorphisms levels
(e.g. from 7 to 5 SNPs)

Nucleotide diversity index: Watterson's Theta
with K SNPs and n chromosomes

$$\theta_w = \frac{K}{a_n}$$

$$a_n = \sum_{i=1}^{n-1} \frac{1}{i}$$

Positive selection

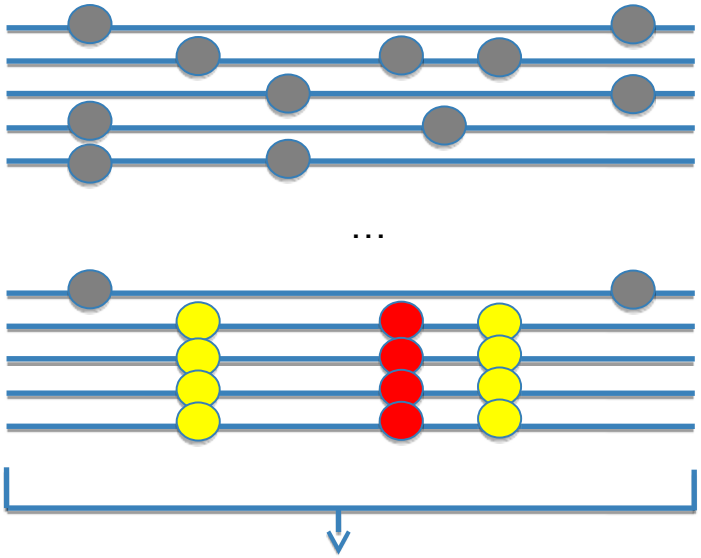


$t<T_{sel}$

$t>>T_{sel}$

- Reduction of polymorphisms levels (Theta)
- ?

Positive selection

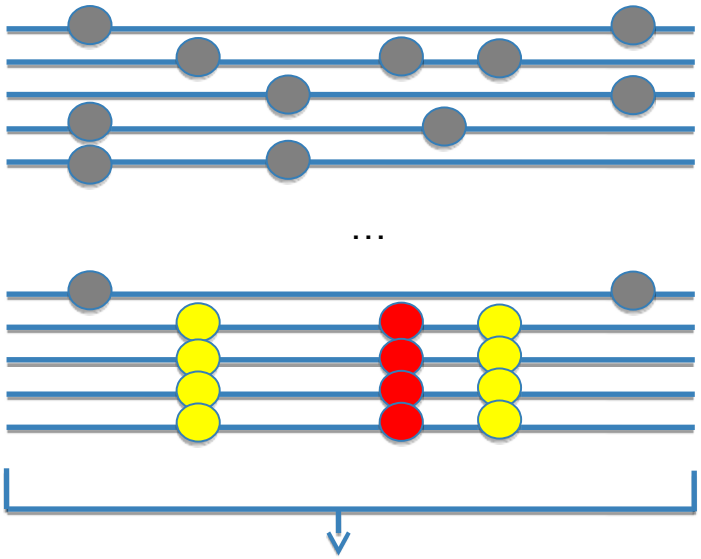


- Reduction of polymorphisms levels (Theta)
- Excess of low-frequency variants

Nucleotide diversity index: average pairwise nucleotide differences (Pi)
with $k_{i,j}$ equal to the number of nucleotide differences between sequences *i* and *j*

$$\pi = \frac{\sum_{i=1}^{n-1} \sum_{j=i+1}^{n} k_{i,j}}{\binom{n}{2}}$$

Positive selection



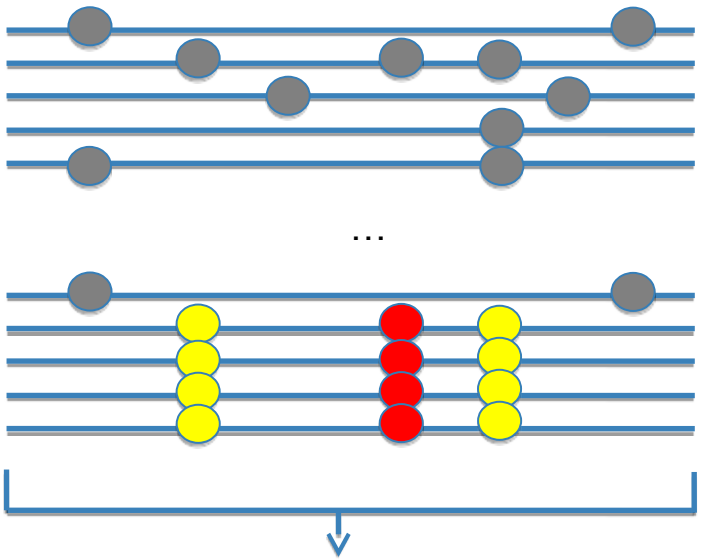
- Reduction of polymorphisms levels (Theta)
- Excess of low-frequency variants (Pi)

Under neutrality, Theta and Pi are expected to be the same.
Tajima's D measures their difference.

$$D = \frac{\pi - \theta_w}{\sqrt{\hat{V}(\pi - \theta_w)}}$$

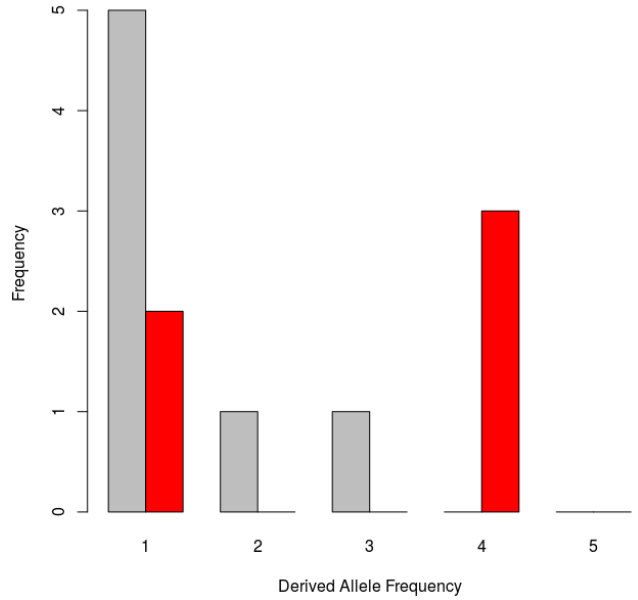
D<0 is suggestive of an excess of low-frequency variants

The Site Frequency Spectrum

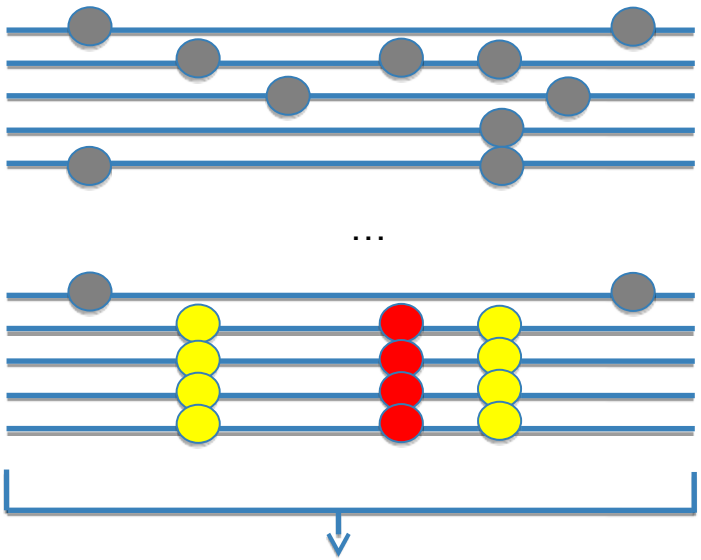


$t<T_{sel}$

$t>>T_{sel}$



The Site Frequency Spectrum



$t<T_{sel}$

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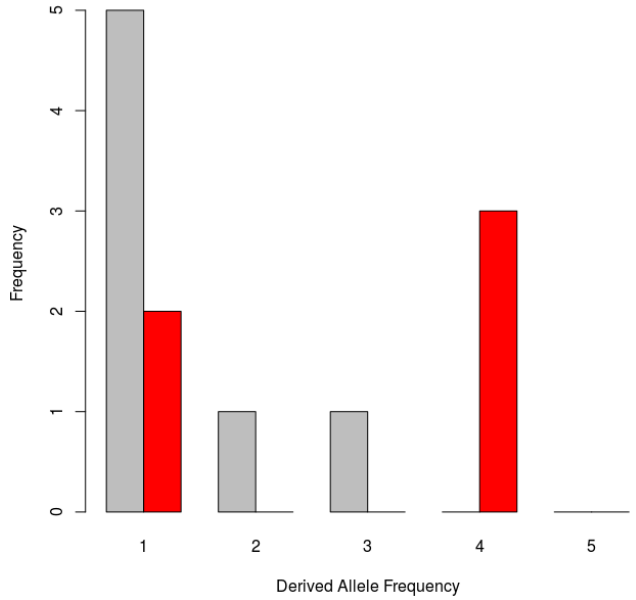


Tajima's D?

$$D = \frac{\pi - \theta_W}{\sqrt{\hat{V}(\pi - \theta_W)}}$$

~0.33=1/3

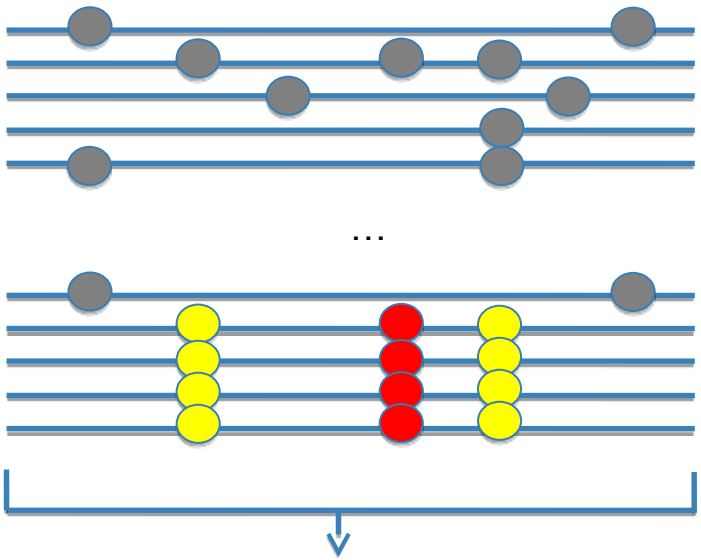
$$\theta_W = \frac{K}{a_n}$$

$$a_n = \sum_{i=1}^{n-1} \frac{1}{i}$$

$$\pi = \frac{\sum_{i=1}^{n-1} \sum_{j=i+1}^{n} k_{i,j}}{\binom{n}{2}}$$

= 10, the number of comparisons you need to make

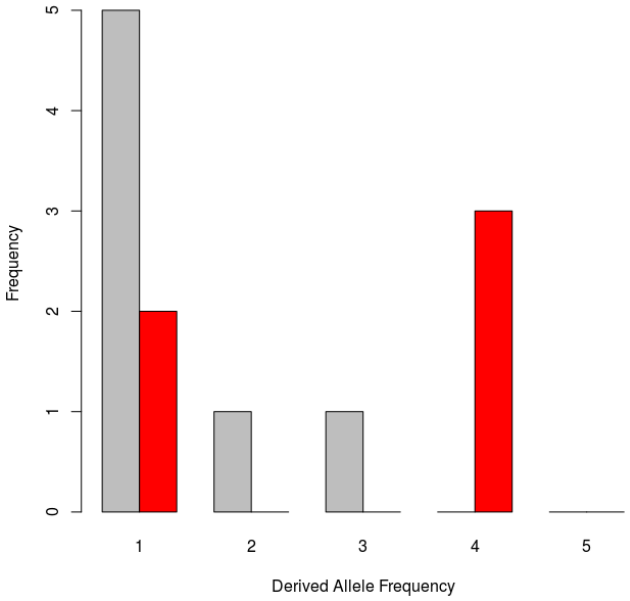
The importance of being…
The Site Frequency Spectrum



$t<T_{sel}$

…

$t>>T_{sel}$



K=5

a_n=1/1 + 1/2 + 1/3 + 1/4=(12+6+4+3)/12=25/12

Theta=5/(25/12)=12/5

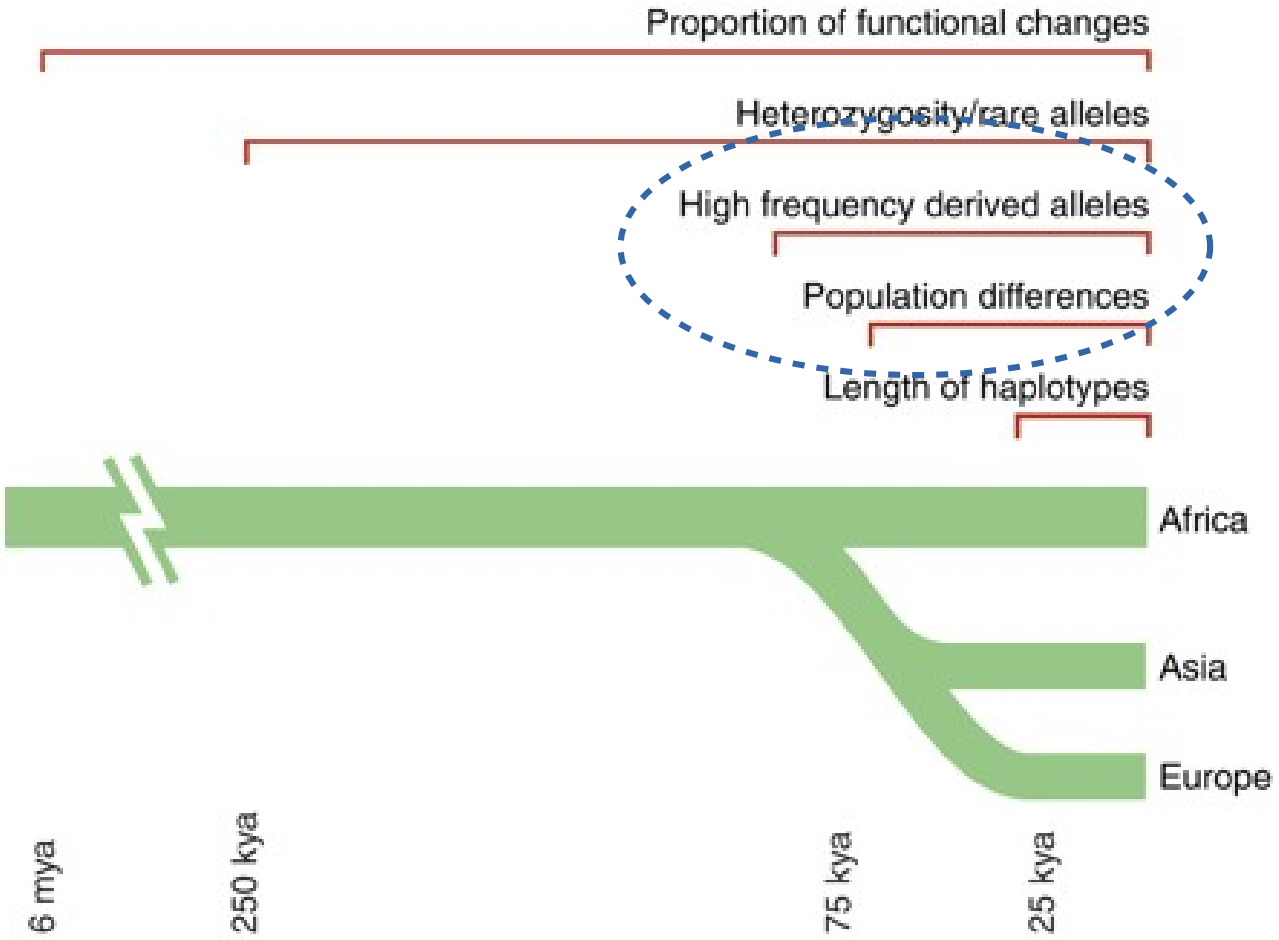
Pi=(5+5+5+5+0+0+0+0+0+0)/10=20/10=2

sd(D)=1/3

D=(2-12/5)/(1/3)=((10-12)/5)*3=-6/5=-1.2

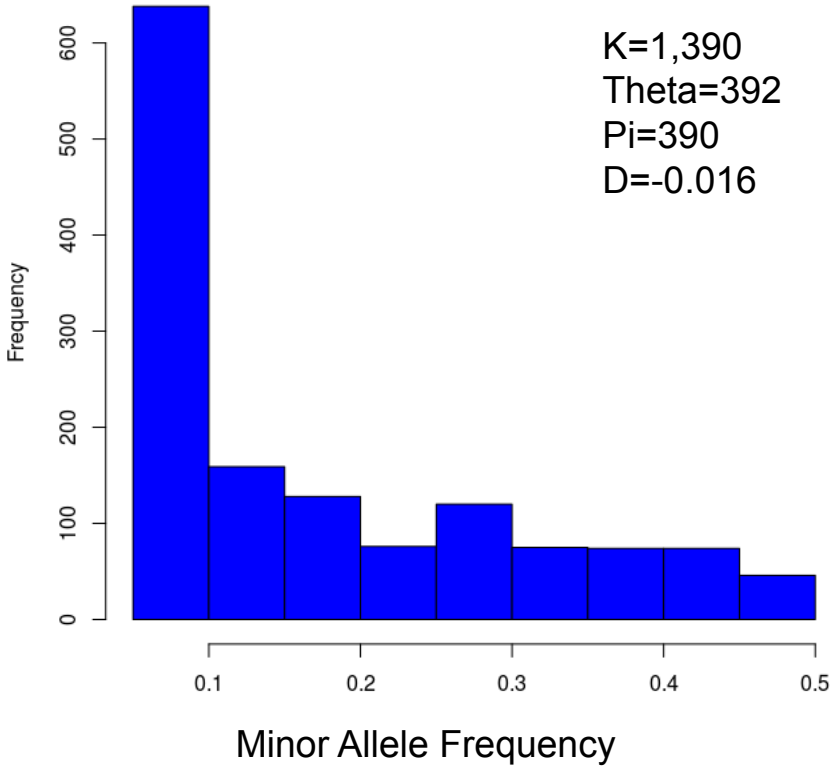
D<0

Inference of positive selection



Confounding factor

n=20; L=500kbp; no selection



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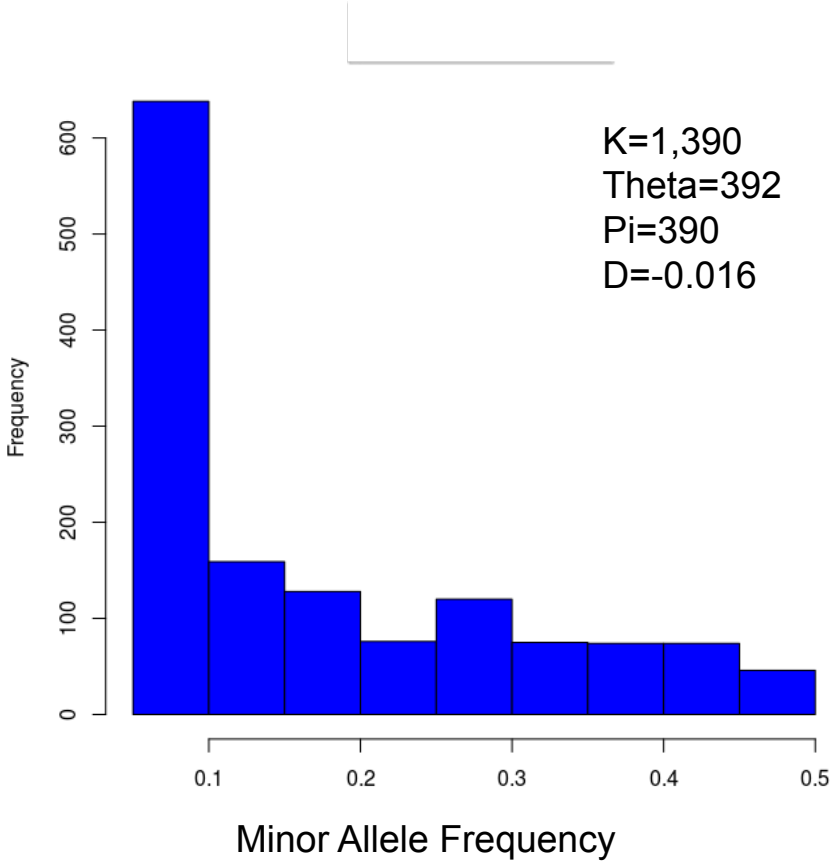
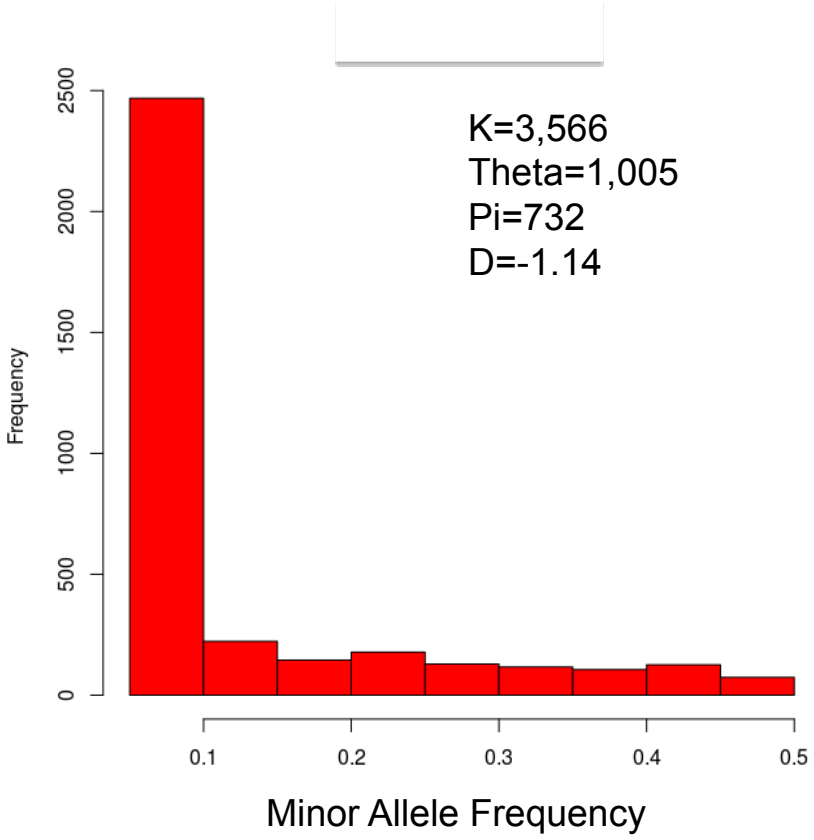
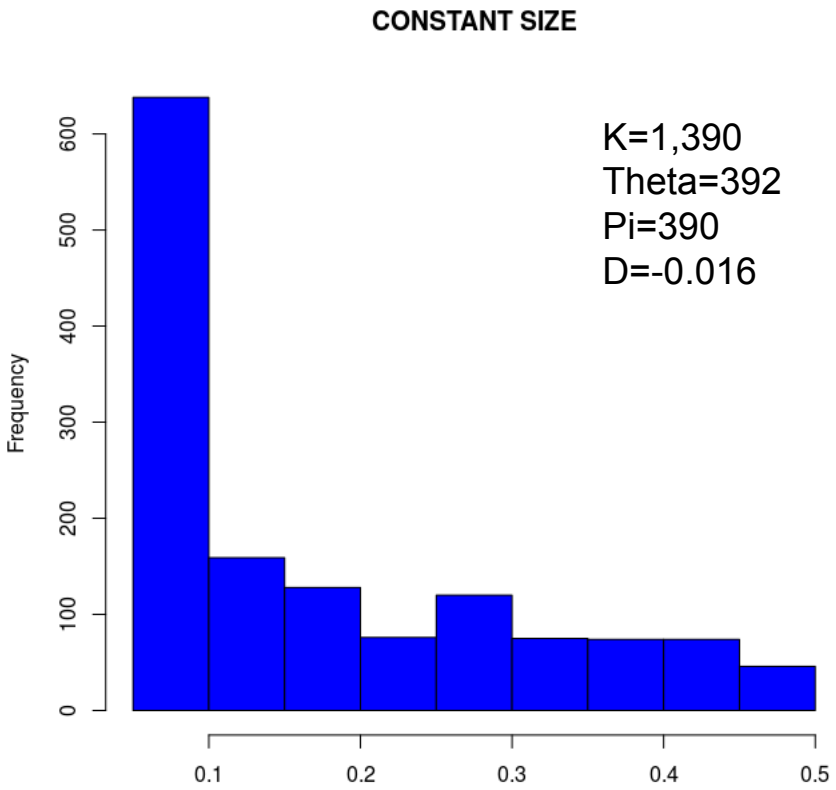


n=20; L=500kbp; no selection



Demography matters!

n=20; L=500kbp; no selection



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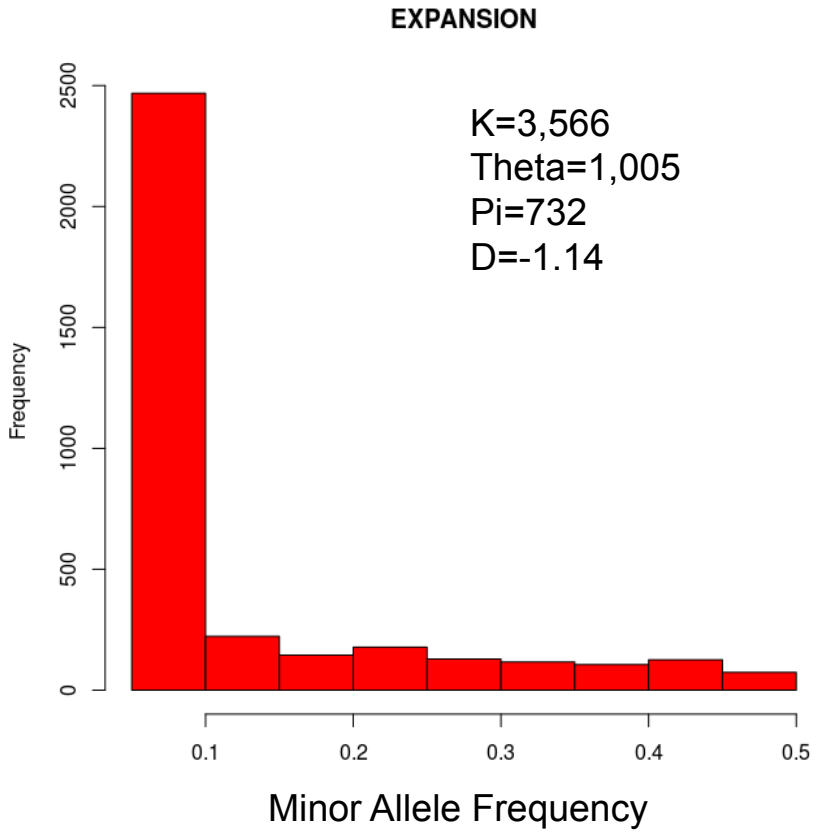

- Excess of segregating sites
- Excess of low-frequency variants
- SFS-derived summary statistics may fail to distinguish between the effects of demography and selection

Demography matters?

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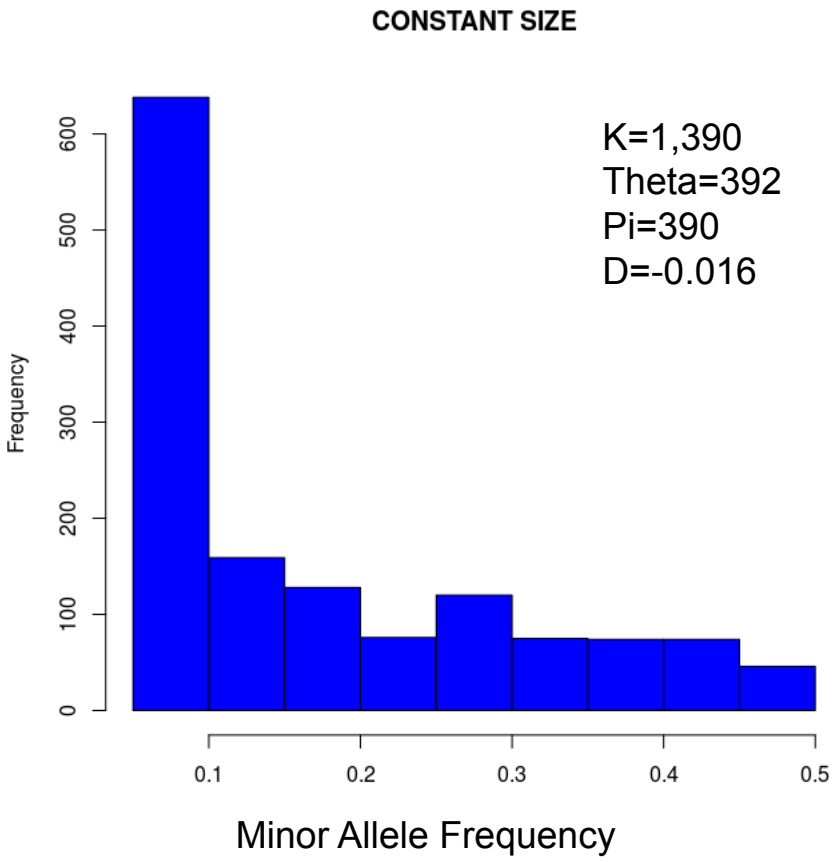
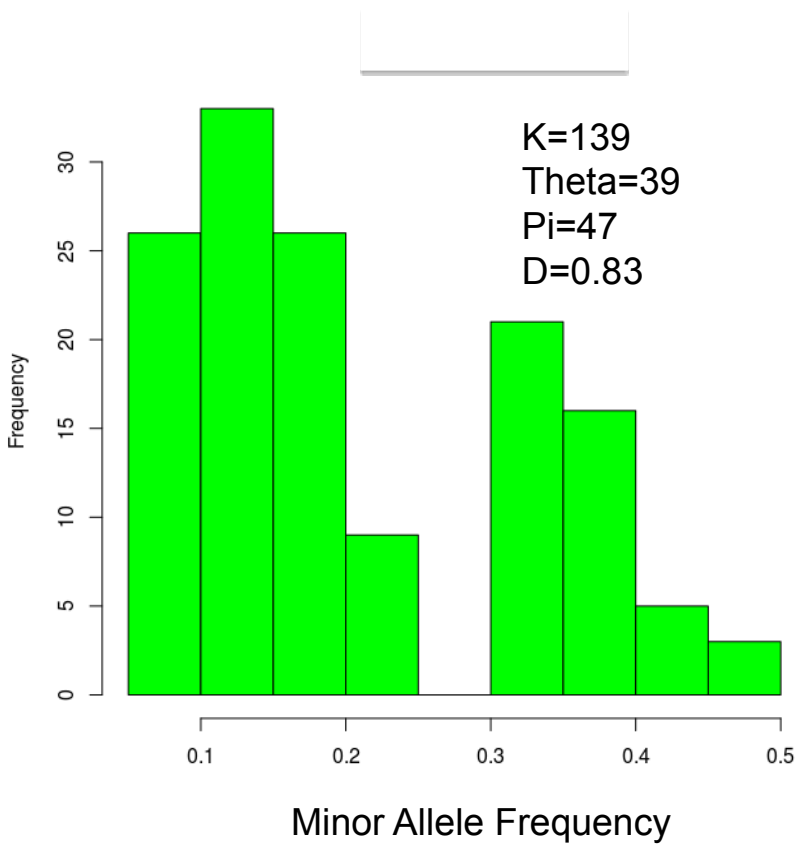


n=20; L=500kbp; no selection



Demography matters!

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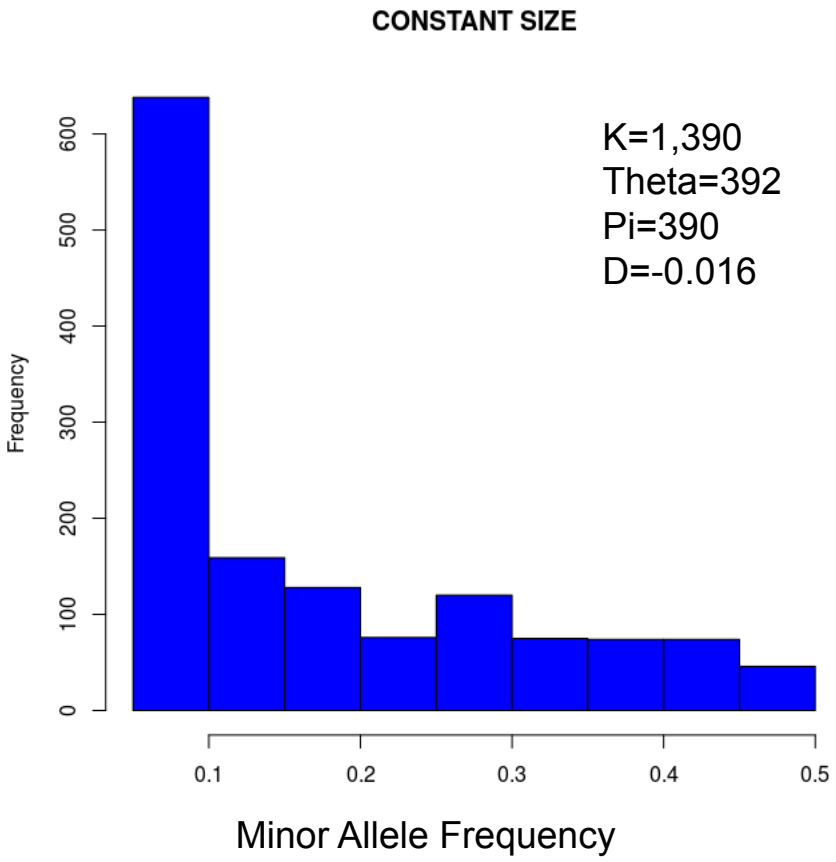
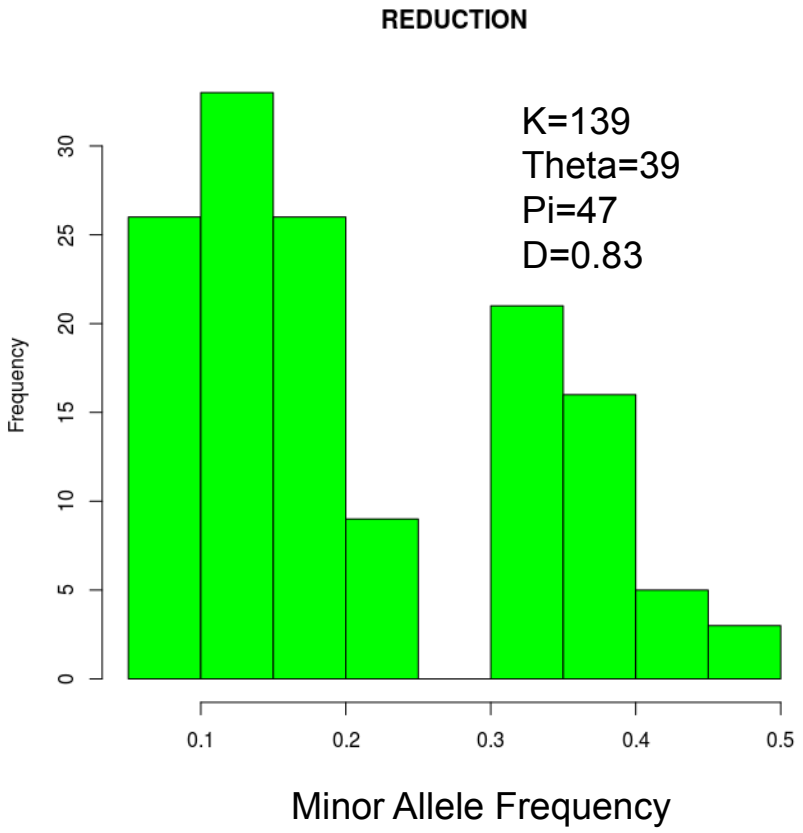


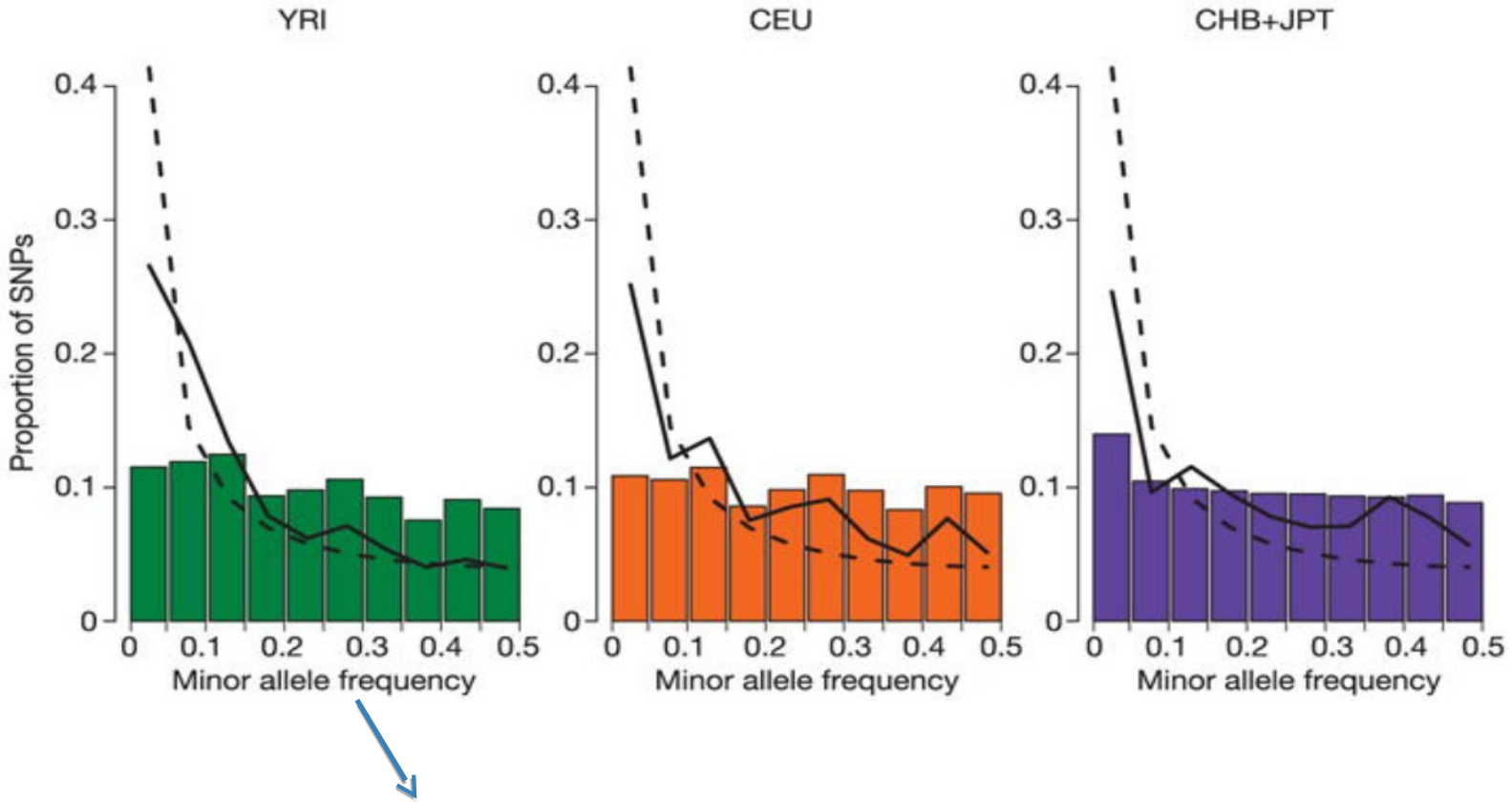
n=20; L=500kbp; no selection



- Depletion of segregating sites
- Excess of intermediate-frequency variants
- SFS-derived summary statistics may fail to distinguish between the effects of demography and selection

Experimental design matters?

The effect of ascertainment bias

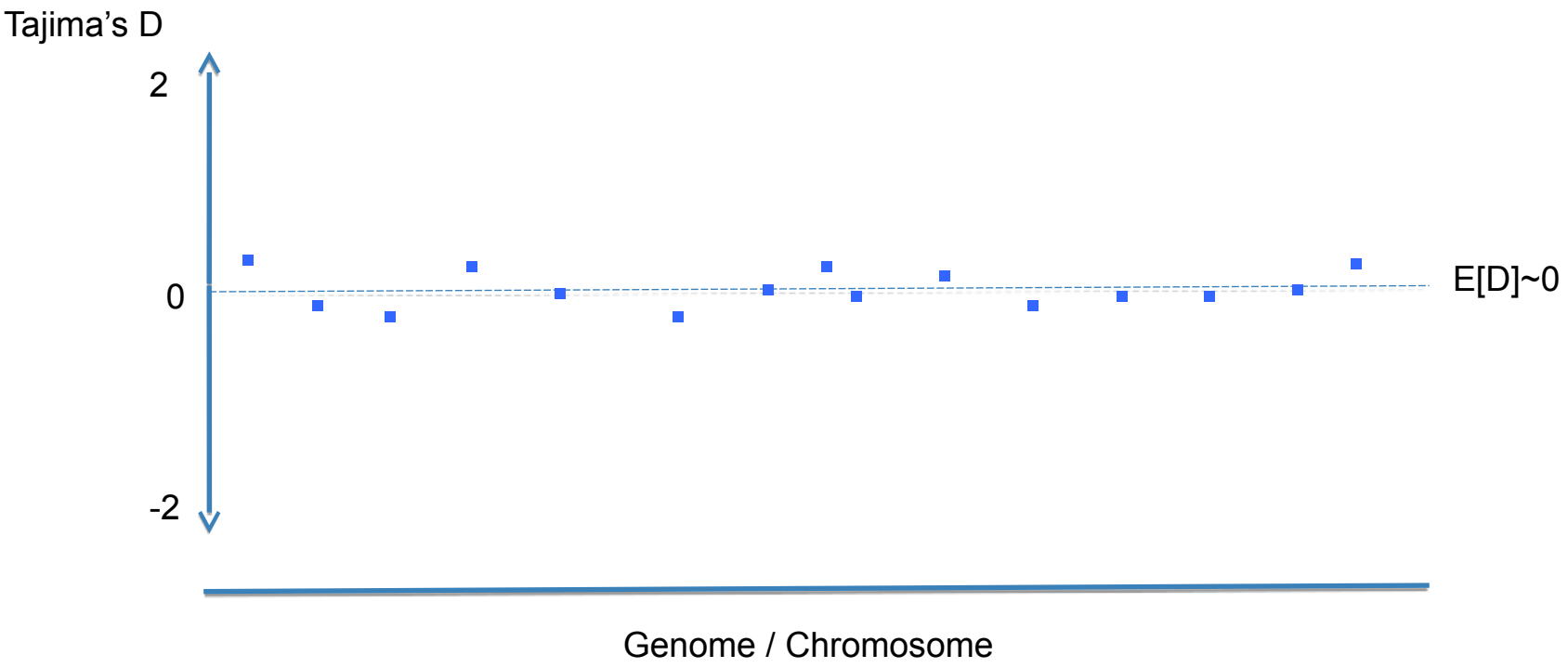


Deficiency of low-frequency variants

HapMap Consortium. Nature 2005

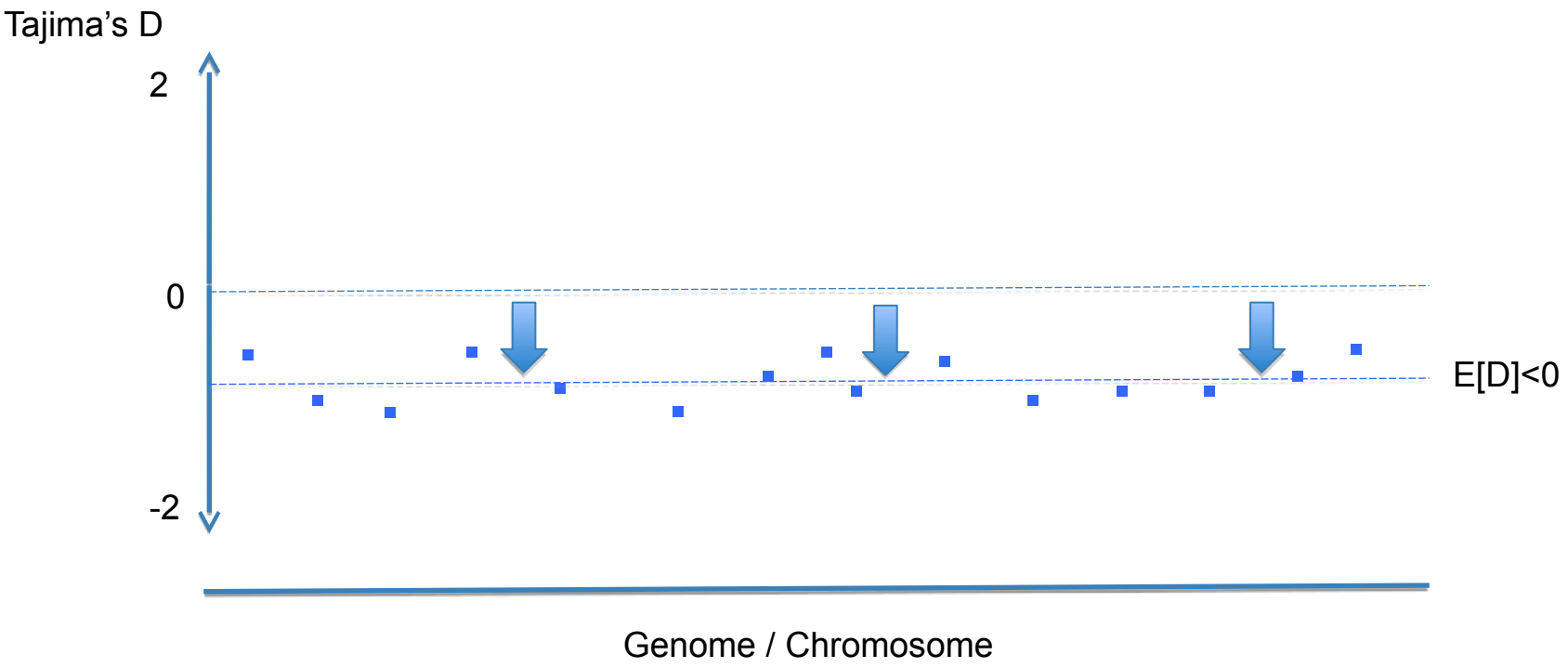
How to take neutral confounding factors into account?

Under constant population size:



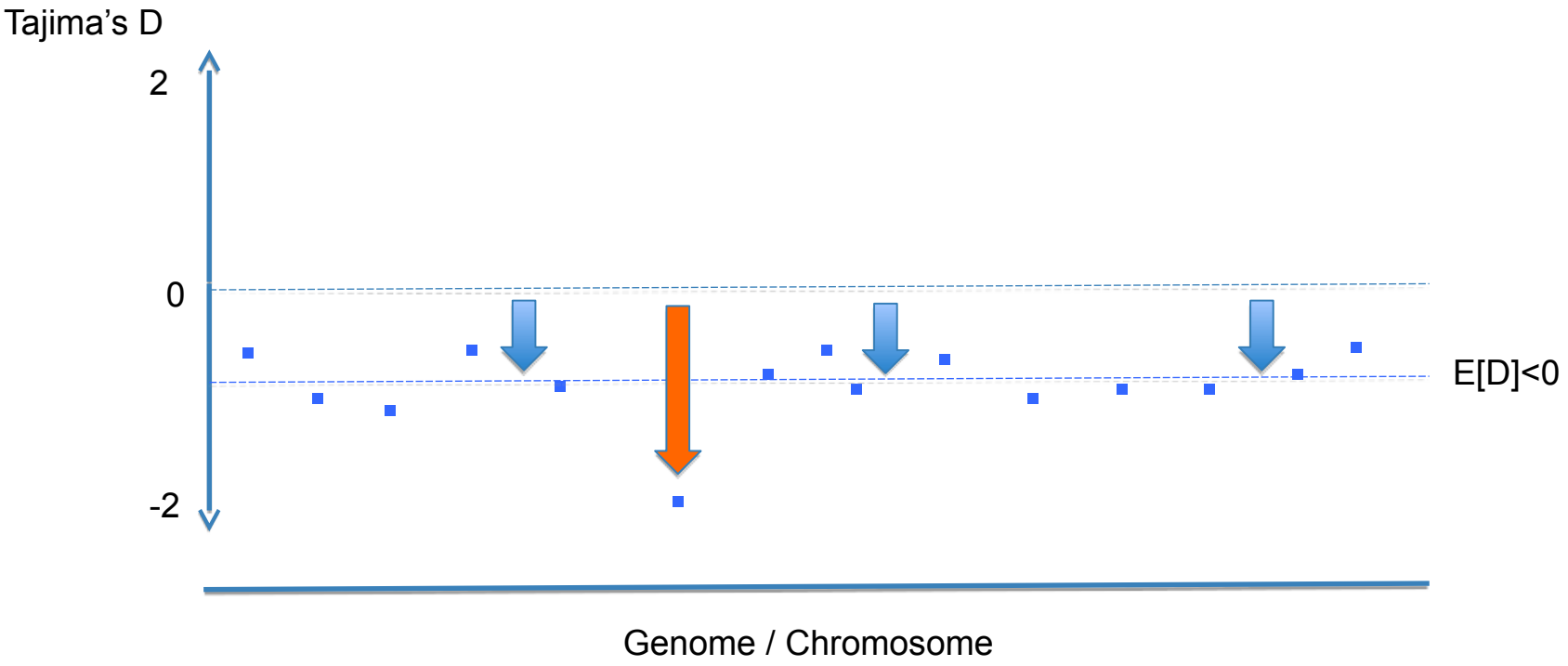
How to take neutral confounding factors into account?

Under expanding population size:



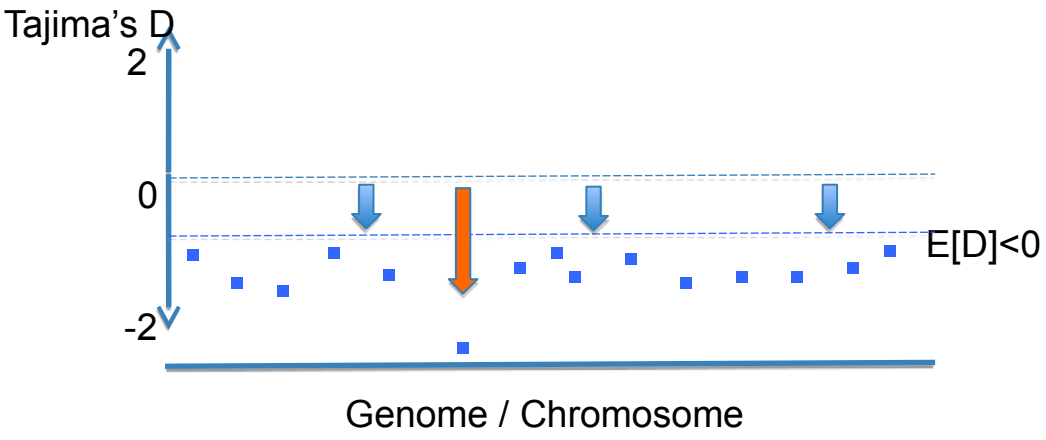
How to take neutral confounding factors into account?

Under expanding population size and positive selection:

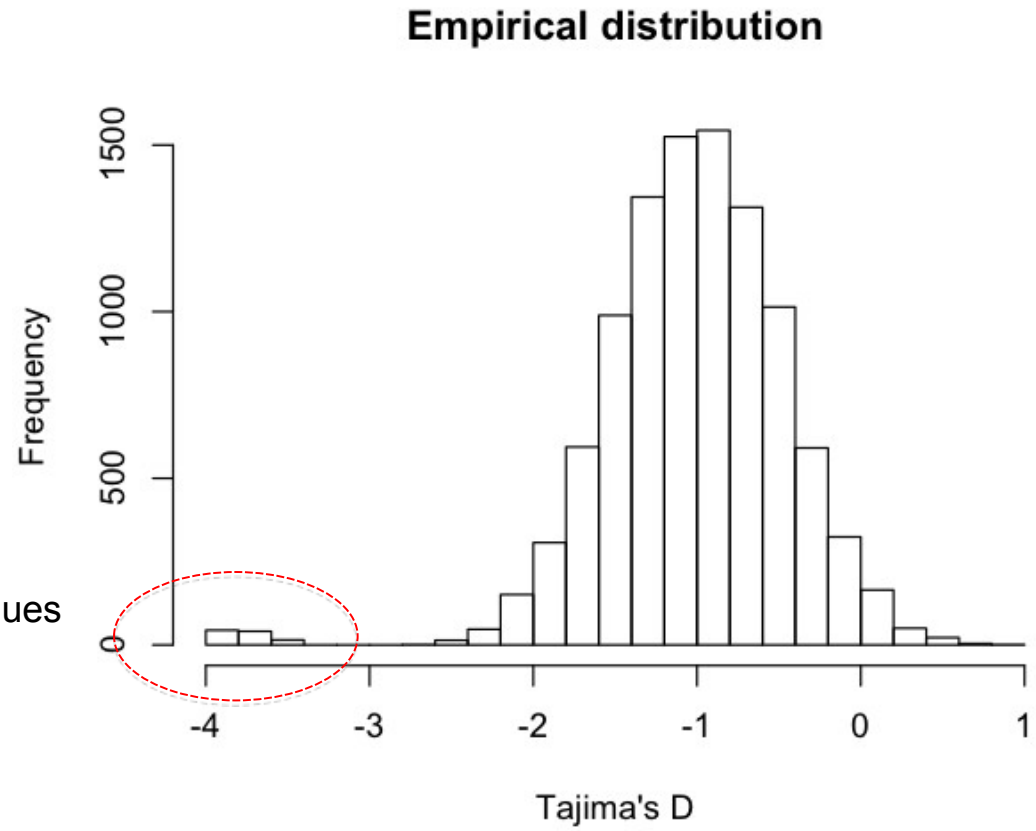


- Demography affects all loci equally, while selection changes local patterns

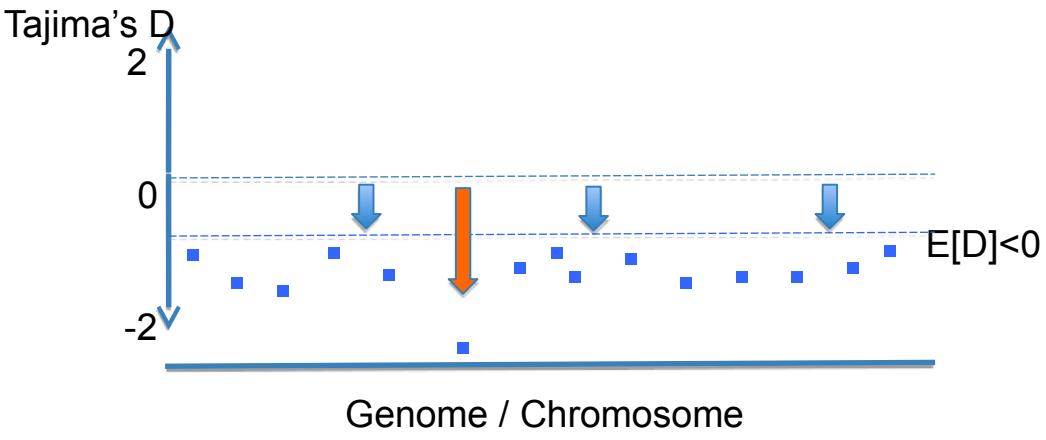
Outlier approach



Assign empirical *p*-values
(ranked percentiles)



Outlier approach



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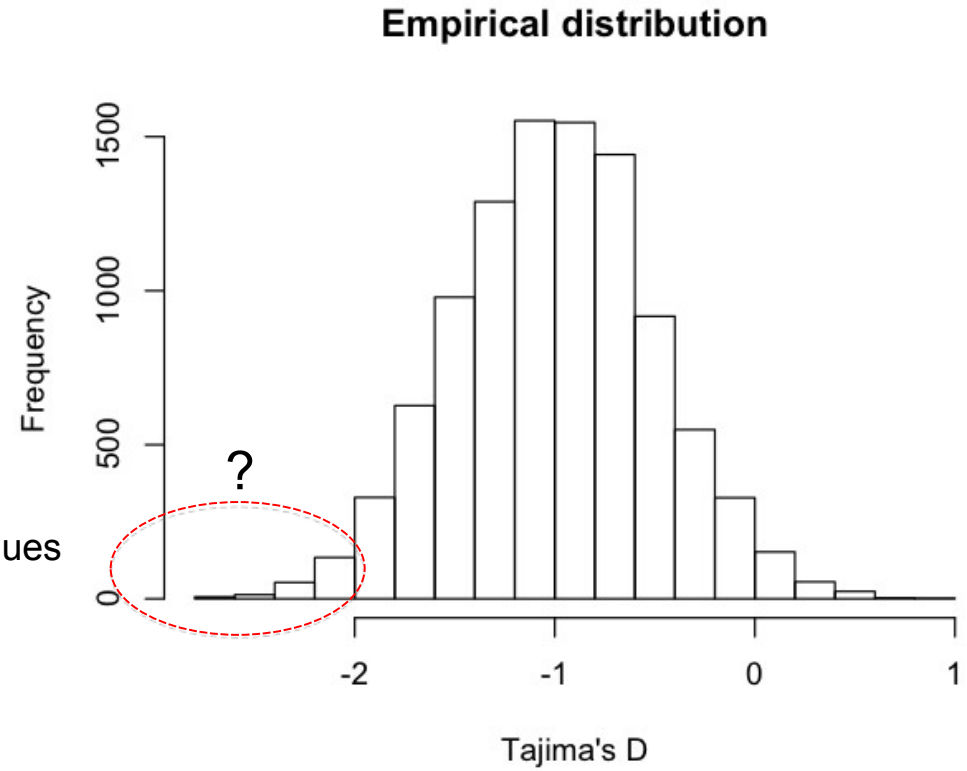
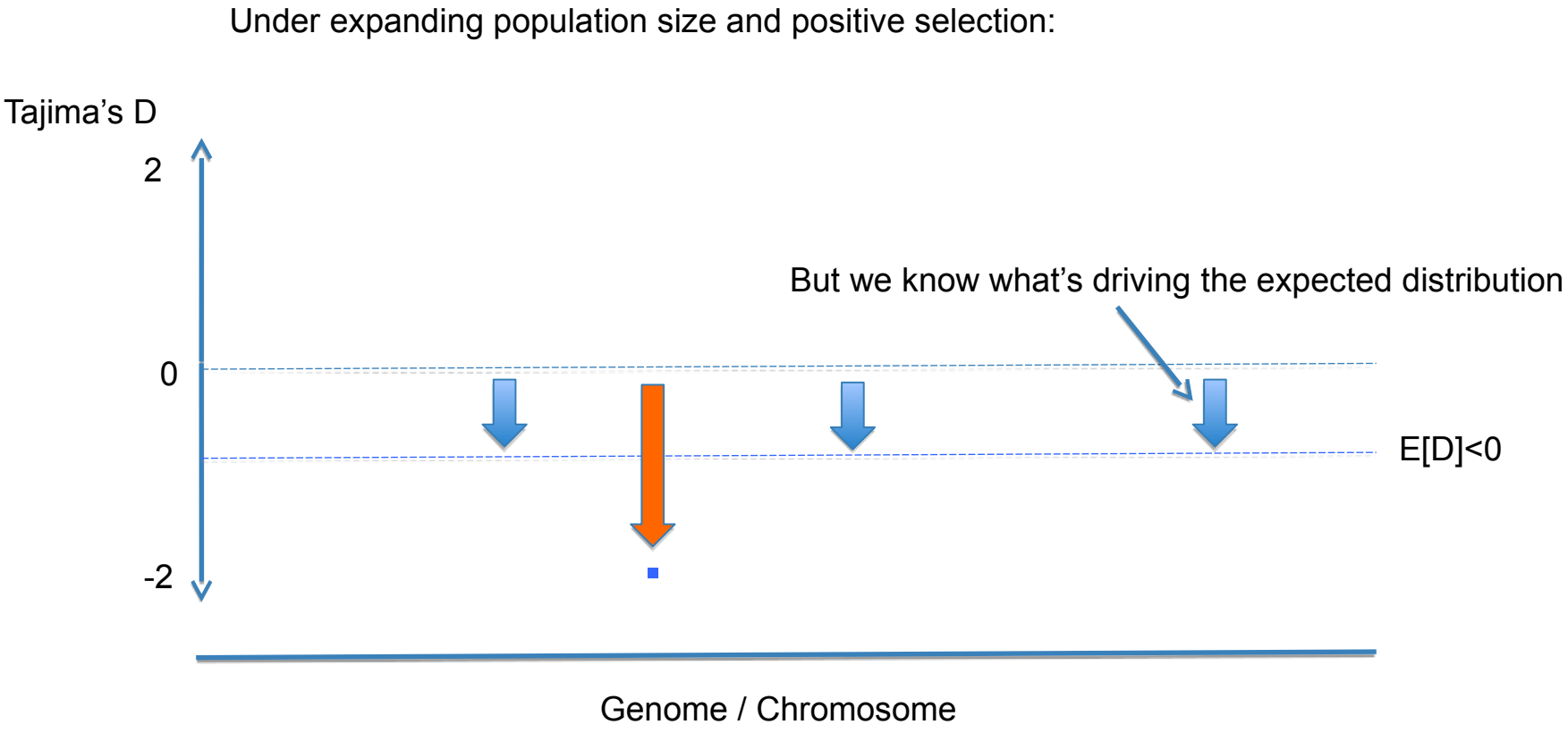
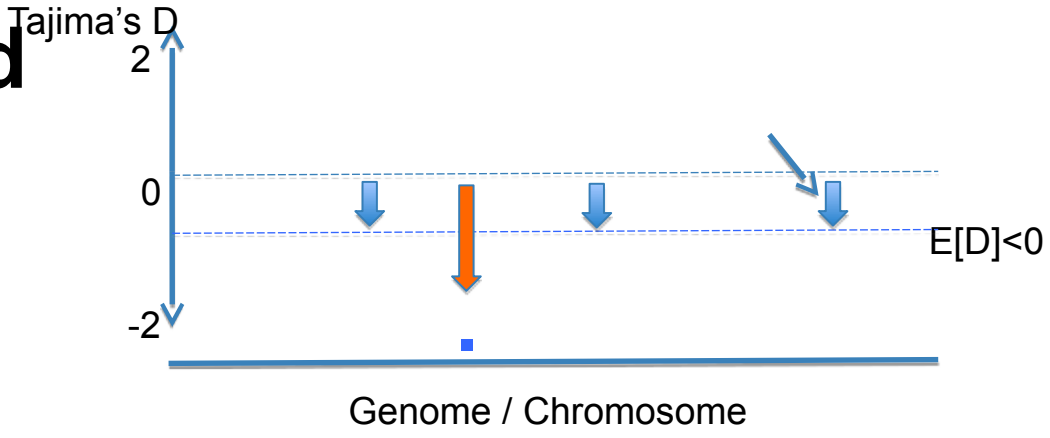


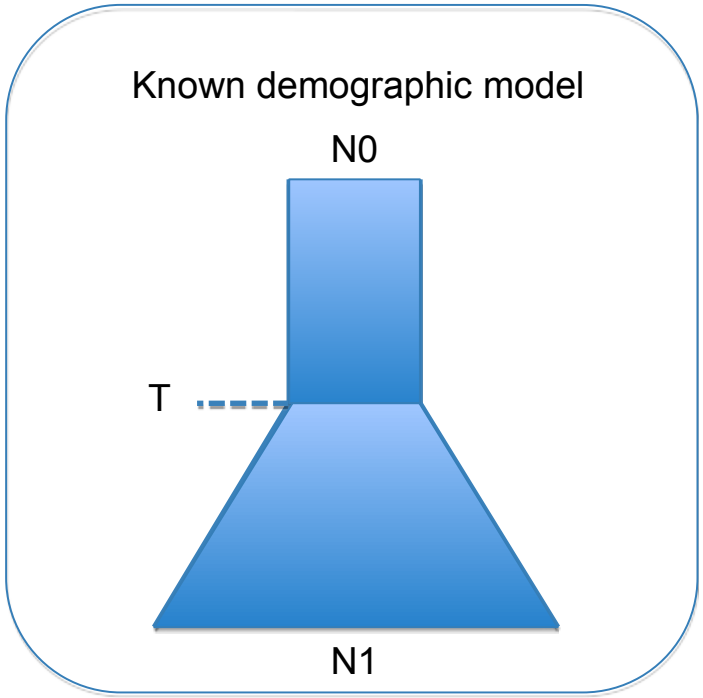
How to take neutral confounding factors into account?



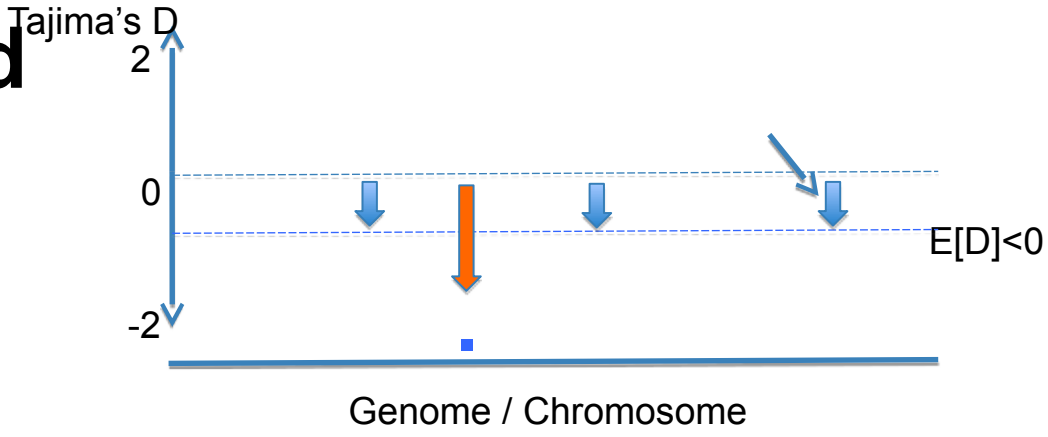
- Demography affects all loci equally, while selection changes local patterns
  What should we do if we don't have genome-wide data?

Simulations-based approach

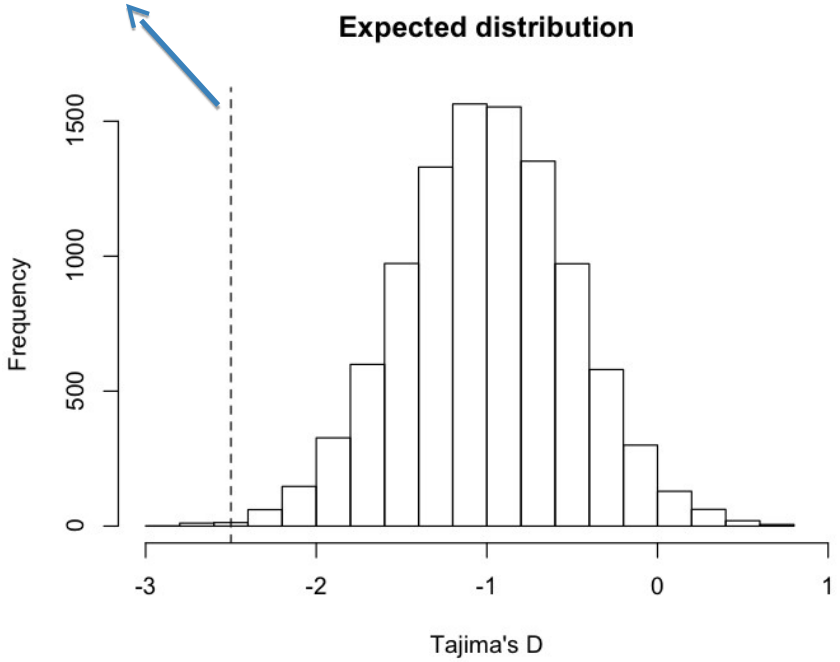


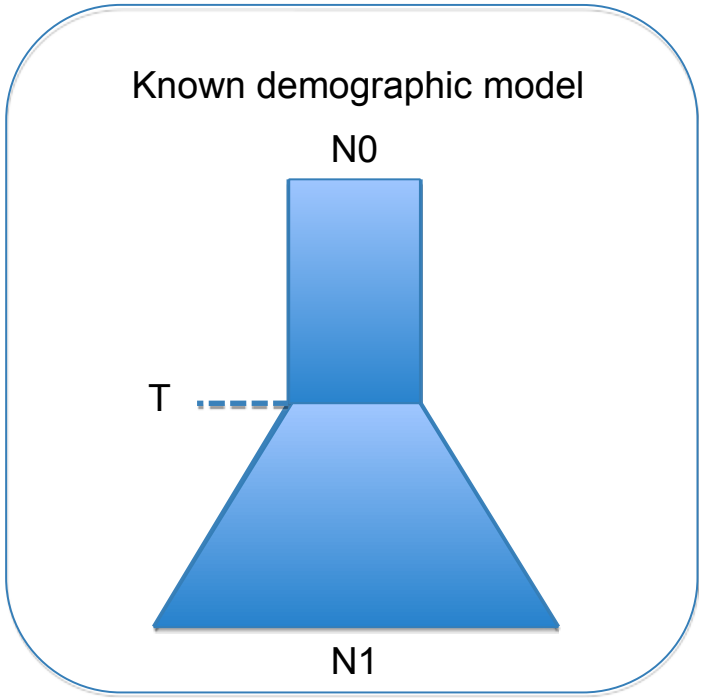


Simulations-based approach

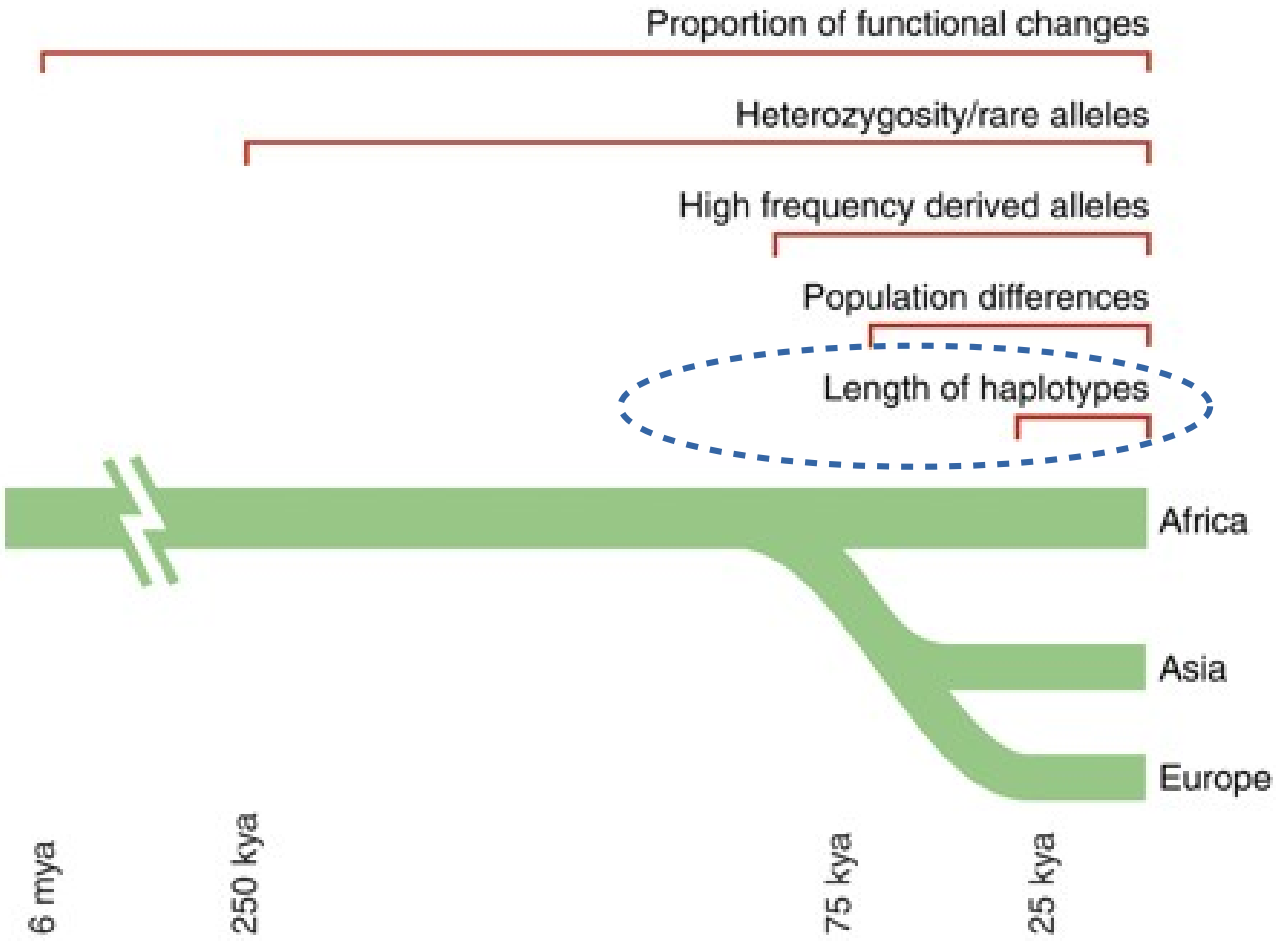


Assign *p*-values
(based on ranked percentile of observed value)

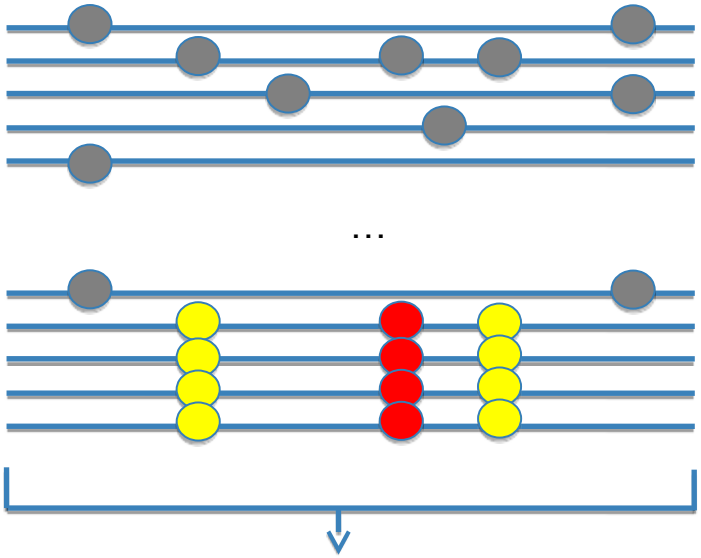




Inference of positive selection



Positive selection

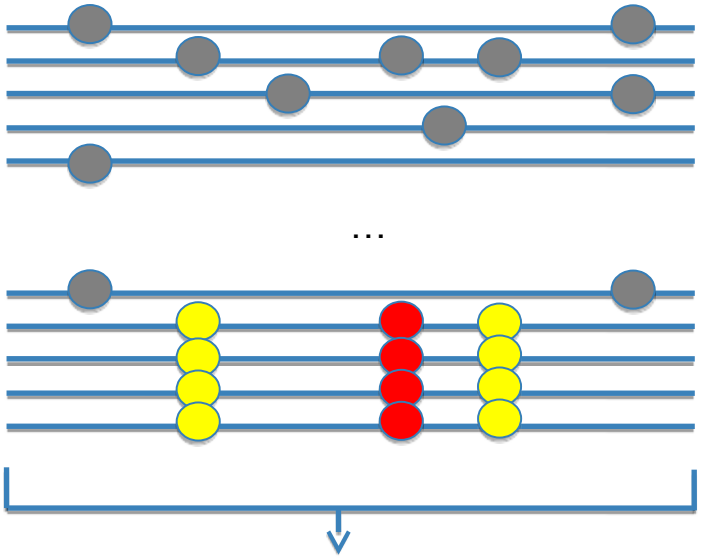


$t<T_{sel}$

$t>>T_{sel}$

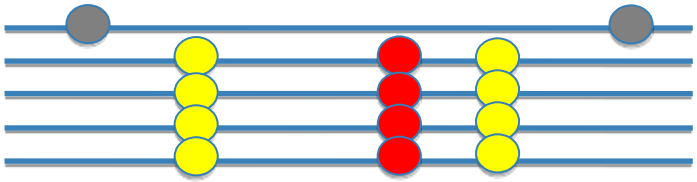
- Reduction of polymorphisms levels (Theta)
- Excess of low-frequency variants (Pi, Tajima's D, SFS)
- ?

Positive selection



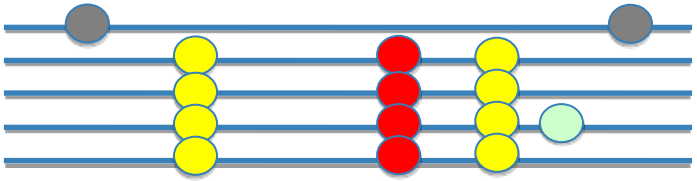
- Reduction of polymorphisms levels (Theta)
- Excess of low-frequency variants (Pi, Tajima's D, SFS)
- Extended haplotype homozygosity / Extended LD

Extended Haplotype Homozygosity



$t >> T_{sel}$

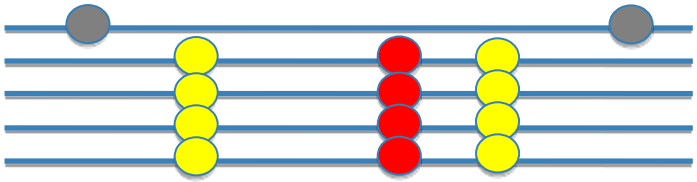
...



$t >>> T_{sel}$

...

Extended Haplotype Homozygosity



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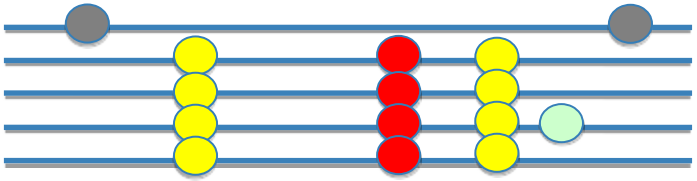
...



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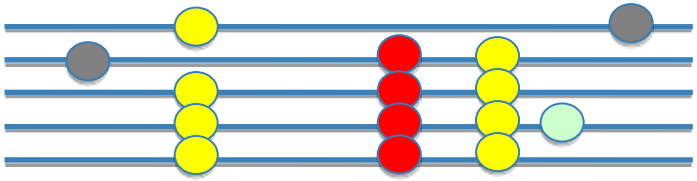
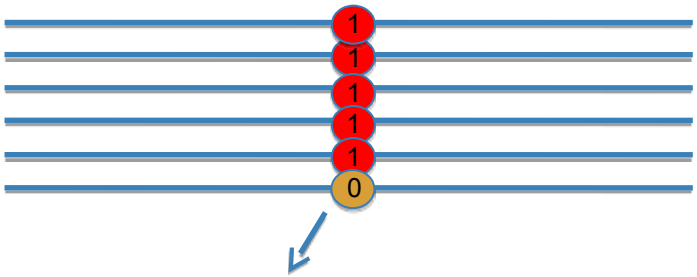


$t >>> T_{sel}$

Extended Haplotype Homozygosity

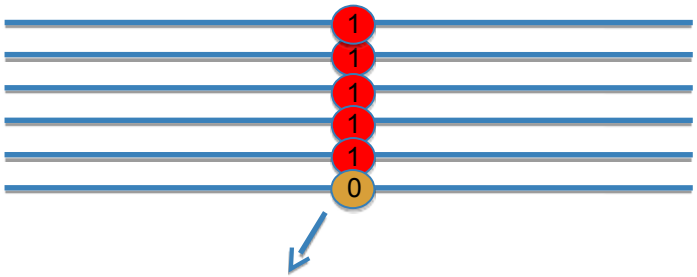


Core haplotype is 1
(Biallelic: 0 is ancestral, 1 is derived allele)

$$EHH_c(x_i) = \sum_{h \in H_c(x_i)} \frac{\binom{n_h}{2}}{\binom{n_c}{2}}$$

Core SNP

Extended Haplotype Homozygosity



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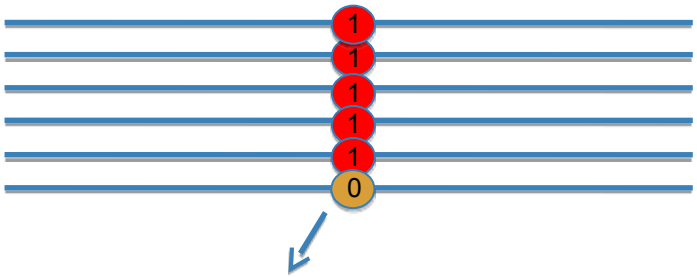
Until marker x_i
(starting from x_0)

Extended Haplotype Homozygosity



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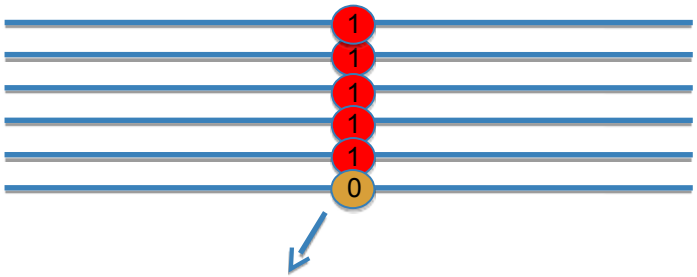
Sum across all unique haplotypes carrying the core SNP

Extended Haplotype Homozygosity



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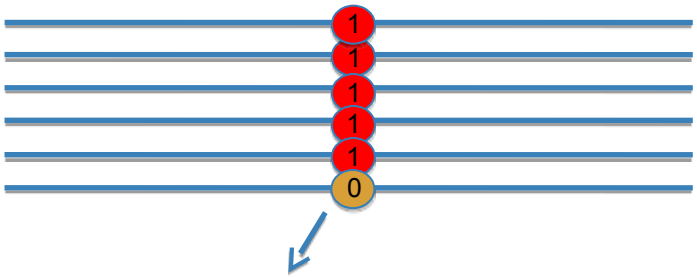
n_h is haplotype frequency of h

n_h is haplotype frequency of the core SNP

Sum across all unique haplotypes carrying the core SNP

Extended Haplotype Homozygosity



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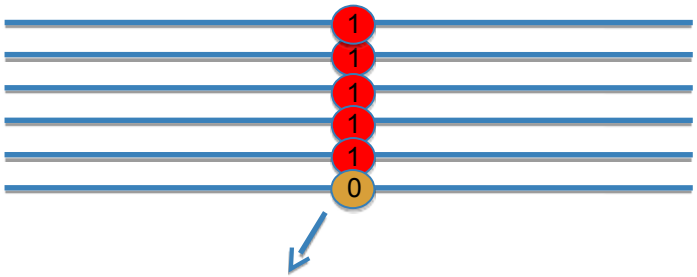
n_h is haplotype frequency of h

n_h is haplotype frequency of the core SNP

Sum across all unique haplotypes carrying the core SNP

$$EHH_c(x_i = 0) = ?$$

Extended Haplotype Homozygosity



Core haplotype is 1
(Biallelic: 0 is ancestral, 1 is derived allele)

$$EHH_c(x_i) = \sum_{h \in H_c(x_i)} \frac{\binom{n_h}{2}}{\binom{n_c}{2}}$$

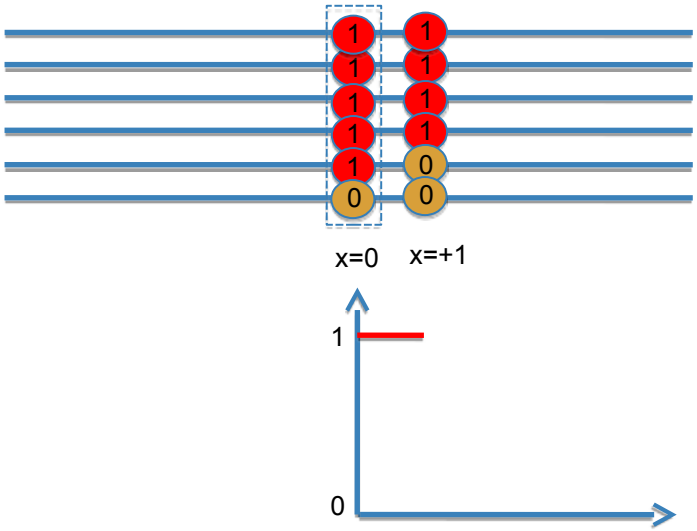
n_h is haplotype frequency of h

n_c is haplotype frequency of the core SNP

Sum across all unique haplotypes carrying the core SNP

$$EHH_c(x_i = 0) = \frac{\binom{5}{2}}{\binom{5}{2}} = 1$$

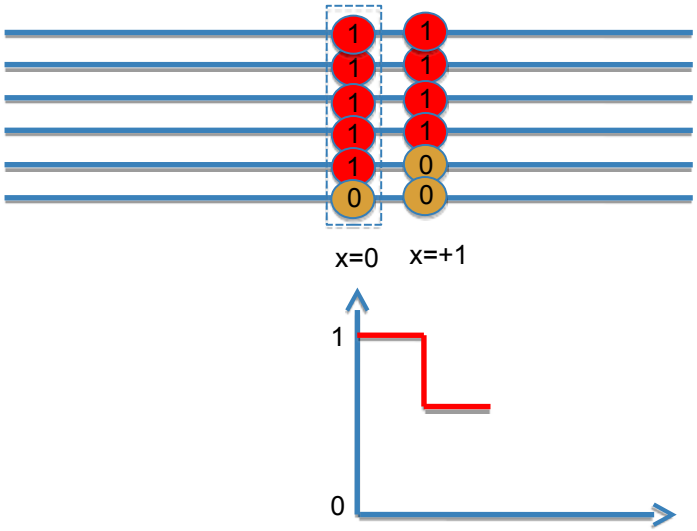
Extended Haplotype Homozygosity



$$EHH_c(x_i = +1) = ?$$

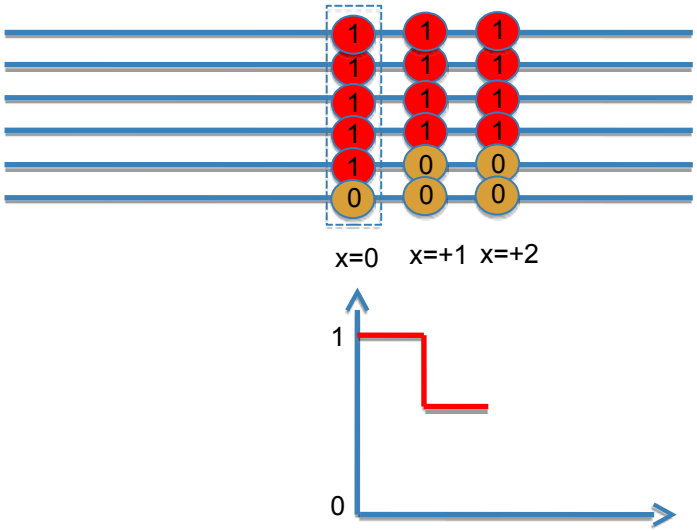
How many unique haplotypes carrying the core SNP?
What is their frequency?

Extended Haplotype Homozygosity



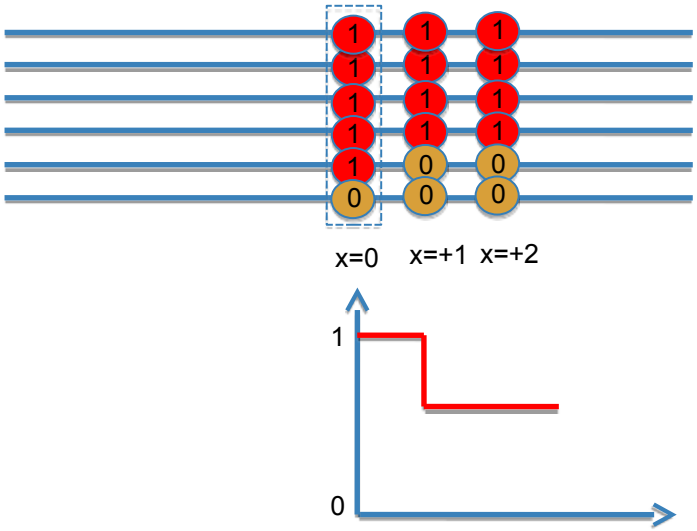
$$EHH_c(x_i = +1) = \frac{\binom{4}{2} + \binom{1}{2}}{\binom{5}{2}} = \frac{6+0}{10} = 0.60$$

Extended Haplotype Homozygosity



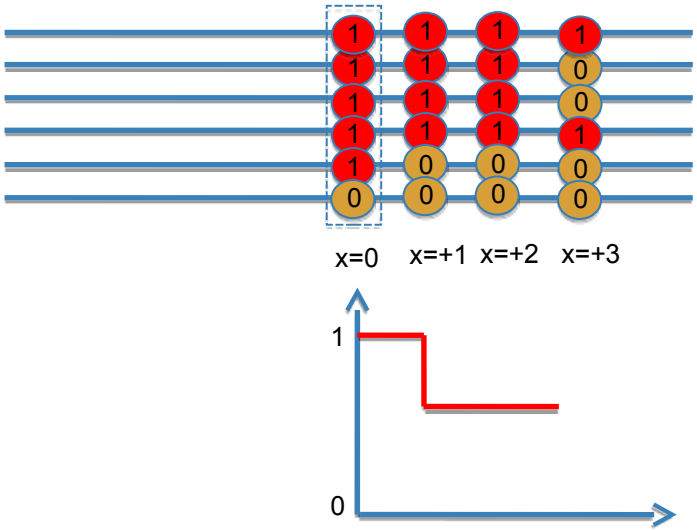
$$EHH_c(x_i = +2) = ?$$

Extended Haplotype Homozygosity



$$EHH_c(x_i = +2) = EHH_c(x_i = +1) = 0.60$$

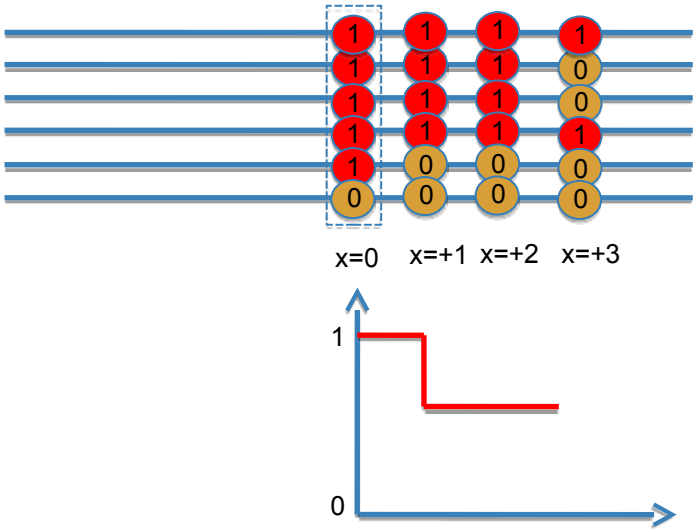
Extended Haplotype Homozygosity



$$EHH_c(x_i) = \sum_{h \in H_c(x_i)} \frac{\binom{n_h}{2}}{\binom{n_c}{2}}$$

How many unique haplotypes carrying the core SNP?
What is their frequency?

Extended Haplotype Homozygosity

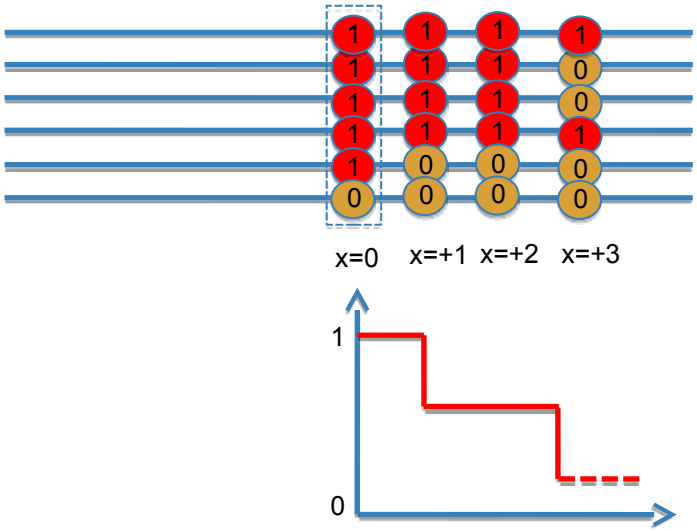


$$EHH_c(x_i) = \sum_{h \in H_c(x_i)} \frac{\binom{n_h}{2}}{\binom{n_c}{2}}$$

How many unique haplotypes carrying the core SNP?
What is their frequency?
1111 with freq=2
1110 with freq=2
1000 with freq=1

$$EHH_c(x_i = +3) = ?$$

Extended Haplotype Homozygosity

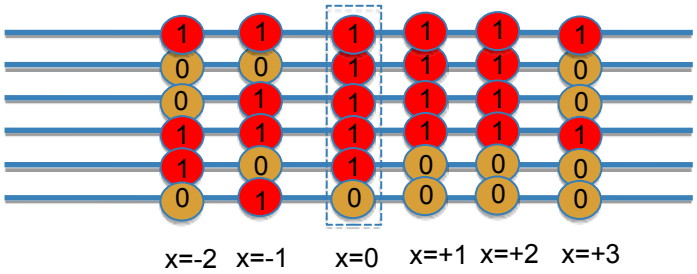


$$EHH_c(x_i) = \sum_{h \in H_c(x_i)} \frac{\binom{n_h}{2}}{\binom{n_c}{2}}$$

How many unique haplotypes carrying the core SNP?
What is their frequency?
1111 with freq=2
1110 with freq=2
1000 with freq=1

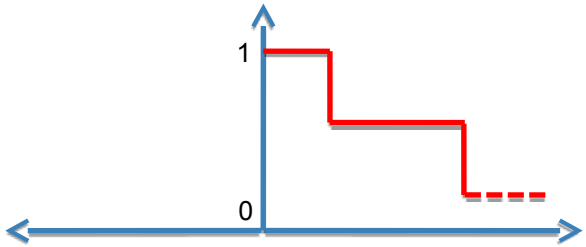
$$EHH_c(x_i = +3) = \frac{\binom{2}{2} + \binom{2}{2} + \binom{1}{2}}{\binom{5}{2}} = \frac{1+1+0}{10} = 0.20$$

Extended Haplotype Homozygosity



$$EHH_c(x_i) = \sum_{h \in H_c(x_i)} \frac{\binom{n_h}{2}}{\binom{n_c}{2}}$$

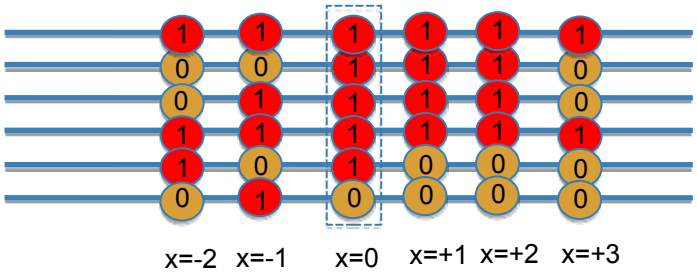
n	*n choose 2*
1	0
2	1
3	3
4	6
5	10
6	15



$$EHH_c(x_i = -1) = ?$$
$$EHH_c(x_i = -2) = ?$$

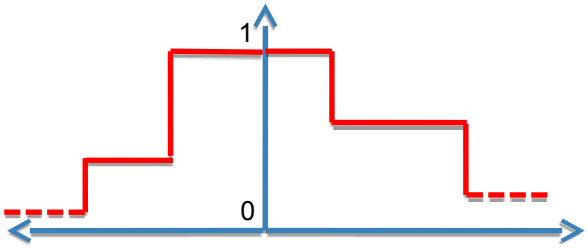
Comment on differences (if any) between *EHH(x=+2)* and *EHH(x=-2)*.

Extended Haplotype Homozygosity



$$EHH_c(x_i) = \sum_{h \in H_c(x_i)} \frac{\binom{n_h}{2}}{\binom{n_c}{2}}$$

n	*n choose 2*
1	0
2	1
3	3
4	6
5	10
6	15



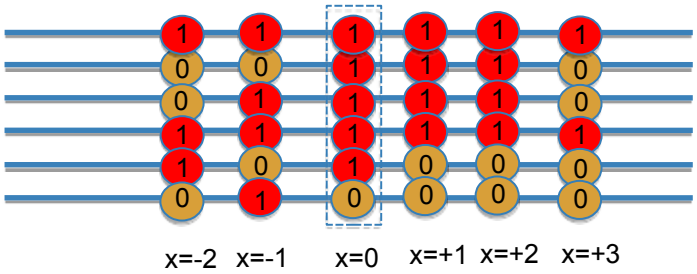
$$EHH_c(x_i = -1) = \frac{\binom{3}{2} + \binom{2}{2}}{\binom{5}{2}} = \frac{3+1}{10} = 0.4$$

+ (1 choose 2)

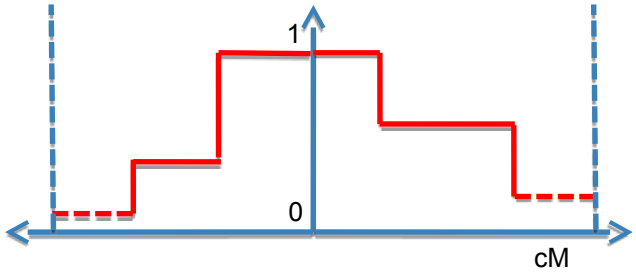
$$EHH_c(x_i = -2) = \frac{\binom{2}{2} + \binom{1}{2} + \binom{1}{2}}{\binom{5}{2}} = \frac{1+0+0}{10} = 0.1$$

Comment on differences (if any) between *EHH(x=+2)* and *EHH(x=-2)*?

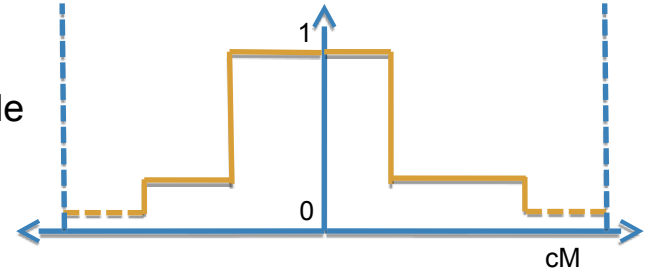
Integrated Haplotype Score



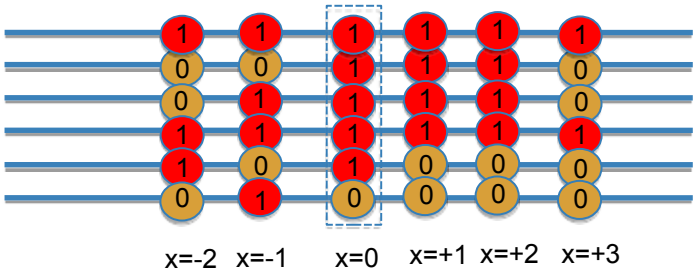
For the derived allele

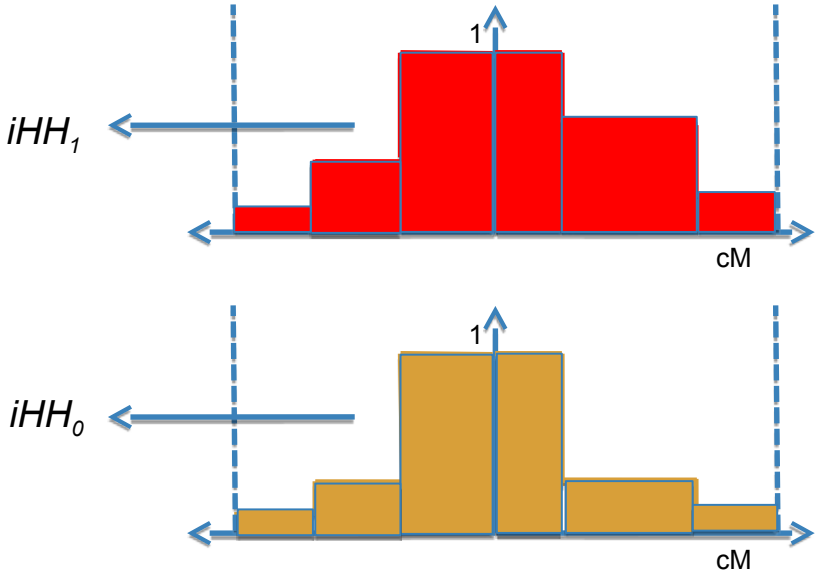


For the ancestral allele



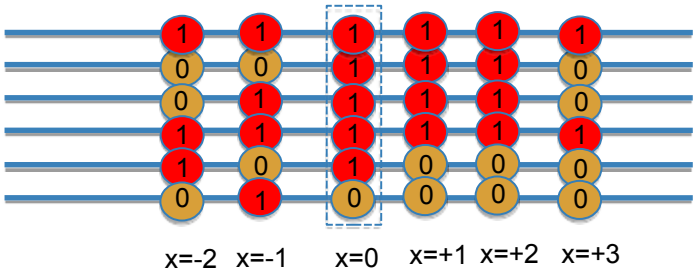
Integrated Haplotype Score

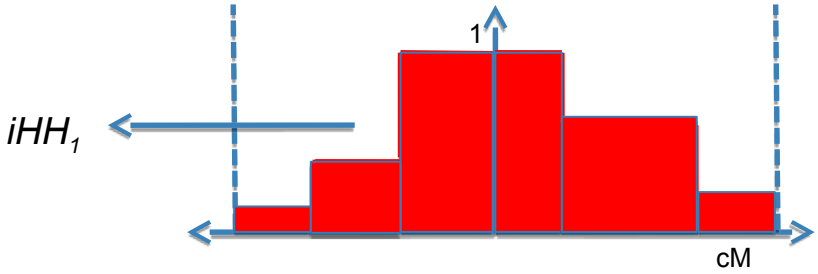




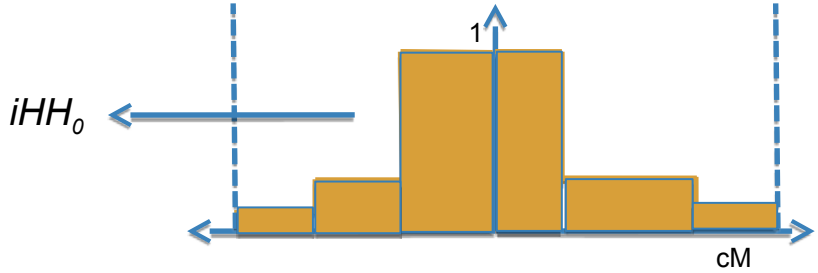
Integrated haplotype homozygosity (*iHH*)

Integrated Haplotype Score





Integrated haplotype homozygosity (*iHH*)

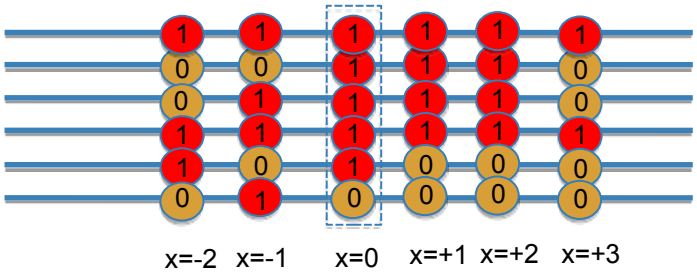


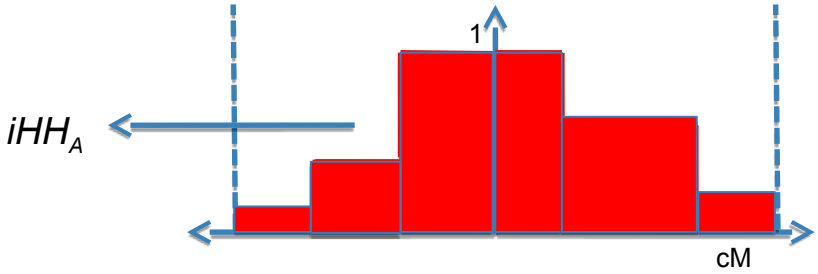
Integrated haplotype score:

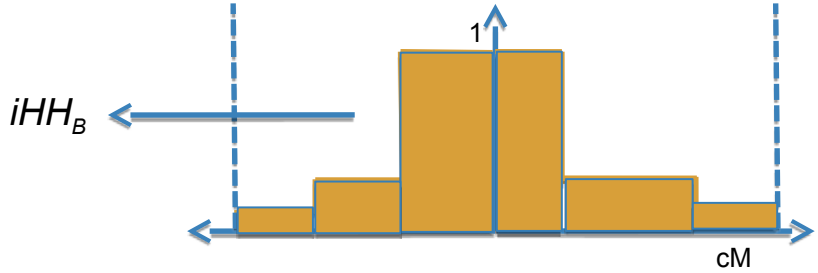
$iHs = ln(iHH_1/iHH_0)$

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

Cross-population Extended Haplotype Homozygosity





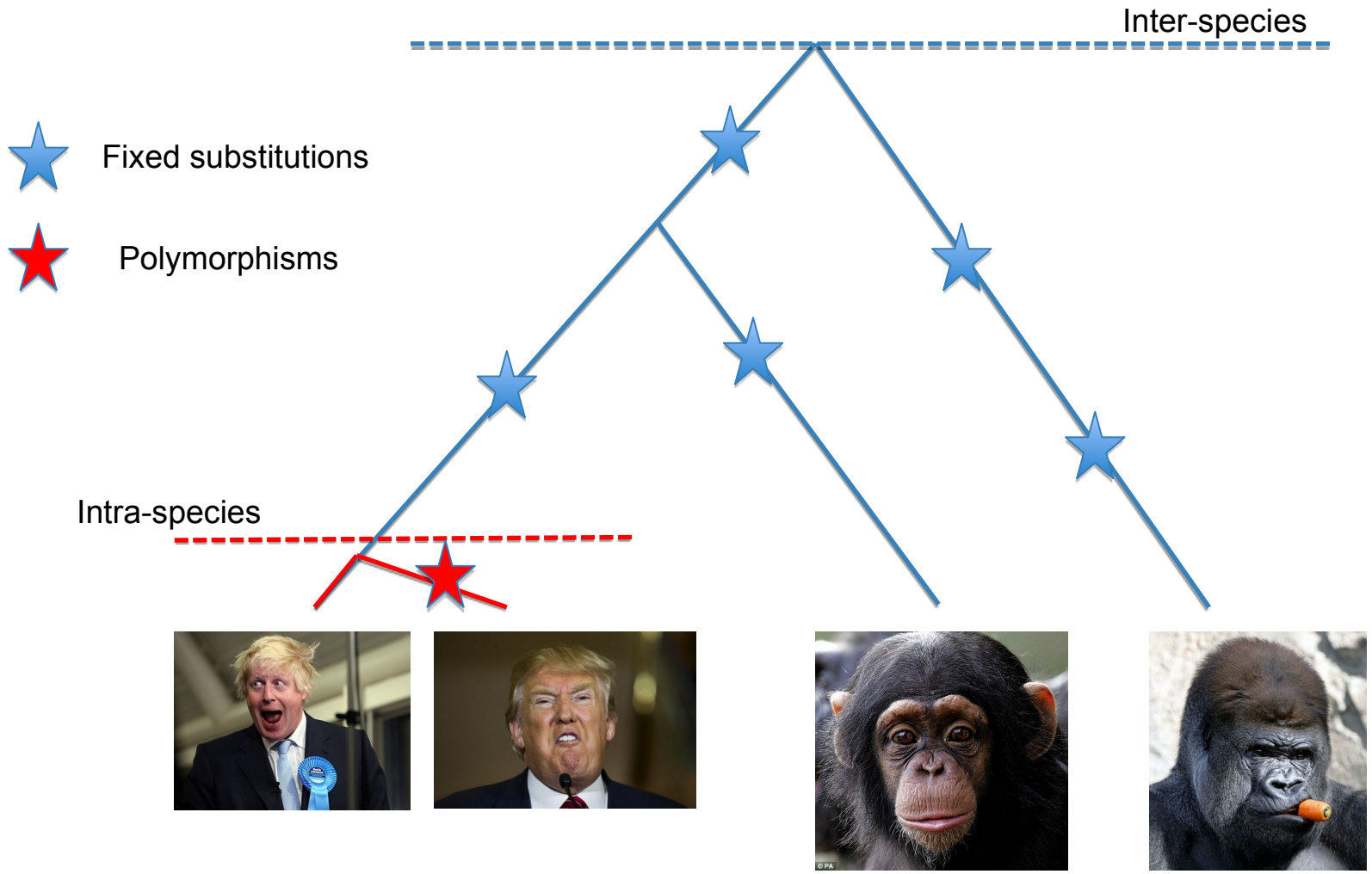


Integrated haplotype homozygosity (*iHH*) for **populations** A and B

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

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

Inferring inter-species selection



State-of-the-art methods to detect natural selection

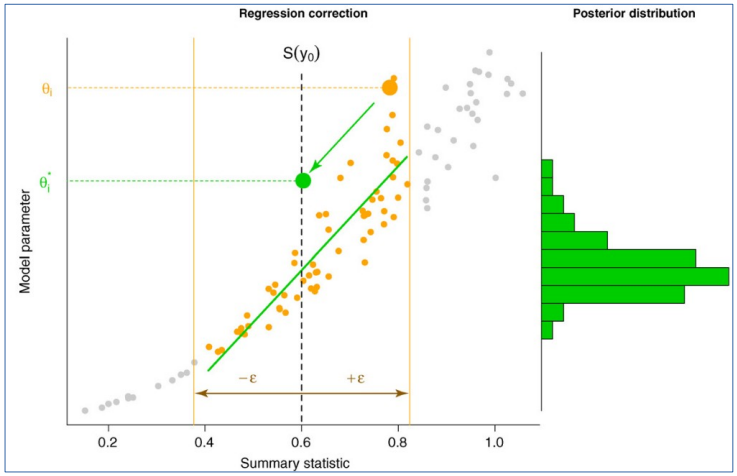
1. Composite scores (Grossman et al. 2013)

$$BF_t = \frac{P(v_t \in bin_{t,k} | selected)}{P(v_t \in bin_{t,k} | unselected)}$$

and defined the composite score as the product of the Bayes factor of each test:

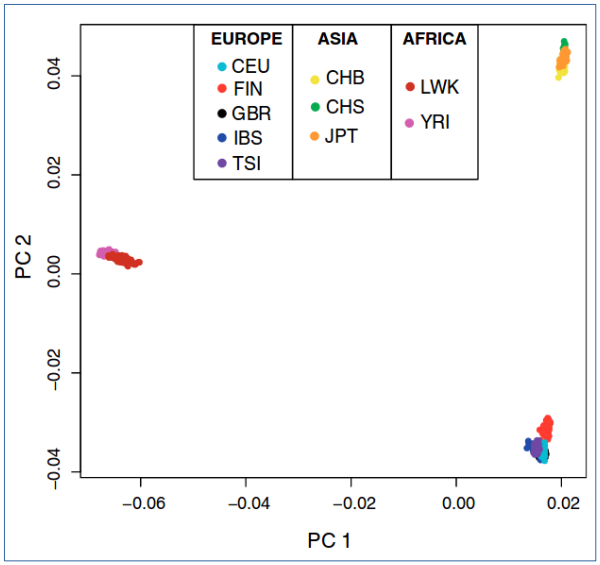
$$CMS_{GW} = \prod_{t \in tests} BF_t$$

2. Simulations-based (rejection, ABC)



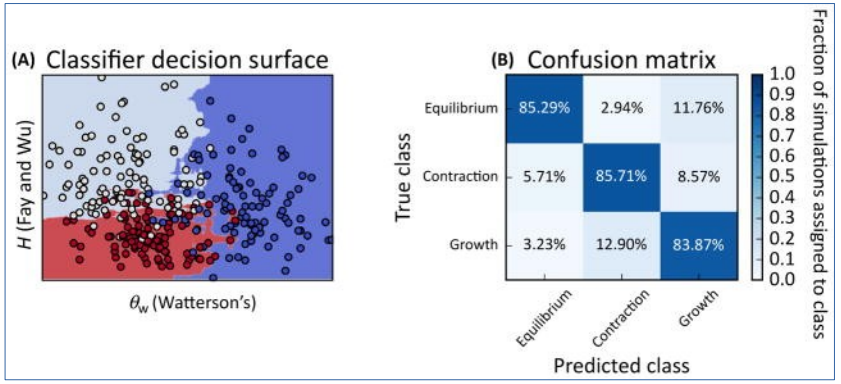
3. Unsupervised machine learning

(PCA, Duforet-Frebourg et al. 2016)



4. Supervised machine learning

(SVM, Schrider & Kern 2018)



How do we infer signals of natural selection from genomic data using machine learning and deep learning?

(let’s move to part 3)

What are the main limitations of currently employed methods to detect selection?